MAIZE GENETICS COOPERATION

NEWSLETTER

77

July 29, 2003

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NOTE: The 2004 Maize Meeting will be held in Mexico City, Mexico.

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I. Foreword

The Maize Genetics Cooperation Newsletter exists for the benefit of the maize community as an informal vehicle for communication. Its inception and continuation has been to foster cooperation among those interested in investigating maize. This cooperation has distinguished our field from others and as a consequence has moved it forward at a pace greater than would have occurred otherwise. Your submissions are encouraged to disseminate knowledge about our field that might otherwise go unrecorded.

During the past two years, maize has emerged as the highest produced crop worldwide based on total metric tonnage according to the United Nations Food and Agricultural Organization. While crop diversity is to be encouraged, this fact illustrates the importance of our endeavors to learn about the maize plant. Efforts to sequence the maize genome are underway and improved methods of transformation have been published. These developments portend exciting times ahead for maize biology.

Because maize is both a commercial species and a genetic model system, the danger exists that the sharing of research materials might be diminished. It is imperative for us to work together to prevent this from occurring. Certainly, basic findings should be transferred to the industrial sector and basic advances in industry should be shared with the academic community for the benefit of both. Published materials must be shared for research purposes with the only restriction being against commercial use.

We remind the readers that contributions to the Newsletter do not constitute formal publications. Citations to them should be accompanied by permission from the authors if at all possible. Notes can be submitted at any time and are entered into MaizeDB. The deadline for the next print copy, volume 78, is January 1, 2004. Electronic submission is encouraged by sending your contributions as attachments, or as text of an email, to Newsletter@chaco.agron.missouri.edu. **Submissions must require minimal editing to be accepted.**

We encourage the community to carry studies of general scientific interest to the formal literature. However, there is a great need to share technical tips, protocols, mutant descriptions, map information, ideas and other isolated information useful in the lab and field.

As in the past, Shirley Kowalewski has been responsible for assembly and correcting of the copy. She has performed this task with speed, precision and a great sense of humor. The maize community owes her much gratitude for her continued service in this capacity.

Mary Polacco
James A. Birchler
Co-editors

AMES, IOWA
Iowa State University

Analysis of the maize Myb gene superfamily: a progress report

--Jiang, C, Peterson, T

Myb proteins contain a conserved DNA-binding domain composed of one to four repeat motifs (referred to as R0R1R2R3); each repeat is approximately 50 amino acids, with constantly spaced Tryptophan residues. Members of the Myb gene superfamily are found in both plants and animals. Interestingly, angiosperms contain large numbers of Myb genes. The functions of most plant Myb genes are unknown, but those studied to date encode transcriptional activator or repressor proteins involved in regulation of secondary metabolism, cellular morphogenesis, pathogen resistance, and in responses to growth regulators and stresses.

To study the Myb gene family in maize, we isolated and sequenced Myb gene sequences derived from a maize BAC genomic library (ZMMBBb; http://www.genome.clemson.edu/orders/lib_desc/ZMMBBb.html). Myb-containing BAC clones were detected using as probe the radiolabeled fragment of a maize Myb gene (*P1-wr*) cDNA covering the R2R3 Myb domain. We detected 143 Myb-hybridizing clones from two filters (NSF B73E, serial# 009687; and NSF B73F, serial# 010186) containing 36,864 BAC clones covering 2 genome equivalents. The BAC clones were initially sequenced using a degenerate primer (5'-GAKGYCSGGSCGVAGGTAGTT-3') complementary to sequences within exon 2 of 78 maize Myb EST sequences (sequence data kindly provided by Dr. Erich Grotewold, Ohio State University). The sequences obtained using the degenerate primer were used to design new primers specific for each clone for further sequencing in the upstream and downstream directions. Further rounds of sequencing followed by specific primer design continued until complete Myb domain sequences were obtained. Using this primer walking strategy, we obtained sequences from 44 BAC clones and detected 31 unique Myb genes (redundancy = 30%). This figure is consistent with previous data indicating that the maize genome contains more than 80 expressed Myb genes (Rabinowicz et al., Genetics 153:427-444, 1999). Obviously, the Myb gene family has expanded broadly during the evolution of flowering plants.

The sequences of the 31 unique Myb genes have been deposited into NCBI. The accession numbers are AF474115 ~ AF474124 (with complete R2R3 domains), AF470072 ~ AF470092 (with partial R2R3 domains due to sequencing difficulties). The maize BAC addresses were also deposited into the Maize Mapping Project (http://www.maizemap.org). It is hoped that the maize Myb gene sequences may assist in the mapping of individual Myb genes, and eventual identification of the specific metabolic pathways and phenotypic traits controlled by each Myb gene.

`Using the Myb genomic sequences, we attempted to identify conserved regulatory motifs in non-coding regions with the assistance of computational tools. First, we constructed a phylogenetic tree and identified clades of closely-related Myb genes. Then, motif-finding tools (MEME and Macaw) were applied to search for motifs within each clade. Besides the Myb domain itself, some highly conserved motifs were identified in the C-terminal coding regions of various diverse Myb proteins. In the non-coding regions, conserved motifs were identified only in the clade containing the maize *p1* and *p2* genes, and orthologs from sorghum and rice. Within this clade, a highly conserved pattern of TATA-box, Transcription Start Site sequences, and 5' UTR CA-box was found. Otherwise, no significant regulatory motifs were detected in non-coding regions of other Myb genes. Our results suggest that it will be difficult to directly identify gene regulatory motifs in non-coding regions using only existing computational techniques. Possibly, the identification of coexpressed genes using microarray analysis will assist in the identification of common regulatory elements.

Molecular analysis of the maize *P1-rw* allele

--Zhang, F, Peterson, T

The maize *p1* gene encodes a Myb-like transcription factor which regulates the synthesis of a phlobaphene-like red pigment in kernel pericarp, cob and other floral organs (Grotewold et al., Cell 76:543-553). Some *p1* alleles elicit differential pigmentation of pericarp and cob: for example, *P1-rr*, *P1-wr*, and *P1-rw* specify red pericarp/red cob, white pericarp/red cod, and red pericarp/white cob, respectively. The *P1-rr* and *P1-wr* alleles have been previously characterized (Lechelt et al., Mol. Gen. Genet. 219:225-234; Chopra et al., Mol. Gen. Genet. 260:372-380); we are now investigating the gene structure and molecular expression pattern of the *P1-rw* allele.

Genomic Southern analysis indicates that, similar to *P1-rr*, *P1-rw* contains a single copy gene flanked by long direct repeats. RT-PCR results showed that the *P1-rw* 5' UTR and 5' coding sequences are identical to *P1-rr* and *P1-wr.* However, the *P1-rw* 3' coding sequences and 3' UTR are identical to that of the *p2* gene, a tightly linked, paralogous gene that regulates the synthesis of 3-deoxyflavones, including maysin, in maize silk (Zhang et al, The Plant Cell 12:1-12, 2000; Zhang et al., Plant Molecular Biology, in press.) To reconcile these results, we screened a genomic lambda library with a probe specific for *P1-rr* (Fragment 15), and a second probe which hybridizes with both *p1* and *p2* (Fragment 8B). Two classes of lambda clones were isolated from the library: the first class resembles *p2;* these clones hybridize only with probe 8B, and they lack an 80 bp indel in the 5' UTR sequence. The second class resembles *p1;* these clones hybridize with both probe 15 and 8B, and they contain the 80bp indel in the 5' UTR sequence. Two overlapping *p1*-like lambda clones were sequenced and found to match the sequences of *P1-rw* transcripts detected by RT-PCR. Interestingly, although *P1-rw* is structurally similar to that of *P1-rr* (both contain a coding sequence flanked by two long direct repeats), *P1-rw* differs from *P1-rr* in two aspects: First, the *P1-rw* coding sequence is chimeric, and consists of a *p1*-like 5' UTR, followed by *p2*-like exons and introns, followed by a truncated *P1-wr*-like exon 3 (Figure 1). This chimeric structure appears to have been generated by recombination between the *p1* and *p2* genes. Second, *P1-rw* has a major polymorphism in the 1.2 kb distal enhancer region which is located 5 kbp upstream of the *p1* transcription start site; specifically, a 339 bp sequence located between the *Pst*I and *Sac*I sites in the *P1-rr* distal enhancer was replaced by a distinct 71bp fragment in *P1-rw*.

Our current hypothesis is that polymorphisms in the coding sequences and/or the distal enhancer region are responsible for the distinct gene expression pattern of *P1-rw*. Nuclear run-on assays

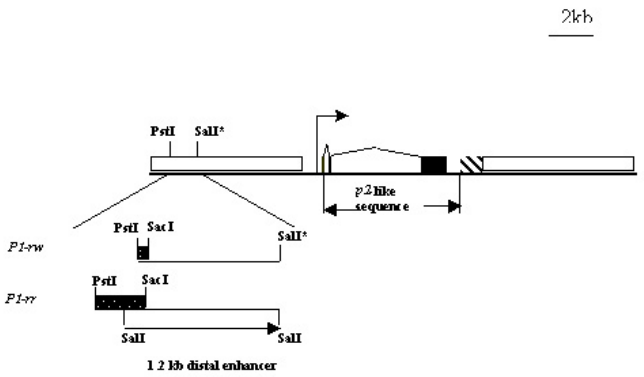

Figure 1. Structure of the *P1-rw* allele. *P1-rw* appears to be a chimeric gene generated by recombination between *p1* and *p2* sequences: the *p2*-like coding sequences are flanked by *p1*-like long direct repeats (open boxes). Exons and introns are indicated by black boxes and bent lines, respectively; the bent arrow indicates the transcription start site experimentally determined for the *P1-rr* allele (Grotewold et al., Proc. Natl. Acad. Sci. 88:4587-4591, 1991). The hatched box indicates a truncated *P1-wr*-like exon3. Sequence polymorphisms in the distal enhancer region are shown as dotted black boxes (339bp in *P1-rr*, 71 bp in *P1-rw).*

are underway to test whether *P1-rw* expression is regulated at the transcriptional or post-transcriptional level, or both.

p1-vv85, a new maize variegated pericarp allele, contains an insertion similar to the CACTA element, *Mpi1*

--Wang, Y, Peterson, T

The maize *p1* gene encodes a Myb-like factor that regulates transcription of structural genes, including *a1* and *c2*, required for red phlobaphene pigmentation in certain floral organs, including kernel, pericarp, and cob. We obtained a new *p1* mutant allele designated *p1-vv85*, from Dr. Peter A. Peterson, ISU. The *p1-vv85* allele specifies variegated pericarp and cob, and exhibits a very high rate of reversion to a state giving red pericarp and cob. Genetic analysis suggested that the mutant phenotype is not associated with *Ac* or *En/Spm* transposable element systems (P.A. Peterson, personal communication). Genomic Southern analysis indicated that *p1-vv85* contains a 1.2 kb insertion in *p1* gene intron 2, compared with its progenitor, *P1-rr107B* (from the Maize Genetics Stock Center). This region was amplified by PCR and found to contain a 1168bp insertion which has characteristics of the CACTA transposable element family: the insertion is bounded by 3 bp target site duplications, and it has 13bp TIR (terminal inverted repeats) which are identical to that of the CACTA transposable element *Mpi1* (Weydemann et al., MNL 62: 48,1988). The insertion also has structured subterminal regions that contain 12 copies and 6 copies of a 12bp motif at the 5'- and 3'-ends of the fragment, respectively. Northern blot analysis revealed that the *p1* gene transcript level is greatly reduced in *p1-vv85* pericarp, while a revertant allele contains a normal level of *p1* transcripts. Surprisingly, Southern blot analysis detected no difference in the structures of the *p1-vv85* allele and two independent revertant alleles. Specifically, no evidence of excision of the 1168 bp insertion could be detected by either genomic Southern blot or PCR. Thus, the insertion in *p1-vv85* may regulate *p1* gene expression by an epigenetic mechanism. Analysis of DNA methylation of the *p-vv85* mutant and a revertant allele revealed some differences in methylation of the insertion sequence, but not in the flanking *p1* gene sequences. This result is consistent with a model in which methylation of the insertion sequence may affect the binding of a suppressor-like factor to the element. In summary, the *p1-vv85* allele contains a CACTA element insertion relative to the progenitor *P1-rr107B* allele. However, the apparent "reversion" of *p1-vv85* to a functional *P1-rr* state does not result from element excision, but rather by relief of suppression, which is correlated with the methylation state of the CACTA element.

BEIJING, CHINA
Chinese Academy of Sciences

su1 type mutant induced by space flight

--Zeng, M, Zeng, Z, Ji, H

In our previous papers, we described a significant influence of space flight of maize seeds on progeny. Some types of traits have been obtained (MNL 74:2-3, 75:4, Chinese Space Science and Techndogy 18(6):63-67, 1998}.In addition, there was a mutant of the *su1* type from the Me141 inbred line of normal maize. The frequency of mutation was the smallest, about 0.06%. Some characters of plant, ear, leaf, tassel and kernel, etc., and some properties are given in Figure 1 and Table 1.

Figure 1 and Table 1 show the situation of the characters and properties of a mutant of the *su1* type. First, it presents some characters of wild maize; for example, the length of the leaf-blade

Figure 1. Ear traits for space induced mutant of the *su1* type (background soybean field)

Table 1. Plant and ear traits for space flight induced maize mutant of the *su1* type

Plant height (cm)	245
Ear height (cm)	101.3
Length of the leaf at the ear site (cm)	101.6
Width of the leaf at the ear site (cm)	9.8
Tassel length (cm)	59.9
Tassel branch number	32.5
Leaf number	21~22
Ear Length (cm)	17.4
Ear diameter (cm)	4.40
Number of kernel row	14.8
Kernel number of each row	38.0
Weight of 100 kernel (g)	21.1
Kernel type, color	*su1*, white
Cob color , ear form	white, spindle
Each ear weight	95.8
Kernel weight per ear	85.2
Day from seedling to kernel maturing	119~121
Length for leaf –blade of husk top (cm)	58-66
Husk number per ear	9~11
Length of ear handle(cm)	16~24
Ear number per plant	3
Resistance to *E. turcicum* & *B. maydis*	HR
to *P. inflatum* , *P. aphanidermatum*, *F.moniliforme* & *F. graminearum*	HR
to *S. holci-sorghi*	HR
to *P. sorghi* & *P. polysora*	HR

of the husk top, and the length of the ear handle is greater than that of normal maize. Second, plant height and ear length were 8.1% and 10.1%, respectively, higher (longer) than Control (CK), width of the leaf at the ear site was 11.4% wider than Ck; there were 31.0% more kernels per row than control, 93.5% greater tassel branch number and 50-100% more ears per plant. Third, there were 21.6% fewer numbers of kernel rows than control, and ear diameter was 23.2% smaller. Fourth, some characters and prooperties didn't have significant changes; for example, ear height, length of the leaf at the ear site, tassel length, leaf number, vegetation period, kernel and ear color, some resistance to diseases, etc.

BELGRADE-ZEMUN, YUGOSLAVIA
Maize Research Institute (Zemun Polje)

Changes in RFLP allele frequencies during recurrent selection for high oil content in maize

--Lazic-Jancic, V, Ignjatovic-Micic, D, Markovic, K, Coric, T, Kovacevic, D, Saratlic, G, Quarrie, SA

Although maize is not classified as an oil crop, oil production from maize has been increasing rapidly. To improve the efficiency of maize programs for increased oil content (i.e., to develop high oil hybrids of high yield and with other agronomically important characteristics) new breeding populations with favorable alleles for high yield have been developed (Micevic, D. et al., Crop Sci. 29:613-617, 1989; Dudley, J. W. and R. J. Lambert, Maydica 37:81-87, 1992).

Oil percentage is a quantitative trait controlled by many loci (Dudley, J. W. et al., Crop Sci. 17:111-117, 1977; Miller, R. L. et al., Crop Sci. 21:433-437, 1981). To help breeders introduce high oil content from such populations into elite lines, we have performed a study to identify genome regions carrying important genes for high oil content.

Genotypes used for this study were two maize populations, YuSSSu and DS7u, created at the Maize Research Institute, Zemun Polje. Selection for nine cycles resulted in a change in oil content percentage from 43.3gkg^{-1} to 128.7gkg^{-1} in YuSSSu and 47.2gkg^{-1} to 136.4gkg^{-1} in the DS7u population (Figure 1) (Dumanovic, J., 1995). By comparing allele frequencies in unselected (cycle 0) and selected (cycle 5 and cycle 9) populations by molecular markers (RFLP), it is possible to locate regions of the genome carrying genes determining oil concentration, thus identifying beneficial and/or detrimental alleles. The identification of RFLP loci that may be associated with selection for oil concentration by comparing population bulks, provides information complementary to RFLP mapping studies designed to identify quantitative trait loci for oil concentration.

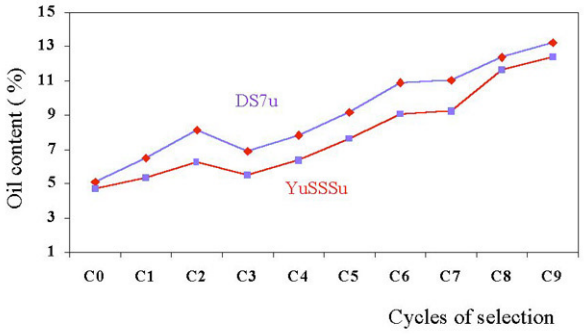

Figure 1. Effect of selection for oil content in DS7u and YuSSSu synthetic populations (nine cycles of selection).

Seedlings of each population and each cycle were raised, and equal weights of 75 plants combined and extracted using CTAB buffer to give DNA bulks. After restriction with three different enzymes (*Eco*RI, *Bam*HI and *Hin*dIII), DNA samples were resolved on agarose gels and Southern blotted.

Restricted DNA was hybridized with DNA probes and labeled by PCR using dig-11-dUTP. Detection was done with anti-digoxigenin, fab fragment, conjugated to alkaline phosphatase and chemiluminiscent substrate CSPD (Dig System Users Guide for Filter Hybridization - Boehringer Mannheim).

Twenty-three RFLP probes known to hybridize to loci distributed around the maize genome were examined. Major allele frequency differences were regarded as likely to be real when they were present in the majority of probe/restriction enzyme combinations.

The results have identified seven regions of the maize genome (Table 1) where major differences in RFLP frequencies had occurred in both populations during selection for high oil content. The example is shown in Figure 2. However, with the probe *umc90*, differences in allele frequencies were present in one population but not in the other. This indicates that the genetic control of high oil content may not be the same in both populations. If the genetic control is found to be different in two sets of populations, then this provides opportunities for increasing oil content yet further by combining beneficial alleles from both populations.

We are currently testing further RFLP markers to study in more detail the genetic determination of oil content in the maize

Table 1. List and effects of the RFLP probes used with DS7u and YuSSSu populations.

Probe	Chromosome	YuSSSu	DS7u
tub1	1	N	N
umc157	1	N	N
umc107	1	C	C
bnl8.45	2	C	C
umc6	2	N	N
umc5	2	N	N
umc49	2	N	N
umc32	3	C	C
umc102	3	N	N
csu25	3	N	N
umc31	4	N	N
npi386	4	N	N
umc66	4	C	C
npi409	5	N	N
umc90	5	C	N
umc59	6	N	N
umc65	6	C	C
umc21	6	C	C
umc38	6	C	C
npi220	8	N	N
csu31	8	N	N
php20075	10	N	N
bnl7.49	10	N	N

N - neutral effect
C - changes in allele frequencies during selction

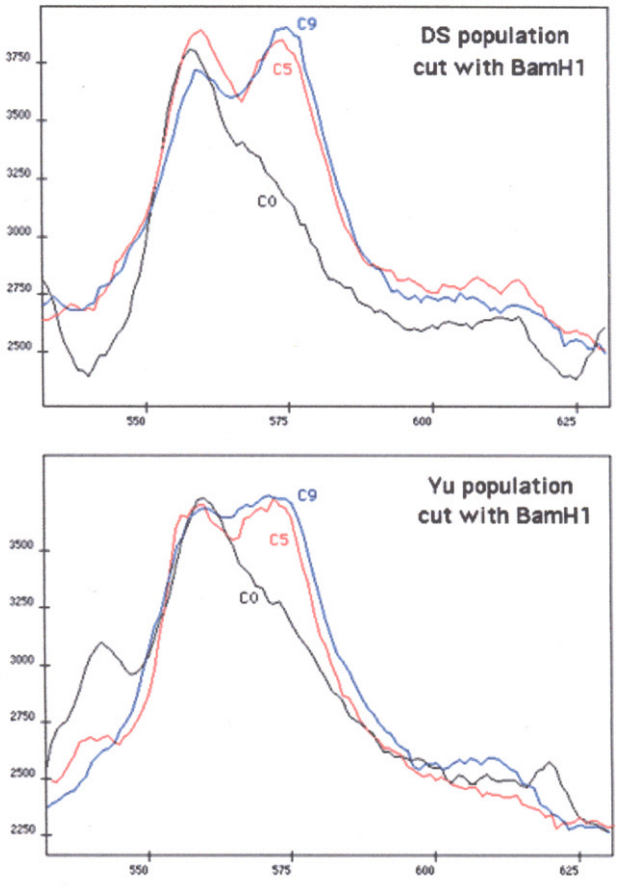

Figure 2. Densitometric traces for pooled DNA from 2 maize populations before (C0) and after selection for high oil content (C5, C9) hybridized with *umc66*.

kernel. The identification of RFLPs associated with oil content may be useful in molecular-marker facilitated breeding programs (MAS) designed to develop high-yielding, high-oil maize hybrids.

The maize variety accession No. 366 from the Yugoslav MRI collection caries a T cytoplasmic male sterility (cmsT)

--Vidakovic, M, Vidakovic, M, Vancetovic, J, Roculj, M

In the first part of the search for the restorer cytoplasm in maize (Vidakovic et al., XVIIth Conference on Maize and Sorghum EUCARPIA, Thessaloniki, Greece, Pp. 138, 1996), 50 randomly chosen late varieties from the Collection of Yugoslav varieties of the Maize Research Institute (MRI), Zemun Polje, Belgrade, Yugoslavia, were crossed with a series of *ms*/+ stocks: *ms1*/+, *ms2*/+, *ms3*/+, *ms6*/+, *ms7*/+, *ms8*/+, *ms9*/+, *ms11*/+, *ms12*/+, *ms13*/+, *ms17*/+, *ms22*/+, *ms23*/+ and *ms24*/+. Crosses were made in 1993, with varieties used as females, and the *ms*/+ stocks as males. Two ears of each cross were taken for further research, and handled separately.

In 1994, F1 ears were sown for further selfing, in order to search for the restorer cytoplasm in 1995 in selfed progenies (100% fertility in such progeny would be an indicator of the restorer cytoplasm for the appropriate *ms* gene). But in a few F1s (with 6 varieties), sterile plants unexpectedly occurred in 1994, indicating some other source of sterility besides the *ms* gene with which it was crossed, i.e., crossing with a *ms*/+ stock to a plant not carrying the appropriate *ms* gene would result in a 100% fertile F1.

In Table 1 there is a list of F1s (variety x stock) where sterile plants were noticed.

Table 1. List of F1s where sterile plants occurred in 1994.

Variety [1]	366	1172	1465	1485	1570	1853
ms stock						
ms1/+	Segr.[2] both progenies					
ms2/+	Segr. both progenies		Segr. 1 progeny			Segr. 1 progeny
ms6/+	Segr. 1 progeny					Segr. 1 progeny
ms8/+	Segr. 1 progeny					
ms9/+	1 progeny 100% sterile	1 progeny 100% sterile	Segr. 1 progeny			
ms11/+	Segr. 1 progeny	1 progeny 100% sterile				
ms13/+	1 progeny 100% sterile	Segr. 1 progeny	1 progeny 100% sterile	1 progeny 100% sterile		1 progeny 100% sterile
ms17/+					Segr. 1 progeny	
ms22/+	Segr. 1 progeny					
ms23/+	Segr. 1 progeny					
ms24/+	Segr. 1 progeny					

[1]Variety is given by an accession number in our gene bank
[2]Segregates on fertile and sterile plants

In the variety accession No. 366, the occurrence of sterile plants was the most obvious. We supposed that this variety contained some kind of cytoplasmic male sterility, and did additional tests: F1 sterile plants of the *ms1*/+ stock were pollinated with the line F-7(R), which is a partial restorer for the S cytoplasm, and F1 sterile plants with the *ms2*/+ stock were pollinated with F-7(R), as well as the line ZPL-217, known as the RfC line.

In 1995, all of the crosses with F-7R and ZPL-217 were ster-

ile, indicating the absence of cms-S, as well as cms-C from population 366. These sterile plants were pollinated with another partial restorer for the cms-S (ZPLB-368/73), as well as with two lines known as restorers for cmsT: R-348 and R455. In 1996, only tests with RfT lines showed full fertility, while others were absolutely sterile. So, variety Zuti zuban from the region of Novi Sad (accession No. 366) carries the T-type of cytoplasmic male sterility.

In this way we checked just the most obvious carrier of cytoplasmic male sterility in this study. Other varieties that showed sterile plants in this experiment are included in a broader checking of the male sterility sources in our gene bank.

Genetic diversity among ZP maize hybrids from different selection cycles obtained by protein markers

--Eric, I, Drinic Mladenovic, S, Konstantinov, K, Stankovic, G

The objective of our study was to identify 30 maize hybrids from different cycles of selection and validate their genetic relationship by protein markers. Since 1964, a total of 439 hybrids, derived at the Maize Research Institute, Zemun Polje, Yugoslavia, have been released or authorised to be included into production by the Federal Commission for the Variety Releasing; the majority of which are single cross hybrids (61%), with triple cross hybrids accounting for 31%, and double cross hybrids for 8%.

Five cycles (periods) have determined breeding and growing of hybrid maize in Yugoslavia. Each period has been characterized by the introduction of new higher yielding hybrids. The increase of genetic yield potential of selected hybrids over these cycles amounted to 1,094 t, or approximately 100 kg per year (Ivanovic et al., Symposium of Maize Breeding, Production and Utilization, pp.3-17, Belgrade, Sept. 1995).

The first cycle of selection is represented by the first local double cross hybrids, replacing the formerly grown American double cross hybrids. They were introduced into broader production at the end of the 50's and the beginning of the 60's. During the 60's, remarkable progress was achieved during the second cycle, when the first single cross hybrids were introduced. They increased genetic potential and uniformity, which led to their predominant use and production during the 70's. The hybrids of the third cycle were introduced at the end of the 70's. These were the new single cross hybrids, which had increased genetic yield potential 10-15% and were more tolerant to high density cropping. Fourth cycle hybrids were introduced at the end of the 80's, and had increased drought tolerance and increased tolerance to stalk lodging. The newly developed hybrids respond better to a higher level of cropping practices and achieve maximum genetic yield potential at greater plant densities (Drinic et al., TOSS 12, pp.1-8, 2001).

Knowledge of the genetic diversity and relationships among maize hybrids is important for planning breeding strategies, hybrid identification, and germplasm identification. The genetic similarity of two genotypes could be estimated indirectly from pedigree information or directly by molecular markers (isozymes, protein, DNA markers). The utility of protein markers to characterize maize hybrids, validate pedigrees, and show association among hybrids was evaluated using a set of 30 ZP maize hybrids from 5 different selection periods (6 hybrids from each cycle).

The proteins were isolated from embryos of hybrids from different selection periods and separated by PAGE (Polyacrylamide Gel Electrophoresis) according to Laemmli (Laemmli, U.K., Nature 227:680-685, 1970). The analysis of embryo salt soluble proteins shows that all genotypes studied have a specific protein pattern. Both quantitative and qualitative differences between protein fraction were determined, and indices of similarity were calculated.

The UPGMA clustering method was used for hierarchical clustering and the necessary computations were performed using the NTSYS-pc program (Rohlf, New York Exeter Publ, 1989). The protein based dendrogram, consisting of three major groups, is presented in Figure 1. The first group is further divided into seven subclusters, assigned from A to F. Twenty-five hybrids were distributed within one large and six small subgroups The main subcluster C includes 13 ZP hybrids, mainly from the third, fourth and fifth cycles of selection. It was comprised of hybrids derived from or related to BSSS germplasm. The hybrids that have Wf9 and Oh43 lines as one parent grouped together in subcluster G and E, respectively. The subcluster A, consisting of two hybrids, one from the first and one from the third cycle of selection, was loosely aggregated with a large group of hybrids.

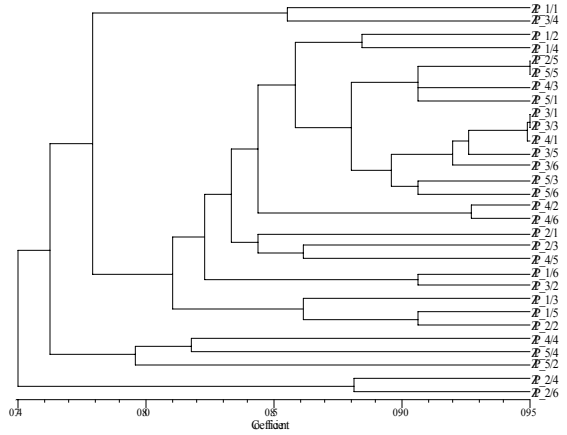

Figure 1. Dendrogram of 30 maize ZP hybrids based on protein markers

The five remaining hybrids with one parent from or related to Lancaster germplasm form two separate groups. Three hybrids, two from the fifth and one from the fourth cycle of selection, form the second group. The third group consists of two hybrids belonging to the second cycle of selection with the common parent line C103.

Grouping of 30 ZP hybrids from different cycles of selection generally agreed with the pedigrees, but some discrepancies in forming subclusters within major groups were noted. One discrepancy was that two double cross hybrids, ZP1/4 and ZP1/3 from the first cycle of selection, which had three of four parental inbred lines in common, were in different subclusters. Also, hybrid ZP2/5, instead of being in the first group, subcluster C, has to be in the third group due to its orgin.

In summary, our study provides information on the molecular basis of polymorphism detected by protein markers in 30 ZP maize hybrids. It demonstrates that protein markers can identify and validate genetic relationships among maize hybrids.

BERGAMO, ITALY
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Nitrogen-induced changes in the metabolism of in vitro grown developing kernels of *defective endosperm* maize mutant

--Balconi, C, Bosio, D, Motto, M

Although the biochemical mechanisms of both C and N synthetic processes in developing maize kernel have been generally elucidated (Moutot et al., Plant Physiol. 80:211-215, 1986; Pernollet et al., Plant Physiol. 80:216-222, 1986; Giroux et al., Plant Physiol. 106:713-722, 1994), the nature of the coordinated regulation of these still remains unclear. In order to improve the understanding of the mechanisms controlling starch and protein synthesis in maize endosperm, and to define genetic functions mediating the state of the metabolism on trascriptional regulation of endosperm-specific genes, the *defective endosperm* (*de*) mutant collection introgressed into the B37 inbred line (Manzocchi et al., Maydica 25:105-116, 1980) and the *miniature* (*mn)* (Lowe et al., Genetics 31:525-533, 1946) mutant, either grown in vivo or cultured in vitro on artificial media containing different levels of nitrogen nutrients, have been studied. For the in vivo evaluation, samples at 15 and 25 days after pollination (DAP), were collected. In order to evaluate a possible role of the cob and pedicel-placento-chalazal tissues (PPCh) in the amino acid supply, in the accumulation of zein and starch synthesis of developing caryopses, *de* and *mn* mutants were harvested at 10 DAP. Ears of the B37 wild-type were used as control. The ears were cut into blocks containing 10 kernels each as described by Gengenbach (Planta 134:91-93, 1977). The blocks were cultured on agar media plus salts as described by Nitsch and Nitsch (Science 163:85-87, 1969) containing NH_4NO_3 (0.72 g/l) as a source of nitrogen (N), 75 g/l sucrose and 0 (Medium A) or 4 (Medium B) g/l asparagine as a source of organic N. Kernels were incubated in the dark at 26 C until 15 or 25 DAP. Dry weights were determined for B37 and *de* mutants' endosperms, at different stages of development on the mother plant and after the in vitro culture. In vivo and in vitro endosperm samples were assayed for protein content (zeins, albumins plus globulins, glutelins), and for starch and soluble sugar content. In Table 1, zein content, as a percentage of dry matter (%/d.w.), of the B37 control, and of the *de* and *mn* mutant kernels grown in vivo or in vitro on the two media with different N content, at 15 and 25 DAP, are reported.

The data indicate that differences exist between B37 and its *de* version and among *de* mutants themselves. A comparison between the in vivo and in vitro developing endosperms, for a given genotype, suggested that the different *de* mutants respond in a peculiar manner to the different N levels. Differences for B37 and the mutants appeared evident relative to the utilization of organic and inorganic N for the protein synthesis. Asparagine in the in vitro culture media, induced, in almost all genotypes tested, an increase in zein content (as %/d.w.) at 25 DAP. More variability in zein accumulation, dependent on the nutrient supply in the media, was noticed at 15 DAP. At 25 DAP, *de37* kernels grown in vitro on both media reached a zein content higher than that observed in field grown kernels at the same developmental stage. The B37 control, *de10*, *de246*, *mn1*, grown in vitro in the presence of asparagine, reached at 25 DAP a zein content similar or very close to that observed in vivo. All the other mutants showed on both culture media a zein content lower than that of field grown kernels. Studies are in progress to analyze if the in vitro culture method tested could mimic the development of defective maize endosperms grown in vivo; in addition these studies are aimed at understanding how the cob and PPCh tissues may be involved in determining the defective phenotype through a less efficient system of amino acid uptake, interconversion, and transport to the endosperm, in comparison with the control.

Table 1. Zein content as percent of dry matter (%/d.w) of in vivo and in vitro (medium A: 0 g/l asparagine and B: 4 g/l asparagine) grown kernels of the B37 + (wild-type), *de* mutant collection and *mn* mutant at 15 and 25 DAP.

	In vivo	In vitro Medium A 0 g/l asparagine	In vitro Medium B 4 g/l asparagine	In vivo	In vitro Medium A 0 g/l asparagine	In vitro Medium B 4 g/l asparagine
Genotype	15 DAP	15 DAP (explant at 10 DAP + 5 days in vitro)	15 DAP (explant at 10 DAP + 5 days in vitro)	25 DAP	25 DAP (explant at 10 DAP + 15 days in vitro)	25 DAP (explant at 10 DAP + 15 days in vitro)
	Zeins (%/d.w)	**Zeins (%/d.w)**	**Zeins (%/d.w)**	**Zeins (%/d.w)**	**Zeins (%/d.w)**	**Zeins (%/d.w)**
B37 +	2.70	2.89	4.22	4.20	2.15	4.25
de1	3.04	2.60	2.10	4.53	2.30	3.52
de 6	2.56	2.20	3.40	6.61	4.41	4.65
de10	2.96	3.29	4.96	4.36	2.40	4.74
de18	3.37	2.05	3.11	7.07	2.20	2.40
de21	4.96	1.90	2.10	9.34	2.30	2.71
de 37	3.07	1.95	2.78	4.92	6.23	7.23
de 110	2.08	3.74	3.18	6.96	3.20	3.69
de 116	3.01	2.56	5.97	7.90	2.17	3.20
de 241	1.99	2.25	1.91	8.16	2.06	2.57
de 246	1.30	2.43	3.19	5.53	2.07	4.71
mn1	1.83	2.40	2.39	4.27	3.26	3.82

Ectopic expression of the endosperm albumin b32 in transgenic maize

--Lanzanova, C, Conti, E, Baldoni, E, Allegri, L, Hartings, H, Lupotto, E

The development of maize plants engineered with defence genes acting against fungal pathogens is a major objective in modern breeding strategies. Pathogen defence genes may provide direct protection of plants in the field contributing to alleviate damages such as ear- and stalk-rot produced by *Fusarium verticillioides (moniliforme)* and subsequent development of storage molds associated with mycotoxin production (*Fusarium*, *Penicillium*, *Aspergillus*). Engineering and correct expression of antifungal genes are therefore the first requirements for such a goal.

The maize endosperm albumin b32 is a Ribosome Inactivating Protein (RIP) normally expressed in the kernel. It has been the subject of extensive studies aimed at investigating and exploiting its action as a defence protein against fungi and insects. Like other RIPs present in the cereal seeds, b32 may play a double role of a storage and a defence protein during seed germination. Ectopic expression of b32 in maize might result in a wider defence action for other tissues. Current work in our laboratories aims to obtain maize plants expressing b32 in various plant parts and during the complete plant growth cycle, with the final goal of verifying its potentiality as a defence gene against fungal pathogens.

A first set of experiments produced a series of transformation events carrying the *b32* gene under the 35S CaMV constitutive promoter. Although not specifically suited for monocotiledonous plants, the 35S promoter correctly drives the expression

of *b32* gene in transgenic wheat and rice (Lupotto, unpubl.). To this purpose, an expression vector carrying the cassette *35S-b32* and *ubi1-bar* as a selectable marker, was constructed. T0 events, obtained from biolistic transformation of A188XB73 F2 immature embryos, were pollinated with B73 plants to obtain T1 plants, which were grown in a controlled environment (notification B/IT/02/02), during 2002 at the Section of Bergamo. A total number of 344 seedlings were sprayed with L-glufosinate 4g/l at the III-leaf stage. After five days, a visual check of surviving seedlings showed 167 resistant plants and 177 dead plants, thus confirming the expected ratio of 1:1 segregation for Basta resistance. Before Basta treatment, a series of 40 randomly chosen plants were analysed in PCR in order to confirm correspondence between Basta resistance and *bar* gene presence, and to evaluate the co-presence of both *bar* and *b32* genes. Results obtained confirmed the co-presence of both genes in each resistant plant: 18 plants were Basta resistant and PCR positive, whilst 22 plants died and were PCR negative.

Young plants at the VI-leaf stage were subsequently analysed for control of ectopic b32 expression in the leaf tissue. All b32 PCR+ plants analysed with immunoblots using anti-b32 antibodies - raised in rabbits against purified GST-b32 obtained in *E.coli* – were positive in western, with the exception of two plants, thus confirming the correct expression of the endosperm protein in leaf tissues (Figure 1a). Plants were grown to complete maturity, were fully fertile and set seeds. Expression of b32 was analysed in adult plants at the stage of flowering, with focus on those tissues more likely to be target sites for fungal invasion: silks, rachis, brace roots and husks. Results obtained gave evidence of expression of the engineered protein in all parts of the b32-engineered adult plants; the two plants which did not express in young leaves were confirmed to be non expressing at later stages (Figure 1b). Current work is focused on b32 expression analysis in germinating seeds and on the interaction between the b32-engineered maize and *Fusarium.*

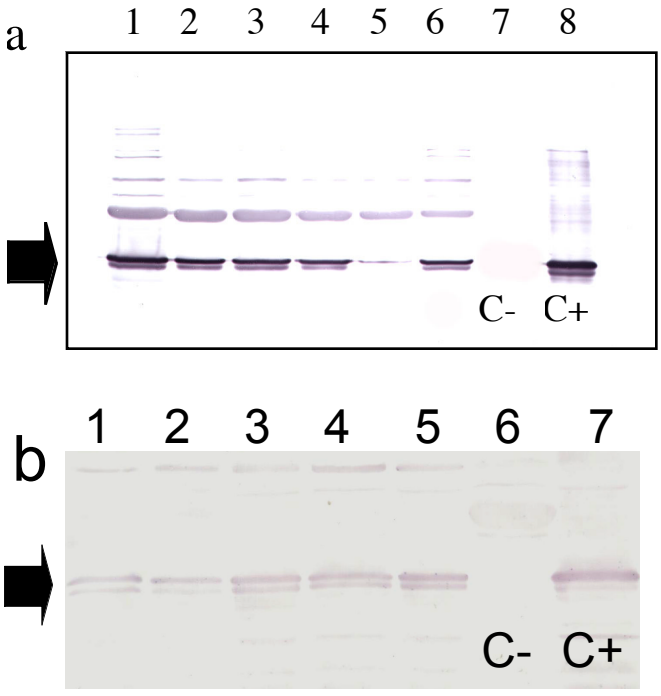

Figure 1. a) Western analysis of T1 plants engineered with 35S-b32, at the VI-leaf stage. Expression was confirmed in all PCR+ plants, except two. The maize control non-transgenic genotype W64A, does not express b32 in leaves (C-) but only in the endosperm (C+). *Lanes*: 1.SM22, 2. SM30, 3.SM35, 4.SM38, 5.SM2, 6.SM43, 7.W64A leaf, 8. W64A endosperm. b) Western analysis for b32 expression in various tissues of plant SM1 at the flowering stage. *Lanes*: 1.SM1 silks, 2. SM1 rachis, 3.SM1 brace roots, 4.SM1 husks, 5.SM1 leaf, 6.W64A leaf, 7. W64A endosperm

The work is developed within the framework of the EU-funded project SAFEMAIZE (ICA4-CT2000-30033) in FP5.

Improving in vitro culture and transformation conditions in *Agrobacterium*-mediated transformation of maize

--Conti, E, Lanzanova, C, Baldoni, E, Allegri, L, Lupotto, E

Agrobacterium-mediated transformation of cereal crops is being extensively investigated because of the many advantages offered by this system of gene delivery over the widely adopted biolistic method. It is indeed now well attested that *Agrobacterium*-mediated transformation –now possible also in monocotiledonous species – results in a higher number of stable, low copy number, correctly expressing transgenic events, than the biolistic system. *Agrobacterium*-mediated transformation of maize, first based on the adoption of supervirulent strains carrying Ti-plasmid engineered with extra copies of the *virB*, *virC* and *virG* genes (Ishida et al., Nature Biotechnol 14:745-750, 1996), can now also be effective using standard binary vector systems and L-cysteine as a transformation enhancer (Frame et al, Plant Physiol 129:13-22, 2002).

Present work in our laboratory aims at extending the methodology of transformation mediated by *Agrobacterium tumefaciens* to maize genotypes of agronomical value. This includes the identification of reliable protocols aimed to enhance the in vitro responsiveness – related to the development of embryogenic callus cultures – and the frequency of transformation.

In a previous work (Lupotto et al., Maydica 44:211-218, 1999), some parameters for the establishment of a transformation system in maize have been explored in the maize A188 inbred line and in a series of Lo inbred lines of agronomical importance (Bertolini et al., Maydica 36:87-106, 1991). In these latter inbreds, the lack of in vitro responsiveness appeared to be the major bottleneck in obtaining transgenic events. As a first step toward our goal, a series of Lo inbred lines belonging to different heterotic groups (Hartings et al., Maize Coop. Newslet. 76:5-6, 2002) was chosen. Their in vitro response to the embryogenic callus induction (EC) and subsequent regenerative capability were evaluated in the Lo per se and in crosses between each Lo and the highly embryogenic maize model genotype A188 (Table 1). With the exception of Lo1010, the induction of E callus did not appear to be a limiting step; E calli were obtained in all cases, although at different rates depending on the genotype. As expected, the in vitro response of F2 immature embryos derived from each cross showed a significantly higher frequency of EC induction. The most important result was the case of Lo1010xA188, in which a complete switch from non-regenerative to regenerative callus culture was obtained. The number of completely regenerated plants varied largely according to the genotype; in addition, plants raised from each cross were not only higher in number, but also more vigorous, with a properly developed root system established in vitro – which is the most important limiting factor for transplantation into soil

Table 1.

Genotype	No. explanted embryos	No. embryogenic calli obtained	% EC	No. regenerating calli	%R	No. plants obtained
Lo1096 x A188	334	266	79.6	89	33.4	76
Lo1095 x A188	253	211	83.3	118	55.9	38
Lo904 x A188	165	124	75.1	60	48.3	23
Lo1124 x A188	163	120	73.7	17	14.1	14
Lo1067 x A188	192	128	66.7	5	3.9	2
Lo1066o2x A188	196	108	55.1	31	28.7	29
Lo1010 x A188	180	131	72.7	11	8.3	9
Lo1010	200	23	11.5	3	13	0
Lo1095	204	134	65.7	96	71.6	6
Lo1096	192	152	79.1	0	0	0
Lo904	194	77	39.7	12	15.6	2
Lo1124	175	97	55.4	0	0	0

– showing a stronger phenotype. Evaluation of the experiment based on the number of completely regenerated plants allowed us to conduct transformations in at least four different crosses.

For *Agrobacterium*-mediated transformation the strain *A.tumefaciens* EHA105 was used. This was engineered with a binary pCAMBIA3301-based vector, containing the *bar* gene as selectable marker, and the *gus* gene as visual marker. The vector also contains the cassette ubi1-b32-nos3' for obtaining the constitutive expression of the maize gene b32 (see above Lanzanova et al.) as a potential anti-fungal gene. Transformation was performed either with immature embryos just after explant or with embryos subjected to a pre-culture period of 5 days. This additional step was introduced with the aim of overcoming the limitation in efficiency due to the deleterious effects of L-cysteine and of the infection process on the subsequent EC induction. As summarised in Table 2, the results obtained strongly supported the adoption of the additional pre-culture. The effect of L-cysteine added during the co-culture period in the case of infection of immature embryos without preculture, varied with the genotype. Of the four crosses evaluated, two were completely inhibited by L-cysteine, while the others were only partially inhibited. In all cases, the absence of L-cysteine raised the rate of EC induction after infection. When a five day pre-culture period before *Agrobacterium* infection was adopted, the negative effect of L-cysteine on EC induction was drastically reduced; it was also evident that the rates of EC induction paralleled those without L-cysteine. Callus culture in general showed a better phenotype and higher rate of callus proliferation (Figure 1). Presence of the engineered cassette was detected in most of the regenerated plants, as shown by PCR analysis in Figure 2. This result is indicative of the efficacy of the protocol adopted, paving the way for a more consistent set of experiments on the selected maize genotypes. The work is developed within the framework of the EU-funded project SAFEMAIZE (ICA4-CT2000-30033) in FP5.

Table 2.

Genotype	No. explanted embryos	% EC obtained +cys	no cys
Infection: T0			
Lo1096 x A188	100	0	85.5
Lo1095 x A188	100	52.8	86.4
Lo904 x A188	100	40	82.6
Lo1124 x A188	100	0	53.7
Infection: T5			
Lo1096 x A188	100	76.8	84.8
Lo1095 x A188	100	87.5	67.9
Lo904 x A188	100	69.5	84.4
Lo1124 x A188	100	98.8	71.7

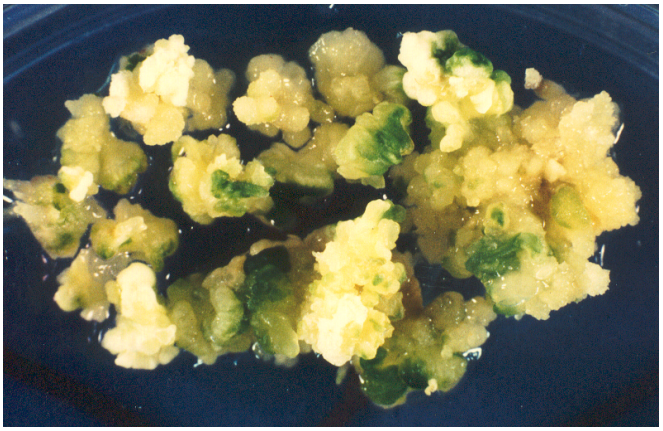

Figure 1. Embyogenic maize callus in regeneration medium, derived from F2 immature embryos of the cross Lo904 x A188, after *Agrobacterium* transformation

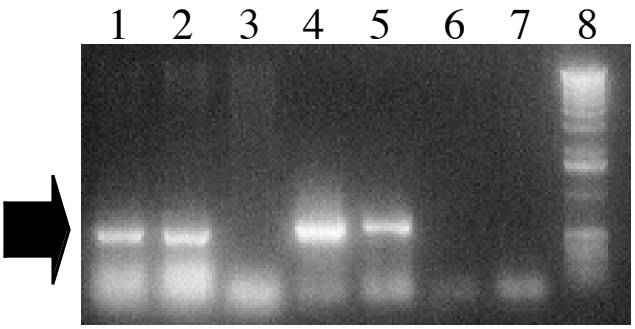

Figure 2. PCR analysis of T0 events of transformation with *Agrobacterium* EHA105(pCAMBIA3301/ubi1-b32). Lanes: 1 to 6 are independent T0 events: plants 1,2,4 and 5 show the expected band for ubi1-b32; 7. A188 negative control, 8.Ladder

Molecular evolution of the regulatory locus *opaque2* from *Zea*

--Lazzaroni, N, Hartings, H

The evolution of the *opaque-2* (*o2*) locus within members of the grass family was analyzed at the molecular level. For this purpose, a segment of the locus ranging from the third to the sixth exon was purified by means of PCR amplification and subjected to sequence analysis. Eleven accessions covering all *Zea* taxa and one *Tripsacum dactyloides* accession were assayed, identifying 21 haplotypes.

Our analyses reveal little evidence of selection at silent sites across the stretch of the *o2* locus considered. First, the distribution of polymorphic silent sites between coding and intron regions was uniform, as was the distribution of polymorphic synonymous sites across the exons examined. Second, the distribution of observed nucleotide frequencies at synonymous polymorphic sites did not deviate significantly from the predicted frequency distributions under a model of selective neutrality. Third, Tajima's D was not significantly different from zero. Selective pressure was measured by means of a sliding windows approach, which revealed a region with a significantly negative D value. This region, in the fourth exon, encodes the basic domain of the O2 protein, which is responsible for DNA binding and is involved in the relocation of the

O2 protein into the nucleus. The preservation of this structure is, therefore, of fundamental importance in order to keep a functional gene product.

The pattern of non-synonymous site variation in the region of the *o2* locus analyzed suggests the operation of natural selection. First, the number of observed nonsynonymous polymorphic sites is significantly lower than expected from synonymous site polymorphism. Second, the distribution of nonsynonymous polymorphism is not uniform across exons. The exons encoding the two functional parts of the active domain of the O2 protein, the basic domain, encoded by the fourth exon, and the zipper domain, encoded by the fifth exon, show an evident reduction of nonsynonymous polymorphic sites with respect to the other exons considered. Third, the use of a sliding windows approach to determine Tajima's D statistic, identified three regions with negative D values residing within the third, fourth and fifth exon, respectively. These results indicate that selection is operating on nonsynonymous sites of the region of the *o2* locus taken into consideration. This selection is most marked within the fourth and fifth exon, the two exons encoding the active domain of the O2 polypeptide. The sixth exon, which exhibits a higher than average density of nonsynonymous polymorphic sites, was found to contain a region showing a positive D value. Since two alternative polypeptide sequences have been identified, the C-terminal region of the O2 protein is probably not exposed to strict structural constraints.

Upper bounds for the time of speciation within *Zea* were recently determined using synonymous polymorphism at the *alcohol dehydrogenase1* (*adh1*) locus. These measures of speciation time can be used to estimate the synonymous site substitution rate at the *o2* locus. Synonymous site substitution rates of 2.2-3.6 x 10^{-8} per site per year were obtained. With the synonymous substitution rate at the *o2* locus, it becomes possible to derive $\hat{N}_e$ the effective population size of *Zea*, which was estimated at 3.9-6.4 x 10^5 by using the equation $\hat{N}_e = \hat{\theta}/4\hat{\mu}$. This value is in good agreement with estimates (8.1 x 10^5) based on *adh1* synonymous polymorphism.

In view of the fact that introgression between teosinte and maize is believed to occur infrequently, the relatively close relationship between the *o2* loci of maize, teosinte, and *T. dactyloides*, as inferred from our molecular analyses, indicates a shared evolutionary history. It is, moreover, probably safe to assume that the variation at the *o2* locus predates the speciation events leading to *Z. perennis*, *Z. diploperennis*, *Z. luxurians*, and *Z. mays*.

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Molecular characterization of mutations resulting in a *liguleless1* phenotype

--Braun, DM, Freeling, M

In our studies on *liguleless1 (lg1)* we have characterized many independent mutations with a liguleless phenotype. These mutants were obtained from the Maize Coop Genetic Stock Center, sent to us by other collaborators, or identified in the Freeling lab. All were determined to be alleles of *lg1* by complementation testing the new liguleless mutants to the *lg1-Reference* allele. All of the F1 progeny showed a mutant phenotype. The F1 were self-fertilized and the F2 displayed a 100% mutant phenotype indicating that the new mutant being tested was allelic to *lg1*. All of the alleles have a phenotype indistinguishable from the reference allele with the exception of *lg1-N2375* which has a much weaker phenotype. The nature of the lesion in the *lg1* gene was determined for many of the alleles (Table 1). To characterize each mutation, a combination of

Table 1. Molecular alterations in various *lg1* alleles.

Allele	Alteration
lg1-Reference	Deletion of entire gene
lg1-64-4	Deletion of entire gene
lg1-6198	Deletion of entire gene
lg1-K16	Deletion of entire gene
lg1-Ds	Deletion of entire gene
lg1-PI200299	268 bp deletion of promoter, transcription & translation start sites
lg1-m1	*Ac* insertion in intron1
lg1-MTM	*Mu* insertion in 5' end
lg1-PI262493	*Tourist* insertion in exon2
lg1-TaiTaiTaSarga	4 bp insertion in exon2
lg1-ZCxGRB	Insertion in 5' end
lg1-128	Insertion in 5' end
lg1-340	Insertion in 5' end
lg1-656	Insertion in 5' end
lg1-N2375	*V173M* mutation in DNA binding domain
lg1-m2	unknown
lg1-ems	unknown
lg1-56-30375	unknown

Southern blot analysis, PCR amplification and DNA sequence analysis of the coding region of *lg1* was performed. Note that for three alleles we were unable to find any changes in the coding region; these alleles likely represent *cis* regulatory mutations.

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Novel meiotic mutants of maize identified from *Mu* transposon and EMS mutant screens

--Golubovskaya, IN, Sheridan, WF, Harper, LC, Cande, WZ

Our goal is to identify maize genes that control key events in meiosis, such as initiation of meiosis, pairing of homologous chromosomes, synapsis, meiotic recombination, and chromosome segregation. A large collection of maize meiotic mutants will allow us to study the genetic control of meiosis and thereby further our understanding of meiosis in large genome organisms.

The first maize meiotic mutants (*as1, am1, dy1, dv1, el1, po1, po1-ms6, st1*, and *va1*) were discovered in the 1930's and have been maintained at the Maize Genetic Stock Center. In 1974, the collection of maize meiotic mutants was doubled in size by screening M3 populations treated with N-nitroso-N-methyl urea. Several new, unique mutants and new alleles of known meiotic genes were isolated from this screen, such as *afd1, am1-pral, dsy1, dsy2, dsy3, dsy4, Mei025, ms28, ms43*, *pam1, pam2,* and *po1-ms4*. All these mutants, except for *Mei025*, are recessive (Golubovskaya, Adv. Genet. 26:141-192, 1989)

New meiotic mutants. As a part of a long-term collaboration between I. N. G. and W. F. S., the collection of meiotic mutants was further increased in number by screening a maize population with active *Mu* transposons. The goal of using an active *Mu* population was to facilitate cloning of the maize meiotic genes. We

screened the same F2 population that was previously used to isolate 51 maize embryo-specific mutants (Clark and Sheridan, Plant Cell 3:935-951, 1991; Sheridan and Clark, Plant J. 3:347-358). From 1991 to 1998, we discovered and characterized 18 new meiotic mutants (Table 1). In addition, in 1993, we isolated three meiotic mutants from active *Ac* stocks; these mutants have desynaptic phenotypes and were designated *dsy9307*, *dsy9308*, and *dsy9309*.

Table 1. Meiotic mutants discovered in screening of *Mu* active stocks at UND during 1991-1998.

Year	Total number of screened Mu active families	Number of families segregated for male sterility*			Symbols of meiotic mutations
		Total*	Independent	Meiotic mutants	
1991	836	80	30	7	*am1-485, dsy483**, dsy485**, dsy523=dsy1-9101, mac1=lar487, po495, sticky485*
1992	584	73	15	5	*am1-489, dsy498=phs1, asy498, segII-513, pam3-495***
1993	738	36	15	6	*dsy9301#, dsy9302#, dsy9303, dsy9304#, dsy9305, dsy9306*

Designations: *Total number of families isolated from a total of 836 *Mu* screening families. If the same mutant phenotype segregated in several (3 –10) self-pollinated siblings we count them as the same mutation event (see Independent column).
**mutants that were lost during propagation;
#these mutants have not been studied since found.
Numbers after gene symbols in years 1991-1992 designate numbers of Robertson's *Mu1* sources. Numbers after gene symbols in 1993 designate year and numerical order of isolated mutants

Abreviations: *am1 – ameiotic1, asy1 – asynaptic, dsy - desynaptic, lar – leptotene arrest, mac1 - multiple archesporial cells, pam3- plural abnormality of meiosis, phs1- poor homology synapsis, po – polymitotic, segII – segregation in II meiotic division.*

Some of the new mutants found in the *Mu* screen have unique phenotypes. For example, in *mac1* plants, multiple archesporial cells undergo differentiation into megaspore mother cells in the ovule instead of one as in normal maize plants (Sheridan et al., Genetics 142:1009-1020, 1996; and Sheridan et al., Genetics 153:933-941, 1999). Other mutants from this screen have phenotypes similar to previously described mutants. Two mutants exhibited phenotypes similar to *ameiotic1* and turned out to be new alleles of the *am1* gene. These alleles were designated *am1-485* and *am1-489* (Golubovskaya et al., Genetics 147:1339-1350, 1997).

Another mutant, *po495,* had a polymitotic phenotype, distinguishable by a precocious post-meiotic mitosis that starts without a preceding S phase. However, it is not allelic to the original *polymitotic1* mutation first described by Beadle (Cytologia 5:118-130, 1933). The *pam495* mutant is similar in phenotype to the *pam1* and *pam2* mutants and is characterized by the presence of multinuclear conglomerates (coenocytes) in prophase I as well as abnormal chromosome synapsis and chromosome missegregation in anaphase I. However, *pam495* is not allelic to either *pam1* or *pam2*. The *sticky485* mutant is similar to the Beadle's *sticky1* mutants. During prophase I, chromosomes in this mutant do not separate but rather condense into a tight cluster and cannot be distinguished individually under a microscope; chromosome fragmentation and missegregation occur in anaphase I. The allelic relationship between *sticky485* and *sticky1* has not been tested. The remainder of the new mutants have abnormal chromosome pairing or synapsis and were designated with a prefix *dsy* (see Table 1). One mutant, originally designated as *segregationII-513 (segII-513)*, turned out to exhibit abnormal homologous synapsis after a more detailed cytological examination. All meiotic mutants found in this screen were completely male and female sterile.

Allelism tests showed that four new mutants with desynaptic phenotypes, *dsy523, dsy9307, dsy9308*, and *dsy9309*, were alleles of the *dsy1* locus, in which two other mutations were previously identified, *dsy1-1*, induced by chemical mutagenesis in 1974 (Golubovskaya and Mashnenkov, Genetika (Russ.) 12:7-14, 1976) and *dsy1-9101,* discovered as a spontaneous mutation in 1991 (Golubovskaya et al., Devel. Genetics, 13:411-24, 1992; Golubovskaya et al., Devel. Genetics, 21:146-59, 1997). However, analysis of the pedigree of the new alleles isolated in *Ac* active families suggested that they likely represented the same mutant allele and they were designated as *dsy1-9307*. The *dsy523* is the *dsy1-9101* allele. Two other new desynaptic mutants, *dsy498* and *asy498,* showed allelism in our test, but pedigree analysis again indicated that they too represented the same mutation event. The other new desynaptic mutants did not show allelism among themselves nor to any of the existing desynaptic maize mutants that we tested (Table 2).

Table 2 Allelism test of desynaptic mutants isolated at UND (1991-1998).

	dsy1	*dsy523*	*dsy9101*	*dsy9307*	*dsy9308*	*dsy9309*	*as1*	*dsy2*	*afd1*	*pam1*	*dsy498*	*segII*	*dsy9303*	*dsy9305*	*dsy9306*
dsy1															
dsy523	A														
dsy9101	A	A													
dsy9307	A	A	A												
dsy9308	A	A	A	A											
dsy9309	A	A	A	A	A										
as1	No	No	No	No	No	No									
dsy2	No	No	No	No	No	No	No								
afd1	No	No	No	No	No	No	No	No							
pam1	No	No	No	No	No	No	No	No	No						
dsy498	No	No	No	No	No	No	No	No	No	No					
segII	No	No	No	No	No	No	No	No	No	No	No				
dsy9303	No	No	No	No	No	No	No	No	No	No	No	No			
dsy9305	No	No	No	No	No	No	No	No	No	No	No	No?	No		
dsy9506	No	No	No	No	No	No	No	No	No	No	No	No?	No	No	

Designation: A – Allelic, No – nonallelic,
Note: *dsy498, dsy9303, dsy9305* and *dsy9306* have been isolated from families with active *Mu. dsy9307, dsy9308* and *dsy9309* have been isolated from families with active *Ac-Ds*

With the new additions during the period of 1991-1998, the collection of meiotic mutants in maize contained 37 mutants. Allelism testing indicated that they represented at least 19 meiotic genes. Most of these meiotic genes (16) were represented by single mutant alleles. Two genes (*dsy1* and *po1*) had three alleles each and one gene (*am1*) was represented by five different alleles.

In 1999, by screening 1260 *Mu*-active families of MTM growouts at the University of California at Berkeley for male and female sterility, four new meiotic mutants were added to the collection. These mutants were designated with a prefix *mtm99 (maize targeted mutagenesis)*. Preliminary cytological characterization showed that *mtm99-14*, *mtm99-25,* and *mtm99-30* are defective in homologous synapsis. The fourth mutant, *mtm99-31*, exhibited normal synapsis but was defective in sister chromatid cohesion, causing the centromeres to separate precociously before metaphase II (Table 3).

Table 3. Meiotic mutants discovered in screening of EMS and MTM* experiments (1999-2000 UC-Berkeley).

Experiment	Total number of families screened	Number of families segregating for male sterility	Number of meiotic mutants	Symbols of meiotic mutations
EMS 1999 (L. Harper)	250	14	3	*dsy9901, dsy9902, dsy9903*
EMS1999 (J. Hollick)	400	11	6	*dsy9904a,dsy9904b, dsy9905a, dsy9905b, dsy9906a, dsy9906b*
MTM1999 (M. Freeling)	1260	20	4	*mtm99-14, mtm99-25, mtm99-30, mtm99-31*
MTM2000 (M. Freeling)	1670	15	In progress	

Abreviations: MTM - Maize Targeted Mutagenesis project; *dsy – desynaptic; mtm – maize targeted mutagenesis*

In the same year, nine meiotic mutants defective in chromosome synapsis were isolated from an EMS treated population at UC Berkeley. In this mutant screen, mature pollen was mutagenized with EMS to induce mutations (Harper et al., MNL 69:22, 1995). All nine EMS mutants exhibited desynaptic phenotypes and were named *dsy9901* through *dsy9906* (Table 3). Preliminary results of allelism testing with the new *Mu*- and EMS-induced mutants indicated that they all represent new meiotic genes (Table 4). This study is in progress.

Mapping meiotic genes. Since 1999, we have mapped five new and old meiotic genes using either the T-waxy series, or molecular markers. *pam1*, *Mei025,* and *afd1* were mapped to chromosomes 1, 5S, and to the distal region of chromosome 6L, respectively. *dsy2* and *dsy498* (renamed *phs1*) were mapped to centromeric regions of chromosomes 5 (Franklin et al., in preparation) and 9 (Pawlowski et al., in preparation) respectively.

Cytology. The majority of the meiotic mutants in our collection display abnormal pairing and synapsis of homologous chromosomes. To classify these mutants, we quantitatively described the patterns of chromosome pairing at diakinesis and metaphase I (Table 5). We used an average number of univalents and bivalents as a criterion to order thirteen mutants from severely desynaptic (e.g., *dsyCS, dsy9906b, phs1,* and *segII-513*) to mildly desynaptic (e.g., *mtm99-30* and *dsy9305*). *mtm99-31* showed normal chromosome pairing and synapsis in meiosis I, consistent with our previous assessment that this mutant is defective in the second meiotic division. A detailed cytological analysis of *dsy498* revealed that it is defective in homologous synapsis.

We are now working toward a comprehensive characterization of the previously known and new mutants using fluorescence in situ hybridization (FISH) coupled with 3-D microscopy to study bouquet formation, pairing of the 5S rDNA loci and the behavior of telomeres and centromeres during chromosome pairing. The *pam1* gene is the first example of successful efforts in this direction (Golubovskaya et al., 2002, Genetics, in press). It appears to be a bouquet mutant. Inhibition of telomere clustering is the earliest lesion detected in *pam1*. The failure to complete the bouquet formation leads to defects in pairing and synapsis.

Table 4. Allelism test of desynaptic mutants.

	as1	*dsy1*	*dsy2*	*pam1*	*dsy498*	*segII513*	*mms25*	*mtm14*	*mtm30*	*mtm31*	*dsy9904a*	*dsy9904b*	*dsy9906a*	*dsy9906b*	*dsy9303*	*dsy9305*	*dsy9306*	*afd1*
as																		
dsy1	No																	
dsy2	No	No																
pam1	No	No	No															
dsy498	No	No	No	No														
segII-513	No	No	No	No	No													
mms25	No	No	No	No	No	No												
mtm14	?	No	?	?	No	?	?											
mtm30	No	No	No	?	No	No	?	?										
mtm31	No	No	No	No	?	No	?	?	?									
dsy9904a	No	?	No	?	No	No	No	?	No	?								
dsy9904b	?	?	?	?	?	?	?	?	?	No	No							
dsy9906a	No	No	No	No	?	No	No	?	?	No	?	No						
dsy9906b	No	No	No	?	No	?	No	No	No	No	No	?	No					
dsy9303	No	No	No	No	No	No	No	?	?	?	No	?	?	No				
dsy9305	No	No	No	No	No	No	?	?	?	?	No	?	No	?	No			
dsy9506	No	No	No	No	No	No	?	?	?	No	No	?	No	?	No	No		
afd1	No	No	No	No	No	No	No	?	?	No	No	?	No	?	No	?	No	

Designation: A – Allelic, No – nonallelic, ? – unknown

Note: *dsy498, segII-513, mms25, mtm13, mtm14, mtm30, mtm31, dsy9303, dsy9305,* and *dsy9306* have been isolated from families with active *Mu*.
dsy9904a, dsy9904b, dsy9906a, and dsy9906b have been isolated from families after treatment pollen grains with EMS.

Table 5. Pattern of homologous synapsis in new desynaptic mutants of maize.

GENOTYPE	METAPHASE I											TOTAL
	Pattern of homologous synapsis (number of univalents and bivalents)											
	20 I	1 II	2II	3II	4 II	5 II	6II	7 II	8 II	9 II	10 II	
A344 STD (CONTROL)									1	3	141	145
MUTANTS												
mtm99-31										2	98	100
mtm99-30							1	10	18	25	36	90
dsy9305		2	0	2	2	2	1	1	1	6	40	57
dsy9901				1	2	4	11	6	9	8	7	48
dsy9902	3	5	10	8	11	10	4	3	3	0	4	61
dsy9906a	31	3	6	12	21	18	17	6	2	1	2	119
dsy2	28	25	50	46	31	21	5	0	0	1		207
dsy9905a	107	15	7	8	10	4	4	7	5	1	0	168
mtm99-14	42	3	7	5	2	1						60
mtm99-25	151	20	8	8	6							193
dsy498=phs1	170	7	6	1								184
dsy9906b	88	4	2									94
dsyCS = mms25	141	15	2									158
segII-513	150	17	4	2								174

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More studies on the expression of the cloning gene in tetraploid maize

--Ting, YC, Tran, L

In the last edition of this Newsletter (MNL 76, 2002), I reported that the study on the day-length effect on the expression of the cloning gene in tetraploid maize was inconclusive. Hence, a repeated experiment was carried out by planting the same material in November and December of the year 2001 and in January of this year. The material was from a selfed progeny of the genotype *Clg clg clg clg*. For each planting, about 25 kernels were sown in the greenhouse. A month later, of the above three plantings, 53 vigorous plants were obtained. They were watered and fertilized as before. Four months later, all of the plants tasselled. However, none of them regenerated into plantlets. This was unexpected. Hence, control of the expression of the cloning gene is still intriguing. Lack of environmental signals may lead to the failure of the expression of this particular gene. In order to identify the signal or signals, a continuing experiment is carried out in the greenhouse during the winter. In addition, four plants of the last year's three plantings were found to be perennial under greenhouse conditions. Since stalks of these plants were cut off three times, regeneration of the propagules in the root stocks continued, and the regenerated plants were vigorous and normal. Thus, this perhaps suggests that a directed genomic restructuring may lead to the development of a successful perennial maize variety. This is encouraging. The next step of the experiment will be growing those putative perennial plants in the field to see how they will respond to the natural condition in the New England Area.

High frequency of parthenogenesis in a cross of tetraploid X diploid

--Ting, YC, Tran, L

In order to produce a triploid perennial maize, several crosses between a tetraploid(*Clg clg clg clg*) and a diploid (*clg clg*) were attempted. In one of the crosses, the F0 progeny kernels were of predominantly defective endosperm, which was unexpected. According to previous observations, pentaploid maize endosperms had normal growth and were like the triploid type. However, in this particular cross, 99 percent of the progeny kernels were defective. It appears that the ovules were not fertilized or fertilizations had occurred without union of the parental gametes. In consequence, the progeny kernels were not fully developed. With the objective of testing this explanation, 10 defective kernels, together with the same number of their normal sibs, were grown in the greenhouse. It was interesting to note that the viability of these two types was surprisingly high, approximately 99 percent. As soon as their root-tips, as well as their male inflorescences, become available for cytological investigations, their chromosome constitutions will be examined.

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Expression of plant height and cob weight in maize haploids

--Mihailov, ME, Chernov, AA

Haploids were obtained from 5 maize inbred lines and 7 of their hybrids by Moldavian Haploid Inducer (MHI). Two quantitative traits, plant height and weight of the top cob, were measured in these 12 diploid genotypes and their 12 haploid analogues to compare gene action in the diploid and haploid states. In 2002 the plants were grown in the field in two replications with a density of 5 plants/sq. meter. In each variant there were 17 plants on average.

The results of the measurements are presented in Table 1. Height of the haploids was highly correlated with height of analogous diploids. The coefficient of correlation within lines was 0.97, within hybrids the coefficient was 0.75. So, distinctions between

Table 1. Plant height and ear weight in diploid and haploid maize plants

	Plant height (cm)		Ear weight (g)	
Genotype	diploids	haploids	diploids	haploids
Rf7	169+4	104+2	16.6+1.4	3.0+0.3
23-245/77V	128+6	72+3	18.6+1.4	1.6+0.3
MK109	178+3	110+5	12.4+1.9	3.0+0.3
W64	133+1	79+8	12.4+0.3	3.7+0.5
Ku123	154+1	101+3	17.2+2.5	6.1+0.2
Rf7 x 23-245/77V	198+5	91+3	21.4+1.6	2.7+0.4
Rf7 x MK109	224+2	115+3	29.5+2.7	3.4+0.3
MK109 x 23-245/77V	215+3	88+2	38.5+1.6	3.1+0.5
W64 x Rf7	200+2	100+4	21.7+1.4	5.0+0.4
Ku123 x Rf7	205+2	106+2	28.1+1.0	3.4+0.4
Ku123 x 23-245/77V	203+4	93+2	26.6+1.3	3.4+0.3
W64 x Ku123	193+2	88+2	21.2+1.1	4.1+0.5

diploid genotypes were reproduced at the haploid level. For weight of cob there was no correlation. For this trait, within lines the coefficient of correlation was -0.06, and within hybrids 0.30. Probably, this result was caused by low kernel set in haploid ears. Low kernel set stimulates formation of additional ears. It leads to decrease of top ear weight and to increase of its relative variation.

In Table 2, values of heterosis are presented. Heterosis was scored as (F1-P)/P, P=(P1+P2)/2. Both traits revealed obvious heterosis in the diploid state. In the haploid state only the W64 x

Table 2. Relative heterosis (%) at the diploid and haploid level

	Plant height (cm)		Ear weight (g)	
Combination	diploids	haploids	diploids	haploids
Rf7 x 23-245/77V	33.3+1.3	2.9+3.4	21.6+10.9	19.4+33.5
Rf7 x MK109	29.3+1.6	7.3+3.8	103.5+20.4	12.3+ 8.0
MK109 x 23-245/77V	40.2+1.2	-3.1+5.8	148.6+12.8	35.5+23.5
W64 x Rf7	32.6+1.3	9.4+3.4**	50.0+11.4	50.1+12.6***
Ku123 x Rf7	26.5+2.7	2.9+2.1	66.3+10.3	-25.9+ 8.6
Ku123 x 23-245/77V	43.5+5.0	6.9+4.9	48.5+10.8	-10.2+ 8.3
W64 x Ku123	33.6+1.0	-2.8+3.9	43.2+11.4	-17.4+12.2
Total	34.1+2.2	3.4+1.9	43.3+16.3	9.1+10.7

** P<0.01, *** P<0.001

Rf7 combination revealed significant heterosis (Table 2). Since at the haploid level allelic interaction (dominance and overdominance) cannot appear, heterosis in this case may only be due to non-allelic interaction. The results for haploids suggest, apparently, the definite role (relatively small) of positive non-allelic interactions in heterosis for some hybrids of maize.

Genetic, phenotypic and ecological correlations between flowering and productivity traits in maize

--Chernov, AA, Mihailov, ME

It is known that in maize the genetic correlations between flowering and productivity traits are, as a rule, positive (Jugenheimer, 1976). The main reason for this effect is considered to be the capability of maize genotypes with long vegetation to use the advantage of favourable growth and maturity conditions.

In our study, the genetic correlations between ear flowering and productivity for 28 different F1 maize hybrids were also positive: 0.45* between ear flowering and total productivity, 0.46* between ear flowering and first ear productivity.

In 2002 we used two maize inbred lines (MK01 and P092) and their F1 and F2 hybrids for correlation studies. The plants were grown in the field in two blocks with a density of 5 plants/sq. meter. The flowering traits are shown in Table 1, the productivity traits in Table 2, and the ecological (for MK01, P092 and F1) and phenotypic (for F2) correlations between flowering and productivity traits in Table 3. The number of plants in blocks is different because some plants in blocks were used for self-pollination or hybridization and so were not measured.

Table 1. Means of flowering traits in maize

		Flowering date (days)		
Genotype	No. of plants in block	tassel	ear	Flowering interval (days)
MK01	26	71.3+0.4	75.2+0.5	3.9+0.2
21	71.5+0.5	75.9+0.7	4.4+0.3	
P092	13	73.5+0.7	73.0+0.8	-0.5+0.4
20	73.4+0.8	73.2+1.1	-0.1+0.5	
MK01 x P092	22	69.5+0.6	70.4+0.7	0.9+0.2
F2(MK01 x P092)	24	68.3+0.7	69.8+0.8	1.4+0.4
	18	70.0+0.8	71.7+1.1	1.7+0.5

Table 2. Means of productivity traits in maize

		First ear trait				
Genotype	No. of plants in block	kernel set (%)	grain weight (g)	cob weight (g)	Grain weight of other ears (g)	Total productivity (g)
MK01	26	99+1	102+4	17.9+0.6	0.9+0.9	103+4
	21	97+1	98+5	18.0+0.8	0	98+5
P092	13	87+4	33+4	6.4+0.5	0.1+0.1	33+4
	20	76+6	26+3	7.2+0.6	0	26+3
MK01 x P092	22	99+1	139+9	24.8+1.5	0	139+9
F2(MK01 x P092)	24	94+3	87+7	15.5+1.1	6.1+3.0	93+8
	18	99+0.4	98+8	16.4+1.5	0	98+8

Table 3. Phenotypic and ecological correlations between flowering and productivity traits in maize (*P<0.05, **P<0.01, ***P<0.001)

Correlation traits	MK01	P092	F1	F2
Kernel set-	-0.53**	-0.06	-0.49*	-0.11
tassel flowering	-0.43	-0.30	-	-0.40
Kernel set-	-0.46*	-0.28	-0.46*	-0.21
ear flowering	-0.57*	-0.47*	-	-0.48
Kernel set-	-0.17	-0.50	-0.16	-0.23
flowering interval	-0.55*	-0.51*	-	-0.40
Cob weight-	-0.61**	-0.62*	-0.72***	-0.32
tassel flowering	-0.70**	-0.74**	-	-0.36
Cob weight-	-0.63**	-0.71*	-0.72***	-0.38
ear flowering	-0.60**	-0.69**	-	-0.42
Cob weight-	-0.45*	-0.27	-0.37	-0.19
flowering interval	-0.16	-0.32	-	-0.31
First ear grain weight-	-0.79***	-0.12	-0.81***	-0.36
tassel flowering	-0.84***	-0.31	-	-0.46
First ear grain weight-	-0.83***	-0.27	-0.74***	-0.54*
ear flowering	-0.92***	-0.48*	-	-0.55*
First ear grain weight-	-0.61**	-0.33	-0.23	-0.44*
flowering interval	-0.66**	-0.50*	-	-0.45
Total productivity-	-0.84***	-0.13	-0.81***	-0.36
tassel flowering	-0.84***	-0.31	-	-0.46
Total productivity-	-0.86***	-0.27	-0.74***	-0.53*
ear flowering	-0.92***	-0.48*	-	-0.55*
Total productivity-	-0.59**	-0.33	-0.23	-0.41
flowering interval	-0.66**	-0.50*	-	-0.45

All correlations in Table 3 are negative. The probable reason for this result is the concurrent capability for favourable growth and maturity conditions, because in our experience, the earliest plants within a definite genotype had the best productivity. This effect may by more essential in concurrent growth and maturity conditions (for example high density), and may be used for revealing the plants with high productivity within a definite genotype.

The estimation of the mutual influence of maize seeds with different germination capacity in pure and mixed genotype groups by changing seed germination capacity during storage

--Maslobrod, SN, Corlateanu, LB, Ganea, AI, Grati, MI, Savasteeva, NL

During long-term storage of crop seeds, their germination capacity deteriorates, which negatively affects both quantitative and qualitative productivity indices of the crops grown from those seeds. This effect can be decreased by regulation of the abiotic environment, in which the seeds are stored: temperature, light, gas composition, etc. (Nicolaeva, Lyanguzova, Pozdova, 1999). We set a goal of determining whether this effect is influenced by the co-storage of seeds of different genotypes and different initial germination capacity, and if the effect can be decreased, and

possibly evaded, by making a special "seed mix" for storage.

The seeds of the local maize hybrids with good initial germination capacity (GG) – M450, P458 and M215A, and bad germination capacity (BG) – M411 and M215 were used in the experiment. The seed mixes were made of the seeds of two genotypes with different germination capacity in a 1:1 proportion – M411+M450; M411+P458; M411+M215A; M215+M450; M215+P458; M215+M215A, and pure groups of seeds of a single genotype – M450; P458; M215A; M411; M215.

In the mixed groups, the seeds of one of the genotypes (BG) were marked with a marker, to make it possible to separate them from the seeds of the other genotype during the following separate germination. The seeds were stored in glass jars with a tight lid. The jars were kept in darkness at +20 C. During storage, the germination capacity was periodically checked with the intervals of 1.5 (1), 3.0 (11) and 4.5 (111) months. The seeds were couched at +25 C. The number of seeds of each variant was no less than 100. In the end of the experiment (stage 111) the chromosome aberrations (%) were counted in 300-700 cells of the germs' roots.

Results and discussion. The seeds of different hybrids, but with the same initial germination capacity and group, showed a similar effect of storage on germination. This allowed us to combine the variants of such seeds and calculate their average germination capacity for each storage period. The seeds of mixed and pure groups were shown to have different germination dynamics. In the mixed group, the germination of the seeds with GG remained practically unchanged during the experiment, while germination capacity of the seeds with BG decreased drastically (Fig. 1). Student value, calculated by studentized test, was $t_{1\text{-}11} = 2.95$ and $t_{1\text{-}111} = 3.92$ for periods 1 and 11 and 1 and 111, respectively. At the same time, according to Fig. 2, in the pure groups, the germination capacity of seeds with GG decreased considerably by the end of the experiment ($t_{1\text{-}11} = 1.68$ and $t_{1\text{-}11} = 7.96$). Germination capacity of seeds with BG in such groups also decreased considerably ($t_{1\text{-}11} = 1.66$ and $t_{1\text{-}11} = 4.63$). The impression is that in the mixed groups the seeds with GG maintained their high germination capacity during the experiment at the expense of the seeds with BG, triggering the decrease of their germination capacity (negative feedback). Apparently, this causes a more rapid decrease of germination capacity of the seeds with BG in the mixed groups than in the pure groups (germination capacity values by periods in mixed groups (%) – 62.0; 51.0 and 45.5; in the pure groups – 64.3; 56.3; 52.3). A totally different pattern is observed in the case of a pure group of seeds with different initial germination capacity. In this case, the seeds with GG maintained a high germination capacity, at the level of the initial one during the experiment, and the seeds with BG showed an increase in germination capacity (Fig. 3). One can assume that the seeds with GG ac

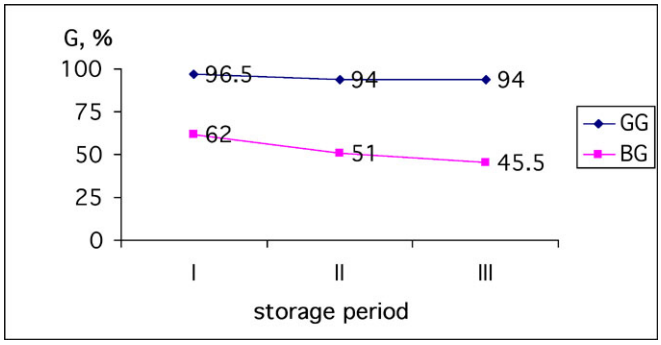

Figure 1. Dependence of germination of the seeds upon their storage periods in the mixture of seeds of different genotypes with different initial germination. GG – the seeds with good germination; BG – the seeds with bad germination; I, II, III – storage period (1.5; 3.0; 4.5 months).

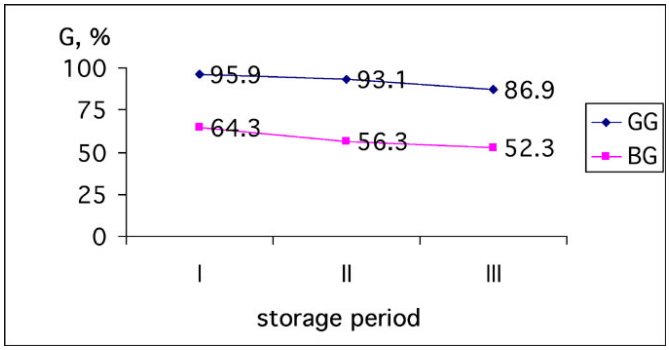

Figure 2. Dependence of germination on their storage periods of seeds of a single genotype and with equal initial germination.

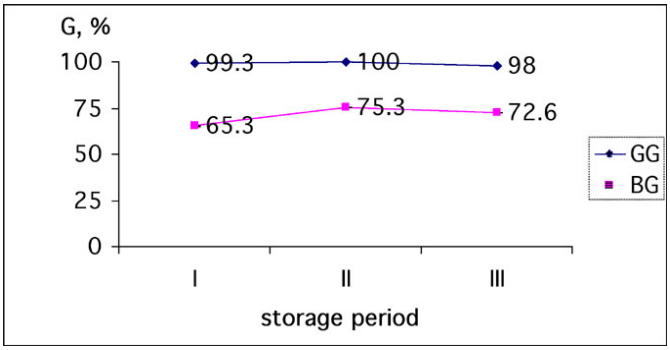

Figure 3. Dependence of germination of the seeds of a single genotype upon their storage period in the mixture of seeds with different initial germination.

tivate the seeds with BG (positive feedback). This confirms our previous data on germination capacity and germination energy stimulation of maize seeds with BG at the expense of the seeds with GG when couched together (Maslobrod et al., 2001; Maslobrod et al., 2002). A hypothesis which has already had its first evidence that the effect of stimulation appears due to electromagnetic (physical) and allelopathic (chemical) channels of interaction of the seeds germinating together, was stated. Apparently, similar mechanisms act during interaction of dry seeds during their co-storage, and become apparent later when the seeds are couched separately. In this case, some kind of seed "memory" is brought about. The stimulation of seeds with BG by the seeds with GG in pure groups, and oppression of the seeds with BG by the seeds with GG in the mixed groups can be considered a result, on the one hand, of the concurrence of the frequencies of electromagnetic fields of the seeds in the group (resulting in a resonance), and, on the other hand, of non-concurrence of these frequencies (no resonance). The work of the chemical mechanism can be pictured, apparently, using as an example a group of seeds with only GG, where the decrease of the seeds germination capacity during storage can be caused by their poisoning by their own products of interaction.

The decrease of the germination capacity of seeds with GG in the pure groups correlates with the increase of chromosome structural abnormalities of the germs of these seeds. The average number of chromosome aberrations of the germs of the seeds with GG was 3.8% in pure groups, 3.1% (t=3.89) in mixed groups. This parameter was the same in both groups (3.8% and 3.7%) of

the seeds with BG.

Thus, seed germination capacity is much influenced by their storage in pure or mixed genotype groups. The first data have been obtained. The research should be continued, as it allows us to demonstrate that the sowing quality of bad seeds can be substantially improved by their storage in a mixture with good seeds.

Detection liquid memory under the influence of electrical appliance fields in changing seed quality and corn sprouts

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In the case of electrical appliances and other things of domestic and production target use we deal with the attributes of our usual environment. The influence on the human being's general state and health is studied very little

We had as a goal to study the action of certain appliances and equipment on plants, with the goal of transferring the results to human beings. It is known that the plant has a great sensitivity to the action of external factors, in some cases being more sensitive than animals (Paturi, 1974). Besides this, there is no nervous system in the plant, and this prevents the receiving of artifacts because of the auto-suggestion effect, and permits us to more objectively discover the first mechanisms of the influences of physi-

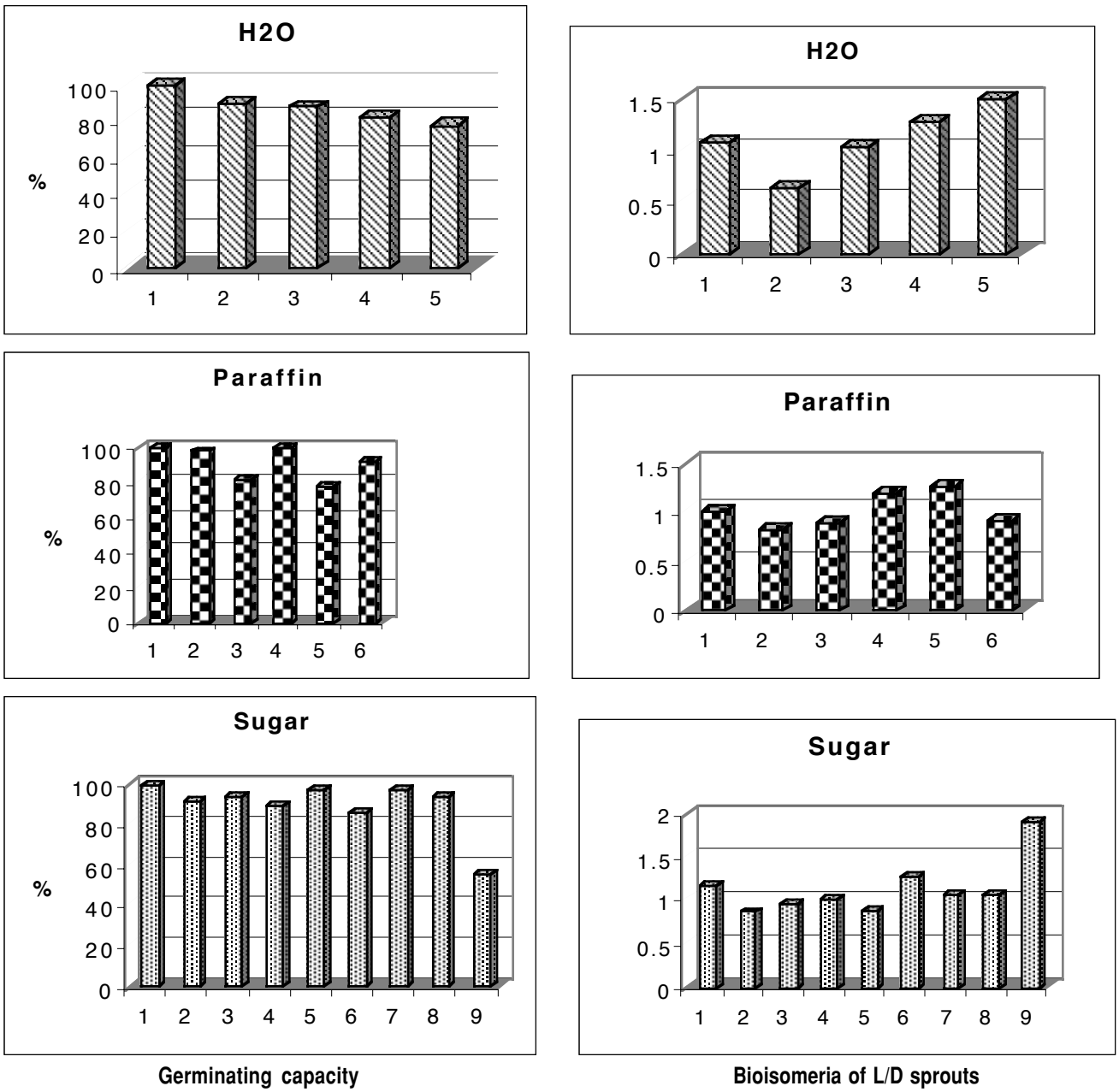

Figure. The change of germinating capacity of corn seeds and bioisomeria of sprouts (L) (D), grown from these seeds, with the influence on the swelled seeds of the liquid theraphim (theraphim was created through the influence of electrical appliance fields on the cooling liquid). Water, paraffin, sugar – theraphim (water, melted paraffin, strong solution of sugar). 1) control (without influence of theraphims); 2) drill with the left (L) rotation of the head; 3) drill with the right (D) rotation of the head; 4) SC; 5) LC; 6) electrical slab; 7) telephone; 8) electrical razor; 9) iron

cal fields on the living system. Finally, such research shows an interest in ascertaining the ecological cleanliness of products of vegetable origin.

In this report the results are shown, not of the direct factor's action on the plant, but through a liquid environment, as a receiver of physical fields generated by appliances and equipment.

Maize and sunflower germs are the indicators of left and right torsion fields of geometrical figures

--Maslobrod, SN, Caranfil, VG*

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In this article, the original results on the influence over the plants' architectonics of torsion fields (TF) generated by different space figures and their combinations, are presented. The bio-effect was judged by the number of left (L) and right (D) germs growing from seeds under the influence of the indicated factors. Quantitatively the bio-effect was evaluated by the ratio L/D germs of maize (hybrid Debjut) and sunflower (sort Sombrerro). In control as a rule L/D=1.00. L – germs have leaves turned up counter-clockwise (L-spiral), D – germs clockwise (D-spiral) (Sulima, 1970). Seeds (at 100 and more in each version) were transplanted in soil in rectangular vessels. The exposition of influence by the factors over the seeds is from 24 hours and more.

We used the following figures:

1. short cylinders (SC) and long cylinders (HC) (ratio diameter (d) – to – length (l) of SC is d>l/2 and of HC is d≤l/2;
2. pyramids (sides and basis are isosceles triangles);
3. cones;
4. domes;
5. combinations of figures;
6. crosses in combination with other figures.

An essential alteration in the correlation of L and D germs was displayed in favour of either leftness (L/D>1.0) or of rightness (L/D<1.0). SC and HC give more L and D germs when the cylinders are disposed under the object (seeds) and more D and L germs when the cylinders are over the object (Table 1).

Table 1. L/D of germs when influenced by torsion fields of short and long cylinders over the germinating seeds.

Disposition of the factor with reference to the object	Maize				Sunflower	
	SC		HC		SC	HC
	Factor manufacturing material				Factor manufacturing material	
	paper	metal	paper	plant (onion stem)	paper	paper
Over	0.72	0.64	1.45	1.67	0.79	1.32
Under	1.32	2.03	0.67	0.85	2.16	0.59

In the case of the disposition of the factor under the object, the TF vector of the figure coincides with the growth vector of the germ. Consequently SC and HC generate from the protrusions accordingly L and D – spiral TFs. In the case of the disposition of the factor over the object, the object perceives the factor in mirror (overturned) version, therefore the bio-effect turns out to be inverse.

The influence of the pyramid, cone and dome caused conformity to natural laws of a common type with clear dependence of the bio-effect on factor orientation with reference to the object (Table 2). The factor being disposed under the object top-upwards induces more D germs, but top-downwards induces moreL germs. Otherwise, D-spiral TFs “flow down” from the tops, but L-spiral from the bases. When the factors are disposed over and under the object becomes functionally polar (Table 2).

Table 2. L/D of sunflower germs when influenced by TF of a pyramid, a cone and a dome over the germinating seeds.

Disposition of the factor with reference to the object	Pyramid (paper)		Cone (paper)		Dome (metal)	
	Factor orientation with the top					
	upwards	downwards	upwards	downwards	upwards	downwards
Over	1.83	0.61	1.69	0.55	1.32	0.74
Under	0.58	2.05	0.64	1.24	0.84	-

The character of the bio-effect doesn’t depend on the genotype and species of the plant (in our case maize and sunflower) nor on the material the factor was made of (Tables 1-4). Since a plant tissue can serve as this material (in our case a hollow onion stem), it can be considered that the genotype architectonics of a plant, and obviously of a man and an animal, also provides generation of TF of different kinds.

The bio-effect doesn’t depend on seed orientation: embryonic radicle up or down (Table 3).

Table 3. The influence of the cylinder orientation and seed orientation on the ratio of L/D of germs.

The character of cylinder orientation in space								
Horizontally					Vertically			
The character of seed orientation with the embryonic radicle								
Disposition of the factor with reference to the object	Down		To the North	To the South	Disposition of the factor with reference to the object	Up		Down
	SC	HC	SC	HC		SC	HC	SC
North	1.85 ----- 0.50	0.85 ----- 2.50	1.34	0.82	Over	0.72 ----- 1.33	1.45 ----- -	0.75
South	1.83 ----- 0.77	0.60 ----- 3.45	0.78	1.03	Under	1.32 ----- 0.36	0.67 ----- 2.25	1.53

Note: in the numerator is the L/D of maize germs from the direct influence of the factor. The denominator is the L/D of sunflower germs from the influence reflected by the mirror.

By influence of the factor along the horizontal the bio-effect depends on the seed orientation: embryonic radicle up or down, to the North or to the South.

By the North orientation the mark of the bio-effect is the same as by the orientation: embryonic – radicle – down. By the South orientation the situation changes into the contrary one. This experiment once more confirmed that SC and HC generate from both protrusions accordingly L and D – spiral TF.

Being reflected by a mirror factor, TF turn the bio-effect as horizontally, as vertically (Table 3). In the direction “east - west” the bio-effect is absent.

We revealed the specification of a cross-figure and a dome influence on the bio-effect by combinaing them with a cylinder. A “pure” cross and dome with a cross on the upper protrusion of a cylinder by the cross orientation “north-south” turn the latter into a new type of TF source, generating horizontally up D TF and down L TF (Table 4).

A dome and a cross additionally give the same function to a cylinder when disposed on the lower protrusion of the cylinder. The influence of a dome without a cross differs from that of a cross without a dome on the lower cylinders protrusion (Table 4). In the “east-west” orientation the effect of transformation is absent. In the given phenomenon in our opinion an unusual energetics of places of worship is displayed.

The quantity of L/D from SC and HC decreases with distance,

Table 4. The modifying influence of the cross-figure with the "north-south" orientation and the dome on the ratio of L/D of sunflower germs induced by the cylinders vertically.

Experimental version	Factor disposition reference to the object	SC *	HC **
Control	Over	0.62	1.24
	Under	1.28	0.59
The cross* on the upper protrusion of the cylinder	Over	0.60	0.96
	Under	0.85	0.79
The cross* on the lower protrusion of the cylinder	Over	0.27	1.39
	Under	1.43	1.15
The dome* on the upper protrusion of the cylinder	Over	-	1.24
	Under	1.55	0.74
The dome* with the cross* on the upper protrusion of the cylinder	Over	0.57	0.62
	Under	0.62	0.70
The dome* with the cross* on the lower protrusion of the cylinder	Over	0.97	0.80
	Under	0.69	0.56

*, ** - materials used were metal and paper, respectively

but can be stabilized with the help of optical means (lenses) forming an obviously nonradiate "ray" of TF. Thus when influenced by SC: a) without a lens and b) with a lens L/D of the sunflower germs ("north-south" direction, embryonic-radicle-down orientation) with the removal of the object from SC in the distance of 0.5; 1.0 and 1.5 m made up: a) 5.25; 2.18 and 1.07 and b) 1.81; 2.34 and 2.25.

We discovered the lessening of the effect right up to its total disappearance when screening TF with the help of: a) crossed polaroid films; b) mirror; c) SC and HC disposed on the same vertical axis but not in contact with each other; d) disposing of the object inside the cylinder in its centre (the latter was received with the standard cylindrical vegetative vessels, when using which plant physiologists unfortunately so far don't take into the consideration the shape effect).

The data observed can be used for the appraisal of availability and mark of TF of natural and artificial origins as a factor of ecology and plant growing, and for the creation of express-procedures when receiving more productive plants (with a needed phyllotaxis spiral). Thus, according to our data, tomato plants grown from L seedlings were more productive than those grown from D seedlings by 15-20%.

COLUMBIA, MISSOURI
University of Missouri

Doubling and quadrupling the chromosome number in endosperm

--Bauer, MJ, Birchler, JA

Akio Kato reported that a prolonged exposure to NO_2 gas could double the maize chromosome number in seedlings (MNL 71:36-37). The same approach was used here to determine if doubling could be accomplished in the maize endosperm as well.

Maize plants were subjected to 600Kpa of nitrous oxide (NO_2) gas from 30-50 hours after pollination. At the end of the time period, the plants were taken out of the NO_2 chamber and grown until 11 days after pollination. By using the chromosome counting technique described by A. Kato (Biotechnic & Histochemistry 73:160-165), slides of endosperm tissue were obtained and the chromosomes were stained with 2.5% acetic orcein. Normal endosperm is a triploid tissue (3x=30; Figure 1). Endosperms treated with NO_2 gas from 30-50 hours after pollination can be successfully doubled creating a hexaploid endosperm (6x=60; Figure 2). In some rare cases, the endosperm genome quadrupled, creating a dodecaploid endosperm (12x=120; Figure 3). At 30 hours after pollination, the endosperm contains four nuclei (Mol, R et al., Plant Journal 5:197-206). In the multinucleated endosperm, it is possible to double one nucleus and not the others. When this

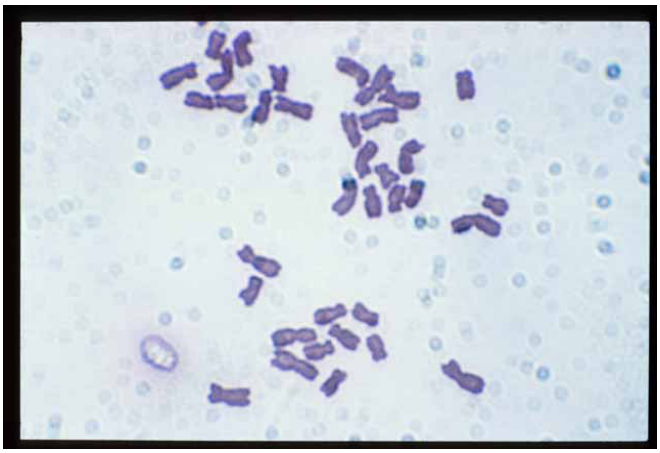

Figure 1. Normal maize endosperm cell containing 30 chromosomes (400X)

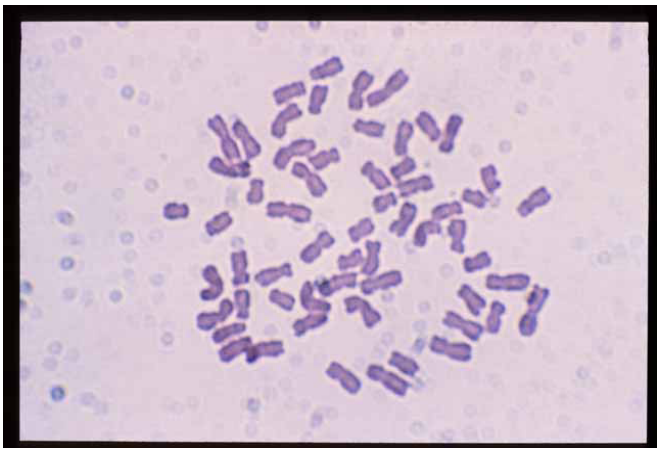

Figure 2. Maize endosperm cell with 60 chromosomes (400X)

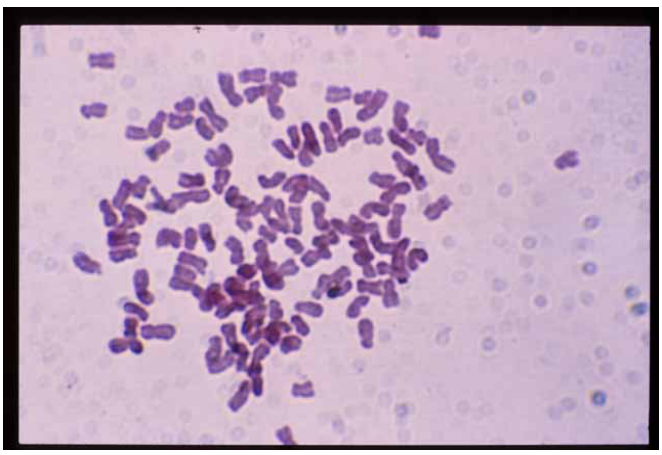

Figure 3. Maize endosperm cell with 120 chromosomes (400X)

occurred, mosaic endosperms were created. We have observed mosaic endosperms that contain some of, or all of the three types of nuclei above. So far, dodecaploid endosperm nuclei have only been observed in mosaic endosperms. It is possible to avoid mosaics by treating with NO_2 gas starting at 14 hours after pollination, which is prior to the first endosperm nuclear division. Hexaploid endosperms have been seen with NO_2 treatment from 14-34 hours after pollination.

In summary, using NO_2 gas from 30 to 50 hours after pollination, it is possible to double the endosperm of maize. Quadrupling the genome also occurred in some few cases. To our knowledge, this is the first time a dodecaploid endosperm cell has been documented in maize.

A first report of mutants mapped using SSR markers at the University of Missouri

--Carson, CB, Robertson, J, Coe, EH, Jr.

We have mapped numerous maize mutants with SSR markers under the Maize Mapping Project (NSF Plant Genome Grant DBI 9872655). This note presents a portion of the results, for genes of visible mutants. Our purpose has been to identify linkage between SSR loci and mutants from the large maize collection, mainly to accelerate the discovery process. One of the goals is to map as many mutants as possible to approximate location, but not to attempt high-resolution mapping. All mutants were mapped in F2 families that were created from crosses between a parent carrying the mutant allele of interest crossed to either: A619, A632, B73, or Mo17. Each F2 was grown and samples collected based on the stage of development of the mutant phenotype.

Classification of mutants for mapping:

1) Kernel, 2) Seedling, 3) Adult plant

For kernel mutants that affect the endosperm, endosperm samples were obtained from maturing F2 kernels on selfed F1 ears before desiccation. For viviparous mutants, the embryo was sampled. Samples of seedling mutants were obtained from F2 seed planted in dense cultures in a sandbench or a groundbed. The plant mutant class has the broadest range of phenotype and samples were obtained from F2 plants growing in larger cultures in the field. Genes of both recessive and dominant mutants were mapped successfully.

Recessive mutants homozygous are mutant, segregating are normal

Dominant mutants homozygous are normal, segregating are mutant

Critical samples of individuals were obtained and placed in 96-well plates. To analyze up to 48 strands for crossing over, up to 24 individual homozygous samples were obtained. Despite attempts to grow enough F2 for samples, there were many cases of less than 24 definite homozygous samples and we collected only as many as possible. For control, an accompanying 8 segregating individuals were collected. To examine for both polymorphism of SSR markers in any F2, and linkage between polymorphic SSR markers and the gene of interest, we first made pools of the homozygous samples to compare with pools of the segregating samples. Based on prior map information for a given mutant, if any, a set of informative SSR marker primer pairs was set up to screen the pools broadly for linkage. For mutant loci that have been previously placed to the correct chromosome, chromosome specific sets of SSR markers were utilized. Otherwise, we used markers that span the whole genome to map unplaced mutants.

The pools were examined for SSR marker polymorphism and linkage using PCR followed by agarose gel electrophoresis. Images of ethidium bromide stained gels using ultraviolet light and an orange filter were examined to identify the band patterns. The pattern of the bands relates to the amount of DNA in the band produced by one allele versus the other. When the polymorphic SSR band pattern of a homozygous pool is similar to the pattern of the segregating pool, there is no linkage. However, when there is linkage between the gene that is homozygous in the pool and a particular SSR allele, the pattern of band accumulation in the homozygous pool is reciprocal to the segregating pool. Greater differences in band patterns indicate tighter linkage. Many times SSR primers might favor one allele over another causing greater accumulation of the DNA in that band; but, when this is taken into account, the analysis is reliable.

Initially, most pool analysis was followed up by a fingerprint analysis on the individuals from the homozygous pool using the polymorphic, linked SSR markers detected in the pool experiments. This provided validation and established linkage distance in map units. Later, we relied more on the pool experiments to report linkage.

The table presents the locus and variation names of the mutants studied as they appeared in the literature (MaizeDB) prior to SSR mapping. It also shows any prior genetic linkage information for the locus. Next, we report the SSR markers that are linked to the locus and the map information for those SSRs. The results from mapping using pools are reported as associations. When individual samples were analyzed the recombination percentage is reported. Then we readdressed the location and name of the locus. Next, we studied the available map information (using MaizeDB) to determine whether the locus is unique from other mutants having similar phenotypes or not. If the new locus is distinct from other mutants, the name is changed (the star is dropped and the next available number is assigned relative to other mutant loci with the same phenotype name). Most often there is some other mutant that is also linked to the locus we mapped and the two cannot be distinguished with the available map data. These are then assigned as candidates for allelism tests in the future. These decisions have been greatly facilitated by additional evaluation from Phil Stinard and Marty Sachs at the Maize Genetics Cooperation Stock Center.

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
	S	pg*-619	1S		umc1160	106.90	1.01	11%	1.01	1.02	pg*-N619		pg15	YES	(pg*-N619 -11-umc1160)
Pheno		y-vp*-85-3101-36	unpl		umc1177	10.50	1.01		1.01	1.03	y-vp*-85 - 3101-36		vp5	NEW	Associated in bulks
Pheno		y-vp*-85-3101-36	unpl		umc1073	206.70	1.03		1.01	1.03	y-vp*-85 - 3101-36		vp5	NEW	Associated in bulks
Pheno		y-vp*-85-3101-36	unpl		umc1166	131.80	1.02		1.01	1.03	y-vp*-85 - 3101-36		vp5	NEW	Associated in bulks

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
Pheno		y-vp*-8419	unpl		umc1177	10.50	1.01		1.01	1.02	y-vp*-8419		vp5	NEW	Associated in bulks
Pheno		y-vp*-8419	unpl		umc1166	131.80	1.02		1.01	1.02	y-vp*-8419		vp5	NEW	Associated in bulks
Pheno		y-vp*-8102	unpl		umc1166	131.80	1.02		1.01	1.03	y-vp*-8102		vp5	NEW	Associated in bulks
	S	sr1	1.02		umc1177	10.50	1.01	24%	1.02		sr1	–		YES	umc1177 -24- sr1 -14- umc1166
	S	sr1	1.02		umc1166	131.80	1.02	14%	1.02						
	S	sr1	1.02		umc1568	140.00	1.02		1.02						
	S	nec*-N495B	1S		umc1568	140.00	1.02	14%	1.02		blh*-N495B		blh1	YES	(blh*-N495B -14- umc1568)
124D	S	v*-5588	1-		umc1166	131.80	1.02	25%	1.02		v*-5588		sr1	YES	umc1166 (v*-5588 -14- umc1568) phi109275
124D	S	v*-5588	1-		umc1568	140.00	1.02	14%	1.02						
124D	S	v*-5588	1-		phi109275	262.20	1.03	12%	1.02						
124D	S	v*-5588	1-		umc1446	696.30	1.08	53%	1.02						
	S	l16-N515	1S		phi109275	262.20	1.03	4%	1.03		l16	–		YES	(l16 -4- phi109275)
	S	wl*-N1930	1S?		umc1568	140.00	1.02	40%	1.04	1.05	wlu7	NEW	w24,wlu5,l16, l17	YES	umc1568 phi109275 umc1144 -17- wlu7 -8- umc1395 umc1590 umc1035
	S	wl*-N1930	1S?		phi109275	262.20	1.03	21%	1.04	1.05					
	S	wl*-N1930	1S?		umc1144	334.00	1.04	17%	1.04	1.05					
	S	wl*-N1930	1S?		umc1395	424.30	1.05	8%	1.04	1.05					
	S	wl*-N1930	1S?		umc1590	469.20	1.06	17%	1.04	1.05					
	S	wl*-N1930	1S?		umc1035	535.10	1.06	27%	1.04	1.05					
124C	S	w*-8345	1S		umc1590	469.20	1.06		1.05	1.06	w*-8345		w20, wlu7	YES	Associated in bulks
124F	S	w*-4791	1L		umc1590	469.20	1.06		1.05	1.06	w20	NEW	wlu7,\w24,wlu 5,l16,l17	YES	Associated in bulks
	S	ppg*-N7A	1S?		umc1395	424.30	1.05	9%	1.05		ppg2	NEW	pg15,pg16	YES	(ppg2 -9- umc1395)
	S	v*-N55	1L		umc1076	401.70	1.05	6%	1.05	1.06	v35	NEW	f1,v22,pg16	YES	umc1076 -6- v35 -10- umc1335 umc1446
	S	v*-N55	1L		umc1335	551.00	1.06	10%	1.05	1.06					
	S	v*-N55	1L		umc1446	696.30	1.08	30%	1.05	1.06					
124H	S	w*-8054	1.08		umc1493	400.60	1.05	21%	1.06	1.08	w24	NEW	wlu5,l16,l17, wlu7	YES	umc1493 umc1335 -19- w24 -3- umc1446 umc1383
124H	S	w*-8054	1.08		umc1335	551.00	1.06	19%	1.06	1.08					
124H	S	w*-8054	1.08		umc1446	696.30	1.08	3%	1.06	1.08					
124H	S	w*-8054	1.08		umc1383	714.80	1.08	6%	1.06	1.08					
124I	S	v*-032-3	1		umc1396	500.50	1.06		1.06		v32	NEW	v22,v35	YES	Associated in bulks
120D	P	ms12	1		umc1245	647.70	1.07		1.07	1.08	ms12	–		YES	Associated in bulks
	S	rgd*-N766B	1L?		mmc0041	699.74	1.08	19%	1.08	1.09	rgd3	NEW		YES	mmc0041 -19- rgd3 -21- bnlg1268
	S	rgd*-N766B	1L?		bnlg1268	794.63	1.08 - 1.09	21%	1.07	1.11					
	S	bl*-N43	1L		umc1335	551.00	1.06	28%	1.08	1.11	bl*-N43		pg16	YES	umc1335 umc1446 -15- bl*-N43 -20- fdx3
	S	bl*-N43	1L		umc1446	696.30	1.08	15%	1.08	1.11					
	S	bl*-N43	1L		fdx3	952.80	1.11	20%	1.08	1.11					
	S	l17-N544	1.09	1.10	bnlg1347	831.44	1.10	17%	1.09	1.11	l17	–		YES	(l17 -17- bnlg1347)
129A	S	w18	1.09	1.10	umc1335	551	1.06	48%	1.09	1.10	w18	–		YES	umc1335 umc1358 -27- w18 -30- fdx3
129A	S	w18	1.09	1.10	umc1358	584.7	1.07	27%	1.09	1.10					
129A	S	w18	1.09	1.10	umc1064	952.8	1.11	30%	1.09	1.10					
129A	S	w18	1.09	1.10	umc1335	551.00	1.06	29%	1.09	1.10	w18	–		YES	umc1335 umc1358 (w18 -4- umc1306) bnlg1347
129A	S	w18	1.09	1.10	umc1358	584.70	1.07	25%	1.09	1.10					
129A	S	w18	1.09	1.10	umc1306	781.94	1.09	4%	1.09	1.10					
129A	S	w18	1.09	1.10	bnlg1347	831.00	1.10	27%	1.09	1.10					
	S	ij2-N8	1.11	1.12	umc1331	951.30	1.11	0%	1.11		ij2	–		YES	(ij2 -0- umc1331) -15- fdx3
	S	ij2-N8	1.11	1.12	umc1064	952.80	1.11	15%	1.11						
	S	spc*-N262A	1L	1.12	umc1331	951.30	1.11	12%	1.11		spc2	–		YES	umc1331 (spc2 -7- phi064)
	S	spc*-N262A	1L	1.12	umc1331	952.30	1.11	9%	1.11						
	S	spc*-N262A	1L	1.12	phi064	957.80	1.11	7%	1.11						
	P	Ts6	1.11		umc1421	880.40	1.11		1.11		ts6	–		YES	Associated in bulks
	S	nec*-N516B	2.02	2.04	umc1542	53.00	2.02	13%	2.01	2.02	nec4	–		YES	(nec4 -13- umc1265 umc1542)
	S	nec*-N516B	2.02	2.04	umc1265	73.10	2.02	13%	2.01	2.02					
	P	d*-N155B	2S		umc1165	42.80	2.01	2%	2.01	2.02	d*-N155B		d5	YES	(d*-N155B -2- umc1165) bnlg1036
	P	d*-N155B	2S		bnlg1036	330.00	2.05	28%	2.01	2.02					
	K	et*-N868A	2S?		umc1265	73.10	2.02	10%	2.01	2.03	et*-N868A		et2	YES	(et*-N868A -10- umc1265)
	K	rgh*-N1013A	"2S?,3L ?"		umc1542	53.00	2.02		2.01	2.02	rgh2	NEW	et2	HIT	
	S	gl2-N718	2.02		umc1552	46.30	2.02	15%	2.02		gl2	–		YES	(gl2 -15- umc1552)
	S	ws3-N453A	2.00	2.01	ole1	202.70	2.03	32%	2.00	2.01	ws3	–		YES	(ws3 -32- ole1)
	S	cb*-N652B	2S?		ole1	202.70	2.03		2.02	2.03	cb2	NEW	al1	YES	Associated in bulks

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
	K	ptd*-N660E	"2S?,3L?"		ole1	202.70	2.03		2.02	2.03	ptd*-N660E		et2	HIT	Associated in bulks
	S	wt*-N178C	2.04		ole1	202.70	2.03	4%	2.03	2.04	wt1		--	YES	ole1 -4- wt1
	K	fl*-N1426	2S		phi109642	214.20	2.03		2.03	2.04	fl*-N1426		fl1	YES	Associated in bulks
	SP	d*-N208B	2S		bnlg108	265.60	2.04		2.03	2.05	d*-N208B		d5	YES	Associated in bulks
	S	wt*-N136A	2S		phi402893	23.8	2.00	56%	2.04	2.05	wt1-N136A			YES	phi402893 (wt1 -0- umc1026) -6- mmc0401
	S	wt*-N136A	2S		umc1026	220.8	2.04	0%	2.04	2.05					
	S	wt*-N136A	2S		mmc0401	315.9	2.05	6%	2.04	2.05					
	S	wt*-N136A	2S		ole1	202.7	2.03-.04	19%	2.04	2.05	wt1-N136A			YES	ole1 -19- wt1-13- bnlg108 umc1080
	S	wt*-N136A	2S		bnlg108	265.6	2.04	13%	2.04	2.05					
	S	wt*-N136A	2S		umc1080	337.2	2.06	13%	2.04	2.05					
224B	S	v*-5537	2-		umc1635	304.2	2.05	7%	2.04	2.06	v*-5537		v24,v4,wlv1	YES	(umc1635 bnlg1887 -7- v*-5537) umc1042
224B	S	v*-5537	2-		bnlg1887	309.17	2.06	7%	2.04	2.06					
224B	S	v*-5537	2-		umc1042	408	2.07	17%	2.04	2.06					
224B	S	v*-5537	2-		bnlg2077	412.1	2.08	14%	2.04	2.06					
224B	S	v*-5537	2-		umc1604	449.1	2.08	21%	2.04	2.06					
224B	S	v*-5537	2-		bnlg1520	514.46	2.07 - 2.09	25%	2.04	2.06					
224B	S	v*-5537	2-		umc1256	516.5	2.09	26%	2.04	2.06					
224J	S	ij-mos*-7335	2-		phi109642	214.20	2.03-2.04	0%	2.04		sr5	NEW		YES	phi109642 -0- sr5 -5- umc2032 bnlg108 umc1635
224J	S	ij-mos*-7335	2-		umc2032	254.50	2.04	5%	2.04						
224J	S	ij-mos*-7335	2-		bnlg108	265.60	2.04	9%	2.04						
224J	S	ij-mos*-7335	2-		umc1635	304.20	2.05	19%	2.04						
224J	S	ij-mos*-7335	2-		umc1080	337.20	2.05	27%	2.04						
224J	S	ij-mos*-7335	2-		umc1042	408.00	2.07	48%	2.04						
224J	S	ij-mos*-7335	2-		umc1604	449.10	2.08	43%	2.04						
224J	S	ij-mos*-7335	2-		umc1552	46.30	2.02	45%	2.04		sr5	NEW		YES	umc1552 phi109642 -5- sr5 -3- umc2032 bnlg108 umc1635
224J	S	ij-mos*-7335	2-		phi109642	214.20	2.03-2.04	5%	2.04						
224J	S	ij-mos*-7335	2-		umc2032	254.50	2.04	3%	2.04						
224J	S	ij-mos*-7335	2-		bnlg108	265.60	2.04	5%	2.04						
224J	S	ij-mos*-7335	2-		umc1635	304.20	2.05	16%	2.04						
224J	S	ij-mos*-7335	2-		umc1042	408.00	2.07	21%	2.04						
224J	S	ij-mos*-7335	2-		mmc0191	415.80	2.07 - .08	24%	2.04						
224J	S	ij-mos*-7335	2-		bnlg1520	514.46	2.07 - 2.09	34%	2.04						
215B	S	gl11	2.03		umc2032	254.5	2.04	28%	2.05	2.06	gl11	--		YES	umc2032 umc1635 (bnlg1887 -18- gl11) mmc0401 umc1080
215B	S	gl11	2.03		umc1635	304.2	2.05	10%	2.05	2.06					
215B	S	gl11	2.03		bnlg1887	309.17	2.06	18%	2.05	2.06					
215B	S	gl11	2.03		mmc0401	315.9	2.05	18%	2.05	2.06					
215B	S	gl11	2.03		umc1080	337.2	2.06	25%	2.05	2.06					
	S	l*-1940	2L		umc1635	304.2	2.05	6%	2.06	2.07	l18	--		YES	umc1635 bnlg1887 -4- l18 -8- umc1042 bnlg2077 mmc0191
	S	l*-1940	2L		bnlg1887	309.17	2.06	4%	2.06	2.07					
	S	l*-1940	2L		umc1042	408	2.07	8%	2.06	2.07					
	S	l*-1940	2L		bnlg2077	412.1	2.08	8%	2.06	2.07					
	S	l*-1940	2L		mmc0191	415.8	2.07	8%	2.06	2.07					
	S	w*-N77	2L		umc1004	338.90	2.06		2.06	2.08	w*-N77			YES	Associated in bulks
	S	w*-N77	2L		bnlg1887	309.17	2.06	13%	2.06	2.08	w*-N77		w3,w21	YES	bnlg1887 -13- w*-N77 -24- umc1042 bnlg1520
	S	w*-N77	2L		umc1042	408	2.07	24%	2.06	2.08					
	S	w*-N77	2L		bnlg1520	514.46	2.07 - 2.09	22%	2.06	2.08					
	S	w*-N77	2L		umc1256	516.5	2.09	22%	2.06	2.08					
	S	v24-N424	2L		bnlg2077	412.1	2.08	9%	2.08		v24	--		YES	bnlg2077 -9- v24 -9- mmc0191 bnlg1520 umc1256
	S	v24-N424	2L		mmc0191	415.8	2.07	9%	2.08						
	S	v24-N424	2L		bnlg1520	514.46	2.07 - 2.09	22%	2.08						
	S	v24-N424	2L		umc1256	516.5	2.09	22%	2.08						
	K	o*-N1195A	2L		umc1516	500.10	2.08	18%	2.08	2.09	o*-N1195A		dek16,\o*-999A	YES	(o*-N1195A -18- umc1516)
	K	o*-N999A	"2L?,1S?"		umc1604	449.10	2.08	20%	2.08		o*-N999A		dek16,\o*-N1195A	HIT	(o*-N999A -20- umc1604)
	S	w*-N332	2L		umc1004	338.9	2.06	43%	2.08		w*-N332		w21	YES	umc1004 bnlg2077 -11- w*-N332 -18- bnlg1520
	S	w*-N332	2L		bnlg2077	412.1	2.08	11%	2.08						

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
	S	w*-N332	2L		bnlg1520	514.96	2.07 - 2.09	18%	2.08						
	S	w*-N1907	2L?		bnlg2077	412.1	2.08	0%	2.08	2.09	w*-N1907		w3	YES	(w*-N1907 -0- bnlg1045 bnlg2077)
	S	w*-N1907	2L?		bnlg1045	555.46	2.07	0%	2.08	2.09					
	K	rgh*-N1112	3S		umc1527	248.60	3.04	12%	3.04	3.05	rgh*-N1112		ref1,dek5, dek24	YES	(rgh*-N1112 -12- umc1527)
	K	smk*-N1230	3S		umc1527	248.60	3.04		3.04	3.05	smk*-N1230		ref1,dek5, dek24	YES	Associated in bulks
329D		yd2	3.06		umc1102	282.10	3.05	26%	3.06		yd2	--		YES	umc1102 mmc0022 (umc1266 -8- yd2)
329D		yd2	3.06		mmc0022	285.00	3.05	24%	3.06						
329D		yd2	3.06		umc1266	358.30	3.06	8%	3.06						
329D		yd2	3.06		bnlg1754	635.00	3.09	34%	3.06						
	P	d*-N282	3L		umc1102	282.1	3.05	33%	3.06	3.07	d*-N282		na1	YES	mmc0022 umc1266 -17- d*-N282 -27- bnlg197
	P	d*-N282	3L		mmc0022	285	3.05	30%	3.06	3.07					
	P	d*-N282	3L		umc1266	358.3	3.06	17%	3.06	3.07					
	P	d*-N282	3L		bnlg197	439.4	3.06	27%	3.06	3.07					
	P	d*-N282	3L		bnlg1754	635	3.09	27%	3.06	3.07					
	S	v*-N1886	3L		umc1102	282.1	3.05	29%	3.06		v*-N1886		v33,et1	YES	umc1102 umc1266 -7- (v*-N1886 -0- bnlg197) -29- bnlg1496
	S	v*-N1886	3L		umc1266	358.3	3.06	7%	3.06						
	S	v*-N1886	3L		bnlg197	439.4	3.06	0%	3.06						
	S	v*-N1886	3L		bnlg1496	638.3	3.08	29%	3.06						
329C		w*-022-15	3-		umc1102	282.10	3.05	36%	3.06	3.07	w*-022-15		y10,wlu1	YES	umc1102 umc1027 umc1266 -17- (w*-022-15 -0- bnlg197)
329C		w*-022-15	3-		umc1027	348.30	3.06	17%	3.06	3.07					
329C		w*-022-15	3-		umc1266	358.30	3.06	17%	3.06	3.07					
329C		w*-022-15	3-		bnlg197	439.40	3.06	0%	3.06	3.07					
329C		w*-022-15	3-		bnlg197	439.40	3.06	0%	3.06	3.07					
	S	wlu1-N28	3.07	3.08	umc1489	484.70	3.07	14%	3.07	3.08	wlu1	--		YES	(wlu1 -14- umc1489)
	S	v*-N1387B	3L?		umc1266	358.3	3.06	27%	3.07	3.08	v33	NEW	et1,v*-N1886	YES	umc1266 (bnlg197 -15- v33) bnlg1754 bnlg1496
	S	v*-N1387B	3L?		bnlg197	439.4	3.06	15%	3.07	3.08					
	S	v*-N1387B	3L?		bnlg1754	635	3.09	25%	3.07	3.08					
	S	v*-N1387B	3L?		bnlg1496	638.3	3.08	25%	3.07	3.08					
	S	w*-N5	3L		phi046	529.56	3.08	10%	3.08		w*-N5		w19,wlu1,y10, wl*-N1906	YES	(w*-N5 -10- phi046) bnlg1182
	S	w*-N5	3L		bnlg1182	577.89	3.09	24%	3.08						
	S	wl*-N1906	3L?		bnlg1182	577.59	3.09	19%	3.09		wl*-N1906		w19,wlu1,y10	YES	(wl*-N1906 -19- bnlg1182)
	S	wl*-N1906	3L?		umc1140	526.30	3.08	12%	3.09		wl*-N1906		w19,wlu1,y10	YES	umc1140 -12- wl* -N1906 -12- umc1594 umc1136
	S	wl*-N1906	3L?		umc1594	685.10	3.10	12%	3.09						
	S	wl*-N1906	3L?		umc1136	712.46	3.10	12%	3.09						
	S	wl*-N1906	3L?		umc1102	282.10	3.05	26%	3.09		wl*-N1906		w19,wlu1,y10	YES	umc1102 -26- wl*-N1906
408J		ra3	4-		bnlg1434	4.3	4.01	21%	4.01		ra3	--		YES	bnlg1434 umc2279 (ra3 -4- cyp3) umc1276
408J		ra3	4-		umc2279	22.9	4.01	23%	4.01			--		YES	
408J		ra3	4-		cyp3	37.50	4.01	4%	4.01			--		YES	
408J		ra3	4-		umc1276	46.08	4.01	25%	4.01			--		YES	
	SP	cb*-N719A	4S		bx1	62.00	4.01		4.01	4.02	cb*-N719A		wt2	YES	Associated in bulks
	S	spt*-N1269A	4S		umc1117	211.90	4.04	17%	4.03	4.05	spt2			YES	(spt2 -17- umc1117)
	S	spt*-N1620B	4S?		umc1117	211.90	4.04	17%	4.03	4.05	spt*-N1620B		spt2	YES	(spt*-N1620B -17- umc1117)
	P	Ysk1-N844	4.04		zp1	225.70	4.04		4.04		ysk1	--		YES	Associated in bulks
	P	smp*-N156A	4S		umc1451	272.50	4.05		4.05		na3	NEW		YES	Associated in bulks
420D;U	S	yel*-8957	4L		umc1132	508.30	4.08	15%	4.08	4.09	l20	NEW		YES	(l20 -15- umc1132)
	P	D*-N2319	5.02		umc1679	48.00	5.00 - 5.01		5.00	5.01	d9	--		YES	Associated in bulks
506L	P	br3	5-		umc1591	280.40	5.04		5.04		br3	--		YES	Associated in bulks
516C	P	ms5	5.04	5.05	mmc0081	351.00	5.05	11%	5.04	5.05	ms5	--		YES	(ms5 -11- mmc0081)
	K	mn*-N1536	5L		umc1224	277.00	5.04		5.04	5.05	mn*-N1536		dek9,dek22,dek27,dek33, prg1,ren1	YES	Associated in bulks
	K	sh*-N1328A	5L		umc1224	277.00	5.04		5.04	5.05	sh*-N1328A		sh4	YES	Associated in bulks
	K	sh*-N887A	5L?		umc1224	277.00	5.04		5.04	5.05	sh*-N887A		sh4	YES	Associated in bulks
	S	wl*-N1393B	5L?		umc1591	280.40	5.04		5.04		wl*-N1393B		v12,vp2	YES	Associated in bulks
Pheno		ps*-85-3288-28	unpl		umc1155	370.90	5.05		5.04	5.05	ps*-85-3288 -28		ps1	NEW	Associated in bulks
Pheno		ps*-Mu85-3061-21	unpl		umc1155	370.90	5.05		5.04	5.05	ps*-Mu85-3061-21		ps1	NEW	Associated in bulks
	S	v*-N1835	5L?		umc1019	411.00	5.06		5.05	5.06	v*-N1835		v12,vp2	YES	Associated in bulks
	P	Hsf*-N1595	5.06		umc126a	411.00	5.06		5.06		hsf1	--		YES	Associated in bulks

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
	K	fl*-N1145A	5L		bnlg609	441.20	5.06		5.06		fl*-N1145A		dek9,dek26,dek27,dek33, prg1,ren1	YES	Associated in bulks
	S	sct*-N206B	5L		bnlg118	549.30	5.07		5.07	5.08	wgs1	–		YES	Associated in bulks
	S	ys*-N755A	5.05	5.06	umc1225	578.20	5.08	12%	5.07	5.08	ys1	–		YES	(ys1 -12- umc1225)
	S	l12	6.01	6.02	umc1006	103.90	6.02	4%	6.01	6.02	l12	–		YES	(l12 -4- umc1006)
	S	wl*-N1848	6L?		bnlg1371	58.7	6.02	8%	6.01	6.02	wl*-N1848		l10,l15,w15	YES	(wl*-N1848 -8- bnlg1371) bnlg1154
	S	wl*-N1848	6L?		bnlg1154	225.8	6.05	31%	6.01	6.02					
	S	pg*-N1885	6L		bnlg1154	225.80	6.05	9%	6.04	6.05	pg*-N1885		cps2,pg11	YES	(pg*-N1885 -9- bnlg1154)
	S	w*-N335	6L		bnlg1154	225.8	6.05	15%	6.05		w*-N335		w1,w14	YES	bnlg1154 -15- w*-N335 -25- dupssr15
	S	w*-N335	6L		dupssr15	371.4	6.06	25%	6.05						
		wl*-N217A	6L		dupssr15	371.40	6.06	3%	6.06		wl*-N217A		w1,w14	YES	(wl*-N217A -3- dupssr15)
	S	gs3-N268	6L		umc1248	422.37	6.07		6.07		gs3	–		YES	Associated in bulks
Pheno	K	vp*-86-1407-15	unpl		bnlg2132	53.3	7.00		7.00	7.03	vp*-86-1407-15		vp9,vp*-8113	NEW	Associated in bulks
Pheno	K	vp*-86-1407-15	unpl		umc1015	300	7.03		7.00	7.03	vp*-86-1407-15		vp9,vp*-8113	NEW	Associated in bulks
		vp*-8113	unpl		c2	115.40	7.01		7.01	7.02	vp*-8113		vp9	NEW	Associated in bulks
		vp*-8113	unpl		bnlg1247	164.40	7.02		7.01	7.02	vp*-8113		vp9	NEW	Associated in bulks
		bu1	7.02		cyp6	158.00	7.02	0%	7.02		bu1	–		YES	(bu1 -0- cyp6)
	S	gl*-N212	7.02		umc1016	143.6	7.02	0%	7.02		gl1	–		YES	(gl1 -0- umc1016) -8- umc1393 umc1015
	S	gl*-N212	7.02		umc1393	212	7.02	8%	7.02						
	S	gl*-N212	7.02		umc1015	253.5	7.03	3%	7.02						
716A	S	v*-8647	7L		umc1015	253.50	7.03		7.02	7.03	v*-8647		v5,v27	YES	Associated in bulks
	S	pg*-N590B	7L?		umc1138	201.30	7.02		7.02		pg*-N590B		l4,o5,sh6,vp9	YES	Associated in bulks
	S	spc*-N357A	7L		umc1001	368.30	7.03-7.04		7.03	7.05				YES	Associated in bulks
	S	spc*-N357A	7L		umc1125	482.51	7.04	21%	7.03	7.05	spc*-N357A		ij1	YES	(spc*-N357A -21- umc1125)
	S	wl*-N629A	7L		umc1295	454.50	7.04	4%	7.04		wl*-N629A		wlu2	YES	(wl*-N629A -4- um1295)
	S	nec*-N249A	8L?		umc1457	250	8.04	22%	8.03	8.05	nec*-N249A		nec1	YES	(umc1457 -22- nec*-N249A -19- umc1858)
	S	nec*-N249A	8L?		umc1858	275.5	8.04	19%	8.03	8.05					
	S	wl*-N203A	8L		bnlg1863	226.3	8.04	25%	8.05	8.06	wlu3	–		YES	bnlg1863 (wlu3 -13- bnlg1782) bnlg1823
	S	wl*-N203A	8L		bnlg1782	382.13	8.05 - .06	13%	8.05	8.06					
	S	wl*-N203A	8L		bnlg1823	440.7	8.07	22%	8.05	8.06					
	S	wl*-N1982	8L?		bnlg1782	382.13	8.05 - 8.06		8.05	8.06	wl*-N1982		wlu3	YES	Associated in bulks
	S	v21-N25	8.06	8.07	umc1268	452.00	8.07		8.06	8.07	v21	–		YES	Associated in bulks
	P	d*-N203D	8L?		gst1	517.40	8.08		8.08	8.09	d12	–		YES	Associated in bulks
	P	d*-N307C	8L?		umc1032		8.08		8.08		d*-N394		d12	YES	Associated in bulks
	P	baf1	9.02		bnlg1810	62.20	9.01	7%	9.00	9.01	baf1	–		YES	(baf1 -7- bnlg1810)
	S	v*-N829A	9S		bnlg1724	11.80	9.00		9.00	9.01	v*-N829A		yg2	YES	Associated in bulks
	S	w*-N1865	9S?		bnlg1724	11.80	9.00		9.00	9.01	w*-N1865		(like wd1)	YES	Associated in bulks
		yg2-N27	9S		umc1279	0.00	9.00		9.00		yg2	–		YES	Associated in bulks
	S	w*-N1854	9S		umc1040	17.7	9.01	0%	9.01		w*-N1854		(like wd1)	YES	(w*-N1854 -0- umc1040 bnlg2122 bnlg1810)
	S	w*-N1854	9S		bnlg2122	21.3	9.01	0%	9.01						
	S	w*-N1854	9S		bnlg1810	62.2	9.01	0%	9.01						
920F	S	w*-9000	9-		bnlg1810	62.20	9.01		9.01		w*-9000		\w11,pyd,l6,l7	YES	Associated in bulks
	S	w11	9.02	9.03	pep1	167.60	9.03		9.02	9.03	w11	–		YES	Associated in bulks
	P	Zb8-N1443	9.01	9.02	bnlg469a	187.60	9.03		9.02	9.03	zb8	–		YES	Associated in bulks
		d*-N1803B			pep1	167.60	9.03		9.02	9.03	d*-N1803B		d3	HIT	Associated in bulks
	S	v*-N53A	9L		sbp4	251.00	9.04	21%	9.03	9.04	v*-N53A		v1,v15	YES	(v*-N53A -21- sbp4)
	S	yg*-N2021	9L?		umc1417	382.61	9.05		9.05	9.06	yg*-N2021		pg12	YES	Associated in bulks
	P	Rld*-N1990	9.08		bnlg619	501.70	9.07		9.07	9.07	rld1	–		YES	Associated in bulks
	S	l19-N425	10.00-10.03		umc1337	104.40	10.02		10.02	10.03	l19	–		YES	Associated in bulks
	S	ij*-N504A	10S		umc1336	178.70	10.03	2%	10.03	10.04	ij*-N504A		sr3	YES	(ij*-N504A -2- umc1336)
	S	gs*-N163B	10S?		umc1336	178.70	10.03	6%	10.03	10.04	gs*-N163B		gs4	YES	(gs*-N163B -6- umc1336)
	S	l*-N1878	10L?		umc1312	141.00	10.03		10.03		l*-N1878		l19	YES	Associated in bulks
	S	v*-N470A	10L		umc1336	178.70	10.03 - .04	3%	10.04	10.05	v*-N470A		v18	YES	(v*-N470A -3- umc1336 umc1506) umc1045
	S	v*-N470A	10L		umc1506	287.50	10.05	3%	10.04	10.05					
	S	v*-N470A	10L		umc1045	308.90	10.06	8%	10.04	10.05					

COOP Stock #	"S, K, or P"	VARIANT MAPPED	PRIOR BIN1	PRIOR BIN2	NEAR SSR	SSR COORD IBM NEIGHBORS	SSR BIN	SSR RECOMB	NEW BIN1	NEW BIN2	LOCUS NAME	NEW NAME?	PROSPECTS (\=not)	LOCATION CONFIRMED?	ORDER
	S	v*-N470A	10L		bnlg2190	354.90	10.06-.07	11%	10.04	10.05					
	S	v*-N470A	10L		umc1084	388.20	10.07	18%	10.04	10.05					
	S	v*-N470A	10L		umc1640	422.50	10.07	3%	10.04	10.05	v*-N470A		v18,v29	YES	v*-N470A -3- umc1640
	S	w*-N24	10L		umc1061	323.60	10.04	33%	10.04	10.06	w*-N24		w2	YES	(w*-N24 -33- umc1061)
	S	wst*-N173B	10L?		umc1506	287.50	10.05	20%	10.05	10.06	wst*-N173B		sr2	YES	(wst*-N173B -20- umc1506)
	S	wst*-N548	10L?		umc1506	287.50	10.05	25%	10.05	10.06	wst*-N548		sr2	YES	(wst*-N548 -25- umc1506)
X10G		v18	10L		bnlg2190	354.90	10.06		10.06	10.07	v18	–		YES	Associated in bulks
	S	l*-N59A	10.07		bnlg1360	408.60	10.07		10.07		l13	–		YES	Associated in bulks
	S	v29-N418	10L		bnlg1360	408.60	10.07		10.07		v29	–		YES	Associated in bulks
	S	Vsr1-N1446	10L		bnlg1360	408.60	10.07	19%	10.07		vsr1	–		YES	(vsr1 -19- bnlg1360)
	S	l*-N1908	10L		bnlg1360	408.60	10.07		10.07		l*-N1908		l13	YES	Associated in bulks
	S	pg*-N1224C	10L?		umc1640	422.50	10.07		10.07		pg*-N1224C		gs4	YES	Associated in bulks
Pheno		vp*-85-3339-25	unpl		umc1038	464.00	10.07		10.07		vp*-85-3339-25		g1,v29	NEW	Associated in bulks
Pheno		vp*-85-3339-25	unpl		umc1084	388.20	10.07		10.07		vp*-85-3339-25		vp13	NEW	Associated in bulks
	S	ppg*-N340B	1S								pg15			NO	Location not confirmed by SSRs
	S	pg*-N526C	1S								pg*-N526C			NO	Location not confirmed by SSRs
	K	o*-N1242A	2S?								o*-1242A			NO	Location not confirmed by SSRs
	S	w*-N346	2L								w*-N346			NO	Location not confirmed by SSRs
	S	v*-N735	5L								v*-N735			NO	Location not confirmed by SSRs
613R	S	wh*-8889	9-								w*-8889			NO	Location not confirmed by SSRs
920E	S	w*-8950	9-								w*-8950			NO	Location not confirmed by SSRs
920L	S	ygzb*-5588	9L?								ygzb*-5588			NO	Location not confirmed by SSRs
920M	S	wnl*-034-5	9.02	9.03							wnl*-034-5			NO	Location not confirmed by SSRs
	S	al*-N427B	7L?								al*-N427B			NO	Location not confirmed by SSRs
	S	l*-N137B	2S?								l*-N137B			NO	Location not confirmed by SSRs
	S	pg*-N1825	10L?								pg*-N1825			NO	Location not confirmed by SSRs
	S	pg*-N330A	1S?2L?								pg*-N330A			NO	Location not confirmed by SSRs
	S	pg*-N36A	3S?								pg*-N36A			NO	Location not confirmed by SSRs
	S	pg*-N380	1S?								pg*-N380			NO	Location not confirmed by SSRs
	S	pg*-N45A	1S?								pg*-N45A			NO	Location not confirmed by SSRs
	K	rgh*-N786	2L?1S?								rgh*-N786			NO	Location not confirmed by SSRs
	S	spt*-N537A	3S?								spt*-N537A			NO	Location not confirmed by SSRs
	S	v*-N142	3L?								v*-N142			NO	Location not confirmed by SSRs
	S	v*-N308	5L?								v*-N308			NO	Location not confirmed by SSRs
	S	w*-N115	10L?								w*-N115			NO	Location not confirmed by SSRs

CORVALLIS, OREGON
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Maize DNA preps for undergraduate students: a robust method for PCR genotyping

--Vejlupkova, Z, Fowler, JE

Our laboratory genotypes thousands of maize plants per year, to analyze our collection of *Mutator* insertion alleles in the *rop* gene family. We routinely use the following method to obtain template genomic DNA for Polymerase Chain Reaction (PCR)-based genotyping. This method is simple, safe, inexpensive, very reliable, and thus easily mastered by the undergraduates who work in our laboratory. The procedure is presented below, with some additional notes based on our experience with undergraduates. We have modified the original method (Cheung, WY et al., PCR Meth Appl 3:69-70, 1993; Rogers, HJ et al., Plant Mol Biol Rep 14:170-183, 1996) to incorporate use of the Eppendorf Repeater Plus pipet-

ter, which significantly shortens the extraction time. We have successfully used this method to extract DNA from maize leaves (both seedling and adult), maize embryos and *Arabidopsis thaliana* leaves.

This method is not only simple and robust enough to be used by inexperienced undergraduates, but also provides extensive pipetting practice and a basic understanding of DNA isolation. The procedure takes us ~2.5 hours for a set of 24 samples, the number of tubes accommodated by our microcentrifuge. Students can work on several sets at once by starting a new set while the samples from the first set are incubating at 60° (step 3). Two sets of samples can thus be completed in ~3.5 hours. It is most efficient to base the number of samples per set on the capacity of your microcentrifuge.

Protocol:

1) Place 20 - 40 mg of tissue in a 1.5 ml tube. Add 150 μL of extraction buffer (2M NaCl; 200 mM Tris-HCl, pH 8.0; 70 mM EDTA, pH 8.0; 20 mM sodium meta-bisulfite) and 50 μL of 5% Sarkosyl (Fisher, Molecular Biology Grade).
2) Grind with drill-mounted plastic pestle for approximately 30 - 40 seconds. Rinse pestle with H_2O between each sample.
3) Incubate in 60 C water bath for 1 hour (30 minutes – 2 hours is OK). Meanwhile, label 0.7 ml tubes for the next step.
4) Spin at full speed (14,000x g) for 15 minutes (room temperature or 4 C). Transfer 150 μL supernatant to a 0.7 ml tube, avoiding the solid debris.
5) Add 150 μL 5M ammonium acetate. Add 300 μL isopropanol and gently mix by inverting the entire rack of tubes.
6) Incubate at room temperature for 15 min. (Tubes can be left overnight at 4 C if necessary.)
7) Spin for 5 min at 9300x g at room temperature.
8) Aspirate the supernatant.
9) Wash pellet by adding 200 μL cold (-20 C) 70% ethanol, spin again (5 min at 9300x g at room temperature) and aspirate supernatant.
10) Air dry for 15 min.
11) Add 200 μL TE, pH 8.0. (Do not vortex!)
12) Incubate at 65 C for 5 min to help dissolve DNA.
13) Done! Store samples at –20 C.
14) We use 5 μL of this DNA prep in a 20 μL PCR reaction; running half of this reaction on a gel results in consistent, strong bands.

Notes:

Sampling: More than 20 - 40 mg of leaf tissue does not improve the results. We do not weigh the samples, but estimate based on sample size ("a pinch-full"). However, it is important to stay fairly consistent. Seedling leaves are easier to grind than older tissue. Therefore, when possible, we use seedlings. Tissue samples can be extracted immediately after collection or stored at –20 C for several weeks. Longer storage increases the difficulty of grinding the samples. We use an Eppendorf Repeater Plus pipetter to rapidly dispense each solution into a set of tubes. To conserve disposables, we label a set of Repeater tips for each solution; these tips are rinsed several times with double distilled H_2O after finishing a set of preps, and can be reused multiple times.

Grinding: Samples are ground with a disposable Kontes pellet pestle (Fisher cat. # K7495211590) mounted in a standard 10mm drill in place of a drill bit. Each pestle lasts for ~10-15 sets of preps. The drill is mounted on a ring stand with the drill/pestle pointing down; a set of ear protectors minimizes exposure to the noise of the drill. While grinding the tissue, we press the tube against the pestle using moderate pressure. However, the tubes and pestle can get hot, so we grind in alternate segments of pressing and slight release. The tissue should be about 80% ground-up, but the grinding time depends on the age of the leaf, with older leaves taking longer. To prevent cross-contamination between samples in a set, the pestle is rinsed by a short burst of "drilling" in a beaker of water and dried with a Kimwipe between each sample. We have not noticed any cross-contamination when using this simple precaution.

Incubation and transfer: Ground samples can be incubated at 60 C from 30 minutes to 2 hours, depending on what is convenient. We have not observed any improvement in yield of DNA upon longer incubation. Following the incubation and spin, supernatant from each tube is transferred using a fresh tip. Tilting the tube while withdrawing supernatant helps keep the tip free of debris.

Precipitation, resuspension and storage: After addition of ammonium acetate and isopropanol, the samples are gently inverted several times in a rack covered with a piece of cardboard. If convenient, the tubes can be stored overnight at 4 C prior to the precipitation spin. After the spin, we carefully remove the supernatant from each tube using a benchtop aspirator with a 200 μL pipet tip on the end. (This speeds up the process significantly, but be careful not to aspirate the pellet!) The aspirator is also used to remove the ethanol wash. Alternatively, the samples can be left overnight in ethanol at –20 C. After drying, the pellets are resuspended in 200 μL TE, pH 8.0. The 5-minute incubation at 65 C helps speed up resuspension; samples can be carefully pipetted up and down if additional mixing is needed. However, there is often a small amount of undissolved debris in the tube; this does not seem to inhibit the subsequent PCR reaction. Samples can be frozen at –20 C for at least several years.

A simple, high-throughput method of DNA extraction for maize using the Matrix Mill

--Vejlupkova, Z, Fowler, JE

The Matrix Mill (Harvester Technology, Inc – http://home.twcny.rr.com/htihome/) is an instrument that uses an electromagnetic field to drive metal dowel pins, which macerate plant tissue for rapid extraction of DNA in a 96-well plate format. We routinely use it in our laboratory to prepare DNA suitable for polymerase chain reaction (PCR) genotyping. The Matrix Mill protocol has the advantages of speed, simplicity and low cost. No special columns or DNA-binding material are required, the solutions are easily made from common reagents, and the 96-well plates can be re-used. With the use of a 12-channel pipetter, the procedure allows for extraction of DNA from 96 samples in about 20 minutes. When extracting from large populations, the time saved by using the instrument more than makes up for the small number (~5%) of unsuccessful extractions. The Matrix Mill has become an indispensable tool in our lab for tracking the inheritance of a set of *Mutator*-induced alleles with no obvious plant pheno-

types. The Matrix Mill is versatile enough that multiple labs needing to extract plant DNA could share it, thus spreading out the initial cost of the equipment.

Although the Matrix Mill manual provides a basic protocol for DNA extraction, we needed to optimize the protocol to increase its reliability with maize leaf samples. The following procedure was developed for seedling leaves, based on our tests, the manual's protocol, and the work of Paris and Carter (Plant Mol Biol Rep 18:357-360, 2000).

Protocol: 1. Collect fresh seedling leaf samples using a paper punch and forceps. Place each leaf disc flat into the well of a 96-well microtiter plate containing 50 μL of sterile water.
2. Place a stainless steel dowel into each well.
3. Cover the 96-well plate with Parafilm and place at –80 C for 5 minutes.
4. Transfer the Parafilm-covered plate to the Matrix Mill; use a strip of Parafilm backing paper to prevent the Parafilm from sticking to the top grinding plate.
5. As soon as samples have thawed, grind for 2 cycles (approximately 4 minutes).
6. Aliquot 50 L of extraction buffer (500 mM NaOH) into each sample well.
7. Grind for an additional 20 seconds.
8. Transfer 5 L of the ground extract from each well into 200 L of neutralizing solution (80 mM Tris-HCl pH 7.5; 1 mM EDTA) that was pre-aliquotted into a 96-well PCR plate. Mix well.
9. Cover the plate with Parafilm and store at –20 C.
10. We use 5 L of each DNA sample in a 20 L PCR reaction; we run half of this reaction (10 L) on a gel.

Notes: *Sampling*: A standard hand-held paper punch works well to collect uniform samples of approximately 4 mg, which fit exactly into the bottom of the well. Broad-tipped forceps are useful for transferring the sample into the well and can be used to flatten the leaf disc. Samples can be extracted immediately or stored in the plate at –20 C for several weeks prior to step 2. We make a "grid map" diagramming the placement of samples in each microtiter plate during collection, and keep the same map with each plate containing finished DNA preps. Although this protocol was optimized for seedlings, it has also been successfully used on adult leaf samples.

Grinding: The dowel pins often have a sharper end, and this end should be placed down against the flat sample. It takes a few minutes for the water in the frozen plate to thaw after placement on the Matrix Mill; you should hear the dowel pins move freely while cycling after the thaw. Samples should be checked between the first and second cycle, as samples will occasionally work their way up the side of the well. These can be readjusted with forceps for the final cycle. Care must be taken to avoid cross-contamination, as some of the extraction liquid can stick to the Parafilm; if this occurs, we use the other side of the Parafilm for the second cycle. Successful maceration produces a pale green fluid.

The addition of NaOH to the extraction (step 6) is not absolutely necessary, but it does improve the DNA preparation, based on a modest increase in PCR band intensity relative to a no NaOH control. However, we found that grinding the samples for extended periods (up to 5 minutes) after addition of NaOH did not affect sample performance, either positively or negatively, for PCR. Therefore, the 20 seconds of additional grinding is merely a convenient way to insure that the samples are well-mixed following addition of the NaOH.

Neutralizing: Our tests indicate that the final step in preparation of the DNA is the most critical for success. The highly basic extraction solution must be diluted appropriately in buffered Tris/EDTA. If too much of the extracted DNA solution is transferred, the PCR fails completely (Figure 1). With a 12-channel pipettor, all 96 samples can be diluted in about a minute. Debris at the bottom of each well should be avoided during transfer.

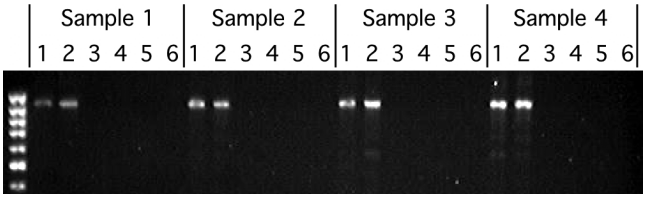

Figure 1. The relative volumes of Matrix Mill extract to neutralization buffer are crucial to the success of PCR amplification. Template DNA for each of the four samples was made for a different maize leaf. The following dilutions (extract:neutralization buffer) were tested: 1) 2 μl: 200 μl; 2) 6 μl: 200 μl; 3) 10 μl: 200 μl; 4) 16 μl: 200 μl; 5) 20 μl: 200 μl; 6) 30 μl: 200 μl. Primers amplified as segment of the wild-type maize *rop6* gene.

PCR and Storage: Diluted samples are ready for use as templates in PCR reactions. We often aliquot 5 μl samples into PCR tubes immediately following the extraction procedure, to avoid having to thaw the entire plate of DNA preps later on. Due to the ~5% failure rate of the procedure, it is important to have a positive internal control in each PCR reaction, to assess the quality of each sample. The extracted DNA can be stored at –20 C for a few months. We have observed decreased performance with 12-month old samples.

A gametophyte factor on chromosome 9 affects both male and female gametophytes

--Fowler, JE

My lab recently became interested in mutations that affect the maize male gametophyte. A search of MaizeDB revealed several *ga** (gametophyte factor) "phenotype only" stocks, which have not been extensively characterized. We obtained these stocks from the Maize Genetics Cooperation Stock Center (Co-op) and are investigating their effects on pollen development.

I confirmed that one of these factors, designated *ga*-94-764*, maps to chromosome 9, near *bz1 sh1*. Exact reciprocal crosses with a homozygous tester showed that the *ga* allele caused a transmission defect through both male and female gametophytes that is significantly different from the expected 1:1 ratio (Table 1). No recombinants in the *bz1-sh1* interval were obtained, so the location of the *ga* factor with respect to these loci is unknown.

Table 1. Reduced transmission of *ga*-linked markers through male and female gametophytes. Each cross shows the results of a *ga* + +/ + sh1 bz1* heterozygote crossed to a *sh1-bz1-m4* homozygote.

	ga through male			*ga* through female		
Cross	bz sh (%)	Bz Sh (%)	Chi-Square	bz sh (%)	Bz Sh (%)	Chi-Square
1	210 (74)	72 (26)	67.5	136 (69)	60 (31)	29.5
2	288 (77)	85 (23)	110	52 (81)	12 (19)	25
3	192 (78)	54 (22)	77.4	36 (71)	15 (29)	8.6

The stock from which these data were derived is marked "from *lo2* stock". Given that *lo2* causes abortion of the female gametophyte, and that it also maps in the vicinity of *bz1 sh1*, *ga*-94-764* could be a derivative of the original *lo2* allele. Alternatively, it could be a new allele of the *ga8* locus, which also

maps to 9S, but is not available from the Co-op; or, this allele could define a novel locus. Until further mapping data allow us to distinguish among these possibilities, I suggest that this allele be referred to as *ga*11*.

Ears in which the *ga** allele was transmitted through the female gametophyte were unfilled (Figure 1A), suggesting that the allele caused a defect in the female gametophyte, in fertilization, or very early in embryonic development.

In addition, transmission of the *ga*-linked *Sh1 Bz1* alleles through the male was reduced at the bottom of the ear, relative to the top (Figure 1B, Table 2). These results indicated that *ga** pollen was at a competitive disadvantage in longer silks, i.e., those leading to the egg sacs at the bottom of the ear. Thus, the *ga** pollen may grow at a slower rate than wild-type pollen. Two other *ga* loci (*ga7* and *ga10*) did not exhibit such a top-to-bottom gradient within the ear (data not shown). Thus, mutations that cause reduced transmission through the male can be separated into two distinct phenotypic classes, based on the distribution of linked kernel markers on the ear.

In similar experiments using two other *ga** stocks from the Co-op (*ga*-Rhoades*, linked to *bt1*; and *ga*-0188*, linked to *pr1*), I was not able to confirm that either of the *ga** alleles adversely affected transmission through male or female gametophytes.

Figure 1. Ears from Cross 2, in Table 1. The top of each ear is to the left. A) The *ga** heterozygote was the female parent. B) The *ga** heterozygote was the male parent.

Table 2. Spatial distribution (top-to-bottom) of kernels of a given phenotype on ears that were derived using the *ga** heterozygote as the male parent. Ears were divided in thirds, based on length. Chi-Square tests rejected the hypothesis that distribution of kernels of a given phenotype is unaffected by their position along the length of the ear (df=2, P value <0.001 for two ears, <0.05 for one ear).

		bz sh	(%)	Bz Sh	(%)	Chi-Square	P
Cross 1							
	Top	62	(64)	35	(36)		
	Middle	68	(72)	26	(28)		
	Bottom	80	(88)	11	(12)		
						14.6	<0.001
Cross 2							
	Top	74	(63)	43	(37)		
	Middle	96	(78)	27	(22)		
	Bottom	118	(89)	15	(11)		
						23.0	<0.001
Cross 3							
	Top	69	(77)	21	(23)		
	Middle	52	(70)	22	(30)		
	Bottom	71	(87)	11	(13)		
						6.20	<0.05

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Anther culture response of maize reciprocal hybrids

--Satarova, TN, Chernousova NM

The investigation of androgenesis of direct and reverse hybrids of maize during several years permits us to estimate the role of reciprocal effects on anther ability to respond in vitro and to produce embryoids.

Tassels from field donor plants before anther culture were preliminarily treated with low temperature (8 C) for 14 days. Anthers were explanted on solid nutrient medium UP according to Genovesi, Collins (Crop Sci. 22:1137-1144, 1982). Up to 1993, the explantation of anthers was made beginning from the 1-cellular vacuolated stage, and after 1993 explantation was made beginning from the stage of the young 2-cellular pollen grain. The analysis concerned the percentage of responsible anthers (anther response, %) and the number of embryo-like structures per 100 anthers (ELS/100 anthers). The results of comparison of androgenic ability of reciprocal crosses are presented in Tables 1 and 2.

Significant differences were observed for H99xWf9 and its

Table 1. Anther response (%) of maize reciprocal hybrids.

HYBRIDS	YEARS					
	1988	**1991**	**1992**	**1993**	**1994**	**1995**
H99xWf9	0.66	0.84	0.59*	0	0.30	1.32
Wf9xH99	0.58	1.17	0	0.34*	0.56	3.78*
$F/F_{0.01}$	0.000	0.41	1.05	1.13	0.20	2.65
	1993	**1994**	**1995**	**1996**	**1997**	**1999**
B14xWf9	1.21	3.43	6.92	0.29	3.39*	1.71
Wf9xB14	3.62*	2.94	10.99*	0.26	0	1.91
$F/F_{0.01}$	1.92	0.000	2.52	0.000	3.32	0.000
	1997	-	-	-	-	-
B14xAnd44	1.74	-	-	-	-	-
And44xB14	0.80	-	-	-	-	-
$F/F_{0.01}$	0.47	-	-	-	-	-
	1997	**2000**	-	-	-	-
And44xWf9	0.22	2.58	-	-	-	-
Wf9xAnd44	0	3.36	-	-	-	-
$F/F_{0.01}$	0.15	0.000	-	-	-	-
	1997	-	-	-	-	-
H99xAnd44	0.37	-	-	-	-	-
And44xH99	0.35	-	-	-	-	-
$F/F_{0.01}$	0.000	-	-	-	-	-

* - Significant exceeding for level 0,01

Table 2. Number of embryo-like structures per 100 cultivated anthers of maize reciprocal hybrids.

HYBRIDS	YEARS					
	1988	**1991**	**1992**	**1993**	**1994**	**1995**
H99 x Wf9	1.03	0.95	0.70*	0	0.30	1.70
Wf9 x H99	0.77	1.45	0	0.34*	0.64	6.33*
$F/F_{0.01}$	0.000	0.88	1.26	1.13	0.31	6.31
	1993	**1994**	**1995**	**1996**	**1997**	**1999**
B14 x Wf9	3.00	5.25	18.26	0.32	7.40*	2.86
Wf9 x B14	4.47	3.73	28.13*	0.44	0	5.08
$F/F_{0.01}$	0.38	0.28	6.60	0.000	6.49	0.41
	1997	-	-	-	-	-
B14xAnd44	3.54*	-	-	-	-	-
And44xB14	0.80	-	-	-	-	-
$F/F_{0.01}$	2.22	-	-	-	-	-
	1997	**2000**	-	-	-	-
And x Wf9	0.22	4.49	-	-	-	-
Wf9xAnd44	0	12.00*	-	-	-	-
$F/F_{0.01}$	0.15	3.12	-	-	-	-
	1997	-	-	-	-	-
H99xAnd44	0.37	-	-	-	-	-
And44xH99	0.52	-	-	-	-	-
$F/F_{0.01}$	0.000	-	-	-	-	-

* - Significant exceeding for level 0.01

reverse combination in 1992, 1993 and 1995 for both indices of androgenic activity. In the other years, reciprocal differences could not be certified. For anther response, differences between B14xWf9 and Wf9xB14 were demonstrated in three of the six years of the investigation, for ELS/100 anthers in two of the six years. Reciprocal effects were not established for anther response between B14xAnd44, And44xWf9, H99xAnd44 and their reverse combinations which had been analyzed during 1-2 years. For ELS/100 anthers, differences between reciprocal crosses were observed only for B14xAnd44 in 1997 and Wf9xAnd44 in 2000.

It is necessary to emphasize that for the same reciprocal crosses in various years, some positive effects were shown by different maternal forms. In crosses H99xWf9 and Wf9xH99, B14xWf9 and Wf9xB14 all the lines being used as female plants caused the exceeding of values in different years. The results have demonstrated not very much exceeding of values due to the exchange of position of lines in the hybrid either. It was 0.34-4.07% for anther response and 0.34-9.87% for ELS/100 anthers.

Thus, reciprocal effect on the development of androgenic induction in maize anther culture was unstable, which led to its manifestation only in some years of the investigation in individual cross combinations. The results represented here show that the main role in the determination of androgenic ability in maize belongs to nuclear genes.

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The study of epidermal replica by oblique illumination microscopy

--Cheng, VC, Cheng, WY, Cheng, PC, Walden, DB

Surface replication is one of the commonly used methods in the study of plant surfaces; since the surface replicating technique allows multiple observations from a living specimen at various developmental stages, the method is thus frequently used in the study of the development of plant surfaces. Nitrocellulose based nail enamel, silicon rubber and methyl methacrylate (PolySciences, 23679-1) resin are among the most commonly used materials for making the surface replica. All of these materials produce flexible, clear, transparent films; therefore, it can be studied by phase contrast or DIC microscopy. Because the replica preserves the surface topography of the specimen, it is also possible to obtain excellent images by using the oblique illuminating method (Greenberg and Boyde, In: Focus on Multidimensional Microscopy, Vol. 1, Eds. PC Cheng et al., World Scientific Publishing, pp 1-24, 1999).

In the study of cell type, shape and size along a developing maize stem (*Zea mays* L., Ohio43/KYS, field grown material), epidermal replicas were obtained by applying a thin layer of clear nail enamel (New York ColorTM 138B) coating on the surface of maize stem and leaf sheath. After allowing the nail enamel to dry, the coating was carefully peeled off from the surface of the specimen and floated on a drop of water on a glass slide. The slide was then heated slightly to flatten the replica and then water was carefully withdrawn. It is important to float the replica with its cell-replicating surface facing away from the microscope slide. Optical microscopy was performed on an Olympus BX51 upright microscope equipped with an Edge dynamic oblique illumination condenser (Boyde et al., Scanning 23, 84, 2001) and an Olympus DP11 digital camera. Figures 1, 2, 3 and 4 show replica images obtained from maize stem surface (c-d region) by oblique illumination at 0o, 90o, 180o and 270 o respectively. In comparing with conventional trans-illuminated wild-field image (Figure 5), the oblique illumination provides significantly better contrast. As a reference, Figure 7 shows the surface and longitudinal section of a maize stem; the nodal region is subdivided into a-b, b-c, c-d regions. The region above “a” bears a surface typical of leaf sheath while the region below “d” consists of a surface typical of internodes (Figure 8). Our microscopy results show complex variations in the arrangement and distribution of cell types from internodes to node to leaf sheath (Figure 8). The epidermal cells on the surface of internodes are aligned in files with rows of stomata. When

approaching the nodal region (Figure 8, d-b region), the stomata (S) become less organized and intermixed with other epidermal cells (c-d region, Fig. 4), then at the b-c region, stomata are completely absent. The a-b region develops a significant number of hair cells, otherwise, the arrangement of epidermal cells remain similar to the b-c region. Above the "a" level, the arrangement of epidermal cells is basically the type found on leaf sheath, with long files of silica cells (Si) demarcating the position of the vascular bundles (Figure 6) (PC Cheng et al., In: Modern microscopy, Eds. P Duke, A Michette, Plenum, 87-117, 1990). Stomata are arranged in between the files of silica cells.

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Aneuploidy as a possible cause of haploid-induction in maize

--Chalyk, S, Baumann, A, Daniel, G, Eder, J

The technology based on utilization of maternal haploid plants induced by special haploid-inducing lines (Eder, Chalyk, TAG 104:703-708, 2002) is used increasingly in practical maize breeding. The mechanism of haploid-inducing capacity of certain lines has not been understood until now. Previously it was supposed that, in the genotypes inducing haploids, two sperms are developed with different speed (Bylich, Chalyk, MNL 70:33, 1996). As a result, one of the sperm develops to a state ready for fertilization, but the other one does not. The existence of only a single normal sperm in a pollen grain could be the reason for a broken doubled fertilization and the development of kernels with haploid embryos (Enaleeva et al., Dokl. Biol. Sci. 353:225-226, 1996). But in contrast to these results, Mahendru and Sarkar (Indian J. Genet. Plant Breed. 60:37-43, 2000) could not find any difference between the two sperms in pollen of a haploid inducing line. Investigation of pollen grains has brought inconsistent results. So, further research has to be initiated to understand what processes make an egg cell develop an embryo without fertilization.

While working with maternal haploids we often observed among them some plants showing an unusual phenotype. These plants did not look like haploids or hybrids, and they expressed the dominant anthocyanin marker genes of the paternal inducer-line. As a rule, these plants developed slowly, were later and often sterile. In different years we observed such plants with a different frequency, usually in a range from 0% to 1%. Root tip-analysis of these plants showed that most of them were aneuploid.

Since the plants were the result of a cross between different breeding populations and a haploid-inducing line it could be supposed that the source of the aneuploid gametes was the haploid-inducing line. When maternal haploids are produced, the haploid-inducing line is used as a paternal parent. Consequently we can suppose that a portion of the pollen grains in haploid-inducing lines has aneuploid sperms.

To test this supposition, chromosome-numbers in microsporocytes of two haploid-inducing lines, MHI and M471H, were analyzed. The cells were analyzed in meiosis at the stage of diakinesis. For comparison, the same analysis was conducted for two normal lines, A619 and MC3. During analysis a number of aneuploid microsporocytes were observed. The results are presented in Table 1. In the line MHI, which was grown in the greenhouse, the frequency of aneuploid cells was 14.7%. When the line was grown in the field the frequency of aneuploid microsporocytes was somewhat lower, 11.0%. In plants from the greenhouse the number of bivalents ranged from 8 to 12. The highest frequency was found for cells with 11 bivalents. Their frequency was 9.7%. There were 4.3% cells with 9 bivalents. From a total of 278 cells in which we determined the number of bivalents, there was only one cell with 8 bivalents and one cell with 12 bivalents. When the line MHI was grown in the field, on analyzing a total of 299 cells we observed 6.4% microsporocytes with 9 bivalents and 4.7% microsporocytes with 11 bivalents.

Another haploid-inducing line, M741H, was grown in the field only. A high frequency of aneuploid microsporocytes was observed in this line as well. In 5.7% of the cells, we observed 9 bivalents, and in 3.6% of the cells, 11 bivalents. Just one cell with 7 bivalents was observed out of 192 microsporocytes.

In the normal lines A619 and MC3, the frequency of aneuploid cells was much lower than in the haploid-inducing lines. One aneuploid cell was observed in line A619 out of 108 cells. In line MC3, four aneuploid microsporocytes were observed out of 253 cells. Among them, three cells possessed 9 bivalents and one cell had 11 bivalents. This result shows that some aneuploid microsporocytes can be found in normal lines as well. This quite agrees with the fact that in normal maize, haploid plants sometimes appear spontaneously. According to Randolph (MNL 12:12, 1938; MNL 14:23-24, 1940), the frequency of spontaneous maternal haploids normally ranges from one to two haploids per one thousand plants.

The facts that the frequency of aneuploid microsporocytes was much higher for haploid inducers than for normal maize, and that among haploids, aneuploid plants appear, let us suppose that haploid-inducing lines do produce some portion of gametes with aneuploid sperms. Aneuploid sperms break doubled fertilization and this can make an egg cell develop into a haploid embryo without being fertilized.

On the basis of the results obtained, it is possible to build a hypothesis that haploid-inducing lines can have a genetic factor, or factors, that cause abnormal division of chromosomes during microsporocyte formation. The factor or factors lead to development of aneuploid sperm. Aneuploid gametes can break doubled

Table 1 . Frequency of aneuploid microsporocytes in meiosis of two haploid-inducing lines, MHI and M741H, and two normal lines, A619 and MC3.

Line	Conditions	Total cells analyzed, no.	Total aneuploid cells		Cells with following number of bivalents									
					7		8		9		11		12	
			No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
A619	field	108	1	0.9							1	0.9		
MC3	field	253	4	1.6					3	1.2	1	0.4		
MHI	greenhouse	278	41	14.7			1	0.4	12	4.3	27	9.7	1	0.4
MHI	field	299	33	11.0					19	6.4	14	4.7		
M741H	field	192	19	9.8	1	0.5			11	5.7	7	3.6		

fertilization and stimulate egg cell division without fertilization. As a result of this process a haploid embryo can be formed from an unfertilized egg cell.

This hypothesis is supported by several experimental results obtained in Germany and in Moldova. Nevertheless, for its complete proof some additional investigations are needed. We would be greatly interested in cooperation with researchers that can make a contribution to the cytological analysis of the mechanism of haploid induction in maize.

Possible effects of heterofertilization on the induction of maternal haploids in maize

--Rotarenco, V, Eder, J

Up to now the mechanism of the induction of haploids in maize by the use of special inducer-lines still remains insufficiently studied. The prevailing hypothesis suggests that the main cause for the development of seeds with a haploid embryo is a single fertilization. According to this hypothesis, a fertilized central nucleus, dividing, stimulates the unfertilized (haploid) egg cell to develop (Chase, 1969; Tyrnov, Zavalishina, 1973; Hohlov, Grishina, 1976; Enaleeva, 1992). The regular double fertilization is distorted after the pollination with pollen of a haploid inducer line.

Bylich and Chalyk (1996) studied the morphological structure of the sperms in the pollen grains of ZMS haploid inducer line. 6.3% of the pollen grains were found to have two sperms morphologically different from each other. According to the authors, morphological defects of one of the sperms influence its functional properties, which often leads to a single fertilization. This, in its turn, results in maternal haploids. It was suggested that the frequency of haploids is, to some degree, related to the frequency of pollen grains of the inducer line having some kind of morphological defects in one of the sperms.

Obtaining haploids every year, we noticed that after natural and artificial pollination their percentage is substantially different. In an isolated plot with free pollination from the inducer line we obtain 2 to 4% of haploids, regardless of the genotype, while after artificial pollination (pollen is applied on ears isolated by bags only once by hand) of the same genotypes, the percentage of haploids is twice and even three times as high.

In our previous research, comparing the output of the haploids after artificial and natural pollination, we concluded that a possible cause of this difference is a delay of pollination (Rotarenco, MNL 76, 2002). But further research in this field showed that the underlying cause is probably different. A possible reason for this difference is assumed to be heterofertilization.

We carried out an experiment comparing the frequency of heterofertilization using MHI haploid-inducer and line X28C, not having haploid-inducing ability. Both lines possess a dominant *R1-nj* gene (anthocyanin coloration of the top of the endosperm and embryo). The presence of this gene in a haploid-inducer-line makes it possible to select maternal haploids at the level of dry seeds.

In the greenhouse, we planted a homozygous line 092 not possessing any marker genes, but which, as had been discovered earlier, expresses the *R1-nj* marker gene well when crossed with a line-carrier of this gene. We prepared two pollen mixtures to pollinate the 092 line – the first mixture consisting of 50% X28C pollen and 50% 092 pollen. The other mixture consisted of 50% pollen obtained from the MHI inducer line, and 50% 092 pollen. The proportion was based on the pollen weight. Each of the pollen mixtures was used for the pollination of three plants of line 092. Each ear pollinated produced over 150 seeds.

After harvest we calculated the percentage of heterofertilization (anthocyanin coloration of the top of the endosperm and white embryo, no anthocyanin coloration of the top of the endosperm and colored embryo). When the first pollen mixture was used for pollination (X28C and 092), on average, 1.5% of heterofertilized seeds were observed. In the second case (MHI and 092), we obtained on average 5.3% heterofertilized seeds.

In the second case, when the inducer pollen was used, seeds with haploid embryos were to be expected. To detect the haploids, we germinated all seeds with colored endosperm and white embryo, both after pollination with the first pollen mixture and after pollination with the second one. Using cytological analysis, we calculated the number of chromosomes in their root meristems. The haploids were found only in the second case, when MHI inducer pollen was used, and the percentage of haploids was on average 7.5% (with respect to the seeds with expressed marker gene). Haploids were not counted in the percentage of heterofertilization, mentioned above.

Thus, when the pollen mixture containing the MHI inducer as a pollinator was used, the percentage of heterofertilization was more than three times as high as in the case when the pollen mixture containing line X28C was used. Most likely, the increase in the percentage of heterofertilization is due to the single fertilization, caused by different defects of one of the sperm of the inducer line, as mentioned before.

It is supposed that the main reason for the decrease in the frequency of haploid seeds in the case of natural fertilization could be heterofertilization. Apparently, more pollen tubes reach the embryo sac applying natural pollination, than during the artificial one. So the probability of heterofertilization is higher, which leads to the observed decrease in the percentage of haploid seeds.

This can be explained by the fact that during natural pollination the pollen that falls on a stigma has a good capability of germination, as there may be an opportunity for its renewal during the whole day. In the case of artificial pollination, there is no opportunity for pollen renewal, so, most likely, fewer tubes reach the embryo sac. So, the probability of heterofertilization decreases, and in the case of single fertilization, the probability of the formation of seeds with a haploid embryo increases.

Of course, further, more extensive studies in this field are needed, but, as we already believe, heterofertilization is an interesting factor related to the mechanism of haploid induction and can have an effect on the percentage of maternal haploid plants induced.

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A 2-oxoglutarate-dependent dioxygenase is involved in DIMBOA-biosynthesis

--Frey, M, Huber, K, Meeley, RB, Simmons, CR, Yalpani, N, Gierl, A

The benzoxazinoids DIBOA [2-hydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one] and its methoxy derivative DIMBOA are natural pesticides, and serve as important factors of host plant resistance

against microbial diseases and insects and as allelochemicals (Sicker et al., Int. Rev. Cytol. 198:319-46, 2000). In maize, a series of five genes, *bx1-bx5* is sufficient to encode the enzymes to synthesize DIBOA (Frey et al., Science 277:696-699, 1997; Gierl and Frey, Planta 213:493-498, 2001). All five oxygen atoms of DIMBOA are incorporated from molecular oxygen (Glawischnig et al., Phytochemistry 45:715-718, 1997). In plants, mainly two classes of enzymes, cytochrome P450-dependent monooxygenases (P450 enzymes) (for review Chapple, Annu. Rev. Plant Physiol. Plant Mol. Biol. 49:311-343, 1998) and 2-oxoglutarate-dependent dioxygenases (De Carolis and De Luca, Phytochemistry 36:1094-1107, 1994), are involved in oxidation reactions using molecular oxygen. The introduction of four oxygen atoms into the indole moiety that yields DIBOA is catalyzed by four P450 enzymes termed *bx2-bx5*. A comprehensive survey of maize P450 enzymes excluded the possibility that a further P450 enzyme is responsible for the hydroxylation at position C-7 of DIBOA.

Prohexadion-Ca (calcium 3-oxido-4-propionyl-5-oxo-3-cyclohexen-carbonic acid) is a specific inhibitor of 2-oxoglutarate-dependent dioxygenases (Rademacher et al., In: Karssen, C. M., van Loon, L. C., Vreugdenhil, D. (Eds.), Progress in Plant Growth Regulation. Kluwer Academic Publishers, Amsterdam, pp. 571-577, 1992). To investigate the participation of this type of oxygenase in the biosynthesis of DIMBOA, seedlings were grown in the presence of prohexadion-Ca. The inhibition of 2-oxoglutarate-dependent dioxygenases by prohexadion-Ca leads to an arrest of the pathway at DIBOA and an almost complete loss of DIMBOA in the seedlings (Figure 1). Hence, the hydroxylation of DIBOA at position 7 is most probably catalyzed by a 2-oxoglutarate-dependent dioxygenase.

The maize EST-data collection of Pioneer Hi-Bred was screened for the presence of 2-oxoglutarate-dependent-dioxygenase sequences. Ten genes were found predominantly in EST-libraries derived from seedling material, the main tissue of DIMBOA biosynthesis. Full-size cDNA clones were retrieved for candidate genes and assayed by northern analysis. One 2-oxoglutarate-dependent-dioxygenase gene displayed co-expression with previously identified *bx* genes.

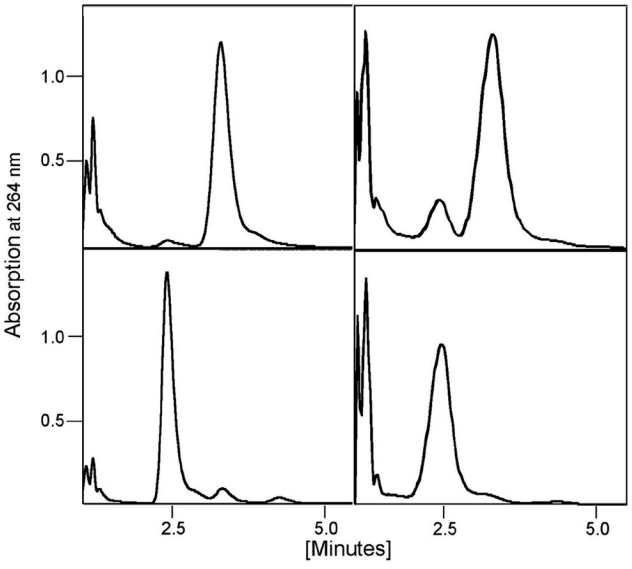

Figure 1. A 2-oxoglutarate-dependant dioxygenase is necessary for DIMBOA biosynthesis in maize and wheat. **A, B** Analysis of benzoxazinones isolated from 4 day old etiolated maize seedlings (A) or wheat seedlings (B) grown in water. The main substance is DIMBOA. **C, D** Maize seedlings (C) or wheat seedlings (D) were grown 4 days etiolated in the presence of the inhibitor prohexadion-Ca. The main benzoxazinone is DIBOA.

A reverse genetic approach was taken in order to verify the function of this 2-oxoglutarate-dependent dioxygenase named *bx6* (GenBank Accession number AF540907). Comparison with the genomic sequence revealed that *bx6* is a gene without introns. Four independent integrations of the transposable element *Mutator* (*Mu*) that are scattered across the cDNA sequence were uncovered in the TUSC population. Four maize lines representing the different *Mu*-integration events were analyzed for the presence of benzoxazinoids. Mutant individuals that no longer synthesize DIMBOA but include DIBOA as the main benzoxazinoid were identified in the F2 progeny of three lines. A total of 42 plants were analyzed, and in all cases, a wildtype phenotype was connected with the presence of at least one wildtype allele of the dioxygenase gene, and the mutant phenotype was displayed only by plants that were homozygous for the integration of a *Mu*-element into *bx6*. This co-segregation provides evidence that the gene responsible for the hydroxylation of DIBOA, *bx6*, in maize has been identified.

A distinct feature of the *bx*-genes of maize is the clustering on the short arm of chromosome 4 (Gierl and Frey, 2001). Therefore, the location of the *bx6* gene in the maize genome is an interesting feature. Mapping of *bx6* using the recombinant inbred population CM37xT232 (Burr and Burr, Trends Genet. 7:55-61, 1991) places *bx6* in close proximity of the other of *bx* genes on chromosome 4. *bx6* and *bx3*/*bx4* are separated by 7 centiMorgan. These results are in good accordance with previous mapping data for the hydroxylation of the C-7 position in DIMBOA-biosynthesis (K. Lobos and P. Sisco, personal communication).

Benzoxazinoids are widely distributed in grasses. The P450 enzymes that convert indole to DIBOA are functionally conserved within cereal species (Glawischnig et al., Phytochemistry 50:925-930, 1999; Nomura et al., Mol. Gen. Genet. 267:210-217, 2002). Prohexadion-Ca incubation inhibits DIMBOA formation in wheat (Figure 1). This indicates that this enzymatic function is also conserved in cereals.

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Further analysis of the regulation of anthocyanin gene expression in maize – influence of *C1, R* and *In1* on *Whp* (*white pollen*) and *C2* expression

--Kirsch, J, Techen, N, Lorbiecke, R, Brettschneider, R, Scheffler, BE, Wienand, U

The influence of *C1, R* and *In1* (intensifier) genes on the expression of *C2* and *Whp* has been analyzed by transient expression assays. *Whp* promoters were isolated either from the Line C (color converted W22 inbred line) or C1-S, and fused to a luciferase reporter gene. Two constructs of each *Whp* promoter (with and without the 5´ untranslated region) were used. In addition, a *C2* promoter, isolated from the mutant *C2-Idf*, was included in the analysis. In particle bombardment assays, using the scutellum of developing embryos, the activity of the reporter gene was analyzed after co-bombardment with the regulatory genes *C1*

and *R*. In parallel, the activity of the endogenous chalcone synthase genes was monitored as red cells, due to anthocyanin accumulation in the bombarded cells. The experiments showed that the expression of the *C2*- and *Whp*-promoters was dependent on the co-bombardment of *C1* and *R*. The activities of the *Whp* promoters were positively influenced by the presence of the 5´ untranslated region of the gene.

In further studies, the *C2* and *Whp* reporter constructs were examined in the presence of a construct coding for the *intensifier* protein (isolated from the *intensifier* mutant *In1-D*). Bombardment of *C1*, *R* and *In1-D* constructs, together with the reporter constructs carrying the *Whp* promoters with the 5´ UTRs, led to considerably reduced promoter activities when compared to the activities without the *In1-D* construct. The same was true using the *C2* promoter. This supports the assumption of *intensifier* being a repressor molecule (Burr et al., Plant Cell 8:1249-1259, 1996).

The possible interaction of *C1*, *R* and *In1* was further analyzed in a yeast two hybrid system. Various constructs of *C1*, *C1-I*, *R*, *In1* and *In1-D* were fused to either the activation or the binding domain of the GAL4 gene and then tested in different combinations in yeast. Whereas strong interaction could be shown for *C1* and *R*, no comparable interaction could be observed between *C1* or *R* with *In1* and *In1-D*. Although, a weak reporter gene expression was detected when *In1* or *In-D1* constructs were used with *C1* or *C1-I* constructs. Nevertheless strong influence of *In1* and *In1-D* on *C1* and *R* dependent chalcone synthase promoter activities could be shown in the transient in vivo studies. The evidence that at least a part of the intensifier repressor activity is linked with transcription is supported by nuclear import experiments, which showed that the In1-D protein is translocated into the nucleus in an onion cell system.

Characterization of *FPF1*-homologous genes in maize

--Pokutta, L, Brettschneider, R, Wienand, U

After flower induction, the *Flowering Promoting Factor 1* (*FPF1*)-gene (Kania, T et al., Plant Cell 9:1327-1338, 1997) is one of the earliest expressed genes in *Sinapis alba* and *Arabidopsis thaliana* plants. *FPF1* is expressed in the peripheral zone of the apical meristems immediately after the photoperiodic induction of flowering. Later in development, it can also be found in floral meristems and in axillary meristems that form the secondary inflorescences. The *FPF1* gene encodes a 12.6 kD protein that has no homology to any protein with a known function. There are indications that *FPF1* is involved in the gibberellin-dependent pathway and modulates the gibberellin response in apical meristems during the transition to flowering. Overexpression of the *FPF1* gene in transgenic *Arabidopsis thaliana* plants led to shortening of the vegetative phase and earlier flowering of these plants (Kania, T et al., Plant Cell 9:1327-1338, 1997).

The cloning of maize genes homologous to the *FPF1* of *Sinapsis alba* revealed the existence of a FPF gene family in maize consisting of at least 9 members. Three of them were used for a genomic and expression analysis. The results of the Northern experiments show that one of the genes, *ZmFPF(L),* is exclusively expressed in immature cobs and immature tassel, whereas *ZmFPF(B)* is predominantly expressed in leaves. No expression could be detected for the third gene, *ZmFPF(E)*, although this gene shows a very high homology to *ZmFPF(B)* in the coding region. These results indicate that individual *FPF* genes of *Zea mays* are expressed in different tissues and may have different functions.

A search of genomic and EST-databases for *FPF*-homologue sequences indicates that this gene family is ubiquitous to the plant kingdom, including the moss *Physcomytrella patens,* gymnosperms, and di- and monocotyledon angiosperms. A dendrogram, analysing the relationship of 28 different putative *FPF*-genes, shows that the sequences are clustered in three mayor subgroups. In the second group, only sequences of monocotyledonous plant species are clustered (see Figure 1)

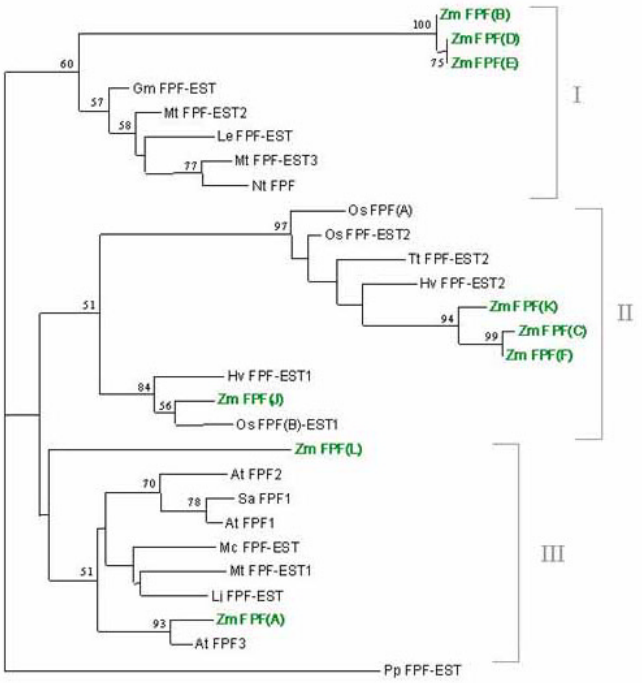

Figure 1. Comparison of FPF-sequences. At: *Arabidopsis thaliana*, Gm: *Glycine max*, Hv: *Hordeum vulgare*, Lj: *Lotus japonicus*, Le: *Lycopersicon esculentum*, Mc: *Mesembryanthemum crystallinum*, Mt: *Medicago truncatula*, Nt: *Nicotiana tabacum*, Os: *Oryza sativa*, Pp: *Physcomitrella patens*, Sa: *Sinapis alba*, Tt: *Triticum turgidum*, Zm: *Zea mays*.

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Genetics of general resistance in tropical sweet corn to *Puccinia polysora* Underw.

--So, YS, Ji, HC, Brewbaker, JL

Epiphytotics of southern corn rust (*Puccinia polysora* Underw.) become severe during Hawaii's wet, cool winter. Most tropical maize displays a mature-plant or general resistance that reduces disease incidence below economic levels. In contrast, essentially all temperate sweet corns are highly susceptible to the rust, and *Rpp* alleles conferring hypernecrotic-type resistance also succumb to tropical races of the pathogen. Sweet corn breeding in Hawaii has been based on conversions of tropical flint

corns, thus providing rust tolerance adequate for growers worldwide. In an evaluation of 120 open-pedigree field corn inbreds in Nigeria and the USA (Texas, Hawaii), we showed general resistance in tropical germplasm to be common, quantitative, and without GxE interactions (Brewbaker et al., Hawaii Res. Ser. 62, 1989).

The current study involved *bt1*-based tropical supersweet corn inbred Hi38-71, an inbred with a high tolerance of *P. polysora* and of corn leaf aphids. A generation mean analysis was conducted with this inbred, rating 3.2 on a 1 to 9 scale, crossed to inbred G24 (rating 6.9). The G24 inbred derives its susceptibility from corn belt dent inbred B68, and is one of the G Set RILs from the cross of Ki14 (a Thailand inbred) and B68 (as Hawaii conversion, Hi31). This G Set of RILs segregated approximately 50% tolerant: 50% resistant (Moon et al., Maydica 44:301, 1999). Many tropical inbreds show greater resistance than Hi38-71, suggesting it to be only intermediate in mature-plant resistance. Data are summarized here from a natural epibiotic in the autumn of 2002.

Mean ratings on the 1 to 9 scale were 2.9 for F1, vs. 3.2 for the resistant parent (Pr) and 6.9 for the susceptible (Ps) parent (Figure 1). These populations were distinguished by extremely low variances. The F2 averaged 4.2 with a broad distribution, and means of backcrosses returned toward those of the parents, 3.8 for BC to Pr and 5.7 for BC to Ps. Heterosis for vigor and yield was very great for these segregating populations, probably obscuring the genetic segregation for rust tolerance loci. For example, the F1 hybrids scored more resistant than their resistant inbred parent. There was no clear distinction of two classes in the BC to Ps.

Generation mean analysis of the 6 generations (Table 1) revealed a large mean effect but no significant additive or dominance

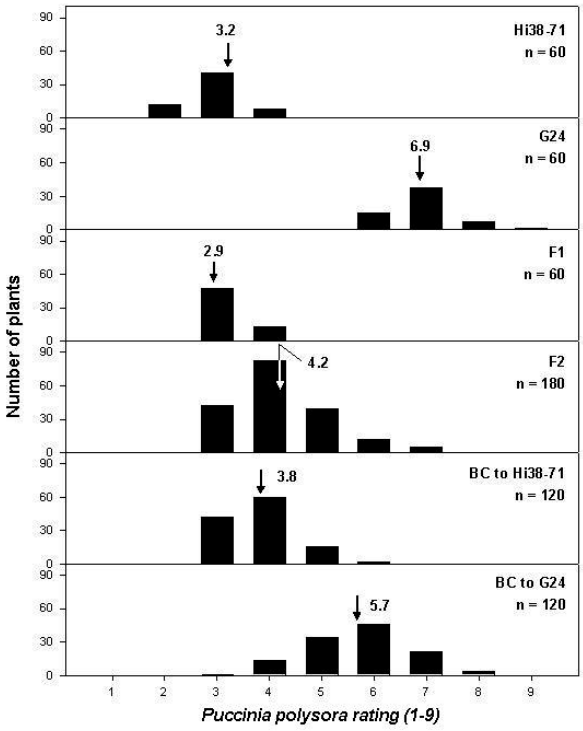

Figure 1. Frequency distribution of *P. polysora* rating on 6 generations.

Table 1. Estimates of additive, dominance, and interaction parameters for the Hi38-71 x G24 family.

Parameter a	Estimate (SE)	t test
m	4.20 0.072	58.373 **
a	-1.88 0.114	-16.450 ns
d	0.11 0.378	0.286 ns
aa	2.23 0.368	6.073 **
ad	-0.04 0.125	-0.334 ns
dd	-5.28 0.570	-9.276 ns

a m=midpoint, a=additive, d=dominance, aa=additive x additive interaction, ad=additive x dominance interaction, dd=dominance x dominance interaction

effects. Additive x additive interaction was highly significant, and the broad-sense heritability was relatively low (31.2%). An estimate of minimum number of gene loci, using Castle and Wright formula, was 2.81.

Hi38-71 was bred from a Cuban-flint derived *sh2*-based sweet corn inbred, AA8sh2, that carries resistance to the corn leaf aphid, *Rhopalosiphon maidis* (Fitch) (Chang and Brewbaker, MNL 48:37-38, 1974). We have confirmed this aphid resistance to be recessive and monogenic, as noted by Lu and Brewbaker (MNL 73:36, 1999). AA8sh2 was converted to *Rp1-d,* derived from W22xB14A, previously suggested to be linked to the aphid resistance locus (Chang and Brewbaker). It appears possible that one or more of the Southern rust resistance loci in Hi38-71 are linked to the aphid and *Rp1* (common rust) loci

Holland et al. (Theor. Appl. Genet. 96:232-241, 1998) reported major QTLs for mature-plant resistance to southern rust on chromosome 10S, with minor QTLs on chromosomes 3 and 4. The 10S locus accounted for 83% of the variation in resistance in their F2:3 populations of tropical x Corn Belt. The hypernecrotic southern-rust resistance locus, *Rpp*9 (Ullstrup, A.J., Plant Dis. Rep. 34:89-99, 1965) is closely linked on Chromosome 10 to gene *Rp1* for resistance to *Puccinia sorghi* Schw. The common sources of *Rpp9* confer little or only partial tolerance to southern rust races in the tropics. We concur with Holland et al. that a few major loci undergird general resistance to southern rust in tropical germplasm, and that *Rpp* alleles may also serve in this capacity.

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Abscisic acid in maize roots at low positive temperature
--Akimova, GP, Sokolova, MG, Nechayeva, LV, Luzova, GB

Identification of abscisic acid (ABA) functioning mechanisms has made considerable progress in the last few years. However, there are still quite a few unclear points, including that relating to ABA participation in the maintenance of plant organism homeostasis in unfavorable environmental conditions. Abscisic acid has been shown to accumulate in the plants in the conditions of osmotic stress, soil drought and supercooling. ABA's role in different plant bodies may vary: in leaves its antitranspiration effect prevails, in roots ABA activity is associated with an influence on ion adsorption and cell permeability for water. Pilet (Plant Physiol. 83:33-88, 1987) demonstrated that ABA amount goes up as the root age increases. The inhibitor is localized in the root apex and affects growth processes.

The present work was aimed at the identification of the impact of a temperature of 10 C on abscisic acid content in the growth zones of maize seedlings in connection with the change of growth

speed with lowered temperature.

Roots of 48-day-old maize seedlings of the Uzbekskaya Zubovidnaya variety (MNL 76:35-36, 2002) were used as the initial material. To clean the extract we used the column chromatography method with polyvinulpyrrolidone. Gas-liquid chromatography was used to identify and determine ABA and IAA content.

The time period during which the cells achieved their final dimensions was used as a criterion for cell comparison in control and test variants. The cells were shown to finalize extension over 8 hours of growth at 27 C. The temperature of 10 C sharply reduced the root growth speed: only after 96 hours of growth at this temperature did the cells cease the extension process. As a result, the root growth speed decreased by 12 times.

ABA content at 10 C (Table) was shown to increase in all the growth zones compared to control (27 C). At the same time the maximum increase was observed in the cells which started extension at 10 C, which is caused by the increase of these cells' volume and may apparently represent a compensatory response to the increase of IAA content. ABA, apparently, does not prevent extension, but is responsible for other functions associated in particular with its participation in the cells' permeability for water. ABA content increase in root meristem is likely to be connected with the formation induction as well as with the slowed tempo of its basipetal transportation to the extension zone. This conclusion is proven by the observed response of root geotropism at 10 C. Pilet observed a similar georeaction in roots exposed to light.

Table. ABA and IAA content in the maize root cells in optimal conditions and at 10 C (mcg 10^{-8} /cell)

Variant	Growth zones	ABA	IAA	ABA:IAA proportion
27 C	Meristem	1.180.05	1.730.06	1:1.5
	Extension initiation	3.510.10	3.120.09	1:0.9
	Extension accomplishment	10.240.72	7.360.64	1:0.7
10 C	Meristem	1.960.06	4.910.12	1:2.5
	Extension initiation	6.180.25	7.870.34	1:1.3
	Extension accomplishment	15.460.91	3.910.11	1:0.3

Plant physiological processes are regulated with the participation of a multi-componental hormonal system, where each hormone is responsible for its own specific function. This is why one should take into account not only the content of an individual phytohormone, but also the balance and interaction of the phytohormones.

Comparison of the data on the dynamics of maize root cell growth with the free IAA dynamics demonstrated that at 10 C, IAA content in the root growth zones undergoes the following changes as compared to control: it increases in the meristem and in the initial extension zone cells and sharply drops in the cells which accomplished their growth. In accordance with the above, it was shown that IAA and ABA proportion in the root cells changes significantly at 10 C. Phytohormone balance in meristem cells and in the cells that started extension shifts towards the decrease of ABA due to an IAA content increase in the cells, thus providing a longer growth impact resulting in the increase of the dimensions of the zone of extending cells. In the cells which accomplished the extension, ABA content grows considerably. In terms of physiological impact, abscisic acid is an antagonist of IAA and inhibits cell extension, which apparently makes a certain impact on the change of these cells growth speed.

Therefore, the change of balance of ABA/IAA in the extending cells of the maize root is one of the ways to control cell extension speed at 10 C.

Maize seedlings accumulate smHSPs in response to water stress but not to treatment by an oxygen radical generating agent

--Korotaeva, NE, Borovskii, GB, Voinikov, VK

Stress proteins ensure plant protection from damages caused by external stress impacts. Stress proteins act at the cell level as chaperones providing protection and restoration of proteins with tertiary structure and degradation of irreversibly damaged polypeptides (Feder and Hofmann, Annu. Rev. Physiol. 61:243-283, 1999). Small heat shock proteins (smHSPs) form a vast group of stress proteins with molecular mass from 14 to 40 kD, which is particularly numerous and diverse in plants. Synthesis of these proteins is induced in response to many types of stresses. SmHSPs, as almost all stress proteins, act predominantly as chaperones (Sun et al., Biochim. Biophys. Acta 1577:1-9, 2002). The role of smHSPs during oxidative and water stress remains unclear, although the study of oxidative and water stress protection mechanisms is an important task. Agricultural plants are often exposed to drought in natural conditions. Oxidative stress is known to accompany many other stress impacts (Davies and Goldberg, J. Biol. Chem. 262:8220-8226, 1987).

Wehmeyer and Vierling (Plant Physiol. 122:1099-1108, 2000) showed that the ability to overcome dehydration correlates with the ability to synthesize smHSPs in mutant drought-resistant *Arabidopsis thaliana* seeds. The same regularity was observed in desiccation-intolerant *Craterostigma plantagineum* callus tissue (Alamillo et al., Plant Mol. Biol. 29:1093-1099, 1995). Nevertheless, up to now smHSP induction in response to water stress has not been directly proven, apart from the work by Almoguera and Jordano (Plant Mol. Biol. 19:781-792, 1992). They demonstrated smHSP accumulation compared to control in sunflower seedlings after 4 and 24 hours of osmotic stress created by mannitol in the vegetation solution.

Oxidative stress was shown to induce smHSP accumulation in rice chloroplasts (Lee et al., Gene 245:283-290, 2000). The key role of smHSPs in the protection of photosystem II of chloroplasts from oxidative stress was proven (Downs et al., J. Plant Physiol. 155, 1999). However, it is still unknown whether smHSPs are accumulated elsewhere in the cell in response to oxidative stress.

The objective of our work was to check whether smHSP accumulation takes place in maize seedlings under long-term and short-term dehydration created by different methods. We also intended to determine whether smHSPs are accumulated elsewhere in the cell, apart from chloroplasts, in response to oxidative stress.

We analyze total cell proteins from etiolated maize seedlings subjected to oxidative and water stress by SDS-PAGE and immunoblotting using antibodies developed for smHSP-specific C-terminal α-crystallin domain (Heckathorn et al., Plant Physiol. 116:439-444, 1998). Simultaneously we monitored water stress. We used three-day-old etiolated maize seedlings grown at 27 C. To provide oxidative stress we submerged the seedlings in the solution containing 100 mM of methyl viologen, a herbicide provoking free oxygen radical production in the cell, for 3 hours. Dehydration was created by two methods. Three-day-old seedlings were left in thermostat for 24, 48 or 72 hours without water. Then the distinct groups of seedlings were incubated in

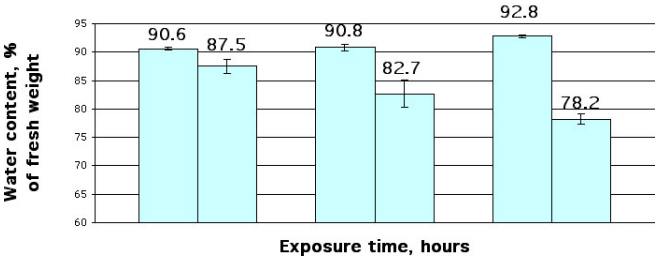
solutions containing 38, 64 or 88 mM of polyethyleneglycol (PEG), which corresponded to 300, 500 and 700 mOsm respectively. To determine moisture content in the seedlings they were dried to dry weight at 80 C for 20 hours with the weight measured before and after drying. Total proteins were extracted from seedlings as described elsewhere (Borovskii et al., J. Plant Physiol. 156:797-800, 2000). Proteins were subjected to SDS-PAGE (14% of acrylamide) using a mini-Protean II cell (Bio-Rad, USA) according to the manufacturer's instructions. Western blot and immunodetection were carried out as was described previously (Timmons and Dunbar, Methods Enzymol. 182:679-688, 1991). Antibodies to the α-crystallin conserved C-terminal domain, common to all eukaryotic smHSPs and to the α-crystallin proteins of the vertebrate eye lens, kindly provided by Dr. Craig A. Downs, were used for detection of smHSPs (Heckathorn et al., Plant Physiol. 116:439-444, 1998).

Significant dehydration of seedlings was shown to take place after PEG treatment and desiccation. Thus, after 24 hours of drought stress water content in the seedlings decreased from 90.6 % (control) to 87.5%. After 48 and 72 hours, water content amounted to 82.7% and 78.2%, respectively (Diagram 1). After incubation of the seedlings with PEG solutions of 300, 500 and 700 mOsm water content decreased from 90.5% (control) to 89.1, 88.1 and 86.6% respectively (Diagram 2).

Immunochemical analysis of total cell protein produced the following results. A small amount of smHSPs were present in the seedlings in the conditions of optimal moisture content, that is, in the control (Fig. 1, Fig. 2). This agrees with our previous results (Korotaeva et al., MNL 75:24-25, 2001). SmHSP accumulation among total cell proteins positively correlated with the duration and intensity of water stress. Thus, well pronounced accumulation of smHSPs with Mr 19 and 22 kD was observed, as compared to the control, after 48 and 72 hours of desiccation, and after incubation with PEG solution of maximal osmotic pressure (700 mOsm) (Fig. 1). However, we did not manage to identify smHSP accumulation among total cell protein with seedlings treated by methyl viologen (Fig. 2). This agrees with the results of Banzet and co-authors (The Plant J. 13:519-527, 1998), shown in tomato suspension cultures, that smHSPs do not accumulate in the cells as a response to treatment by O_2 (o-) generating agents methyl viologen and digitonin, though smHSP accumulation happens with H_2O_2 treatment. Nevertheless, other researchers showed that pea leaf treatment by methyl viologen still brings about the consequences pointing to the presence of oxidative stress. This was witnessed by the decrease (compared to control) in concentration of some antioxidant enzymes, and the accumulation of oxidized proteins and catalytic Fe in pea leaf parenchyma (Iturbe-Ormaetxe et al., Plant Physiol. 116:173-181, 1998). Therefore, the consequences resulting from methyl viologen treatment do not induce smHSP accumulation. It is still unknown what kind of oxidative stress consequences lead to smHSP accumulation in the cell.

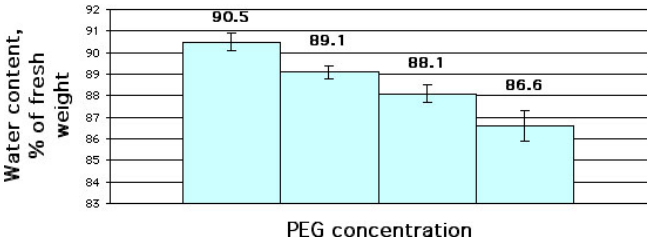
This work was supported by the Russian Fund of Basic Research (projects 02-04-06022 and 02-04-48599).

Diagram 1. Water content in control maize seedlings and after 24, 48 and 72 hours of desiccation.



Seedlings were grown at 27 C in optimal water conditions. One group of three-day-old seedlings was kept without water at 27 C for 24, 48 or 72 hours (columns 2, 4, 6, respectively). Other seedlings were kept 24, 48 or 72 hours in optimal water conditions at the same temperature (columns 1, 3, 5, respectively). After that we carried out detection of water content in seedlings. Each replication contained three measurements of water content in groups of 40-50 shoots. Mean ± S.D (n=3; P=0.95).

Diagram 2. Water content in control maize seedlings and after incubation with different PEG solutions.



Seedlings were grown at 27 C in optimal water conditions. Three-day-old seedlings were cut and divided into four groups of 30-40 shoots. Each group was distinctly incubated 3 hours with PEG solutions of 300 mOsm (column 2), 500 (column 3) or 700 mOsm (column 4). Seedlings incubated with distilled water were used as control (column 1). After that, detection of water content was carried out. Each replication contained three measurements in groups of 30-40 shoots. Mean ± S.D (n=3; P=0.95).

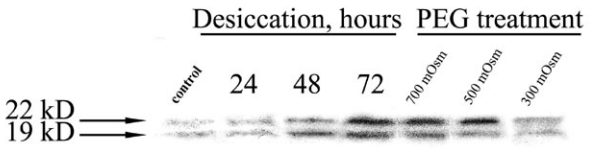


Figure 1. Accumulation of smHSPs in maize seedlings during desiccation and PEG treatment. Seedlings were grown at 27 C in optimal water conditions. One group of three-day-old seedlings was kept without water for 24, 48 or 72 hours. Others were cut and incubated 3 hours with PEG solution of 300, 500 or 700 mOsm. Seedlings kept without treatment were used as control. Total protein fraction was divided by SDS-PAGE (14% of acrylamide), and proteins were transferred from gel to nitrocellulose membrane, which was incubated with primary antibodies (1:500 dilution), elaborated to the α-crystallin domain (Heckathorn et al., Plant Physiol. 116:439-444, 1998). Molecular masses of smHSPs are given on the left.

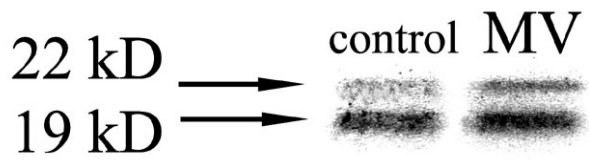


Figure 2. SmHSPs of maize seedlings at control conditions and after methyl viologen treatment. Three-day-old seedlings were cut and incubated 3 hours either with 100 mM of methyl viologen dissolved in 0.01% of Tween 100 (MV) to induce oxidative stress, or in 0.01% of Tween 100 for control. Total protein fraction was divided by SDS-PAGE (14% of acrylamide), and proteins were transferred from gels to nitrocellulose membrane, which was incubated with primary antibodies (1:500 dilution), elaborated to the α-crystallin domain. Molecular masses of smHSPs are given on the left.

The functioning of different electron transport pathways of the respiratory chain during low-temperature stress in maize mitochondria

--Grabelnych, OI, Funderat, SP, Sumina, ON, Pobezhimova, TP, Kolesnichenko, A, Voinikov, VK

It is known that the plant mitochondria respiratory chain has different electron pathways. Some of them are in common with mammal mitochondria (complexes I – IV). Other of these complexes, such as alternative oxidase (AO), internal rotenone-insensitive, and external NADH-dehydrogenases are unique to plant mitochondria (Vanlerberghe and McIntosh, Annu. Rev. Plant Physiol. Plant Mol. Biol. 48:703-734 1997; Soole and Menz, J. Bioenerg. Biomembr. 27:397-406 1995). Complex I of the mitochondrial respiratory chain is the most unstable under different stresses and pathologies (Lee, Biochim. Biophys. Acta 1271:21-28 1995; El-Wadawi and Bowler, J. Therm. Biol. 21:403-408 1996); in maize mitochondria complex I is the most thermosensitive (Pobezhimova et al., Membr. Cell Biol., 10:269-274, 1996). On the other hand, it is known that in protein spectrum maize mitochondria there are such proteins as AO (Karpova et al., Plant Cell, 14:3271-3284 2002), and different plant uncoupling proteins (the UCP-like plant uncoupling mitochondrial protein – PUMP and cold shock protein CSP 310 and CSP 310-like proteins) (Jezek et al., Biochim. Biophys. Acta, 1365:319-327, 1998; Kolesnichenko et al., J. Therm. Biol., 25:203-209, 2000). Because the activity of these proteins can change during low-temperature stress, the aim of the present work was to study the participation of the main cytochrome and alternative electron transport pathways in oxygen uptake of maize mitochondria during short-term low-temperature stress and hardening.

Three-day-old etiolated shoots of maize (*Zea mays* L. cv. Rossiyskaya) germinated on moist paper at 26 C were used in this work. Shoots were cold-stressed at 0 C for 1 h or were hardened at 8 C for 7 days. After cold treatment, mitochondria were isolated from seedlings shoots by differential centrifugation (Pobezhimova et al., J. Therm. Biol. 21:283-288 1996) and their energetic activity was studied. The mitochondria isolated were resuspended in the following medium: 40 mM MOPS-KOH buffer (pH 7.4), 300 mM sucrose, 10 mM KCl, 5 mM EDTA, 1 mM $MgCl_2$. The activity of mitochondria was recorded polarographically at 27 C using a platinum electrode of a closed type in a 1.4 ml volume cell. The reaction mixture contained 125 mM KCl, 18 mM KH_2PO_4, 1 mM $MgCl_2$ and 5 mM EDTA, pH 7.4. During NADH oxidation to incubation media, Ca^{2+} was added (0.06 mM $CaCl_2$) (Moller et al., Biochem. J. 194:487-495 1981). The concentration of mitochondrial protein was analysed by the Lowry method (Lowry et al., J. Biol. Chem. 1059:265-275 1951). Polarograms were used to calculate the rates of phosphorylative respiration (state 3), non-phosphorylative respiration (state 4), respiratory control by Chance-Williams and the ADP:O ratio (Estabrook, Methods Enzymol. 10:41-47 1967). All the experiments were performed on 3-6 separate mitochondrial preparations.

It was found that maize mitochondria that used malate as oxidation substrate were the most sensitive to cold shock and cold hardening, as compared with succinate and NADH oxidizing mitochondria. Cold shock and hardening caused about a 40% increase of state 4 respiration, a 26% decrease of RC coefficient, and a 10% decrease of ADP:O ratio. Such changes in mitochondrial energetic activity are typical for a low-energetic mitochondrial state.

To study the participation of cytochrome and alternative electron transport pathways, the effects of sequential additions of benzhydroxamic acid (BHAM) (an inhibitor of AO) and antimycin A (an inhibitor of complex III electron transport) on the activity of isolated maize mitochondria were used. It was shown that mitochondria isolated from control, stressed and hardened seedling shoots differ in their reaction when these inhibitors were added. Indeed, the addition of BHAM to control mitochondria oxidising malate in state 4 caused a slight decrease (18%) in the rate of oxygen uptake (Fig. 1A). A subsequent addition of antimycin A inhibited the rate of oxygen consumption up to 14%. The remaining oxygen consumption was fully inhibited by the addition of anti-

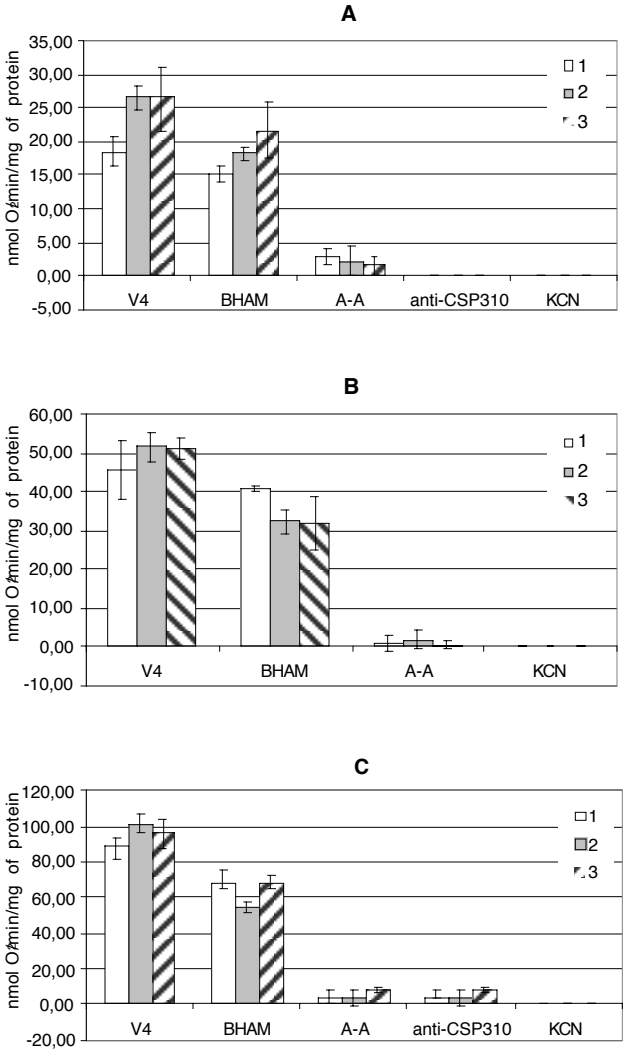


Figure 1. The effect of different respiratory chain inhibitors on state 4 oxygen consumption by maize mitochondria isolated from control (1), stress (2) and cold-hardened (3) shoots. The inhibitors were added in the sequence shown reading left to right. Their final concentrations were: - BHAM (1 mM), antimycin A (A-A) (20 mkM), KCN (0.4 mM) and CSP 310 antiserum (1 mg/mL).

A. 10 mM malate in the presence of 10 mM glutamate was used as a substrate of oxidation.

B. 8 mM succinate in the presence of 5 mM glutamate and 3 mkM rotenone was used as a substrate of oxidation.

C. 1 mM NADH in the presence of 3 mkM rotenone was used as a substrate of oxidation.

CSP310 antiserum (Fig 1A). So, in non-stressed maize mitochondria the following pathways are functional: cytochrome pathway (66%), AO (18%), and CSP 310 (16%). Cold shock caused the decrease of the main cytochrome pathway (60%), a significant increase of the AO pathway (31%), and a slight decrease of the CSP 310-pathway (8%) (Fig. 1A). Hardening caused an increase of the main cytochrome pathway (77%), did not influence the AO pathway (18%), and caused a slight decrease of the CSP 310-pathway (5%) (Fig. 1A).

On the other hand, an addition of BHAM to control succinate-oxidizing state 4 maize mitochondria resulted in a 10% inhibition of oxygen uptake (Fig. 1B). A subsequent addition of antimycin A fully inhibited mitochondrial respiration. So, in succinate-oxidizing maize mitochondria, both the main cytochrome (90%) and AO pathway (10%) function. Cold stress caused a decrease of the cytochrome pathway (60%) and an increase of the AO pathway (38%) (Fig. 1B). Cold hardening caused the decrease of cytochrome pathway (62%) and an increase of AO pathway (38%) too (Fig. 1B). In all cases, the sequential addition of BHAM and antimycin A to succinate-oxidizing mitochondria fully inhibits the oxygen uptake.

The addition of BHAM to NADH-oxidizing state 4 control maize mitochondria resulted in a 23% inhibition of oxygen uptake, and addition of antimycin caused about a 73% inhibition of mitochondrial respiration (Fig. 1C). The remaining oxygen uptake after BHAM and antimycin A addition was about 5%, and was not affected by anti-CSP 310 antiserum addition. It is possible that this oxygen uptake depends on the presence of the external antimycin A-insensitive NADH-cytochrome *c* reductase (Soole et al., Physiol. Plantarum 78:205-210 1990). This residual respiration was fully inhibited by cyanide (Fig. 1C). The addition of BHAM to cold-stressed maize mitochondria caused a 46% inhibition of oxygen uptake, and subsequent antimycin A addition inhibits mitochondrial respiration up to 4% (Fig. 1C). Cold hardening caused the decrease of the main cytochrome pathway (63%), a slight increase in the AO pathway (29%), and an increase in the antimycin A and anti-CSP310 resistant pathways (8%) (Fig. 1C). So, in NADH-oxidizing maize mitochondria the main cytochrome pathway, the AO pathway and the “external” antimycin A-resistant pathways are present. The main cytochrome pathway is the most active in maize mitochondria (73%), but it decreases during short-term cold stress and cold hardening.

So, based on the data obtained we can detect the presence of different electron transport pathways in maize mitochondria. The combination of different NAD(P)H dehydrogenases, AOX and CSP 310 should make plant mitochondria more tolerant to different stress factors.

Acknowledgements: The work has been performed, in part, with the support of the Russian Foundation of Basic Research (projects 00-04-48093 and 02-04-06096) and the Siberian Division of Russian Academy of Sciences Youth Grant (project 78).

Effects of redox conditions on DNA binding activity of mitochondrial topoisomerase I

--Konstantinov, YM, Katyshev, SI, Subota, IY, Tarasenko, VI, Kobzev, VF

Redox-based control of gene expression has recently emerged as a fundamental regulatory mechanism in cell biology. It is very likely that such regulation exists in plant organelles, taking into account their redox nature. We have previously shown (Konstantinov et al., Biochem. Mol. Biol. Intern. 36:319-326, 1995) the effect of redox conditions on mitochondrial transcription. An activation of RNA synthesis in organello under oxidising conditions, and its significant supression under reducing conditions was reported. Hence, it is a very interesting task to identify redox dependent proteins potentially involved in regulation of mitochondrial genome expression.

Assuming mitochondrial DNA topoisomerase I (topo I) as one of the candidates for playing such a regulatory role, we have shown (MNL 73:39-40, 1999) the modulation of mitochondrial topo I activity under different redox conditions: an activation of DNA relaxation driven by topo I in the presence of reduced glutathione (GSH), and its significant repression following the addition of oxidised glutathione (GSSG). The aim of the present work was to verify our hypothesis that this redox modulation is realized at the level of DNA binding activity of enzyme.

Mitochondria were isolated from 4-day-old etiolated maize seedlings of hybrid VIR42 MV by a standard method of differential centrifugation. The method of topo I isolation was described earlier (MNL 73:40-41, 1999), with an additional stage of purification on non-denaturing PAGE. EMSA was carried out as described by Ikeda and Gray (Mol. Cell. Biol. 19:8113-8122, 1999), with minor modifications. Assays employed double stranded DNA probes containing regions recognized by eukaryotic topo I, as well as *coxI* and *atp9* promoter fragments.

We have not found any DNA binding activity of purified topo I to DNA probes used in the standard assay conditions in the absence of redox agents. However, we have shown that the enzyme is able to form the stable complex with double stranded DNA in the presence of 5 mM GSH in the incubation mixture (Figure 1). In

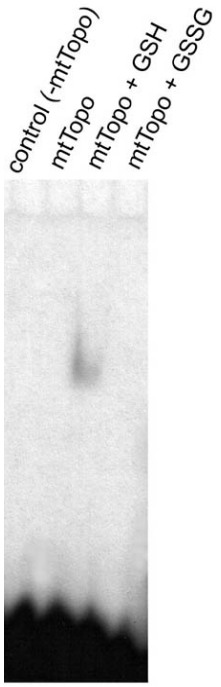


Fig.1

Figure 1. The effect of reduced and oxidised glutathione on DNA binding activity of mitochondrial topoisomerase I.

contrast, oxidised glutathione appeared not to be able to stimulate DNA binding activity of topo I. Furthermore, the presence of such redox agents as sodium dithionite and potassium ferricyanide has not led to induction of DNA binding (data not shown). Thus, data obtained point to a potential regulatory role played by the glutathione system in relation to mitochondrial topo I. This influence exists at the level of topo I DNA binding, which is the first stage of enzyme-DNA interaction. GSH might modulate topo I activity by favouring DNA-protein non-covalent complex stabilization.

It is not clear why we have not detected any DNA binding of topo I in the absence of GSH. We suppose that the complex formed between enzyme and DNA in such conditions is much less stable, and readily dissociates during the process of electrophoresis. It is also possible that the presence of GSH leads to changes in topo I affinity to one or another nucleotide sequence. Further investigations are needed to verify this hypothesis.

Financial support from the Russian Foundation for Basic Research (Grant No. 01-04-48162) is acknowledged.

RNA editing affects the potential protein kinase phosphorylation sites in mitochondrial proteins

--Konstantinov, YM, Arziev, AS

It is well known that both transcriptional and post-transcriptional events play important roles in governing the expression of the maize mitochondrial genes (Finnegan, Brown, Plant Cell 2:71-83, 1990). RNA editing in plant mitochondria involves post-transcriptional conversion of hundreds of different cytidine residues to uridine, or uridine-like, residues. Moreover, few uridine to cytidine transitions have been detected (Cattaneo, Annu. Rev. Genet. 25:71-88, 1991). From 668 editing sites in plant mitochondria transcripts studied so far, it appears that 60% of the edited codons correspond to Ser and Pro codons (Araya, Bégu, Litvak, Physiol. Plant. 91:543-550, 1994). We propose that part of these changes of Ser codons under RNA editing may lead to the damage of some protein kinase phosphorylation sites in mitochondrial proteins. Mitochondrial proteins are potential targets for the catalytic action of at least three types of protein kinases: protein kinase C, casein kinase II and tyrosine kinase. Therefore the change of protein kinase phosphorylation sites may also be the result of substitution of some other amino acids in the pattern of phosphorylation sites under transcript editing. If partially edited transcripts are translated, such an alteration of the phosphorylation state of definite mitochondrial proteins may be a part of a special physiological regulation mechanism.

The aim of this work was to check the hypothesis that the editing events in primary transcripts may influence the protein kinase phosphorylation pattern of genomically deduced proteins through alteration of protein kinase phosphorylation sites. For that purpose, we studied the presumed protein kinase phosphorylation site patterns in the genomically encoded proteins, and proteins translated from an edited mRNA.

Amino acid sequences of mitochondrially encoded polypeptides (ATP6, COX2, NAD4L, NAD3, NAD9), before and after editing of the appropriate mRNAs, are taken from the EMBL Nucleotide Sequence Database (the nucleotide sequence data under the accession numbers M16223, Z11843, V00712, J01425, X52865, AB015175, X52200, AF279446, AF279447, AB020062) (http://www.ebi.ac.uk/). The analysis of protein kinase phosphorylation patterns in mitochondrial proteins was performed using the PROSCAN (PROSITE SCAN) program (http://npsa-pbil.ibcp.fr/).

The sequence comparison of *Zea mays* and other plant species' mitochondrially encoded polypeptides, before and after editing of the appropriate mRNAs, reveals a significant number of amino acid replacements leading to alteration of presumed protein kinase phosphorylation sites (Table). Thus, in maize, RNA editing

Table. The alteration of potential protein kinase phosphorylation sites in mitochondrial proteins through RNA editing

Species	Protein	Protein kinase	Number of phosphorylation sites per molecule	Sites and their location
Zea mays	ATP6	Protein kinase C	2	69TKK 213SVK
		Casein kinase II	3	25SPLD 83SLVE 247TGLE
	ATP6*	Protein kinase C	1	207TKK
		Casein kinase II	3	163SPLD 221SLVE 385TGLE
	COX2	Protein kinase C	2	119TIK 243TLK
		Casein kinase II	4	81TTIE 138SSDE 183TPAD 243TLKD
		Tyrosine kinase	1	129RSYEYSDY
	COX2*	Protein kinase C	2	119TIK 243TLK
		Casein kinase II	4	81TTIE 138SSDE 183TPAD 243TLKD
		Tyrosine kinase	0	-
Beta vulgaris	ATP6	Protein kinase C	2	32TKK 176SVK
		Casein kinase II	2	46SLVE 210TGLE
	ATP6*	Protein kinase C	1	32TKK
		Casein kinase II	2	46SLVE 210TGLE

	NAD4L	Protein kinase C	2	2SIK 83TFR
		Casein kinase II	1	52SSDD
	NAD4L*	Protein kinase C	2	2SIK 83TFR
		Casein kinase II	1	52SSDD
Oenothera berteriana	NAD3	Protein kinase C	1	115SDR
		Casein kinase II	5	34TYPE 40SAYE 54SRFD 106SLYE 115SDRE
		Tyrosine kinase	1	53RSRFDIRFY
	NAD3*	Protein kinase C	0	-
		Casein kinase II	3	34TYPE 40SAYE 54SRFD
		Tyrosine kinase	1	53RSRFDIRFY
Sorghum bicolor	ATP6	Protein kinase C	4	26TRR 61TGR 172TKK 316SVK
		Casein kinase II	4	7SLTD 128SPLD 186SLVE 350TGLE
	ATP6*	Protein kinase C	3	26TRR 61TGR 172TKK
		Casein kinase II	4	7SLTD 128SPLD 186SLVE 350TGLE
Lupinus luteus	NAD9	Protein kinase C	2	66SRK 79STR
		Casein kinase II	4	33TNTD 90TSAD 91SADE 182SPWE
		Tyrosine kinase	2	69RRFEVVY 68KRRFEVVY
	NAD9*	Protein kinase C	2	66SRK 79STR
		Casein kinase II	4	33TNTD 90TSAD 91SADE 182SPWE
		Tyrosine kinase	2	69RRFEVVY 68KRRFEVVY

Protein abbreviations without asterisks correspond to sequence-deduced protein. An asterisk designates protein translated from an edited mRNA.

damages one protein kinase C phosphorylation site in the mitochondrial ATPase complex subunit 6 gene transcript of the C male-sterile cytoplasm (Kumar and Levings, Curr. Genet. 23:154-9, 1993), and one phosphorylation site for tyrosine kinase in subunit II of cytochrome *c* oxidase. A similar situation was revealed for *Beta vulgaris* ATPase subunit 6 transcript editing, with alteration of the protein kinase C phosphorylation site. RNA editing of subunit 3 NADH dehydrogenase transcript in *Oenothera berteriana* decreases the number of phosphorylation sites for casein kinase II from 5 to 3, and damages the site for protein kinase C. The alteration of protein kinase C phosphorylation site number was also shown for ATPase subunit 6 in *Sorghum bicolor*. Therefore one consequence of RNA editing in plant mitochondria is to change protein kinase phosphorylation site patterns in mitochondrial enzyme subunits.

We suggest also that the change in potential protein kinase phosphorylation site numbers in mitochondrial proteins under RNA editing is a remnant of some evolutionary mechanism to alterate or modify the functional activity of proteins in plant mitochondria.

Some molecular characteristics of ORFs in S1, S2 and 2.3 kb linear mitochondrial plasmids in VIR42 MV hybrid

--Verbitski, DS, Koulintchenko, MV, Konstantinov, YM

Mitochondria of S-cytoplasm contain linear plasmids S1 and S2 of 6.4 and 5.4 kbp (Pring et al., PNAS 74:2904-2908, 1977). There is also a 2.3 kb (S3) linear plasmid in other types of maize cytoplasm (Bedinger et al., Mol. Gen. Genet. 205:206-212, 1986). All of these mitochondrial linear plasmids contain their own open reading frames, encoding proteins presumably relating to their replicon function. Little is known about the genetic variability of these genes in mitochondrial extra-chromosomal DNAs. The aim of the present work was to investigate the nucleotide structure of ORFs in S1, S2 and S3 plasmids in a VIR42 MV hybrid.

The nucleotide sequences of ORF3 in a VIR42 MV hybrid and from the genotype reported earlier are almost identical. The only difference was found in position 963 of the sequence (guanine instead of cytosine). This minor alteration in nucleotide sequence leads to amino acid substitution (histidine ➔ aspartic acid) in the polypeptide product of ORF3 (see Fig. 2).

```
              tctagaa actcttttat taaaaagacg agacacggat gtcgacaaaa     900
              ******* ********** ********** ********** **********

  ctcacgtgcc ctacgcaggg gggtatatga tggttgatat ggaaaagcgg gttaacgcgg     960
  ********** ********** ********** ********** ********** **********

  accatattac gacgttctat gcacatgact actcaaaagt gtgccaggat tttcacgata     1020
  **g******* ********** ********** ********** ********** **********

  tgagtgaaaa gatgctcaca gagatgatta atagaatagt aaaggatgtt caaagaagag     1080
  ********** ********** ********** ********** ********** **********

  gaagttcaat ggttgtatac tttcacaatt tatctcagtt cgacggtatt atgatactct     1140
  ********** ********** ********** ********** ********** **********

  ctttttaac taaaagttat aaaaactgtc atatagagcc catcatgaga aacgactgta     1200
  ********** ********** ********** ********** ********** **********

  tttattccat aaaactgtat aaggtatcca aaaatgggga taaaaggctt gttttaacgt     1260
  ********** ********** ********** ********** ********** **********

  tcatggattc gtacctcctg ttgaaagtaa agctcgctga tctagccgat agtttttgcc     1320
  ********** *********
```

Figure 1. The nucleotide sequence of ORF3 in S1 plasmid of a VIR42 MV hybrid. The strand shown corresponds to the EMBL Database sequence accession X02451. Primers for PCR amplification of the ORF3 region used were the following: 5'-primer, 5'-AGAAATGAAAAACAAAACTC-3'; 3'-primer, 5'-CAAAAACTATCGGCTAGATCAG-3'. Purified double-stranded amplification product was sequenced using the dideoxy chain termination method (Sanger et al., 1977) as described in Promega's Technical Protocol. The nucleotide sequence was determined on both strands of DNA in triplicate. The products of sequencing reactions were resolved by 5 and 8% polyacrylamide-8 mol/L urea gel electrophoresis, and autoradiographed for 24 hours at room temperature.

```
VADLETLLLKRRDTDVDKTHVPYAGGYMMVDMEKRVNADHITTFYAHDYSKVCQDFHDM
************************************D*******************

SEKMLTEMINRIVKDVQRRGSSMVVYFHNLSQFDGIMILSFLTKSYKNCHIEPIMRNDC
************************************************************

IYSIKLYKVSKNGDKRLVLTFMDSYLLLKVKLADLADSFCPELGGKGSFDHQNVTVDKL
************************************************************
```

Figure 2. Deduced amino acid sequence of ORF3 product in a VIR42 MV hybrid.

```
                                                          agtct
                                                          *****

1741 atgattttat acaaaaacat tggagtgtat tagtgtccgt ggggcttctc aggccgaaga
     ********** ********** ********** ********** ********** **********

1801 atctagcttt atttaaacga aaggaggcgc tcaggctact atctagcctt ttgtttaaac
     ********** ********** ********** ********** ********** **********

1861 acgaggagct ttcaacgatt tatcgatata gtgagttgaa atctgtattg ttaaaaaata
     ********** ********** ********** ********** ********** **********

1921 tacacgcgtc aaccttcgaa ctatatacta tgaaaatagc tgaggcttat ctagattata
     ********** ********** ********** ********** ********** **********

1981 aaatctattt tccaatcttt ctggacttca gggggcgaaa ttaccgccat ggacccttcc
     ********** ********** ********** ********** ********** **********

2041 atttccacga acgtgattta gtgagatcac tcatcatatt tgatgaaagt gatgactcag
     ********** ********** ********** ********** ********** **********

2101 cagcacatac tataaatagt gatgttgggg atagaatcct ccataatttc cttatatcag
     ********** ********** ****a*a*** ********** ********** **********

2161 cgg
     ***
```

Figure 3. The nucleotide sequence of ORF1 in the S2 plasmid of a VIR42 MV hybrid. The strand shown corresponds to the sequence from EMBL Database (EMBL J01426).

The results of sequencing of an ORF1 fragment in the S2 plasmid in a VIR42 MV hybrid are shown in Figure 3.

Two nucleotide changes in the ORF1 sequence in the S2 plasmid of a VIR42 MV hybrid were revealed (T ➔ A and G ➔ A). Both S1 and S2 plasmids are in the integrated state in this hybrid, but the 2.3 kb linear plasmid behaves as an autonomous replicon. The ORF1 transcript in the S3 plasmid was detected by RT-PCR (Fig. 4). At the moment we are sequencing this RT-PCR product. We have been unable to detect the ORFs product in S1 and S2 plasmids in this hybrid.

The data presented demonstrate that ORFs in linear plasmids of maize mitochondria in different genotypes have a rather conservative nature.

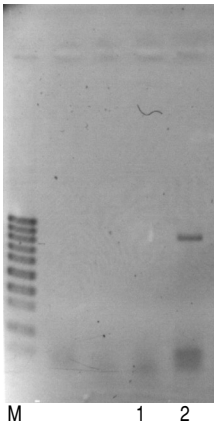


Figure 4. Electrophoretic analysis of the RT-PCR product of ORF1 in 2.3 kb plasmid-like DNA in a VIR42 MV hybrid. 1, control; 2, RT-PCR product. M, molecular weight markers.

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Cornell University

Will the real Maize Genetics Garden please stand up?

--Kass, LB, Murphy, RP

While writing a history of Cornell's Plant Breeding Department and conducting research for an intellectual biography of Barbara McClintock, we have located documents that clear up the confusion surrounding the location of two corn growing fields at Cornell University during the Golden Age of Corn Genetics, 1928-1935. These areas identified as the "Emerson Garden" and "the hole" are currently part of the Cornell Plantations arboretum, botanical gardens and natural preserves. We present evidence that these areas, misrepresented as one local (May 1991), were two separate fields.

In early 1927, R. A. Emerson, Head of Cornell's Plant Breeding Department wrote to his former student Milislav Demerec at Cold Spring Harbor about growing his white seedling stocks at Cornell the following spring: "I do not know as yet whether the farther garden, which we call the hole, will be available." Emerson was most concerned that the University might take over this area and "construct part of their new water system on it" (Emerson to Demerec March 30, 1927).

In fact, the Carnegie Filtration Plant, near Emerson's office and originally built in 1904 following the typhoid epidemic of 1903 (Anon 1905, Cornell campus map, 1914), was no longer large enough to meet the new demands on the system. Consequently, an enlarged filtration plant was erected in 1927 and 1928, and located in a more convenient place, "where it would not interfere with the expanding main campus and where there would be enough land for future expansion" (Plant Managers Report). The new water system unfortunately occupied part of the Plant Breeding Department's "farther garden," thus limiting land for growing the important corn stocks maintained by Emerson's department. This area was used primarily for corn genetics or breeding from the 1920s to 1960s, when it was ultimately and completely transferred to the water filtration plant (Murphy unpub. ms. p. 12).

Plant Breeding's nearer experimental maize garden, named Emerson Garden ca. 1949, was less than a five minute walk down gymnosperm slope from Emerson's department in the Forestry building (later named Fernow Hall). This Garden is located near the headquarters of the Cornell Plantations. The "farther garden," known in the department as "the hole," was east of the Garden, between Judd Falls and Caldwell Roads, about a half hour's walk from the Botany and Plant Breeding Departments (see map in Haine 1995:74-75). In these fields, faculty and students in both departments grew their maize crops and laid the foundations for our current understanding of maize genetics.

It was in the Emerson Garden where George Beadle, Barbara McClintock, Marcus Rhoades, Charles Burnham, Harriet Creighton

Figure 1. Cornell's Plant Breeding Garden from gymnosperm slope overlook along Tower Road (ca. 1932). Photo courtesy of J. H. Srb. from A. M. Srb's papers.

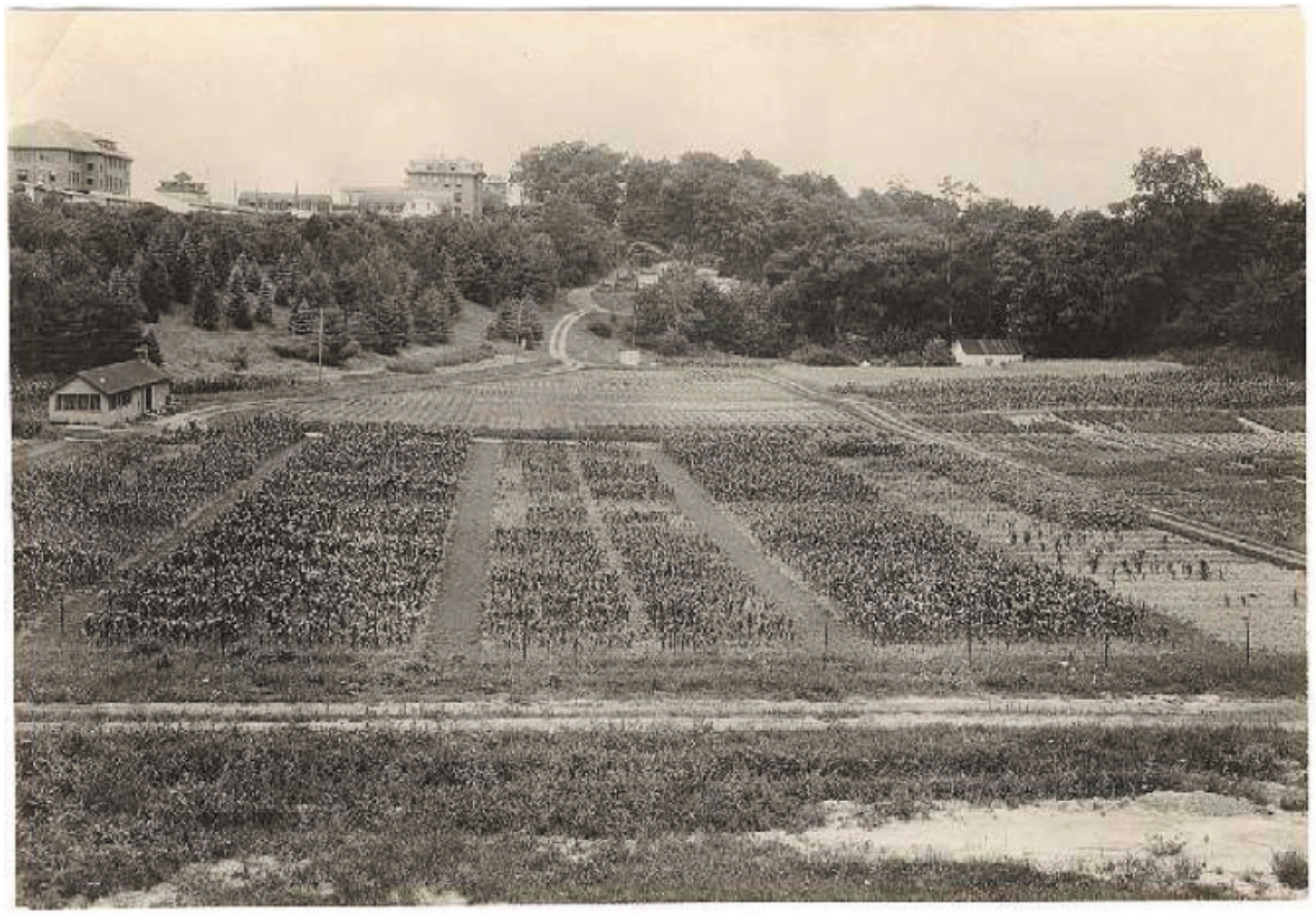

Figure 2. Cornell's Plant Breeding Garden, facing west from Judd Falls Road, with"McClintock Shed" on left and Forestry Building above (ca. 1932). Photo courtesy of J. H. Srb. from A. M. Srb's papers.

and others grew and harvested their special maize plants, providing the first connections of chromosomes with linkage groups, semi-sterility, crossing-over, translocations, etc. (Emerson, 1932; Emerson, Beadle and Fraser, 1935; Kass and Bonneuil, in press). The Garden area was quite convenient -- only a few minutes walk from their cytology lab in Stone Hall. It was protected from early frosts in winter, which also permits earlier plantings in spring. The shed adjacent to their plot (known fondly as McClintock Shed, Haine 1995: 54-55), not only provided storage for crops and equipment but also shade for a cooler and secluded lunch. During a break from pollinations, the famous 1929 photograph of Emerson and his colleagues was taken in back of this shed (Emerson's maize group 1929).

The inception of the Plant Breeding Garden has an interesting history. In 1909, L. H. Bailey, then dean of Cornell's College of Agriculture turned over the entire garden to H. J. Webber, head of Cornell's recently established Department of Plant Breeding. Webber had previously shared the field with Farm Crops, but he requested use of the whole area, expecting his "breeding garden to be the most interesting spot on the University Campus" (Webber to Bailey, 16 March 1909). Bailey had always dreamed of a good outdoor laboratory and he hoped it would be "one of the best laboratories at Cornell" (Bailey to Webber, 25 March 1909). Emerson inherited the Garden in 1914, when he succeeded Webber as department head. By 1932, Emerson and his students had more than fulfilled Bailey's and Webber's expectations (Emerson 1932).

The confusion about the location of the two plant breeding fields seems to have emerged from a 1991 publication by May, who relied on memoirs and recollections by the early maize geneticists. R. P. Murphy, co-author of this report, was Head of Cornell's Plant Breeding Department from 1953 through 1964. His records and experiences in both localities were most valuable for this interpretation. Other faculty and students in Cornell's Plant Breeding department had also grown plants in both the "Emerson Garden" and "the hole." They were most surprised to find that these areas had been misrepresented as one locality by May, who was never a student in their department. Their comments provoked us to seek records documenting the locations of these corn fields. We were fortunate to find letters in the Cornell Archives that provide a clear picture of where the exciting history of maize genetics had its origins. The glory of maize genetics is memorialized by the Emerson Garden at the Cornell Plantations -- the hole remains hidden in the records of the past.

Acknowledgments: We thank Plant Breeding Department Professors Elizabeth Earle, Margaret Smith, Henry Munger, and Ronnie Coffman, for bringing this question to our attention. We give special thanks to Tom Rapalee, Al Loomis and Jan Slattery for giving us a tour of the filtration plant on April 29, 1998, and for sharing its documented history.

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Plant Managers Report. Undated. The Cornell University Water System--From the 19th Century to the Present Day. Tom Rapalee gave a copy of this report to Lee Kass and R. P. Murphy on 29 April 1998.
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Comparison of mRNA structure and expression between high and low GC mode maize genes

--Simmons, CR, Navarro, PA, Li, AD

Maize and other cereals, such as rice and wheat, have a distinctly bimodal gene GC content distribution. Using a dataset of 1831 public and private full-length cDNAs, we investigated various aspects of mRNA structure and expression between the high and low GC mode genes. Among the key findings are the following.

Other taxonomic groups such as dicot plants, animals, fungi, bacteria, and archaea, do not have bimodal GC content distributions, although vertebrate animals come close. Arabidopsis, with its unimodal distribution centered at 44% ORFGC, is therefore not a representative model system for this chiefly monocot (cereal) phenomenon. [Note, abbreviations are: GC, G+C% nucleotide content; ORF, open reading frame from ATG to stop; 3GC, third codon position GC%].

The low and high ORFGC maize gene modes peak at about 51% and 67% GC, with circa a 2/3 majority of genes found in the lower GC mode. This GC bimodality is a product of nuclear-encoded genes: 111 chloroplast-encoded ORFs have a unimodal distribution with a low 39.1% average ORFGC content, and 16 mitochondrion-encoded gene ORFs averaged 43.4% GC.

Most bimodal GC content variation is in the coding region, especially the third codon position, where GC ranges up to 100%, with obvious affects on codon usage. Third codon position C predominates over G by a ratio of 1.3 among high GC mode genes. In the ORF overall, however, G% is nonetheless slightly higher than C% among high GC genes, primarily due to the high frequency of G in the non-synonymous 1st codon position, evidently related to amino acid frequencies. The 5'-UTRs and 3'-UTRs of GC-rich genes are more GC-rich, but only slightly more so, 1.8% and 2.6% respectively, than their counterparts from low GC mode genes.

Maize genes generally have a negative GC gradient along the transcript, from the 5'-UTR, through the coding region, and the 3'-UTR. (See also Wong, GK-S et al. Genome Res. 12:851, 2002). Nonetheless, most high GC mode genes, and a subset of the low GC mode genes, have only slightly negative ORFGC gradients. The remaining genes from the low GC mode have marked negative GC gradients, but this negative gradient tends to rebound to a positive gradient before the end of the ORF. The gradient and its reversal are more pronounced for the ORF3GC than the ORFGC. Interestingly, because of these differences, a plot of ORF3GC gradient tendencies versus GC content (as ORF3GC) reveals a tri-modal maize gene distribution: 1) high GC mode, little gradient; 2) low GC mode, little gradient; and 3) low GC mode, negative gradient and rebound.

Like GC content, the CpG methylation site frequencies are also bimodal, as might be expected given this site is comprised of G and C. However, importantly, if the observed (direct count) and expected (calculated from GC content) CpG site frequencies are determined for each gene in a codon-position-specific manner (i.e., separately for codon positions 1,2; 2,3; and 3,1), a bimodal pattern still emerges. High GC genes have a generally balanced CpG ratio of about 0.9, but low GC genes tend to have a deficit CpG ratio of about 0.6. It should be emphasized that this represents a two-order separation in CpG site frequencies between low and high GC genes, because for the low GC mode genes their expected CpG frequency is already low due to their own intrinsically lower GC content.

A plot of the obs/exp CpG ratios is thus bimodal, and a plot of these CpG ratios in turn versus the bimodal ORFGC content, results in a diagonal distribution anchored with two clusters at each end. The correlation of the CpG ratios versus GC content is fairly high (r2=0.72). Nonetheless, the plot is slightly curved, with the slope declining with higher GC content. Like the GC content, the CpG ratios also show a generally negative gradient along the ORF length, with a rebound from the negative gradient towards the C-terminus, especially among low GC mode genes. The more balanced CpG ratios of high GC genes also extends to the 5'- and 3'-UTRs, indicating it is not limited to the coding region. The frequencies of the alternative methylation site CpNpG do not vary as much as CpG sites between high and low GC mode genes, and the obs/exp CpNpG ratios are balanced (1.0) for both high and low GC mode genes in all three codon positions (1,3; 2,1; and 3,2), and in both the 5'- and 3'-UTRs.

While most GC content variation is manifest in the third codon position, the first two non-synonymous codon positions are nonetheless also higher in GC content among high GC mode genes. This is therefore reflected in shifts in amino acid composition. High GC mode genes are richer in necessarily GC-rich codon amino acids, such as alanine (GCX), glycine (GGX), and proline (CCX). Low GC mode genes, conversely, are richer in the necessarily GC-poor codon amino acids, and moderate GC codon amino acids are

found at similar frequencies between high and low GC mode genes. Like GC content and the obs/exp CpG ratios, the frequencies of GC-rich amino acids generally decline 5'-3' (N-terminal to C-terminal) along the ORF, but rebound toward the C-terminus among low GC genes. This is especially true for alanine, which being found at higher levels near the N-terminus, contributes to higher signal peptide prediction rates for high GC genes, because alanine is often scored as a signal peptide cleavage site. These compositional biases thus have implications for automated gene functional annotation, and might also complicate protein evolutionary comparisons.

Maize GC-rich genes tend to be more compact, having shorter coding regions (by 18%), encoded predicted protein MWs (by 20%), 5'-UTRs (by 10%), and 3'-UTRs (by 14%), relative to the counterparts from low GC genes. The 5'-UTRs of high GC genes also contain nearly four-fold fewer non-coding ATG sites. Using rice as a surrogate cereal to investigate introns (because there are yet few maize full-length genes with annotated introns), we found that total intron length of GC-rich genes is markedly shorter, primarily due to only 40% as many introns present in high GC mode genes relative to low GC mode genes. High GC mode rice genes are also 18.2 intronless, compared to 7.9% for GC-poor mode rice genes. Similar trends will presumably hold when comparable numbers of maize introns are available for study.

The compact and simpler structure of GC-rich gene transcripts, the extreme codon bias, and the fewer ATG sites in 5'-UTR (which the ribosomal apparatus could confuse with bona fide start sites), together might suggest that GC-rich genes may be adapted to more efficient gene expression, both in terms of transcript production and processing, and in protein translation. The Kozak translational initiation site frequencies, however, do not differ greatly between high and low GC mode genes: both favor "GCCATGGC". Kozak context is therefore not a good marker for bimodal gene GC content. In humans, on the other hand, Kozak context does vary between high and low GC genes (Pesole, G et al., FEBS Lett. 464:60, 1999).

We investigated mRNA expression of high and low GC mode genes using both EST distribution analysis (over 400,000 ESTs) and Lynx MPSS technology (63.4 million 17-mer tags) (Brenner, S et al., Nat. Biotech. 18:630, 2000). We found that while gene expression varied widely within high and low GC modes, considering the average expression levels among 12 key distinct tissue categories, the overall average tissue expression level of high and low GC genes was similar; only 1.1- and 1.2-fold higher for high GC mode genes, in EST and MPSS analyses respectively. We observed, however, a tendency for higher magnitude tissue-preferred expression of GC-rich genes, especially in vegetative tissues (root, mesocotyl, stalk, leaf; averaging 1.6- and 3.0-fold higher, EST and MPSS respectively) and in non-kernel reproductive tissues (silks, tassel, and pollen; averaging 2.5- and 4.3-fold higher, EST and MPSS respectively). In contrast, in endosperm, pericarp, and R1 kernel tissues, expression of low GC genes was higher than the high GC mode genes by an average of 1.9- and 2.0-fold, EST and MPSS respectively.

High and low GC mode genes were expressed constitutively in similar frequencies: 4.8% and 9.1%, respectively, by EST analysis; and 7.8% and 8.9%, respectively, by MPSS analysis. For this study constitutive expression was defined for the EST analysis as expression in at least 10 of the 12 tissue categories at a level of at least 25 PPM in each of the 10 tissues, with an overall average expression among all 12 tissues of 100 PPM. For the Lynx MPSS technology the definition was similar, but it was set to a 12.5 PPM minimum and 50 PPM average. However, the constitutive expression levels (i.e., magnitude in PPM) of the GC-rich genes averaged higher by 1.7- and 2.1-fold, in EST and MPSS analyses respectively.

Inspection of gene identities for high and low GC mode genes revealed diverse biological and biochemical functions of the gene products, both within and between the high and low GC modes. Protein relationships were higher within genes of each GC mode, no doubt contributed to by close gene family relationships, however substantial protein relationships existed for predicted proteins between high and low GC mode genes as well. Highly conserved proteins (that is, conserved in other distant taxonomic groups such a bacteria, fungi and animals) were readily found among both high and low GC mode genes. It had been argued that since methylated CpG sites mutate at a high rate, then high GC genes would tend to be relatively new (e.g., see Moore, G et al., Genomics 15:472, 1993). There was little indication of bimodality arising from pre-existing GC differences in parental genomes of polyploids. For example, among 11 loci pairs attributed to maize tetraploid ancestry (Gaut, BS and Doebley, JF, PNAS 94:6809, 1997), the GC content differed by only 0-3% (average 1.2%). Of course, all cereals investigated to date have the bimodality, indicating its origin precedes the maize lineage.

The cellular locations of high and low GC gene products appeared to be similarly diverse, and gene plots of presumed cellular location (nuclear, cytoplasm, chloroplast, mitochondria, plasma membrane, and extracellular), versus ORFGC content were all generally bimodal. The extracellular proteins investigated on average had higher GC contents however. Looking in more detail at one cellular compartment, the nucleus, we investigated the 45 transcription factor families of maize using 2384 members from among 84,085 "UniGene" EST assemblies. The transcription factor genes as a whole differed little from the overall gene GC content or bimodal tendency. Yet, while most families showed a broad or somewhat bimodal GC content distribution, some families displayed an upper or lower GC bias. For example, the Wrky transcription factor family (IPR003657), averaged 59% GC with the mode peak at 67%GC (N=67).

While the cause of the bimodal gene distribution is unknown, these investigations have directed our attention to CpG sites and methylation. Of all the gene characteristics we investigated, the obs/exp CpG ratios had the best correlation to the GC content variation, and these ratios differed not only within the ORF, but also along the ORF length, and outside the ORFs in the non-coding regions. The gradients in GC content suggest an organizing 'force' emanating from the 5' end of the transcript region. The rebound at the 3' end among some genes may be a compensational recovery from this 5'-end pressure. After all, the amino acid bias rebounds sooner (i.e., closer to the N-terminus) than does the base composition, which might be expected with a 'force' declining with distance from the 5'-end. Yet, other features associated with high GC genes, such as their compact structure and fewer 5'-UTR ATG sites, are not obviously related to a 5'-end emanating force or methylation, and instead, at least superficially, suggest expression efficiency could somehow relate to GC content as well. Whether these varied characteristics are the product of one or multiple evolutionary trends is unknown, but this data suggests there is an important organizing principle at play in cereal genomes. Perhaps it relates to how genes are registered in chro-

mosomes and disposed towards developmental or temporal expression. Analysis of 129 of the 1831 genes that were genetically mapped indicated that they were distributed throughout the genome on all 20 chromosome arms; however more extensive physical maps and genomic sequencing will be needed to affirm or refute any relationship of maize bimodal gene GC content to chromosomal position.

Codon bias is still assumed to be a key condition for optimizing (translational) expression in eukaryotes such as maize - presumably because some microbes have correlations between codon usage, iso-accepting tRNA pools, and expression levels. Codon biases have accordingly figured into gene re-engineering methods for transgene expression (e.g. Koziel, M et al., US Patent 6121014, 2000). The findings here cast further doubt upon this assumption and the need for this practice. First, maize does not have one codon table, but in effect two. Second, high and low GC genes have generally similar levels of mRNA expression. Third, high and low GC mode genes are both expressed within the same tissues, and presumably the same cells, even while there are some differences in tissue preference. Fourth, the GC content variation is not limited to the ORF, and within the ORF it presses beyond merely codon usage to affect amino acid content itself. Fifth, the correlation of obs/exp CpG sites to GC content is unlikely related to translation. And sixth, the codon usage varies along the ORF length with GC content. It is not apparent how the codon-anticodon coadaptation hypothesis can account for all these varied observations. We have, however, developed and applied computerized methods for reengineering ORFs from any source into configurations at least compatible with the natural structures of maize genes revealed by this study, for subsequent reintroduction into transgenic crops, by drawing upon a more elaborate combination of attributes such as GC content, ORFGC gradients, obs/exp CpG ratios, and codon biases.

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The premature senescence mutant (*pre1*) maps to the long arm of chromosome 1

--Multani, DS, Lee, Y, Johal, G

Senescence is the last stage of plant development. The biological role of this process is believed to be in the recruitment or salvage of nutrients from the senescing tissues to developing reproductive tissues. In an effort to understand the senescence at the genetic and molecular levels, we are studying the premature senescence-1 (*pre1*) mutant of maize.

Steve Briggs first observed this mutant in a randomly *Mu*-tagged population in 1991 at Pioneer Hi-Bred Int., Inc. The senescing phenotype of *pre1*, which is inherited in a recessive manner, is apparent 2-3 weeks prior to anthesis (Neuffer, Coe and Wessler, eds., Mutants of Maize, pp. 275-276, 1997). A wave of diffuse chlorosis and necrosis begins at the tip and margins of the leaves and then spreads toward the leaf base. Like natural senescence, the *pre1* phenotype starts from the lowermost leaves and then spreads to the top of the plant in a progressive fashion (Fig. 1), causing *pre1* plants to senesce completely within weeks after

anthesis. Although *pre1* plants largely stay male sterile, they do shed pollen occasionally, especially under cool dry conditions. Like most maize mutants that affect tissue integrity, *pre1* is easily influenced by genetic backgrounds. For instance, *pre1* plants can be maintained in homozygous condition in the B73 background, and its phenotype almost disappears if the *brachytic-2* mutation is also in the background.

In order to map *pre1* to a specific chromosome, a set of B-A translocation stocks (received from Jim Birchler, University of Missouri-Columbia) was used. Plants heterozygous for this mutation (*pre1*/+) were pollinated with pollen from hyperploid TB-stocks covering 16 different chromosome arms. The premature senescence mutants (12 out of 62 plants) were observed only in the progeny of crosses involving TB-1La, indicating that *pre1* is located on the long arm of chromosome 1.

***bk3*, a new brittle stalk mutant of maize**

--Multani, DS, Johal, G

A brittle stalk mutant was identified from the self-pollinated population of a plant known to have *Mutator* activity in 1997 (MO97-08-626). The true breeding nature of the mutant was

confirmed by growing self-pollinated progeny of the WT-sib. Leaves of this mutant are highly brittle and snapped readily when pressed between fingers (Fig. 1). All other parts of the plant, such as the stalk and roots, are also brittle and easily breakable. In addition, this mutant is weak, dwarf and has leaves that develop a reddish tinge especially towards at the tip. The inheritance of this mutant was studied by crossing with the inbred B73. The F1 was normal in phenotype and in an F2 population of 108 plants, 82 were normal and 26 were mutant. These data agree with a 3 normal: 1 mutant ratio. Thus, the new brittle stalk mutant phenotype is due to a single recessive gene. To determine its allelic relationship with another known brittle stalk mutant, *bk2* (Langham, MNL 14:21-22, 1940), the two were crossed (*bk2* was acquired from the Maize Genetics Coop). The resulting F1 was normal in phenotype; the appearance of both brittle stalk mutants in F2 indicates that the new brittle stalk mutant is non-allelic to *bk2*.

Figure 1. *bk3*, brittle stalk mutant: brittle plant parts after 4-leaf stage are easily broken. Lower leaves also have reddish tinge more at the tip.

Many features of this new mutant resemble those described for *bk1* (Brewbaker, MNL 69:58-59, 1995). However, because of the unavailability of seed for *bk1*, which appears to have been lost from the Maize Genetics Coop, allelic relationships between the two can never be established. Therefore, the new brittle stalk mutant has been designated as *bk3*.

It is difficult to maintain this mutant as a homozygote, and only occasionally has it been seen to shed pollen. Thus, it is maintained as a heterozygote. In an attempt to map *bk3* to the specific chromosome arm, we used B-A translocations. Plants heterozygous for *bk3* (*bk3*/+) were used as females and crossed with TB-stocks (received from Jim Birchler, University of Missouri-Columbia) representing 16 (TB-1Sb, TB-1La, TB-2Sa, TB-3Sb, TB-3La, TB-4Sa, TB-4Lb, TB-5Sc, TB-5Lb, TB-6Lc, TB-7Sc, TB-7Lb, TB-8Lc, TB-9Sd, TB-9Lc, TB-10Sc, and TB-10L19) out of 20 chromosome arms. Except for TB-9Lc, progeny of all crosses was normal in phenotype. In the case of the cross with TB-9Lc, 11 out of 126 progeny plants tested were mutant, suggesting that *bk3* is located on the long arm of chromosome 9. Interestingly, *bk2* also maps to 9L (Langham, 1940).

As *bk3* was isolated from a *Mutator* population, a segregating F2 population was analyzed by co-segregation analysis to identify the *Mu1* element that segregated completely with the mutant phenotype. This *Mu1* element, along with the flanking genomic DNA (5.4 kb/NotI fragment), was cloned and subject to a higher resolution of linkage with the mutant allele. One out of 96 plants tested gave us an exception to the tight linkage between the clone and the mutant phenotype, indicating that the clone we have isolated does not come from the *bk3* locus. However, the two are localized within 1-2 cM of each other. This information was used to reconfirm the chromosomal location of *bk3* using the collection of oat-maize addition lines. Two gene specific primers from this *bk3*-linked clone were designed and used to amplify the target sequence from DNA derived from each of the ten oat-maize addition lines. An amplification product, which hybridized positively with a clone-specific probe, was obtained only from the oat-maize addition line 9 (Fig. 2). This result, along with data from the B-A study, clearly established that like *bk2*, *bk3* is localized to 9L.

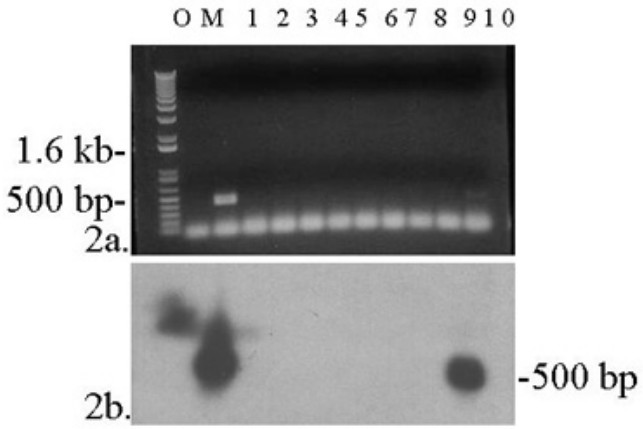

Figure 2. Chromosomal location of DNA fragment showing tight linkage with *bk3* in corn: a) PCR amplification using oat-maize addition lines DNA; b) Southern blot of PCR products.

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Yield of waxy and high quality protein maize hybrids developed in Argentina

--Corcuera,VR, Naranjo,CA

It is commonly believed that waxy maize hybrids, as well as quality protein ones, yield less than their normal counterparts. This premise is set upon the lower density of their starch, soft endosperm, and consequently lower grain weight. During 1990, a maize breeding program aimed at obtaining waxy maize hybrids, as well as quality protein ones, in Argentina, was initiated at the Instituto Fitotécnico de Santa Catalina in Llavallol. Since then, several inbreds have been developed and tested. Crosses among the best inbreds were done, and finally during the growing season 2001/02, numerous single-cross hybrids were first tested at this location, situated at 35°S and 58°W. The hybrids tested can be classified into three categories: waxy hybrids, quality protein hybrids and double recessives combining modified starch with quality protein. The single-crosses, as well as their parental inbreds, were arranged in a 3 replicate complete randomised block design field trial. Each plot consisted of a single row of 5.5 m, sown at a density of 71,500 plants/ha (see Figures 1 and 2). At maturity, each plot was hand harvested, and many ear and kernel traits were

Fig.1:Field trial

Fig. 2: Field Trial

Fig. 3: Waxy ear

Fig .4 :Waxy Hybrid

Fig. 5: QPMH

Waxy and Quality Protein Hybrids. Left: 2001/02 field trial. Upper right: original waxy inbred. Center: waxy hybrid. Bottom right: quality protein maize hybrid.

measured. Some of these traits are summarized in Tables 1, 2 and 3 according to the type of hybrid. Potential yield was calculated as the product of ears/plant x grams of kernels/ear x plants/ha. Yields ranged from 8.9 to 20.9 tons/ha, 1000-kernel-weights varied from 200 to 350 grams, and 91 to 171 grams of kernels/ear were obtained (see Figures 3 to 5). Generally, lower yields are consistent with lower 1000-kernel-weights, smaller ears and/or a lower number of ears/plant. Thus, the yield of individual plants is an important factor to be considered, and comes not only from specific ear traits, but also from prolificity. It must be said that the parental inbreds used to develop these single-cross hybrids were selected among other traits because of their high prolificity. New trials at multiple locations must be made to verify the surprisingly good preliminary results obtained. By breeding, high yielding parentals may be selected, and choosing the most appropriate single-crosses among them will make it possible to develop high yielding modified starch or quality protein maize hybrids adapted to our growing conditions.

Table 1. Waxy maize hybrids.

Hybrid No	Number of rows	Kernels/row	1000-kernel-weight	Grams of kernels/ear	No. Ears/Plant	Potential Yield(1)
3123	16	34	300.0 grams	102.1	"1.7"	12.0
3166	16	17	330.0 grams	134.7	"1.7"	16.0
3167	14	27	310.0 grams	107.0	"2.0"	14.1
3168	14	36	350.0 grams	149.1	"1.9"	18.4
3170	16	33	350.0 grams	147.1	"1.6"	15.8
3172	12	38	340.0 grams	146.8	"1.5"	15.2
3173	14	31	310.0 grams	131.3	"1.6"	14.1
3175	18	33	265.0 grams	136.3	"1.8"	15.9
3176	16	34	340.0 grams	170.2	"1.8"	20.9
3177	16	30	270.0 grams	113.8	"1.5"	11.7
3178	disordered	disordered	380.0 grams	90.2	"2.0"	12.5
3179	15	36	210.0 grams	81.8	"1.7"	9.0
3180	16	36	310.0 grams	125.9	"1.5"	12.4
3182	14	31	310.0 grams	119.6	"1.2"	9.4
3184	14	36	320.0 grams	159.2	"1.5"	15.5
3185	16	36	320.0 grams	146.2	"1.7"	16.6
3186	16	31	290.0 grams	140.4	"1.6"	14.8
3187a	16	33	330.0 grams	130.9	"1.7"	13.7
3187b	16	35	350.0 grams	134.3	"1.7"	16.2
3190	16	30	270.0 grams	118.4	"1.3"	10.0
3192	16	33	330.0 grams	171.0	"1.3"	14.1
3196	14	37	320.0 grams	132.4	"1.2"	10.7
3197	16	30	310.0 grams	121.8	"1.5"	12.1

(1) Tons/hectare corrected at 15% moisture content in kernels.

Table 2. High quality protein maize hybrids.

Hybrid No.	Number or rows	Kernels/ row	1000-kernel-weight	Grams of kernels/ear	No. Ears/Plant	Potential Yield(1)
3126	18	32	230.0 grams	119.2	"1.3"	10.8
3145	14	28	290.0 grams	96.1	"2.0"	14.9
3146	14	32	290.0 grams	129.3	"2.0"	18.4
3147	16	27	250.0 grams	91.3	"1.4"	8.9
3148	16	32	260.0 grams	127.6	"1.6"	13.8
3150	14	28	200.0 grams	99.0	"1.7"	10.6
3151	14	31	280.0 grams	120.5	"1.6"	13.0

(1) Tons/hectare corrected at 15% moisture content in kernels.

Table 3: Modified starch and quality protein (double recessives) maize hybrids.

Hybrid No.	Number of rows	Kernels/ row	1000-kernel-weight	Grams of kernels/ear	No. Ears/plant	Potential Yield(1)
3159	14	35	280.0 grams	129.5	"2.0"	17.1
3160	14	36	345.0 grams	115.3	"1.9"	14.7
3161	16	33	280.0 grams	140.3	"1.7"	16.4
3163	14	36	300.0 grams	140.1	"1.7"	16.4
3164	18	31	330.0 grams	162.0	"1.3"	13.8
3165	16	32	280.0 grams	135.7	"1.1"	9.9
3198	14	27	340.0 grams	111.4	"1.3"	10.0
3199	14	35	340.0 grams	145.0	"1.7"	18.8

(1) Tons/hectare corrected at 15% moisture content in kernels.

Phytosanitary behaviour of waxy and high quality protein maize hybrids developed in Argentina

--Corcuera, VR, Naranjo, CA

The phytosanitary behaviour to Maize Common Leaf Rust (*Puccinia sorghi* Schw.) and Ear Smut (*Ustilago maydis* DC Corda) of several waxy, high quality protein and double recessive hybrids evaluated during the growing season 2001/02 are summarized in Tables 1 to 3. The trial was sown in Llavallol (35° S, 58° W) according to a 3 replicate complete randomized block design. The response to the attack of *Ustilago maydis* under field conditions was evaluated through % *frequency* of galls in the leaves (A), galls in the ears (B) and male flowers in the ear apex (C). Response to *Puccinia sorghi* was measured through 1) % *frequency* of weak plants, 2) attack *severity* or % of leaf area with pustules (based on the visual scale developed by Peterson et al., 1948 for Wheat Orange Rust) and 3) type or *degree* of infection based on a modification of Cobb´s scale as follows:

No. Pustules/leaf	Severity %	Degree of Infection	Response to Pathogen
< 11	< 5	I	VERY RESISTANT
12 to 19	6 to 10	II	RESISTANT
20 to 38	11 to 25	III	MID-RESISTANT
39 to 67	26 to 40	IV	MID-SUSCEPTIBLE
68 to 83	41 to 65	V	SUSCEPTIBLE
> 84	66 to 100	VI	VERY SUSCEPTIBLE

Table 2. Phytosanitary behaviour of high quality protein maize hybrids

	Frequency%			Maize Common Rust		
Hybrid No.	(A)	(B)	(C)	Frequency%	Degree	Severity %
3126	0	0	0	100	II-III	6 to 25
3145	0	6.7	0	100	I-III	< 5 to 25
3146	0	0	0	26.7	I-III	< 5 to 25
3147	0	0	0	100	I-III	< 5 to 25
3148	0	0	0	66.7	I-III	< 5 to 25
3150	0	0	0	80	I-III	< 5 to 25
3151	0	6.7	0	100	III-V	11 to 65

Table 3. Phytosanitary behaviour of double recessive maize hybrids.

	Frequency %			Maize Common Rust		
Hybrid No.	(A)	(B)	(C)	Frequency %	Degree	Severity %
3159	0	0	0	0	0	0
3160	0	0	0	86.7	I-III	< 5 to 25
3161	0	0	0	53.4	II-III	6 to 25
3163	0	6.7	0	86.7	II-IV	6 to 40
3164	0	0	0	33.4	II	6 to 10
3165	13.4	0	0	0	0	0
3198	0	11.2	0	11.2	I	< 5
3199	0	0	0	77.8	II-VI	6 to 100

Measurements in the field were taken over 30 days after anthesis, and 3 leaves/plant (those of the upper ear and one leaf up and down) were considered to evaluate response to Leaf Common Rust under natural field conditions. The data shown in the Tables let us conclude that eleven hybrids were VERY RESISTANT to *P. sorghi*, as no symptoms were detected in any plant. All of these 11 hybrids include at least one parental also classified as resistant to the pathogen in previous years, and in some of them the Oh43 genetic background was included during inbreeding and ear-to-row selection process. On the other hand, nine hybrids behaved as SUSCEPTIBLE or VERY SUSCEPTIBLE to *P. sorghi*. Twenty-three hybrids were VERY RESISTANT to *U. maydis*, as no symptoms were detected in the plants under field conditions. These single-crosses were developed using at least one of the eleven inbreds reported as resistant to ear smut in previous is-

sues. Nevertheless, more than 13% of the plants of the hybrids 3185, 3186 and 3197 showed symptoms and exceed the historic value of 13% historically registered at the Experimental Station. Seven hybrids were VERY RESISTANT both to *P. sorghi* and *U. maydis*, and their potential yield exceeds 10 tons/ha, yielding up to 18.4 tons/ha. In the case of Maize Leaf Common Rust, the lineal regression coefficient (byx) for yield over degree of infection was calculated.The value was negative for all hybrids: -0.20 for waxy hybrids, -0.29 for high quality protein hybrids, and -0.46 for modified starch and high quality protein (*double recessive*) hybrids. According to the values found for byx, yields decrease in average 200 to 460 kg/ha for each grade of infection. Considering an average yield of 1.7 tons/ha for all hybrids evaluated, it can be stated that yield decreases caused by attack of *P. sorghi* may range from 1.6% to 3.6% for each grade of infection. This means that a hybrid showing an infection grade III (25% of foliage wounded) may yield 5 to 11% less than if no infection were present. Although new multilocation trials must be run to complete the evaluation of the performance of these hybrids, the preliminary results obtained during 2001/02 are really very promising.

GISH affinities between subspecies of *Zea mays*

--Gonzalez, G*, Confalonieri, V*, Comas, C*, Naranjo, CA, Poggio, L*
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Zea mays (L.) is composed of four subspecies (Doebley, Maydica 35:143-150, 1990): *Zea mays* ssp. *mays* (maize), *Zea mays* ssp. *mexicana*, *Zea mays* ssp. *parviglumis* and *Zea mays* ssp. *huehuetenanguensis*. The last two taxa have a disjunct geographic distribution (Doebley and Iltis, Amer. J. Bot 67:982-993, 1980; Iltis and Doebley, Amer. J. Bot 67 (6):994-1004, 1980), and were considered as varieties of *Zea mays* ssp. *parviglumis* until 1990, when Doebley separated them as subspecies.

Isoenzymatic and molecular marker studies (Doebley et al., Econ. Bot. 42:120-131, 1989; Hilton and Gaut, Genetics 150:863-872, 1998; Matsuoka et al., Proc. Natl. Acad. Sci. USA, 99 (9):6080-6084, 2002) showed that *Zea mays* ssp. *mays* would have more affinity with the annual teosinte *Zea mays* ssp. *parviglumis*. Nevertheless, in a previous study (Gonzalez et al., MNL 75:36, 2001) we demonstrated that there are divergent chromosome regions between these two taxa, by means of GISH (Genomic In Situ Hybridization) experiments on chromosome preparations of *Zea mays* ssp. *parviglumis*.. The present work intends to further investigate the genomic homology between *Zea mays* ssp. *mays* (native race of Argentina, cult. 6484, Instituto Fitotécnico Santa Catalina - IFSC) and two of the other subspecies: *Zea mays* ssp. *parviglumis* (Balsas, cult. 6836, IFSC, provided by CIMMYT) and *Zea mays* ssp. *huehuetenanguensis* (cultivated at IFSC, provided by CIMMYT). The study was performed by means of GISH, without applying a blocking procedure, and using chromosomes of *Zea mays* ssp. *mays* as the target of hybridization.

Chromosome preparations and GISH were carried out according to Poggio et al. (Genome 42:993-1000, 1999).

When maize chromosomes were hybridized with labelled genomic DNA from *Zea mays* ssp. *parviglumis*, we observed hybridization signals of variable intensities throughout all of the chromosomes, with the exception of the centromeric and nucleolar organizer regions, where the hybridization is weak or absent, indicating that these are zones of less homology between both taxa. Then, when genomic DNA of *Zea mays* ssp. *huehuetenanguensis* was used as a probe on maize chromosomes, we observed that in addition to the absence of hybridization signals in the centromeric and nucleolar organizer regions, many other chromosome regions were unlabelled. In fact, at least 3 chromosomal pairs display similar patterns of hybridization, showing one chromosome arm highly labelled and the other one unlabelled or weakly hybridized. These results indicate an important divergence between both subspecies.

We conclude that a greater general homology is evident between maize and *Zea mays* ssp. *parviglumis* than with the other subspecies analyzed. These results are in agreement with previous molecular studies that propose *Zea mays* ssp. *parviglumis* as the closest related taxa of maize, although they do not corroborate the ancestor–descendant relationship proposed by some authors cited above. On the other hand, the degree of divergence observed gives further support to the last subdivision of the *Zea mays* species made by Doebley (1990).

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Selection of popcorn hybrids as an alternative crop in a non-traditional maize production region in Argentina

--Burak, R, Broccoli, AM

Fourteen hybrids of popcorn were tested in 5 locations of the non-traditional maize production region known as “Cuenca del Salado”, Buenos Aires (Argentina), during two years (1998 and 1999). The objective was to select those of better grain yield and expansion capacity to be incorporated as an alternative product for the region. Kang´s methodology was applied to select simultaneously for yield, expansion capacity, and stability across environments. Combining both characteristics, hybrids C2 and C3 were the recommended genotypes for this region.

Popcorn belongs to the botanical species *Zea mays ssp. mays* L.. There are several hypotheses described for its origin and evolution. Erwin (1949) suggests that popcorn recently originated as a mutation within the flint maize type, but this proposal was critiziced in view of archeologic evidence. Another author quoted by Mangelsdorsf (1974) suggests that popcorn originated from hybridization between the *Euchlaena* and *Zea* genera, due to the fact that crossbreeding the two results in an ear with sharp, small and hard kernels. Additionally, it was observed that “teosinte” may explode like “popcorn”.

Popcorn was classified into two primary types of kernels: pearled and riced. Pearled kernels have a slight crown and riced are sharp. Both types are hard and small, and the endosperm contains a reduced proportion of farinaceous starch, because most of the starch-producing cells only produce corneous starch and a little farinaceous starch around the embryo.

Expansion capability, defined as expanded volume of 1 g. of grain, is the most important trait for selection in popcorn, because an enhanced expansion is associated with increased palatability. Another important factor is grain yield and type of grain (there

are little white, little yellow and big yellow kernels; each type may be preferred more than the others). For quantifying grain size, the number of grains in 10 g. must be considered (large type has 52-67 grains, medium 58-75 and little 76-105). Paired maturity of crop also must be considered, because this has a big influence on expansion capability.

The problem situation focused on by plant breeding scientists is in breaking the negative correlation that exists between traits of cultivation interest and expansion volume, for getting a product which can satisfy producers' and consumers' demands simultaneously. Farmers desire one genotype with large yield, stability, disease resistance and increased expansion capability. Consumers demand tender, soft, tasty popcorn flakes, with an attractive color and without pericarp.

The aim of this work was to analyze this quest, in order to identify cultivars with the highest grain yield and increased expansion capability, resulting in recomendations to "Cuenca del Río Salado" (Buenos Aires Province, Argentina) farmers.

Trials were carried out in a region of Buenos Aires Province known as "Cuenca del Río Salado", where dairy farming is the major activity. It is located at 34 degrees, 38 minutes of South latitude and 58 degrees, 48 minutes of West longitude, and topographically is 23 m. above sea level. This region has heterogeneous soils and for trials parcels classified as Molisols were used, with a molic epipedon of 27 cm. of depth, 4.5% of organic matter and use of the soil capability types I and II.

Fourteen cultivars were sown (simple hybrids), named C1 to C14, in 5 locations, during 2 years (1998 and 1999). A statistical design was used of randomized complete blocks with a factorial arrangement: 14 treatments x 3 replications x 10 environments, according to the following model:

$$Y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha \times \beta)_{ij} + \rho_{k(j)} + \varepsilon_{ijk}$$

Where :

Y_{ijk} = Observation corresponding to i treatment in j environment of k replication

μ = General mean of evaluated trait

α_i = Fixed effect of i genotype

β_j = Random effect of j environment

$(\alpha \times \beta)_{ij}$ = G x E interaction effect

$\rho_{k(j)}$ = Replications nested within environmental effect

ε_{ijk} = Random variable corresponding to experimental error

The experimental unit consisted of 2 furrows of 5 cm of longitude with a distance between rows of 0.70 m.

Evaluated variables were:

YIELD: Grain yield (kg.) / experimental unit

EXVOL: Expansion volume (cc/g)

For selection of cultivars the method of Kang was applied (Agron. J. 85:754-757, 1993), who defines a stability-yield statistic Y_{si} that considers type II error for both components, yield and stability. The stability component of Y_{si} is substantiated in stability variance by Shukla σ_i^2 (Heredity 29:237-245, 1972) and variation statistics by Lin and Binns (Can J. Plant. Sci. 68:193-198, 1988), that is a relative dependent measurement of genotypes included in the work and shows the contribution of a genotype to G x E interaction, which is assumed to all genotypes included in this experiment.

Results of the combined analysis are presented in Table 1, where significant effects for environments and genotypes are observed for the EXVOL variable, without detecting significant effects in G x E interaction; by contrast, for the YIELD variable, this interaction was significant.

Table 1. Mean squares from the combined anova for EXVOL and YIELD.

	Environment (E)	Genotype (G)	Interaction (G * E)	Heterogeneity	Residual	Pooled error
DF#	93	13	117	13	104	260
EXVOL	479.2**	25.3**	8.19 ns	8.48 ns	8.15 ns	7.92
YIELD	93.4**	0.82**	0.19**	0.21 ns	0.18**	0.098

#Degrees of freedom.

**p< 0.01; *p<0.05; ns: non-significant.

Table 2 shows mean values of genotypes in all environments, Shukla´s variance of stability and selection index. The selection index for the EXVOL variable, will be based only in mean values ranking, because G x E interaction and therefore stability variances, are not significant.

Genotype C5 recorded the highest index (Y_{si} = 16), followed by C2 (Y_{si} = 14), C9 (Y_{si} = 13), C3 (Y_{si} = 12), and C11 (Y_{si} = 11).For the YIELD variable, genotypes which made the major contribution to G x E interaction sum of squares were observed. They are the most non-stable genotypes: C1 (σ^2_i = 0,44), C6 (σ^2_i = 0.41), C5 (σ^2_i = 0.29), then, with minor values C9 (σ^2_i = 0.23) and C10 (σ^2_i = 0.22). The highest selection index resulted from C7 (Y_{si} = 15), followed by C3 (Y_{si} = 14), C10 (Y_{si} = 12), C2 (Y_{si} = 11) and C13 (Y_{si} = 9).

This work allows us to establish which are the genotypes with the most promise, considering the ecological conditions of the region studied. If yield, as weight variable, is preferred, the best genotype is C7; if stability is preferred, C3· and C13 are the best genotypes; for both factors, C3 is the best genotype. For selecting by yield and expansion volume simultaneously, the highest index corresponding to both variables must be combined. In this case, C2 and C3 were selected. The C5 genotype showed high expansion capability, low yield and low adaptability. This phenomenon

Table 2. Stability statistics corresponding to the two variables studied.

Gen	EXVOL			YIELD			Gen	EXVOL			YIELD		
	μ_i	σ^2_i	Y_{si}	μ_i	σ^2_i	Y_{si}		μ_i	σ^2_i	Y_{si}	μ_i	σ^2_i	Y_{si}
C1	25.33	3.38	3	2.67	0.44**	5	C8	25.44	6.56	4	2.44	0.13	4
C2	26.77	8.87	14+	2.65	0.11	11+	C9	26.73	10.45	13+	2.57	0.23*	6
C3	26.57	7.23	12+	2.69	0.065	14+	C10	25.48	3.56	5	2.78	0.22*	12+
C4	24.04	5.36	-1	2.44	0.12	3	C11	26.07	8.16	11+	2.46	0.11	5
C5	27.07	11.47	16+	2.25	0.29**	-10	C12	25.62	14.38	4	2.26	0.14	-1
C6	25.10	10.13	2	2.49	0.41**	-2	C13	24.11	4.86	0	2.55	0.063	9+
C7	25.88	13.19	7	2.74	0.12	15+	C14	25.92	7.05	10	2.40	0.19*	-2

** p< 0.01; * p<0.05; Gen= genotype; μ_i = general mean of each genotype; σ^2_i = stability variance by Shukla; Y_{si} = selection index by Kang; + = selected genotypes.

may be explained by the negative correlation that exists between yield vs. expansion volume, according to reports in most papers on popcorn.

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Identification of glucosidase-transferase enzyme in developing maize endosperms that affects starch synthesis in the *glt1* mutant

--Pan, D

We report the identification of an enzyme in developing maize endosperms that has both alpha-1,6-glucosidase and transferase activities. The transferase transfers oligosaccharides forming largely alpha-1,4-glucan bonds, although we cannot exclude the possibility that some alpha-1,6 linkages are formed. The spectrum of the amylopectin component of *glt1* starch following reaction with an I2, KI stain has its absorption peak displaced from that of glt1 amylopectin, while the spectra of the amylose components are identical. This result indicates that glucosidase-transferase function is likely linked to the amylopectin synthesis pathway rather than the amylose pathway. The Brabender amylograms reveal that the starch produced by mutant endosperms differs markedly from that produced by nonmutant endosperms. The enzyme is coded by the nonmutant alleles of a gene on the short arm of chromosome 4 that we are designating *glucosidase-transferase1* (*glt1).* The homozygous mutant seeds (*glt1*/*glt1*) have deeply dimpled crowns, somewhat shrunken, and are easily distinguished from their nonmutant sibs segregating on the same ear (Fig. 1). The mutant seed weight, on average, is only 81% as much as the nonmutant. The catalytic activities of this enzyme are reminiscent to some extent of the glycogen debranching enzyme from rabbit muscle investigated by Brown. The purest preparation of that enzyme retained both glucosidase and transferase activities, and it is concluded that both activities were the properties of a single protein. The molecular weight of the maize enzyme is about 89,000 on SDS electrophoresis gel. The observations that starch production is reduced in mutant seeds and the amylopectin component is altered indicate a role in starch synthesis for this enzyme in maize. The relationship of the number of nonmutant alleles per endosperm to enzyme activity was investigated in a gene dosage series (zero to three nonmutant alleles/endosperm) made by selfing the *glt1/glt1* and *Glt1/Glt1* stocks and also crossing them reciprocally. The endosperms from each genotype were assayed for alpha-1,6-glucosidase activity using partially purified enzyme preparations (20 to 50% ammonium sulfate fraction). Fig. 2 shows the results expressed as nmol maltose released per endosperm over a 100 min incubation period. Such a linear relationship between enzyme activity and gene dosage would be expected if the Glt1 alleles encoded the enzyme, although it does not constitute definitive evidence of such a relationship. A bifunctional enzyme of this type has been investigated in rabbit muscle where it was presumed to be involved in the catabolism of glycogen. The maize enzyme can be shown to differ in some specifics from the mammalian enzyme although it also is an indirect debranching enzyme as classified by Lee and Whelan since it does not attack long glucose chains originating at an alpha-1,6-branch point. The enzyme in maize evidently has a role in starch synthesis in the developing endosperm as shown by the reduction in starch content of

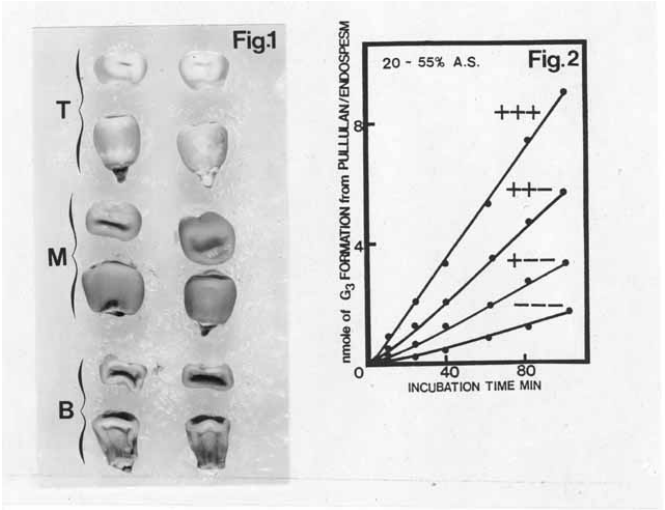

Fig. 1. Phenotypes of Glt_1 nonmutant and glt_1 mutant seeds.
Top two rows: Top and side view of Glt_1–W22N seeds.
Middle two rows: Top and side view of glt_1-(W22N) seeds.
Bottom two rows: Top and side view of glt_1–9101 (W22N) seeds.

Fig. 2. The digestion over time of pullulan by partially purified enzyme preparations (through ammonium sulfate precipitation) from endosperms representative of the gene copy number series from homozygous nonmutant (+/+/+) endosperms to homozygous mutant (-/-/-) endosperms

mutant endosperms, as well as alteration of amylopectin component. Thus, it is therefore suggested that four enzymes: branching enzyme (Ae), isoamylase/debranching enzyme (Su1), and alpha-1,4-glucosidase-transferase (Glt1) together play an important role for the modification of starch structure/synthesis during the development of maize endosperms.

Defect of phosphofructose kinase activity in a *sugary2* mutant

--Pan, D

Several genes are known in maize which affect the quality and quantity of various carbohydrates found in the endoperms. The *su2* mutant was originally described by Eyster in 1943, and the starch extracted from endosperms of this mutant is 10 to 15% higher in apparent amylose than in normal endosperms. Although the starch compositions of the *su2* mutant are altered, purified *su2* amylopectin and amylose have properties similar to those of normal amylose and amylopectin, suggesting that the direct mechanism of polyoligosaccharide synthesis is probably not altered, but likely the pathway relevant to the starch synthesis pathway has been regulated. In this report we would like to demonstrate that the biochemical lesion of *su2* is likely due to the defect of phosphofructose kinase (PFK) enzyme activity (Fruc-6-P + ATP Fruc-1,6-bisphosphate + ADP). Table 1 shows the PFK activity of enzyme preparations obtained from nonmutant and mutant maize endosperms at 23 DAP.

Protein precipitate between 20% and 45% $(NH_4)_2SO_4$ satu-

Table 1.

Genotypes	Phosphofructose Kinase Activity umole/mg/min
Su2Su2Su2	0.172
Su2Su2su2	0.142
Su2su2su2	0.119
su2su2su2	0.063

ration was applied onto DEAE-Cellulose column. After washing the column with 50 mM Tris-HCl buffer, pH 7.0; the enzyme was eluted with 0.15 M KCl in 50 mM Tris-HCl buffer. The fractions containing enzyme activity were pooled and collected by 60% $(NH_4)_2SO_4$ precipitation. After dialysis, the enzyme preparation was assayed for PFK activity.

The results in Table 1 demonstrate the proportionality of the PFK activity with the copy number of the *Su2* gene, suggesting that the *su2* locus could be a structural gene for the fructose-1,6-bisphosphate kinase enzyme. If the mutation of *su2* is the result of the defect of PFK activity, one might expect that there will be an alteration of the metabolites accumulated in the amyloplast of the *su2* mutant as compared to the nonmutant. The study of the distribution of metabolites in the amyloplast isolated by a nonaqueous technique was therefore carried out. As expected, the results in Table 2 show a lower activity of PFK activity in the *su2* mutant, causing the reduction of fruc-1,6-bisphosphate synthesis, and therefore a reduction of 3,P-glyceraldehyde. As a result, the accumulations of glucose-6-phosphate and fructose-6-phosphate are increased in the mutant amyloplast. Based on these results, we consider that the gene encoding PFK activity had been affected in the *su2* mutant. However, we do not rule out the possibility that other protein components in *su2* have also been modified as a result of mutation, since quite often in maize, mutants with aberrant starch synthesis are usually linked to multiple defects on biochemical pathways linked to the synthesis of polysaccharides. Details of this study have been submitted for publication elsewhere.

Table 2. Levels of soluble fructose-1,6-bisphosphate, glucose-6-phosphate, fructose-6-phosphate and 3,P-glyceraldehyde in *su2* mutant and nonmutant amyloplasts isolated by a nonaqueous technique.

Metabolites	Nonmutant	*su2* Mutant
	nano mole/gram of endosperms (wet weight)	
Fructose-1,6-bisphosphate	23.00	7.68
Glucose-6-phosphate	960.00	1790.00
Fructose-6-phosphate	450.00	750.00
3-P-Glyceraldehyde	77.00	20.00

Which loci in kernel-spotting collection *R-r:Venezuela 594* are unstable?

--Kermicle, J

Venezuelan accession 594 PI302363 is polymorphic for colorless, pale, spotted and full-color kernels. Recurrent backcrosses with a *r-g* tester (W22 background) of the spotted class produce progenies with the nominal ratio of 1/2 colorless: 1/4 pale: 1/4 spotted. Tested similarly the pale class produces 1/2 colorless: 1/2 pale. This pattern of inheritance constitutes prima facie evidence for an *r*-mutable allele whose instability depends on an independently assorting factor.

Inheritance of the full-color kernels in this collection suggests an alternative interpretation. Crossed recurrently with *r-g* the full-color class produces 1/2 colorless: 1/4 pale: 1/4 full color. Testcross progeny of the pale class again are 1/2 colorless: 1/2 pale. Thus an independently assorting amplifier of *r* action is responsible for full color. Were such an amplifier unstable, its action on a responsive but stable hypomorphic *r* allele would give the same pattern of inheritance described in the preceding paragraph.

Germinal revertants were sought to help distinguish between the two categories of interpretation. The question posed is whether revertants would segregate as alleles of *r* or of an unlinked amplifier locus.

Full-color revertants proved uncommon. Five were established among 102,700 testcross progeny of a true-breeding spotted strain. Serial backcrosses of full color with *r-g* produced 1/2 colorless: 1/4 pale: 1/4 full color. When tested similarly, the pale segregants produced 1/2 colorless: 1/2 pale, as before. When pollinated with an *r-g* strain carrying the unstable amplifier (provisionally *arv-m*) the pale class was replaced by spotted. Hence the revertant class behaved as the polymorphic full-color class present in the original collection. This outcome is consistent with germinal reversion occurring not at *r* but at the unstable amplifier locus.

One revertant (NI-5874) was tested for allelism with the unstable amplifier by pollinating their F1 with stable, pale *R-r:Ven594*. The resulting kernels were all either dark or spotted, none light pale, the class expected had there been recombination between the revertant and *arv-m*.

Not all hypomorphic *r* alleles respond to *arv-m*. When the *r-g arv-m* stock was pollinated with *R-g:8 pale* -- a second-generation mutation of *R-r:standard* -- light pale kernels lacking spots resulted, similarly with the *Ds* insertion mutant *r-sc:m1*. In contrast, parallel crosses using the pale segregants of Venezuelan accession 694#16037 produced spotted aleurone superimposed on pale. Thus like certain other modifiers of kernel coloration, the effect of *arv-m* is *r*-allele specific.

To what class of instabilities does *arv-m* belong? Standard *Ac* is excluded since *arv-m* did not activate *r-sc:m1*. Similarly, the F2 of crosses between *r-g arv-m* and the *Spm*/*En*-dependent *bz1-m13* reporter allele did not include a spotted class. However, pollination of *r-g arv-m* with *R-spotted dilute 2* did give a positive result. The *R-sd2* stock used included the *Dilute* factor but not autonomous activator *Spf* of that system (Sastry and Kurmi, Newsletter 44:101, 1970). Again, this outcome can be interpreted in either of two ways. Perhaps *arv-m* activates an element in *R-sd2* to transpose or otherwise change. Alternatively, response occurs by means not involving DNA-level alteration at *R-sd2*. Germinal revertants have not been obtained from this combination and tests for reciprocal activation, i.e. *R-r:Ven.594* response to *Spf*, have yet to be made.

R-sd2 is known to respond to the *Fcu* element characterized in a Colombian strain (Gonella and Peterson, MGG 167:29, 1978). Thus the *R-r:Ven* + *arv-m* system may be related to *r-cu* + *Fcu*. Both derive from northern South America and their spotting and stable pale phenotypes appear similar, as does their two-factor pattern of inheritance.

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Wind-stress induces the initiation of crown roots

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We have discovered that wind load on plants induces the initiation of crown roots. A total of 32 plants (Ohio 43 inbred,

two plants per 12 inch pot) were used in this study. Eighteen plants were grown under strictly no air movement conditions, while the other 18 were grown under a constant wind of 9 km/hr (day and night). Two box-fans were used to generate air movement in a growth chamber; pots were rotated every day to simulate changes in wind direction. Plants were grown under 16/8 hours day/night scheme with a high-low temperature of 27/20C, and RH was set at approx 50%. Lighting was provided by a combination of fluorescent lights, high pressure Na and metal halide arc lamps, resulting in an intensity of 1500 foot-candle at the pot level. The results show that the Ohio 43 inbred grew two rows (Figure 1a, 1 and 2) of crown roots from the soil level under no wind conditions, while the wind-blown plants initiated an additional row (Figure 1b, 3) of crown roots at a higher node. Our results suggest that the initiation of crown roots is influenced by the bending stress of the stem resulting from wind load. As indicated by our earlier stem model (Cheng, WY et al., MGCNL 76:27-28, 2002), the maize stem can be described as a "foam stick," a reinforced outer shell, with a spongy interior. The peripheral region can be considered as the steel reinforcing bars and cylinder, and the interconnecting nodal networks (Cheng, WY et al., MGCNL 76:28-29, 2002) are the steel bracings ("rebar") found in a concrete pillar. In the early stage of development, the vasculatures act as the tensile element, while the highly turgid parenchyma cells are the compression element in the model. In the later stage when the parenchyma cells become air-filled, developing a "foamy" texture, the highly lignified para-epidermal bundles become the structural element. The binding between individual para-epidermal vascular bundles by lignified sclerenchyma cells is an important structural development. This binding transforms those loosely parallel arranged vascular bundles into a solid cylindrical structure. Bending of the stem exerts tensile stress in the nodal elements ("rebar"), which may be responsible for orientating the cell division for the initiation of crown roots.

This work was supported by undergraduate scholarships from the Microscopy Society of America and SPIE to WYC.

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SCAR marker creation for maize somaclones using some specific RAPD and ISSR fragments

--Osipova, ES, Trotskij, AV, Dolgikh, Yul, Shamina, ZB, Gostimskij, SA

Two groups of somaclones were obtained from callus of maize inbred A188 in a different series of experiments after two and eight months' subculturing. The regenerants of the first group (families R11, R14, R27 and R54) diverged from initial plants in a number of quantitative traits such as: height, size and number of branches of the tassel, and the number of kernel rows in the ear. Besides the alteration of some quantitative traits, somaclones of the second group (families R105, R106, R107 and R119) diverged from the initial A188 line in flowering time, kernel color and their ability to form embryogenic callus in an in vitro culture. The inheritance of the somaclonal variations revealed was followed through R1-R4 generations.

The deviations of the somaclones from the initial line A188 at the molecular level have been determined by RAPD analysis (Osipova et al., MNL 74:52, 2000). The main objective of this investigation was to reveal some unique RAPD- and ISSR-fragments specific both for every group of somaclones and for individual regenerants, and to transform these fragments into SCAR markers (Sequence Characterized Amplified Region). To extend a choice of the specific markers, 28 RAPD and 10 ISSR primers were synthesized. Some polymorphism was found using 14 RAPD and 6 ISSR primers. The fragments specific for 1) all the somaclones, 2) individual somaclones, 3) each of the regenerant groups, were revealed among the products of amplification.

To quantify RAPD and ISSR polymorphism, the data obtained were constructed as a matrix of the binary character states. There the presence or absence of amplified fragments of a certain size in RAPD and ISSR patterns was considered as state 1 or 0 respectively. Index 1 was conferred to the amplified fragments revealing with high intensity and steadily repeating in all the experiments. Jacquard coefficient was used to calculate the matrices of differences based on the matrix of states. The difference between the somaclones and their initial line varied from 6.5 to 23%. The diversity among plants of the second group (R105-R119) was 5-12%, whereas the plant deviation from each other was only 2-6% in the first group (R11-R54).

Based on the matrix of differences, a dendrogram was constructed by the neighbor-joining method (Fig. 1). This dendrogram reflected the diversity between the RAPD and ISSR patterns of nine subjects studied with the usage of 24 primers with respect to 161 binary traits comprising presence or absence of the amplified fragments. The initial line A188 was used as a root in the dendrogram.

Two somaclone clusters could be marked in the constructed dendrogram. One of them was quite similar to the first group of

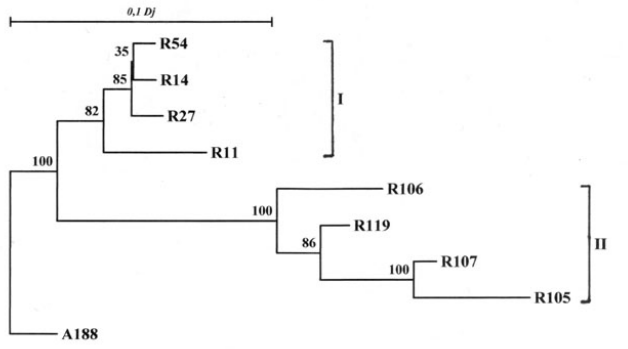

Figure 1. Dendrogram based on the genetic differences between the initial A188 line and A188-derived somaclones constructed using the NJ method.
Dj- Jacquard distance, I and II – two clusters of somaclones.

regenerants and involved families R11, R14, R27 and R54. The other cluster involved lines R105, R106, R107 and R119 forming the second group. Somaclones R105-R119 were more distant both from the initial line and from each other. The results obtained completely corresponded to the morphological data, according to which, the second group of somaclones, regenerated after the longer-term subculturing, displayed the greater range of variation. This fact confirmed the assumption that accumulating mutations had resulted from the lengthening of subculturing. Thus, the investigation carried out using the random primers resulted in revealing somaclonal deviations both from each other and from the initial line. Also, some somaclone specific fragments were found. These fragments' specificity was examined in 4-8 individual R1 plants for every somaclone.

Six polymorphic amplified fragments, five RAPD and one ISSR, were used to create SCAR markers. All the regenerants carried a 1050-bp fragment amplifying with the QR-2 primer, which was absent in the A188 line (Fig. 2). The common band for the first somaclone group was found with the M10 primer and for the second group, with the Q-20 primer. Primers OPC-09, NO-15 and Leb-10 revealed some amplified fragments, characteristic for individual somaclones (Table 1).

The specific fragments were cloned in vector pGem-T and their terminal regions were sequenced. Based on the nucleotide

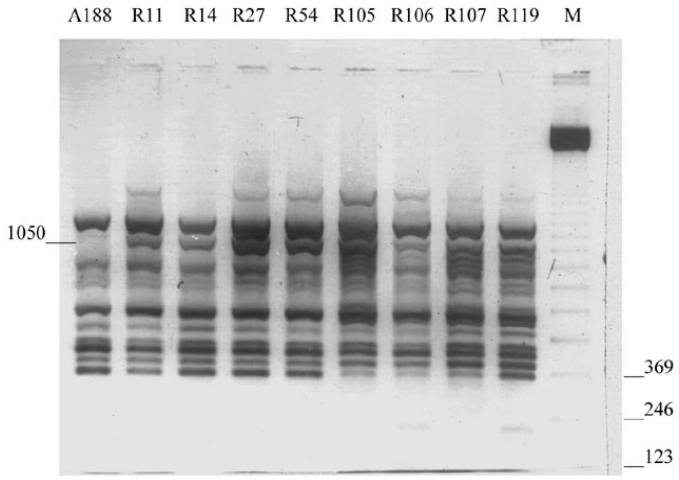

Figure 2. DNA fragments amplifying with RAPD QR-2 primer.
Note: M - marker (123 bp DNA Ladder) "GIBCO BRL"

Table 1. Polymorphic fragments selected for cloning.

Primer	Nucleotide sequence	Total fragment quantity	Polymorphic fragment quantity	Somaclones with polymorphic fragment	Polymorphic fragment size bp
QR-2	CGG-CCA-CTG-T	11	1	All somaclones (R11-R119)	1050
M-10	(CA)6AGG	9	1	First group (R11-R54)	860
Q-20	TCG-CCC-AGT-C	10	1	Second group (R105-R119)	860
OPC-09	CTC-ACC-GTC-C	9	1	188, R106	670
NO-15	CAG-CGA-CTG-T	7	1	R105, R107	420
Leb-10	AGC-CGC-AGC-T	10	1	R105	920

sequence, primer pairs of 20-30 bp in length were selected using the OLIGO computer program and synthesized to obtain SCAR markers. To optimize the conditions of amplification, the annealing temperature for each pair was determined experimentally. Using the SCAR primers obtained we confirmed polymorphism for five of the six fragments (Table 2). Fragment Leb-10 with SCAR primers amplified both in all the somaclones, and in the initial A188 line.

Table 2. SCAR primers, synthesizing polymorphic fragments

Primer	Nucleotide sequence	Somaclones comprising SCAR fragment	Fragment size	Annealing temperature
QR-2	5'-CGG-CCA-CTG-TCT-AGT-GCT-AA-3' 5'-CGG-CCA-CTG-TAC-CTA-GAT-TTT-3'	A188 All somaclones	1300 1050	54/55
M-10	5'-CAA-AAT-CAG-AGC-AAC-AAT-ACG-CAC-ACA-AGT-3' 5'-CAC-ACA-GGT-TCA-CAT-TAA-TAT-AAA-T-3'	First group (R11-R54)	840	54/55
Q-20	5'-TGT-TCC-AAG-AAA-AAG-GAA-TCG-AAC-TGC-TTG-3' 5'-AAC-GGA-TGC-GCT-AAC-GTT-TTC-CTC-TTG-CAG-3'	Second group (R105-R119)	840	56/57
OPC-09	5'-CTC-ACC-GTC-CAA-ATC-AAG-GG-3' 5'-CTC-ACC-GTC-CCA-GTG-CAC-T-3'	188, R106	660	58
NO-15	5'-ACC-TTC-CAT-GAT-TCA-TTC-CAT-TGC-TTC-TAG-3' 5'-ACT-ATT-CTT-ATA-TTT-GAA-ATT-TGA-A-3'	R105, R107	250	54/55
Leb	5'-TGT-ATA-GAC-TCA-TCA-AAA-GCC-TGG-ACC-CAT-3' 5'-CAG-AGT-GGT-CCC-GAT-GCA-TGG-GTC-TCC-GAG-3'	A188 and all somaclones	900	58

The inheritance of six SCAR-fragments was examined in the R2 generation of each somaclone. In some cases, we examined the R3 and R4 generations and, also, F1 and F2 of R27xA188 and R105xA188 hybrids. The dominant inheritance of these fragments was established.

Besides the expected fragment, characteristic only for somaclones in R1, the heavier amplified fragment was revealed in the A188 line by using a pair of SCAR QR-2 primers (Fig. 3). In this case, the deletion probably took place in the genome of the initial line A188 as a result of somaclonal variability. But the final conclusion could only be done after comparing the sequences of these fragments. Investigating F1 hybrids (R27xA188) and (R105xA188) with QR-2-primers, both amplified fragments were found (Fig. 4a). These data supposed co-dominance. The following segregation was found in the F2: 8 plants only comprised a light fragment, 8 plants only comprised a heavier one, and

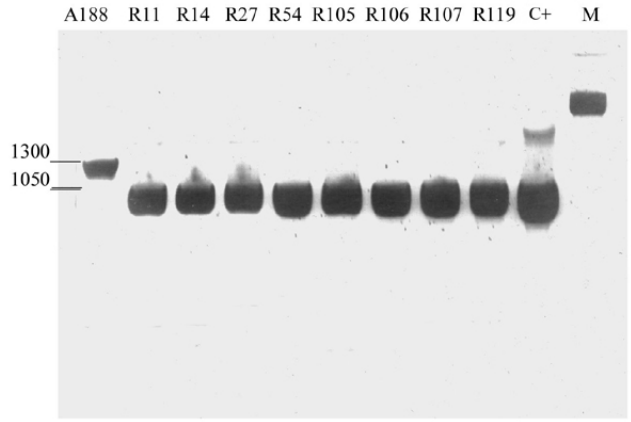

Figure 3. DNA fragments amplifying with SCAR QR-2 primer.
Note: M - marker (123 bp DNA Ladder) "GIBCO BRL"

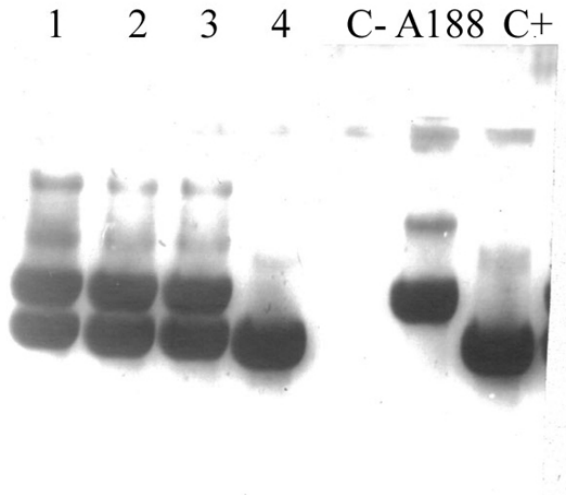

Figure 4a. DNA fragments amplifying with SCAR QR-2 primer in F1 hybrid R105xA188.
Note: 1-4 – individual plants; C- - negative control (instead of DNA-sample, some water was added); C+ - positive control (cloned specific fragment); M - marker (123 bp DNA Ladder) "GIBCO BRL"

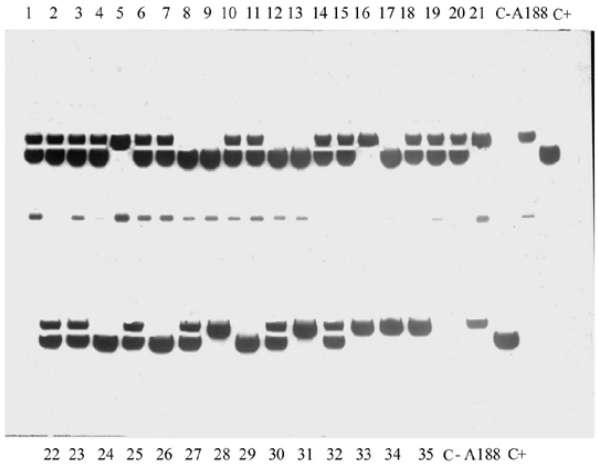

Figure 4b. DNA fragments amplifying with SCAR QR-2 primer in F2 hybrid R105xA188.
Note: 1-35 – individual plants; C- - negative control (instead of DNA, water was added); C+ - positive control (cloned specific fragment); M - marker (123 bp DNA Ladder) "GIBCO BRL"

19 genotypes synthesized both fragments. That result corresponded approximately to a 1:2:1 ratio (Fig. 4b).

Studying SCAR Leb-10 inheritance, it was found that the fragment was present in all plants of line A188 investigated, whereas the segregation and sometimes the loss of this marker were noticed in R1, R2 and F1 somaclones. Thus, although SCAR Leb-10 is not unique for R105, as it had been supposed earlier, it can distinguish all the somaclones from the initial line in accordance with the inheritance pattern.

The segregation in the R1-R4 generations was found for fragments OPC-09, NO-15 and Leb-10. This indicated heterozygosis of the regenerated plants. SCAR Q-20, M-10 and QR-2 fragments were present in all the plants investigated in the R1-R4 and F1 generations. The segregation according to the dominant pattern of inheritance was only determined in the F2. That result is supposed to be due to the homozygous nature of the regenerants.

Thus, the results of this investigation confirmed the genetic nature of the regenerant variability, and also, several molecular markers were produced both for maize line A188 and for all the somaclones, each group of the somaclones and individual genotypes.

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Tripsacum SR5: Shatter Resistance study population

--Blakey, CA[1], Goldman, SL[2], Dewald, CL[3], Frutiger, K[2]

In a collaborative arrangement with Stephen Goldman (PSRC, University of Toledo), and Chet Dewald (USDA-ARS-SPRRS), preliminary steps have been made towards the development of a study in diploid *Tripsacum dactyloides* (2n=2x=36). The new population has been designated as the SR5 population. The population has been involved in a large-scale seed shattering and forage

quality studies currently being conducted by the USDA-ARS-SPRRS, Woodward, OK (Chester Dewald, personal communication). Large tissue samplings of parental and F1, and a set of 240 out of 1250 SR5 F2 individuals, were harvested during the summers of 2000 and 2001. Samplings of tissue were collected from each F2 individual from the same field for two successive years to reduce possibility of sampling error. These F2 samplings provide both a back-up population tissue set for the BSU on-site map population, and a set of QTL materials scored for seed shattering studies and eventual molecular analysis. The tissue harvested from this subset of 240 individuals of the SR5 F2 has limitations as the actual mapping population. Additional tissue harvests were not possible with the commencing of seed shattering studies in summer 2002, which allowed for nursery contamination by shattered seed. The QTL study materials remain in storage while characterized markers are assembled using the *Tripsacum* SR5 F2 mapping nursery at Ball State University, Muncie, IN.

As of August 2001, DNA had been isolated and a set of 72 parental/F1 screening blots for the eight enzymes *Eco*RI, *Eco*RV, *Bam*HI, *Bgl*II, *Dra*I, *Sac*I, *Xba*I, and *Hin*dIII had been constructed. Initial screening results of 5 of seven UMC maize bin markers revealed clearly mappable polymorphisms. These five markers include: *umc31* (4-6 bands), *umc38* (1 bright monomorphic band + 3-7 polymorphic bands), *umc44* (4-6 bands), *umc65* (4-8 bands), *umc66* (4-8 bands). While *Tripsacum* typically has a more complex band pattern than that seen in maize, previous experience with *Tripsacum* mapping has shown that inter-specific probes reduce data complexity. Addition of other markers, particularly *Tripsacum* genomic markers (TDA), and cDNAs, will be added as they become available through collaborative efforts. The advantage of these materials is that they have the same parentage as the F2 mapping population being established at Ball State University, Muncie, IN, and represent one of the first molecular QTL sample sets extensively scored/rated for analysis of seed shattering and forage quality in *Tripsacum*.

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Isolation of stage- and ploidy-specific floral RNA in *Tripsacum dactyloides* for cDNA library construction - a pilot study for large-scale isolations

--Blakey, CA[1], Houghteling, B[1], Goldman, SL[2], Dewald, CL[3], Sokolov, VA[4], Hammersmith, R[1]

A pilot study was designed and conducted at Ball State Univ. and incorporated into part of a Master's thesis project (B. Houghteling, 1998, " Isolation of differentially expressed messages in sexually reproducing *Tripsacum dactyloides*." M.Sc., BSU.). The aim of the study was to determine the physical stages of floral development for the isolation of pre-emergent ovules of greenhouse plants for both WW1582 (sexual) and WW1008 (asexual, apomictic) in the range of 0.5 to 3.0 mm, and to develop the step-by-step procedure for harvesting tissues containing these ovules with minimal contamination for high quality RNA isolations, necessary for later large-scale isolations from field nurseries. The field total RNA isolations would be used in the creation of stage- and ploidy-specific cDNA libraries, therefore the preservation of the RNA, particularly rare mRNAs, was a primary goal of the project. Harvested pre-emergent spikes were sized and ovules were excised to determine an approximate physical correlation between fruitcase width and ovule width within the fruitcase. Based on these findings a set of pre-emergent spikes with fruitcases were divided into three classes, <0.5 mm (E), 1.0-3.0 mm (M), and > 3.5 mm (L) (all fruitcases used were less than 5 mm in width). Total RNA was isolated from these sample classes using a Trizol™ RNA isolation protocol (as provided by Sigma).

Stage-specific cDNAs were generated using the SMART™ PCR cDNA Synthesis Kit (CLONTECH Cat# K1052-1). Small quantities of cDNAs were detected for each class, but in insufficient quantities for library construction. In order to enhance total RNA isolations, larger quantities of staged tissues of these accessions would be required. Based on the work at Ball State, it was determined that the fruitcase width measurements would be altered to compensate for the higher quantities of advanced maturity sexual spikes relative to the availablity of early apomictic spikes during the limited RNA isolation experiment time-window in Oklahoma.

Racemes with maturing terminal inflorescences were harvested from multiple clones of the sexual diploid (2x=2n=36) *Tripsacum dactyloides* plant WW1582 from Ottawa, KS, and from multiple clones of the tetraploid (4n=4x=72) *Tripsacum plant* WW1008 from Baird, TX, by Dewald and crew in Woodward, OK. Lateral pre-emergent inflorescence spikelet sections were then isolated from these racemes. Proximal cross-sectional cuts were made immediately below the node of inflorescence development, and the distal cuts were made 5-7 cm above the node. Outer leaves were removed from these sections by lateral incisions on the side opposite the inflorescence structure. The final layer of immature leaves encasing the inflorescences was left intact to maintain tissue sterility.

The encased spikelet sections were placed on ice until the floral structure was removed and sized, under sterile conditions, to reduce RNA and/or RNase contamination of female floral tissues. The immature spikelet sections were size-sorted according to the width of the ovule fruitcase. The classifications were as follows: "E" for early stage (<1.5 mm), "M" for middle stage (1.5-3.5 mm), and "L" for late stage (>3.5 mm). Ovules were not excised from surrounding maternally-derived tissues (fruitcase and stem); thus, the entire floral section was used in subsequent RNA isolations. It is important to note that these sections did not contain any male floral structures. The actual Trizol™ RNA isolation was performed on-site in Woodward, OK, by Blakey, according to the Trizol™ RNA isolation protocol provided by Sigma. Total RNA was stored under 75% EtOH in DEPC-H2O at 20 C and transported to Ball State University (BSU), Muncie, IN, for quantitation. Following resuspension, the total RNA samples were quantitated by UV at 260/280 nm. Resuspended total RNA samples were stored at -80 C until samples were divided. A portion was placed in permanent storage at BSU. The remainder of the RNA was shipped to the PSRC facilities, University of Toledo for 5 of 6 cDNA library constructions, and residual U.Toledo RNA subsequently sent to Miami University, Oxford, OH, for suppression

subtraction hybridization library construction.

Homology searches from sequenced cDNAs obtained from the U. Toledo libraries, to date, will continue to be analyzed at Ball State University. Update searches and re-analysis of novel clones will also be undertaken relative to any newly released *Oryza*, *Arabidopsis*, and *Zea* sequences will continue to be performed.

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Ball State University[1]
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Tripsacum SR5 Genetic Map - a new generation

--Blakey, CA[1], Dewald, CL[2]

The establishment of a single-site location for the new molecular genetic mapping work and mapping population of *Tripscaum dactyloides* was undertaken at Ball State University. This map will build on information gained in the construction of a previous map in *Tripsacum dactyloides*, which had been limited by a combination of sample size and field-nursery contamination. All plants are being maintained at Ball State in a non-flowering, vegetative growth stage to avoid these problems and allow for a continuing supply of F2 tissue for research. Currently, the only source of the paternal plant material of this F2 is housed at Ball State University. The primary focus of this project will be to derive a cross-genera marker genetic map of the warm season perennial forage grass *Tripsacum dactyloides,* a relative of modern maize, as a genetic resource for crop improvement in the Gramineae. The map will combine data from three sets of markers: 1) the TDA markers (derived from genomic DNA of *Tripsacum dactyloides*) developed by the PI while at the Univ. of Missouri; 2) the UMC RFLP maize bin markers; and 3) the Cornell Anchor marker set, which includes markers from several genera of the Gramineae. A broad-based marker map in *Tripsacum*, as a member of the Gramineae, utilizing a combination of species-derived and cross-specific markers will provide an enhanced basis for trait specific investigations, such as apomixis and seed shattering. The mapping population will eventually consist of 120 - 150 F2 individuals from the parental cross WW1673 x WW1760, and is known to segregate for the distinct recessive floral genotype *gynomonoecious sex form-1* (a known homolog to the floral gene *ts2*, in *Zea mays*, Li et al. PNAS 1997). The mapping individuals are a subset of a population currently under evaluation by the USDA for quantitative trait analyses of seed shattering and forage quality.

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Analysis of genetic relationships in elite maize inbred lines and their relationship to heterotic grouping

--Kumari, J, Gadag, RN

In view of current emphasis on single cross hybrids in maize breeding strategy in India, we attempted comprehensive characterization and genetic analysis of maize inbred lines being used by a maize improvement unit. The ten parental lines (originating from four source populations) were characterized using eighteen easily identifiable morphological traits and molecular (SSR) markers. Very few morphological markers were found to be unique to the parental lines, implying restricted utility of morphological data in accurately differentiating the inbred lines. Polymorphism at the genomic level in these lines was analyzed using 27 polymorphic SSR markers, and it revealed eight unique or rare alleles specific to four inbred lines (DMB 101, 105, 106 and 109). This can help in identification and differentiation of inbred lines by multiplexing SSR markers having different size-ranges. Three inbred lines, DMB 102, DMB 104 and DMB 106, were found to be highly homozygous on the basis of molecular marker analysis also. Analysis of genetic relationship was attempted using the data sets generated by morphological and SSR markers individually, and in combination by cluster analysis. The ten inbred lines were grouped into three clusters (Fig. 1).

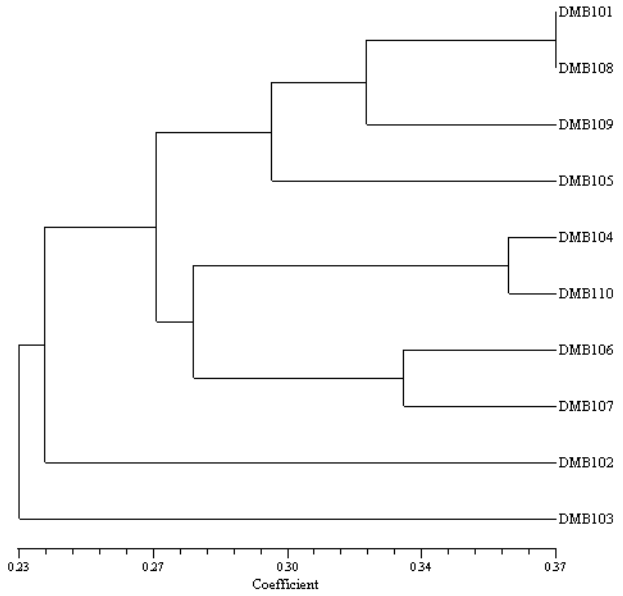

Figure 1. Dendrogram depicting genetic relationships among selected inbred based on morphological and SSR data

DMB 107 and DMB 108 (derived from A-64 source population) clustered together. Also, the similarity of DMB 110 and DMB 104, which shared a common source population, was implied. However, many discrepancies were noticed in the general clustering patterns (on the basis of morphological and SSR markers individually or in combination). This could be possibly due to a limited number of traits, low SSR markers, multiple underlying genes for these traits and scoring errors. The broad base of the source population, as well as over-representation of a particular source population (for example, five of the ten genotypes were derived from A-64), might be the reason for the low level of conformity between genetic relationships vis a vis pedigree information. It is not uncommon to expect inconsistency between SSR grouping and genetic background of corn inbreds, and this may be attributed to many factors (Yu et.al., Maydica 46:133-139, 2001).

Superior heterotic single cross combinations in comparison to PEHM-2 (the check with comparable maturity) were identified (DMB 101 x DMB 109, DMB 102 x DMB 103, DMB 102 x DMB 110, DMB 103 x DMB 104 and DMB 104 x DMB 110) on the basis of per se performance (Table 1). Of the five elite hybrid combinations identified over two locations, three crosses (highlighted) involved the parental line belonging to different clusters generated

Table 1. Particulars and performance of promising maize single cross hybrids

		Heterosis for Gr. yield/plant over PEHM-2 (%)		Days to 50%			
				Tasseling		Silking	
S. No	Cross	Delhi	Karnal	Delhi	Karnal	Delhi	Karnal
1.	DMB 103 X 104	17.9	8.3	51	53	54	56
2.	DMB 101 X 109	17.9	4.2	49	50	52	53
3.	DMB 102 X 103	10.3	3.9	49	47	51	49
4.	**DMB 104 X 110**	7.7	2.5	53	52	56	54
5.	DMB 102 X 110	2.6	12.5	51	48	54	51

by the combined data of morphological and molecular markers. Hence, the clustering pattern can be taken as a general indicator for choosing potential heterotic combinations. The relationship between hybrid relatedness and/or pedigree information, in terms of heterosis performance, can be explained and interpreted (Smith and Smith, MNL 63:86-87, 1989; Smith et.al., Maydica 45:235-241, 2000)

The fact that all parental inbred lines involved in these crosses (except DMB 110) were derived from the same source population, A-64 (Table 2), gave further credence to the broad base of the source population.

Table 2. Particulars of maize inbred lines involved in elite single cross hybrids

Inbred No.	Pedigree	Source Population
DMB 101	IPA 3-6-10-3-1-1-1-2-1-#	A-64
DMB 102	IPA 3-f (-1)	A-64
DMB 103	IPA 3-f (-2)	A-64
DMB 104	IPA 1-f-16-2-#-f-1	A-64
DMB 109	TCA 22-3-1-1-1-f-#-f-1	A-64
DMB 110	SC 7-2-1-1-7-1-1-1-1	Derived from MDR-1 X A-64

In the present investigation aimed at characterization of selected maize inbreds, SSR markers were instrumental in finer discrimination of inbred lines, as well as more precise analysis of homozygosity. Though differentiation of maize lines on the basis of morphological traits is presently contemplated, for finer discrimination between the parental lines, molecular markers like SSRs will be used. Some discrepancy in clustering could be accounted for by various factors. Molecular markers can serve as an invaluable aid for a variety of applications in maize breeding (Dudley et.al., Crop Sci. 31:718-723, 1991).

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About similarities between the *Bg-rbg* and some other transposable element systems of the hAT superfamily

--Koterniak, VV

Similarities in properties of the *o2-lf*, *o2-hf* receptive alleles and the mutable *an3* alleles of petunia. Two receptive alleles, *o2-lf* and *o2-hf*, significantly different in their frequencies of reversion to the normal allele (reversion frequency of *o2-hf* is more than 12 times higher than that of *o2-lf*) were described earlier (Koterniak, Maydica 44:195-203, 1999; Koterniak, MNL 73:76-79, 1999). Some similarities were observed between their properties and the petunia *an3* class 1 and class 2 alleles (described in van Houwelingen, A., et al., Plant Cell 11:1319-1336, 1999). The mutable petunia alleles indicated arose due to insertions of the non-autonomous element *dTph1* (belonging to the hAT superfamily) into the *anthocyanin3* (*an3*) locus of petunia (van Houwelingen, 1999).

Both petunia *an3* class2 alleles and the maize *o2-hf* allele are characterized by a high frequency of reversions. Reversion of the class 2 petunia alleles occurs by epigenetic interaction between three *dTph1* elements, situated in two homologous chromosomes (van Houwelingen, 1999). The high frequency of reversion of the *o2-hf* allele is characterized by the epigenetic interaction as well, but between the receptor element *rbg*, present in this allele, and the regulatory element *Bg-hf* (Koterniak, Genetika, in press). The similarity between the maize and petunia alleles mentioned could indicate a similarity in the mechanisms of their reversions. Therefore, by analogy with the class 2 *an3* petunia alleles, in the case of the *o2-hf* allele, at or near the *o2* locus, two receptor *rbg* elements could be expected. The loss of one *dTph1* element leads to suppression of the class 2 allele reversions (van Houwelingen, 1999). Existence of the analogous suppression for the *o2-hf* allele in case of the loss of one of the *rbg* elements could explain significant variability in revertant content and effectiveness of reverse selection for revertant frequency observed in the strains containing this allele (Koterniak, in press; Koterniak, MNL 75:51-53, 2001).

Reversion of the petunia class1 *an3* alleles is characterized by the absence of epigenetic effects and by a low frequency (van Houwelingen, 1999) similar to the *o2-lf* allele. It is necessary to mention that excisions of *dTph1* elements from the class 2 *an3* alleles, in contrast to their excisions from the class 1 alleles, lead to a perfect restoration in a majority of cases of the wild-type gene sequence (van Houwelingen, 1999). We expect that the determination of the character of restoration of the wild-type sequence in the case of the *rbg* reversion from the *o2-lf* and *o2-hf* alleles could confirm similarity in reversion mechanisms of the maize and petunia alleles mentioned.

Similarity in dosage effects expression between the regulatory elements *Bg* and *Ac*. Earlier it was reported that two regulatory elements, *Bg-lf* and *Bg-hf*, significantly differ in their ability to cause *rbg* excision in different doses (Koterniak, 1999). For the *Bg-hf* (in contrast to the *Bg-lf*) a strong positive dependence was characteristic between its dose and the frequency of revertants.

However, further studies show that there exists a non-linear and quite complicated dependence (Koterniak, in press; unpublished data) between the frequency of revertants and the dose of the *Bg* regulatory elements. As in earlier experiments, the frequency of revertants observed at 1 dose of the regulatory element *Bg-hf* was much lower than the frequency observed at 2 and 3 doses (revertant frequency conditioned by one dose may be on the same level with the revertant content observed in the crosses involving the regulatory element *Bg-lf* and the *o2-lf* allele) (Koterniak, 1999; Koterniak, in press). Increase in the dose of the *Bg-hf* from 1 to 2 or 3 increases the frequency of revertant formation by 6-19 times (calculating per one dose of the regulatory element) (Koterniak, 1999; Koterniak, in press). However, the increase in *Bg-hf* doses from 2 to 3 does not lead to significant enhancement of revertant content; moreover, it is accompanied by a decrease in revertant frequency counting per one dose of the regulatory element (Koterniak, in press).

Such a non-linear dependence between the reversion frequency and the dose of *Bg-hf* resembles to a certain degree the dosage

effects observed for the *Ac-Ds* system of transposable elements, where an increase in the *Ac* dose leads to a decrease in somatic mutations at the *Ac* controlled loci. For the *Ac-Ds* interaction it is supposed that the maximum excision frequency is observed under a certain optimal level of the *Ac* encoded transposase, deviation from which leads to a decrease in excision frequency of the receptor element *Ds*. It is assumed that the inhibition of excisions under the high transposase concentration may be connected with the aggregation of transposase molecules and the regulation of transposase activity on its substrate site (see reviews in Heinlein, Genetics 144:1851-1869, 1996; Brutnell, Genetics 147:823-834, 1997). Taking into account sequence similarity between *Ac* and *Bg* (Hartings, Mol. Gen. Genet. 197:209-218, 1984), it is possible to suppose that the mentioned decrease in excision frequency of the receptor element *rbg* also could be connected with a certain kind of association of the *Bg* encoded transposase.

Activity in ontogeny. One of the characteristic features of the *Bg-rbg* system of transposable elements, observed under the control of expression of the mutable alleles at the *o2* locus, is the fact that excisions of the receptor element *rbg* from this locus take place at postmeiotic mitotic divisions during mega- or microsporogenesis or during endosperm development, but not during embryo or sporophyte development (Montanelli, Mol. Gen. Genet. 227:91-96, 1984).

However, it is well known that the activity of regulatory elements (e. g. *Ac*) can show high developmental and tissue specificity. Such properties could be connected both with their DNA sequences and the positional effect of transposable elements (Peterson, Mol. Gen. Genet. 149:5-21, 1976; Fedoroff, pp. 1-63 in Mobile Genetic Elements, New York: Academic Press, 1983). Data available allow concluding that the specificity of the *Bg-rbg* system in relation to the mutable alleles at the *o2* locus also may be connected with the properties of the *Bg* regulatory element sequences and with the positional effect of the *Bg* and *rbg* insertions.

Thus, the study of a *Bg*-induced allele at the *wx1* locus showed that the *Bg* activity is not restricted to the endosperm tissue (Motto, Maydica 34:107-122, 1989). Besides, in the studies of the *Bg*-controlled receptive alleles at the *o2* locus it was established that the reversion of the *o2-hf* allele can occur in the late stages of the ear development before meiosis (Koterniak, MNL 76:54, 2002).

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Maize alpha zein genes map to seven positions in the maize genome

--Song, R, Ward, K, Messing, J

Maize alpha zeins are the most abundant fraction of maize storage proteins and encoded by a large gene family, which amounts to 41 members in inbred B73 (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002; Song, R and Messing, J, manuscript in preparation). Usually the alpha zeins are also referred to as 19 kDa and 22 kDa zeins according to their apparent molecular mass on SDS-PAGE. For a long time, the exact genomic organization of individual family members and their map position was unknown. Mapping data based on protein analysis provided map positions of certain expressed alpha zeins, which only represented a small portion of the entire gene family. Recent genomic approaches, however, have facilitated the isolation and complete sequencing analysis of regions containing all the alpha zein genes (Song, R et al., Genome Research 11:1817-1825, 2001; Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002). The entire alpha zein gene family contains four gene subfamilies based on sequence homology. Three of those (z1A, z1B and z1D) belong to the 19 kDa zein and one to the 22 kDa zein (z1C) protein class. A total of seven genomic locations were determined based on BAC clone contig analysis, two for z1A, two for z1B, two for z1C and one for z1D, respectively.

The 22 kDa zein (z1C) gene subfamily has two different genomic locations. The z1C gene cluster contains most family members except for one, and is physically linked to the *php200725* RFLP marker on maize chromosome 4S (~55 kb apart). The single copy member of the 22 kDa zein genes (*asz22;16*) has translocated to a different position on the same chromosome arm. Using a single-nucleotide-polymorphism (SNP) in the 22 kDa zein gene coding region between two different inbred lines, BSSS53 and Mo17, we were able to map this gene member by a (Mo17xBSSS53)xMo17 backcross mapping population. A primer pair: (5' primer: TCACTTGCTCCTAGTGGCAG; 3' primer: TAGATGAAAGTAGTTGTAGGTAGA), which will only give a PCR product from *azs22;16* of BSSS53 but not that of Mo17, was used for scoring the recombinant events from the population. The same population was also used to map the *php200725* and *cdo520* loci relative to the location of the zein genes. Out of 107 samples, we found 21 recombinant events between *php200725* and *azs22;16*, which gave a genetic distance of 19.6 cM. We also found four recombination events between *php200725* and *cdo520*, and 17 recombination events between *cdo520* and *azs22;16*. Therefore *cdo520* was placed in between *php200725* and *azs22;16*, with 3.7 cM genetic distance to *php200725*. Sequence homology comparison indicated that *azs22;16* is the normal allele of *floury2*.

The 19 kDa zeins consist of three gene subfamilies (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002). According to BAC clone analysis, the two larger subfamilies, z1A and z1B, both have two different genomic locations. The smallest subfamily, z1D, only comprises one genomic location. Using a z1D subfamily-specific probe, we found that the z1D subfamily is located on maize chromosome 1 by using oat-maize addition lines (data not shown). Previously, Woo, YM et al. (Plant Cell 13:2297-2317, 2001) mapped the two z1D genes, *az19D1* and *az19D2*, to positions 123.3 and 122.4, consistent with our results. The 0.9 cM genetic distance between the two z1D genes reflects a ~200 kb physical distance according to our sequence analysis of the z1D gene subfamily (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002).

The other two 19 kDa zein gene subfamilies both comprise two different genomic locations. Each genomic location contains gene clusters with high sequence homology indicating recent gene amplifications within short physical intervals. The subfamily-specific probes that were used to isolate the BAC clones were not sufficient to distinguish the two locations. Therefore instead of mapping the two locations by location-specific probes, we decided to map them based on their co-segregation pattern using a subfam-

ily-specific probe. The subfamily-specific probe will detect all the bands from both genomic locations on a Southern blot, but only those bands belonging to the same location will co-segregate. We used the z1A and z1B-specific probes that were previously described (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002) to check for sequence polymorphism of the parental lines of two maize recombinant inbred lines (Burr, B et al., Genetics 118:519-526, 1988). Based on a maximum of polymorphism detected by Southern blot analysis (number of bands and their polymorphism), we chose the Tx303xCo159 population cut with *Eco*RI for z1A subfamily. One band does not show polymorphism between the two parental lines. However, other bands could be sorted into two co-segregating groups (Fig. 1). One group contains most of the bands detected by Southern blot analysis and has the following mapping score:

212222121121112222121212111112112112222222

This gave us a map position of 40.90 on chromosome 4S according to the BNL map. At the same position, *uaz149(zp19)*, a 19-kDa zein gene has previously been mapped. Because this position contains most members of the z1A gene subfamily, it corresponds to the z1A-1 location as previously defined (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002).

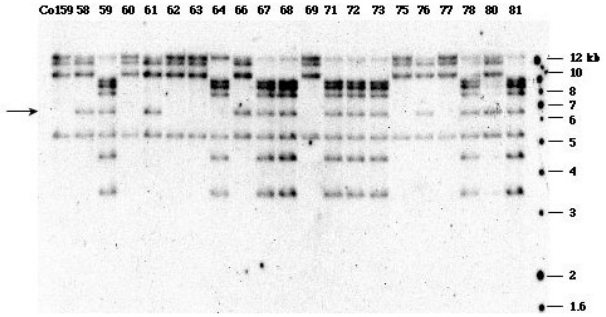

Figure 1. Co-segregation analysis of gene clusters of the z1A subfamily.

The other group contains a single band (Fig. 1, arrow indicated band) and has the following mapping score:

112122211121112121112111121222222122211221

This gave us a map position of 70.20 on chromosome 4S according to the BNL map. At the same position, *zpl3a*, a zein protein has previously been mapped. This position only contains a few zein gene copies and corresponds to z1A-2 location (Song, R. and Messing, J, Plant Physiology 130:1626-1635, 2002).

The same approach was taken for mapping the z1B subfamily. In this case, the Tx303xC0159 population cut with *Hin*dIII was selected for mapping. To our surprise, only one co-segregating group was detected by Southern blot analysis (Fig. 2), with the following score:

112222312211122211121211222212111211122222

This resulted in a map position of 52.30 on chromosome 7S. The same map position is also occupied by *uaz68a(zp19)* and *zpl2b*, two alpha zein genes. Even though we found two physically unlinked locations for the z1B subfamily in inbred line B73, they could still be tightly linked in terms of genetic distance because of the low resolution provided by the mapping population (only 41 samples).

A summary of all seven map positions is included in Table 1.

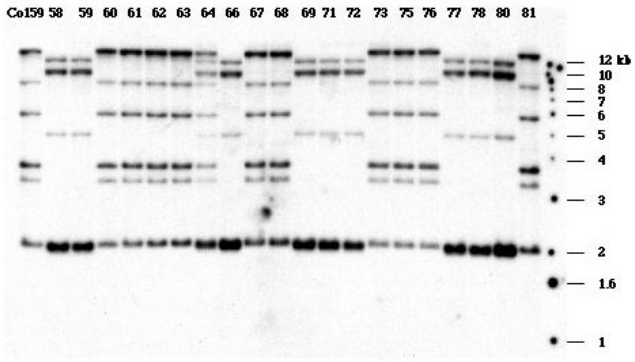

Figure 2. Co-segregation analysis of z1B subfamily.

Table 1. Genetic locations of the alpha zein gene family.

alpha zein subfamily	map position	mapping population	mapping method
z1A-1	chr 4, 40.90	C0159xTx303 RI	RFLP
z1A-2	chr 4, 72.20	C0159xTx303 RI	RFLP
z1B-1/z1B-2	chr 7, 52.30	C0159xTx303 RI	RFLP
z1C-1	chr 4, *php200725**	(Mo17xBSSS53)xMo17	RFLP
z1C-2	chr 4, *floury 2**	(Mo17xBSSS53)xMo17	SNP
z1D	chr 1, 122.4; 123.3**	N/A	RFLP

*please, refer to these two markers for relative positions in different genetic maps.
**segregating population not known (Woo, YM et al, Plant Cell 13:2297-2317, 2001).

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Paramutation in traditional varieties from Brazil

--Gardingo, JR, Mondin, M

Among the traditional varieties of maize, neither the occurrence of kernels showing different patterns of coloration nor the predominance of stippled phenotypes is unusual**.** During a germplasm survey on ethnovarieties from Paraná State, we detected some ears of the variety Carioca with variegated and full colored kernels, while ears of other varieties had only yellow kernels, among them Piranão, Cayano, Ferrinho and IAPAR 50.

Analysis of the variety Carioca showed that the sectors were localized in the aleurone. Different levels of pigmentation could be observed, and five classes were characterized as being full, near full, stippled, near colorless and colorless (Fig. 1). Comparing the phenotypes found in the Carioca original population with others described in the literature, we concluded that these phenotypes should be comparable to a paramutation event. All the other varieties are known to be *bb;rr*. In the summer of 1999-2000 we conducted a field experiment with all varieties without pollination control to analyze the occurrence of colored and stippled kernels.

Figure 1: Four phenotypic classes. (a) colorless, (b) near colorless, (c) stippled and (d) near colorfull. The colorfull phenotype has not been shown here.

The wind direction was favorable to lead the pollen grain of the Carioca onto other varieties. The results are presented in Table 1 with only three phenotypic classes. In the class Mot/Stt "near full", "stippled" and "near colorless" are included. The ear with paramutation means that at least one kernel was mottled. Interestingly, no kernel with a stippled phenotype was observed in the Ferrinho variety. Its position in the field was favorable to present at least one kernel with a stippled phenotype. Our hypothesis is that the alleles of color were completely null. These varieties have been analyzed carefully in order to verify why they did not show such a stippled phenotype. We have conducted controlled crosses between Ferrinho and Carioca as a complete diallel to check out possible differences when Ferrinho was used as female or male.

Table 1: Frequency of different color classes in the kernels of etnovarieties from Brazil

	Phenotypes				Ears		
	Color	Mot/Stt	Colorless	Total of kernels	Paramutation	Normals	Total
Carioca	118	304	10712	11134	30	29	59
Piranão	30	40	12844	12914	38	119	157
Ferrinho	-	-	-	-	0	34	34
Cayano	9	11	3725	3745	10	37	47
IAPAR 50	4	7	3401	3412	8	29	37
Piranão x Cusco	22	36	5999	6057	16	39	55
Sintético	5	23	2574	2602	10	21	31

Our results show that the allele was transmitted to other varieties, and the paramutation event was observed by the kernels showing different color levels or reduced expression of the dominant allele. The low level of introgression in some varieties such as IAPAR 50 and Cayano is a result of its position in the field. This low introgression reinforces the hypothesis of a null expression of the alleles, because these varieties were more distant from Carioca in the field than Ferrinho. The detailed analysis was not presented because we are conducting experiments with inbred lines and backcrosses derived from these varieties.

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TIGR Maize Gene Index

--Lee, D, Quackenbush, J

Overview. The most comprehensive resource for the cataloging of transcribed genes is the vast body of data generated by the sequencing of Expressed Sequence Tags (ESTs). ESTs are single-pass, partial sequences of cDNA clones, and they have been used extensively for gene discovery and genomic mapping in various species. Similar to the other TIGR Gene Index databases, the Maize Gene Index uses assembly algorithms to first cluster, then assemble EST and gene sequences to produce tentative consensus (TC) sequences that represent the underlying mRNA transcripts. The resulting TCs can be used for eukaryotic genome sequence annotation, EST sequence annotation, integration of complex mapping data and identification of orthologous genes in other crop plants.

Building Maize Gene Index. Maize TCs were assembled by treating ESTs and Expressed Transcripts (ET) sequences as elements of a transcriptome shotgun sequencing project. Maize ESTs are downloaded daily from dbEST, cleaned to remove untrimmed vector, linker, ribosomal, mitochondrial, low quality, poly(A/T) and contaminating bacterial sequences. Maize ETs are extracted from annotated mRNA and CDS features in GenBank records. Cleaned ESTs and ETs are compared pair-wise to identify overlaps using megablast . Sequences sharing a minimum of 95% identity over a 40 nt or longer region with 20 bases or fewer of mismatched sequence at either end are grouped into a cluster. Each cluster is then assembled separately using CAP3, the resulting TC sequences are annotated to provide a provisional functional annotation, and the assemblies and their annotations are stored in a Sybase relational database that allows versioning and heritability to be maintained. All nonclustered, non-overlapping sequences remain as singletons. The resulting Gene Index is released through the TIGR maize gene index web site (www.tigr.org/tdb/tgi/zmgi/). Each TC reports (example TC160405, http://webtest.tigr.org/docs/tigr-scripts/tgi/tc_report.pl?species=maize&tc=TC160405&display=1) includes: the assembled TC sequence, the predicted open reading frames (ORFs) from ESTscan, DIANA and framefinder, coordinates of each EST and ET in the assembly, information about each EST and ET with links to a variety of databases, alternative splicing cluster, an expression summary by counting number of ESTs from different libraries, SNP detection, orientation determination, functional annotations including matches to a known protein and GO annotations, and tentative orthologous gene identifications in other species from the EGO database, and maps to rice and Arabidopsis genomes .

Using TIGR Maize Gene Index. There are a variety of means by which a user might gain entry to the Maize Gene Index database. Users can search the database using a variety of sequence identifiers, such as GenBank Accession or TC number, or by searching gene name or for TCs that are preferentially expressed in specific tissues.

However, the most common entry point for most users is the sequence search page (<http://tigrblast.tigr.org/tgi/>). Both BLASTN and TBLASTN versions of the WU-BLAST package have been implemented allowing DNA and protein queries to be used. Alignments to high scoring TCs and singleton ESTs are returned and users can view the individual target sequences by clicking on the TC number or EST_id. From the TC reports (see Figure 2), users can view the annotation provided for the sequence and its evidence, link to orthologues in EGO, or view genomic sequence alignments with rice and *Arabidopsis*.

In addition to the Web interface, the TIGR Maize Gene Index is available as a set of flat files. The TC consensus sequences are provided in a FASTA format file; the ESTs comprising each TC are specified in a separate file. Many users involved in the annotation of genomic sequence and in the analysis of cDNA microarray data have found these to be particularly useful. In addition, we provide a putative annotation of all the assembled and singleton ESTs in the database through the EST Annotator feature available through the main maize gene index page.

TIGR Maize Gene Index release data. The current release of the Maize Gene Index, ZmGI 11.0, was released on February 1, 2003, and contains 188,973 ESTS, 173,826 in TCs and 15,147 as singletons, as well as 3,463 expressed transcripts. New releases will be available every 120 days, provided a minimum 10% increase in the number of available ESTs.

Acknowledgements. We would like to thank the members of the maize EST cloning and sequencing community whose data made this project possible. This work was supported by National Science Foundation, grant DBI-9983070.

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A novel maize ditelosome 10 addition to oat cv. Sun II for use in radiation hybrid mapping

--Kynast, RG, Okagaki, RJ, Granath, SR, Rines, HW, Phillips, RL

A complete set of disomic oat-maize chromosome additions, each with an individual maize chromosome pair added to a complete genome of hexaploid oat, is desirable for chromosomally dissecting and mapping the maize genome and studying maize genes and markers in the genetic background of oat (Kynast et al., Funct. Integrative Genomics 2:60-69, 2002). To date, a total of 46 disomic addition lines have been produced by pollinating more than 80,000 florets of eight different oat lines with four different maize lines. Fertile F1 (oat maize) hybrids and their F2 and subsequent generations were recovered, and the added maize chromosomes cytologically and molecularly identified, as described elsewhere (Kynast et al., Plant Physiol. 125:1228-1235, 2001). The series of fertile disomic addition lines (2n = 6x+2 = 44) include ones for maize chromosomes 1, 2, 3, 4, 5, 6, 7, 8, and 9, with seed and/or DNA available upon request. The maize chromosome 10 has been recovered as a monosomic addition to haploid GAF-Park oat; however, to date it has failed to produce F2 offspring. The chromosome 10 addition is being maintained vegetatively by tiller-cloning for DNA/RNA production. In an attempt to complete the set of disomic oat-maize addition lines for use in the production of radiation hybrids, we extended our crossing program to additional genotypes and culture conditions. From about 8,000 crosses between oat cv. Sun II and maize cv. Seneca 60, we generated 51 new proembryos. Of these, 11 proembryos developed into plantlets of haploid oat with one or more maize chromosome(s) added; 36 proembryos developed into haploid oat plants without maize chromosomes. Four proembryos did not develop enough tissue for an analysis.

Plant 'F1-0289-1' retained the maize chromosome 10, in addition to all oat chromosomes, based on a positive test for the maize-specific LTR-type retrotransposon Grande 1 and maize chromosome 10 SSR markers. The plant was allowed to self-pollinate, and four maize-positive panicles were found to set seeds (Table 1). Genomic DNA samples of ten F2 offspring from each maize-positive panicle of the F1-0289-1 plant were assayed for presence versus absence of the maize-specific LTR-type retrotransposon Grande 1 (Figure 1). PCR using Grande 1-specific primers detected maize chromatin in nine offspring plants of F1-0289-1/a (designated F2-3776/a-1 to F2-3776/a-9; F2-3776/a-10 was negative), nine offspring plants of F1-0289-1/b (designated F2-3776/b-1 to F2-3776/b-10; F2-3776/b-4 was negative), no offspring plant of F1-0289-1/c (all F2-3776/c-1 to F2-3776/c-10 were negative), and ten offspring plants of F1-0289-1/d (designated F2-3776/d-1 to F2-3776/d-10). We verified the

Table 1. Seed set of the first fertile oat-maize chromosome 10 addition F1 (Sun II Seneca 60) 0289-1.

			Number of Seeds		
F1 Plant/Panicle	Grande 1-SSR	Florets	Harvested	Analyzed	F2 Offspring IDs
F1-0289-1/a	+	222	51	10	F2-3776/a
F1-0289-1/b	+	264	59	10	F2-3776/b
F1-0289-1/c	+	156	48	10	F2-3776/c
F1-0289-1/d	+	154	31	10	F2-3776/d

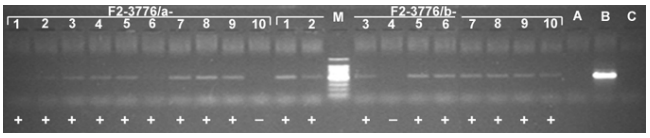

Figure 1. Selected examples of oat offspring possessing maize-chromatin shown by PCR with Grande 1 primers. The presence of the 500 bp band (+) indicates presence of maize chromatin in the DNA extract of the corresponding F2 plant; M=Molecular Weight Marker, A=Sun II, B=Seneca 60, C=No-DNA Control.

maize chromosome identities by assaying the corresponding DNA samples of the maize-positive F2 offspring plants with two sets of SSRs genetically mapped to maize chromosome 10 from the MaizeDB (http://www.agron.missouri.edu/) (Figure 2). We selected the markers: p-phi041, p-phi117, and p-umc1293 from bin 10.00, and p-umc1249, p-umc1196, p-umc1176 and p-umc1084 from bin 10.07. Since most of the maize-positive plants showed consistent presence of the three markers from the bin 10.00, but absence of the four markers from the bin 10.07, we conclude that the maize chromosome present in each of these offspring is likely a telocentric derivative of the chromosome 10 retained in the original plant 'F1-0289-1'. GISH analysis on root-tip cells using labeled genomic DNA from maize revealed the disomic status and the telocentric nature of the added chromosomes in most of the plants analyzed by PCR (Figure 3). The line was given the designation OMAdt10.20S in accordance with the proposed nomenclature for oat-maize chromosome addition lines (Kynast et al. 2001: Maize Genetics Coop. Newsl. 75, 54-55).

Since there are more seeds to be analyzed for the possible telosomic addition of the long arm of chromosome 10, we will test

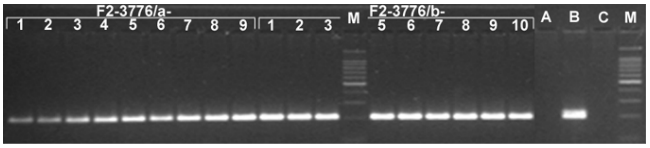

Figure 2. Telocentric maize chromosome identification with the short arm-specific SSR, p-phi041 (bin10.00). The presence of the 200 bp band is diagnostic for the short arm of maize chromosome 10 as shown in DNA extracts of the corresponding F2 plants; M=Molecular Weight Marker, A=Sun II, B=Seneca 60, C=No-DNA Control.

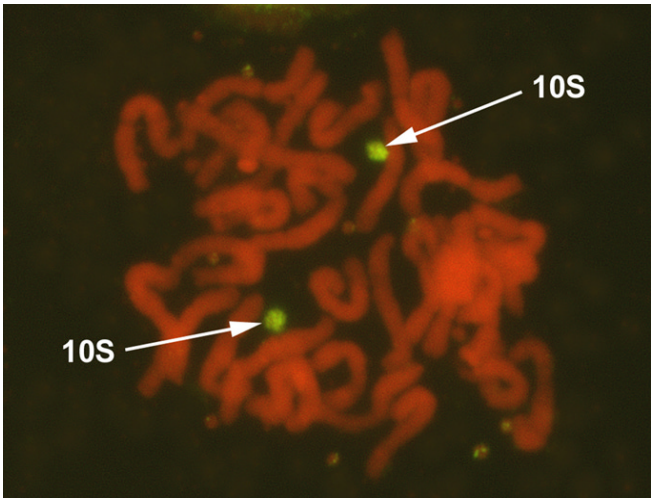

Figure 3. GISH of fluorophore-labeled genomic maize DNA to root meristem cells of plant F2-3776/b-6. Arrows point to the two telocentric maize chromosomes (green), which are formed from the short arm of chromosome 10 (smallest maize chromosome). Oat chromosomes (red) are counterstained with propidium iodide.

all seeds with larger numbers of chromosome arm-specific SSRs. At present we are propagating the identified disomic telocentric F2 offspring plants to test for chromosome stability and transmission to F3 offspring. Once more seed are produced, the new addition lines will be available upon request to the scientific community.

This material is based upon work supported by the National Science Foundation under Grant No. 0110134.

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New genetic map of *Zea mays* mitochondrial genome (nb) derived from sequence data

--Fauron, C, Gibson, M, Clifton, S, Minx, P, Spieth, J, Newton, K, Rugen, M

A National Science Foundation-funded Plant Genome Project focused on the organization, evolution and expression of the mitochondrial genomes of maize and its relatives, has resulted in the preliminary data analysis presented here. Currently, six mitochondrial genomes within the genus *Zea* are being sequenced, including fertile (NB and NA genotypes) and male sterile (CMS-T and CMS-C genotypes) maize, *Zea parviglumis* (the probable progenitor of maize) and *Zea perennis*. In addition, the mtDNA sequences of related grasses, *Tripsacum dactyloides* and *Sorghum bicolor*, are being determined.

The sequencing of the *Zea mays mays* NB mitochondrial genome is now complete. The final assembly generated a circular map of 569,630 basepairs with an average G+C content of 43.9%. The size compares well with the previous restriction enzyme analyses (Fauron and Havlik, NAR 16:10395, 1988), which generated a map of 570kb.

The previous arbitrary start point of the NB map (shown in the last update published in MNL70:133, 1996) was defined at a *Sma*I site internal to the 5.2 kb repeat in NB. For sequence annotation purposes, it was decided that the start point should be located in a region devoid of any features (including repeats); therefore, a new starting point (labeled start on the figure) is the first base of the *Xho*I site located 5' to the previous *Sma*I start point (shown as an asterisk* on the figure). This region seems to be conserved among other maize cytotypes.

Sequence data can be found at the Washington University Genome Sequencing Center web site (genome.wustl.edu/pub), and additional information about this genome project can be found at our project web site (grassmt.genetics.utah.edu).

Table 1. List of known genes for the mitochondrial genome of normal NB maize.

Genes	Synonym	Product
atp1		ATPase subunit 1
atp1		ATPase subunit 1
atp6		ATPase subunit 6
atp8	orfB	ATPase subunit 8
atp9		ATPase subunit 9
ccmB	ccb206	cytochrome c biogenesis B
ccmC	ccb256	cytochrome c biogenesis C
ccmFC	ccl1	cytochrome c biogenesis FC (2 exons)
ccmFN	ccl1	cytochrome c biogenesis FN
cob		apocytochrome b
cox2		cytochrome c oxidase subunit 2 (2 exons)
cox3		cytochrome c oxidase subunit 3
coxI		cytochrome c oxidase subunit 1
mat-r		maturase
nad1 exon 1		exon1 of NADH dehydrogenase subunit 1
nad1 exon 1		exon1 of NADH dehydrogenase subunit 1
nad1 exons 2, 3		exons 2 & 3 nad1
nad2 exons 1, 2		exon 1 and 2of NADH dehydrogenase subunit 2
nad2 exons 3, 4, 5		exons 3, 4 and 5 of NADH dehydrogenase subunit 2
nad2 exons 4, 5		exons 4 and 5 of NADH dehydrogenase subunit 2
nad3		NADH dehydrogenase subunit 3
nad4		NADH dehydrogenase subunit 4 (4 exons)
nad4L		NADH dehydrogenase subunit 4L
nad5 exon 1, 2		exons 1 and 2 of NADH dehydrogenase subunit 5
nad5 exon 3		exon3 of NADH dehydrogenase subunit 5
nad5 exon 4, 5		exons 4 and 5 of NADH dehydrogenase subunit 5
nad6		NADH dehydrogenase subunit 6
nad7		NADH dehydrogenase subunit 7 (5 exons)
nad9		NADH dehydrogenase subunit 9
orf25		protein orf25
orfX		protein orfX
pseudo trnL		pseudo tRNA-Leu (2 exons)
rpl16		ribosomal protein L16
rps1		ribosomal protein S1
rps12		ribosomal protein S12
rps13		ribosomal protein S13
rps2A		ribosomal protein S2
rps2B		ribosomal protein S2
rps3		ribosomal protein S3
rps4		ribosomal protein S4
rps7		ribosomal protein S7
rrn18		18S ribosomal RNA
rrn26		26S ribosomal RNA
rrn5		5S ribosomal RNA
trnC		tRNA-Cys
trnD		tRNA -Asp
trnD		tRNA-Asp
trnD		tRNA-Asp
trnE		tRNA-Glu
trnE		tRNA-Glu
trnF		tRNA-Phe
trnH		tRNA-His
trnI		tRNA-Ile
trnL		tRNA-Lys
trnL		tRNA Leu
trnL		tRNA Leu (2 exons)
trnM		tRNA-Met
trnM		tRNA-Met
trnM		tRNA-Met
trnN		tRNA -Asn
trnN		tRNA-Asn
trnP		tRNA-Pro
trnP		tRNA-Pro
trnQ		tRNA-Gln
trnR		tRNA-Arg
trnR		tRNA-Arg
trnS		tRNA-Ser
trnS		tRNA-Ser
trnY		tRNA-Tyr

Figure 1. The mitochondrial genome of normal NB maize. The outside circular ring shows the known genes. Genes that are encoded on the plus strand are located on the outside and genes encoded in the minus strand on the inside. The middle circle shows *Sma*I and *Xho*I restriction fragments sites derived from the sequence. Start (*Xho*I site-see text) is located at the 12 o'clock position. The inside ring shows the homologous regions between maize NB mtDNA and the maize chloroplast genome.

Table 2. List of repeats larger than 0.5 kb.

Repeats	Size (bp)	copy1 start	copy1 end	copy2 start	copy2 end
17 kb - inverted	16870	113649	130518	59371	42502
15 kb -direct	14946	453701	468636	522638	537573
11 kb - direct	11092	164398	175489	63778	74869
5.3 kb - direct	5277	245065	250334	1555	6824
0.7 kb - direct	689	21428	22152	541232	541950
0.5 kb - direct	549	13415	13963	499862	500410

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Development of haploids on haploids of parthenogenetical maize lines in crosses n x 2n by different pollination delay terms

--Smolkina, YV, Tyrnov, VS

It was demonstrated earlier that kernels with both haploid and diploid embryos may develop on haploids of parthenogenetical maize lines pollinated by pollen of diploid plants. Haploids on haploids were produced successively in 5 generations (Tyrnov, MNL 71:74, 1997).

In our work we investigated the influence of different terms of haploid pollination delay on setting of kernels and ploidy level of plants, developed from them. We used parthenogenetical lines AT-1 and AT-3, described earlier in MNL, 1997 (Tyrnov, 71:73-74; Enaleeva, Tyrnov, 71:74-75). For haploid producing, these lines (and further the haploids themselves) were pollinated by an embryo marker, which is characterized by low haplo-inducing ability (about 0.05%). Therefore, almost all haploids arose as a result of a genetically conditioned predisposition to parthenogenesis of maternal forms. Haploids were discovered by the method of genetic marking, morphometric and cytological analysis (Khokhlov, Tyrnov, Methods of Diagnosis of Haploids. Haploidy and Selection. Moscow, pp. 14-25, 1976). The experiments included “ideal” and “not ideal” variants. The ideal variants were characterized by an equal number of haploids in different experimental seasons (2000, 2001), by equal sizes of plant and ears, and by similar conditions of cultivation. Pollination was made in 2-3 and 7-8 days after appearance of silks. Not ideal variants included the smaller plants, with different sized ears. The terms of pollination can be conditionally divided into “early” (1-3 days) and “late” (5-9 days). Sometimes pollination was made on the first day, and repeatedly on the second or third day. Such differences are connected with the use of haploids, which for some reason were not discovered in other experiments. Haploids might grow in thickset crops and in the shadow of powerful diploids. It is possible that some haploids were a part of twins such as n-n and n-2n. We suppose that variants that are not ideal are not less valuable than ideal ones, since in further work it is impossible to be sure that haploids will always appear in perfect conditions.

Ideal variants of both lines on 20 haploids, early and late in terms of pollination, were examined yearly. The differences in the different years were not discovered. So, we give the data for 2 years. In line AT-1, 248 kernels were set on 40 haploid ears, on average 6 on one ear, with a variability from 1 to 20. With pollination delay, only 18 kernels were set on 40 ears. In line AT-3, according to pollination terms, 186 and 16 kernels were set. Consequently, pollination delay led to a reduction of kernel setting of more than 10 times. With early pollination, kernels were produced on all 80 haploids. Nine ears gave one kernel, 14 gave two. Other ears had 3-9, 14, or 16-21 kernels. With pollination delay in line AT-1, 65% of the ears did not form kernels, in line AT-3 – 72.5%. The maximum number of kernels on an ear did not exceed 2.

The differences were observed in ploidy level of seedlings, obtained by growing kernels which set on haploids. Early pollination of the AT-1 and AT-3 lines resulted in 3.6 and 2.7% haploids, late pollination resulted in 78 and 75%. Taking into account that on a majority of ears pollinated late only haploids have been set, we may speak about a 100% frequency of parthenogenesis. However, it is necessary to remember that we are discussing single specimens, not mass production of haploids with such a frequency. Nevertheless, this index can be used as a diagnostic sign in selection on parthenogenesis.

Enough similar results were obtained in variants that were not ideal. With late pollination, kernels set 8-15 times more seldom, but the occurrence of haploids among them reached 50-60%. With early pollination, the frequency of haploidy did not exceed 5%.

Besides haploids in all variants, the occurrence of twins was noted with a frequency of 1-12%. The types of twins were n-n and n-2n. The phenomenon for haploids was noted first. It connects with parthenogenesis and probably can be its diagnostic sign.

It was noted above that in line AT-1, haploids on haploids were produced successively in 5 generations (1986-1990). Beginning with 1990, an analogous experiment was conducted with haploids of the AT-3 line. We could produce haploids on haploids this time in 11 generations. Signs of degeneration were not established.

Hence, some conclusions may be made from the data obtained. With pollination delay, signs of reduced parthenogenesis manifest most clearly: the set of haploids on haploids, 100% occurrence of haploidy, polyembryony of n-n and n-2n types. However, taking into account that about 70% of ears do not form kernels, and on the rest only single kernels develop, pollination delay will be expedient only in those cases when a line gives many haploids or if a single haploid can be cloned.

The work was supported by a grant from the Russian Foundation for Basic Research (01-04-49385).

Production of unreduced apomicts by diploidization of lines predisposed to reduced parthenogenesis

--Tyrnov, VS, Smolkina, YV

Maize lines, characterized by reduced pseudogamous parthenogenesis were produced (Tyrnov, MNL 71:73-74, 1997; Enaleeva, Tyrnov, 73-75). In these lines, we obtained haploids successively in 5-10 generations from kernels set on haploids. This was practically regular reproduction by haploid apomixis.This points to the principal possibility of production of unreduced apomicts. There is a probability, that this can be realized by the introduction of unreduction genes into parthenogenetical lines. But before starting work in this direction on a large scale, it was necessary to see if parthenogenesis manifests on a diploid level and how endosperm develops in that case. We checked this in a model system. We treated kernels and seedlings of the AT-3 line with colchicine to produce tetraploid plants. Colchicine-treated plants were pollinated by pollen of tetraploids, having genes *a B Pl R* or *A B Pl R*. The AT-3 line had gene *A1*, so all hybrid plants had a purple colour, and hybrid endosperm had a purple aleurone. Maternal diploids were green with white roots. By autonomous development, the endosperm must have a colour of maternal form.

1126 kernels were set on 42 colchicine-treated plants. Almost all of them appear larger than in the initial line AT-3. It has not been ascertained exactly if this is connected with polyploidy, heterozygosity or a small number of kernels on ears. Most of the kernels had purple colour. Only 8 yellow kernels were found. However, it is impossible for the present to confirm an apomictic origin. 1118 kernels were germinated on moist filter paper. Normal seedlings were developed from 423 kernels. 268 of them (63%)

were diploids of the maternal type. Among the rest of the plants, 34 were abnormal in appearance. They did not produce ears. Weakly developed panicles did not form pollen. The rest of the plants were hybrid tetraploids. Part of the plants were analyzed in winter, another part in spring. Therefore, only 76 plants of the maternal type were grown in the field. Most of them were like plants of the initial line AT-3. However, 8 of them had some distinctions in height, form of panicle, and terms of blossom. It is possible that this could be a consequence of colchicine's mutagenic action. Part of the plants were self-pollinated, and another part pollinated by pollen of the embryo marker (*ACR-nj:cudu, g11*). More than 10% of haploids were discovered by kernel germination. Thus, this experiment allows the following conclusion: Parthenogenesis can manifest on diploid level as well as on a haploid level. Diploid apomicts, produced experimentally, do not lose the ability for reduced parthenogenesis. Hybrid endosperm is well-developed and is, probably, hexaploid. It is known that pollination of a tetraploid by reduced pollen gives a weakly-developed pentaploid endosperm. Defective endosperm is an extremely undesirable phenomenon. So, in further work, we plan to discover and use genes to provoke unreduction simultaneously in both female and male spheres. In line AT-3, the initial stages of endospermogenesis (some few nuclear divisions) can be realize without fertilization, but further development is blocked (Enaleeva, Tyrnov, MNL 71:74-75, 1997). Therefore, we plan work on intensification of the tendencies to autonomous endospermogenesis by selection, creation of optimal ploidy level, and overcoming the effect of imprinting.

This work was supported by a grant from the Russian Foundation for Basic Research (01-04-49385).

The starting mechanism for paramutation: cytoplasm as a factor

--Zavalishina, AN, Tyrnov, VS

The phenomenon of paramutation in maize has been investigated for a long time and on a large scale, on both the genetic and the molecular levels. However, to this day the reasons and mechanisms of the origin of paramutation have not been ascertained.

Study of progeny of androgenesis in vivo demonstrate that in lines with substituted cytoplasm, paramutations arise as a regular phenomenon. By transference of the genome, including dominant genes *B1* and *Pl1*, onto different cytoplasms, in some generations these genes transferred from a state of active expression to reduction of expression, from the state *B1* and *Pl1* to the state of paramutagenic genes *B`* and *Pl`* (MNL 69:120-121, 1995; MNL 72:74-75, 1998). It happened, more often, after 2-3 generations, rarely 4-5, since genome and different cytoplasm were joined in the initial androgenic plant. Such regularity in the transformation of the genome was observed by transference of the genome by the method of androgenesis both on sterile and on normal cytoplasms. Sometimes genes *B1* and *Pl1* became paramutagenic in the first generation by the union of different cytoplasms and genomes and manifested in the phenotype of the initial androgenic plant. It is possible this happens because of a significant difference in the substituted cytoplasm from the initial one. For example, paramutagenic genes *B`*or *Pl`* or both, manifested relatively often in androgenic haploids produced on S-type cytoplasm. An exclusive case was observed when, in progeny of androgenic plants with normal cytoplasm, paramutagenic genes were not discovered in 15 generations. Probably in this case, both substituted and initial cytoplasms did not differ from one another. In the initial maize lines, which were donors of the genomes for the androgenic plants, paramutagenic genes were not discovered in more than 20 generations.

Confirmation that the cytoplasm, but not androgenesis, influences the origin of paramutagenic genes, comes from results obtained by crossing of lines with subsequent backcrossing or selfing. In our experiments with the transference of genomes, including the dominant genes *A1, B1, Pl1, R1* or *a1, B1, Pl1, R1*, in a line with CMS, paramutagenic genes *B`, Pl1`*, *R`* also manifested in backcrossed progeny. It must be noted that, as well as by androgenesis, paramutagenic genes more often manifested in some years after the beginning of backcrossing and their expression decreased to a state of *B`, Pl`, R`*. Analogous results were also obtained by self-pollination. From the hybrid, the maternal parent of which was line W23 with normal cytoplasm, and the male parent was a line with the genes *a1, B1, Pl1, R1*, a line was picked out with these genes in a homozygous condition. This line preserves active expression of color genes in three generations. In subsequent generations, expression of these genes first decreases in solitary individuals, and then in all plants up to full suppression of expression of *B`, Pl`*.

Once more, confirmation of cytoplasm participation in the origin of paramutations was obtained in an experiment in which reversion of paramutagenic genes to a state of complete expression on the initial cytoplasm was observed. For that purpose, a special experiment was organized in which two lines were used – the initial Brown marker line with the genes *B1* and *Pl1* in a state of complete expression and its line-analogue, produced by the method of androgenesis in vivo on cytoplasm of line W23, in which paramutagenic genes *B`* and *Pl`* then manifested. We carried out a series of direct and reverse saturating crosses between these two lines. In progenies, both in direct and in reverse crosses, only plants with paramutagenic genes *B`* and *Pl`* first appeared. Partial reversion to a state of active expression of paramutagenic genes *B`* and *Pl`* was discovered after the third backcross, and complete reversion after the fourth backcross, on the initial cytoplasm of the Brown marker line. In spite of the same heterozygosity (normal and paramutagenic genes) on cytoplasm W23, reversion was not discovered.

Additional arguments, confirming indirectly, that namely the initial cytoplasm, but not heterozygosity, influences reversion of paramutagenic genes, follow our experiments. By both backcrossing and androgenesis in vivo we produced analogous lines with sterile cytoplasms. Initially, genomes of these analogues included all or part of genes *A1, B1, Pl1, R1.* The fact is well-known, that for production of progeny from analogous lines with CMS they must be pollinated by pollen of the initial lines. This procedure was used every year. As a result, in some generations in all analogous lines on sterile cytoplasms, irrespective of its production by androgenesis or by backcrossing, paramutagenic genes *B', Pl', R'* were manifested. The more generations were produced in analogous lines, the more strongly suppressed was expression of genes *B1, Pl1, R1,* which came with pollen. They also became paramutagenic. In all these numerous experiments, which continued sometimes more than dozens of years, we not once discovered reversion of paramutagenic genes to a state of complete expression, in spite of constant heterozygosity in result of pollination.

Obviously, starting or switching of expression of nuclear genes is in some manner associated with cytoplasm. This connection was not discovered till now, probably, for several reasons. First of all, changes of genome arise, as a rule, in some generations after the union of the genome with a different cytoplasm, and often these changes first manifest not in complete expression, but as a small decrease of expression of some color genes. Secondly, after this process has happened and genes become paramutagenic, they that was for some generations, irrespective of the cytoplasmic background.

The importance of research into the role of the cytoplasm is also that substituted cytoplasm influences a change in quantitative signs. In our experiments with change of color genes' expression, a change in quantitative signs influencing crops was observed (MNL 75:57-58, 2001). It is possible that by transference of the genome onto different cytoplasms, one may obtain not only changes of selectively significant signs, but a fixation of these changes.

Probably, cytoplasmic factors play a more important role, than has been considered till now, in the instability of the genome and in the formative process, having evolutionary and selective value. We are ready to cooperate for discussion of this problem and joint research.

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Reciprocal cross effects for grain yield and content of raw protein in the maize grain

--Bonea, D, Urechean, V

The creation of new maize cultivars that are more productive and with a high content of raw protein in the grain poses the next question: is it possible that the crossing directions may be analyzed in order to obtain a maximum effect for the characters studied?

The simultaneous improvement of the quantitative characters (the production capacity and the content of raw protein in the grain), involves the "per se" previous analysis of the inbred lines for the characters studied; on the basis of this analysis, the best lines are included in a diallel system, that establishes the direction of the reciprocity effects.

The knowledge of the direction of the reciprocity effects for both characters is possible only by analysing the direct and reciprocal hybrids.

In this work there 8 inbred maize lines have been used, which were crossed in a [n(n-1)] diallel system. Fifty-six direct and reciprocal hybrid combinations have been obtained.

Knowing the grain yield and the percentage of raw protein in the grain for the 8 parental forms (Table 1), the reciprocity effects for the 2 characters in the 28 pairs of inbred lines have been determined and analysed.

The results obtained show that there are significant differences between the direct hybrids and the reciprocal ones regarding the grain yield and the content of raw protein in the grain.

Concerning the grain yield, the reciprocity effects have statistical significance thresholds for 9 pairs of inbred lines (Lc 257 and Lc 402; Lc 257 and Lc 403; Lc 257 and Lc 407; Lc 402 and Lc 407; Lc 403 and Lc 404; Lc 403 and Lc406; Lc 403 and Lc 407; Lc 403 and Lc3/Dxx; W153R and Lc3/Dxx) (Table 2).

Table 1. The grain yield and the content of raw protein

Genotype	Grain yield(q/ha)	% raw protein
Lc 257	25.3	10.00
Lc 402	28.4***	10.5
Lc 403	31.6***	10.6
Lc 404	17.4000	12.1***
Lc 406	16.4000	11.4*
Lc 407	18.800	10.3
W 153R	26.8**	10.8
Lc 3/Dxx	21.4	10.00
Average (control)	23.3	10.7
Dl 5%	2.6	0.6
Dl 1%	3.4	0.7
Dl 0.1%	4.5	1.3

Table 2. Reciprocity effects concerning the characters grain yield (x_1) and the content of raw protein in the grain (x_2).

Pairs of inbred lines (i. j) from hybrid combinations	X_1 Grain yield (q/ha)			X_2 % raw protein in the grain		
	Combination			Combination		
	Direct i x j	Reciprocal j x i	r_{ij}	Direct i x j	Reciprocal j x i	r_{ij}
257x402 402x257	52.4	39.8	6.3***	9.9	10.6	-0.3
257x403 403x257	51.5	43.3	4.1*	9.8	11.3	-0.7^{0}
257x404 404x257	44.5	37.9	3.3	10.8	10.6	0.1
257x406 406x257	43.3	40.5	1.4	10.9	10.9	0
257x407 407x257	48.4	35.0	6.7***	10.1	11.3	-0.6^{0}
257xW153R W153Rx257	50.1	45.1	2.5	9.8	10.2	-0.2
257x3/Dxx 3/Dxxx257	37.6	40.0	-1.2	10.2	12.1	-0.9^{00}
402x403 403x402	39.5	48.0	-4.2^{0}	11.0	10.1	0.4
402x404 404x402	41.5	34.4	3.5	11.0	10.6	0.2
402x406 406x402	41.0	36.6	2.2	9.7	10.7	-0.5
402x407 407x402	52.3	34.4	8.9***	10.0	11.5	-0.7^{0}
402xW153R W153Rx402	44.3	39.6	2.3	10.3	11.0	-0.3
402x3/Dxx 3/Dxxx402	34.8	47.3	-6.2^{00}	10.8	9.9	0.4
403x404 404x403	48.6	38.1	5.2**	12.0	11.2	0.4
403x406 406x403	44.6	30.3	7.1***	10.7	11.8	-0.5
403x407 407x403	38.5	30.3	4.1*	10.8	11.0	-0.1
403xW153R W153Rx403	33.3	34.5	-0.6	10.1	11.6	-0.7^{0}
403x3/Dxx 3/Dxxx403	44.9	32.3	6.3***	10.2	11.4	-0.6^{0}
404x406 406x404	28.8	32.0	-1.6	11.7	12.7	-0.5
404x407 407x404	31.8	32.7	-0.4	12.2	12.6	-0.2
404xW153R W153Rx404	35.2	31.0	2.1	10.8	12.8	-1.0^{00}
404x3/Dxx 3/Dxxx404	35.5	31.6	1.9	12.0	12.2	-0.1
406x407 407x406	30.3	28.7	0.8	11.7	11.8	0
406xW153R W153Rx406	33.5	37.0	-1.7	11.5	11.6	0
406x3/Dxx 3/Dxxx406	29.2	40.7	-5.7^{00}	11.8	11.6	0.1
407xW153R W153Rx407	31.7	42.7	-5.5^{00}	10.9	10.3	0.3
407x3/Dxx 3/Dxxx407	37.2	31.5	2.8	10.6	11.1	-0.2
W153Rx3/Dxx 3/DxxxW153R	43.6	30.0	6.8***	10.2	9.5	0.3
Dl 5%	3.6			0.6		
Dl 1%	4.8			0.8		
Dl 0.1%	6.3			1.1		

In the combinations studied, the inbred Lc 257 has the ability to transmit the production capacity character when it is used as female, but has no negative effects on the percentage of raw protein in the grain. The same thing is true of the lines Lc 402 and Lc 403 in the combinations Lc 402 and Lc 407; Lc 403 and Lc 406; Lc 403 and Lc 407; Lc 403 and Lc3/Dxx.

But in the combination Lc 403 x Lc 404, the line Lc 403, when used as a female, transmits to the descendent F1 both production capacity and the percentage of raw protein in the grain characters.

This aspect is more obvious for the inbred line W 153R, which in combination with line Lc 3/Dxx, transmits in the maternal form a production capacity very significant from a statistical point of view, and also transmits the percentage of raw protein in the grain character.

For this character (% raw protein in the grain), the negative

reciprocity effects that turn up in most of the pairs of inbred lines suggest that the inversion of the parental forms would improve the percentage of raw protein in the grain in the descendant F1.

We could say that, for the set of analysed lines, the reciprocity effects were more frequent for the production capacity (grain yield) character, than for the procentage of raw protein in the grain.

For two or more characters that are going to be improved simultaneously we can infer the necessity of preservation of the reciprocity effects in a positive direction for all the characters. In our case, this fact is obvious for the pairs of lines Lc 403 and Lc404; W 153R and Lc3/Dxx.

The existence of some positive effects of reciprocity that are simultaneous for the production capacity and the percentage of raw protein in the grain characters permits us to obtain some maize cultivars that are able to join harmoniously the two characters in the same genotype.

The influence of climatic conditions upon the grain yield and the content of raw protein in the maize grain

--Bonea, D, Urechean, V, Naidin, C

Maize is a plant with vast usage but it is also very diverse.

From the dent grain to the flint, sweet, popcorn, waxy, or floury, the breeders and the users have the possibility to choose in concordance with various industrial goals.

Corn with more and better quality protein for improved nutrition appears promising.

Both the grain yields and the content of raw protein in the grain are governed by a complex of genes, which can be expressed or not depending on the multitude of factors that act in the maize plant through the entire vegetative period.

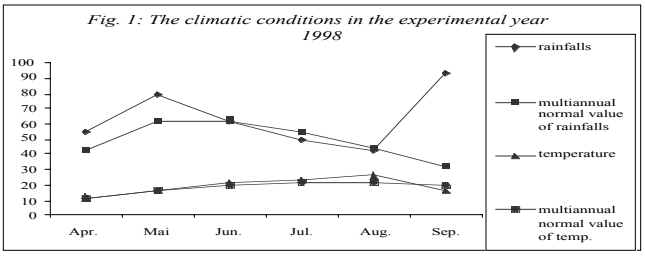
The climatic conditions (temperature, rainfall) represent only a part of the factors that influence the metabolic processes.

In order to obtain commercial maize hybrids with a high content of raw protein, the breeder must know their parental forms (inbred lines) well.

In our study, we analysed the grain yield and the content of raw protein in the grain for 8 inbred lines over the course of 2 years (1998, 1999), with different climatic conditions, in order to use these genotypes as parental forms for commercial hybrids with a high content of protein.

The agricultural year 1997-1998 was an excessively rainy year, both in the cold period (October 1997-March 1998 = +52.8 l/mp. in comparison with the multiannual average) and in the maize vegetative period.

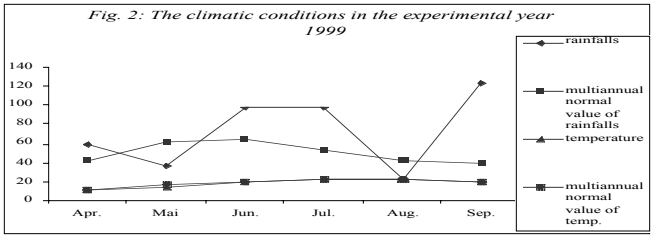
The rain separated two intervals of drought: the first, in the third week of June and the first week of July (Figure 1), when the development of the flowery parts and the flowering of the maize takes place; the second interval of drought, in the first and second weeks of August, when the development and the filling process of the grains takes place.



The thermic regime was the limiting factor prevalent in the production's realization. We can say that the thermic stress which the plants had been submitted to nullified the excess of rainfall to a great extent so that, after the flowering period, the plants dried off visibly because of the stifling heat (when the temperature was 38 C in the meteorology shelter and over 50 C at the level of soil and leaves).

In these circumstances, we can say that 1998 was an unfavourable year for the maize culture (droughty year). 1999 was a favourable year for maize culture.

In the period of maximum vegetative development, flowering and grain development (in June-July) the rainfall amount was excessive (Figure 2) and permits the realization of a good grain yield.



The difference between the grain yield of the two experimental years in the 8 genotypes (inbred lines) studied is obvious.

The drought year 1998 is a remarkable one from the point of view of production capacity. Lc 403 produced 31.6 q/ha, Lc 402 produced 28.4 q/ha, W153R produced 26.8 q/ha, and the lowest production was obtained in Lc 404 and Lc 406 (Table 1).

Table 1. The grain yield and the content of raw protein in the grain

Genotype	Grain yield (q/ha)		% raw protein	
	1998	1999	1998	1999
Lc 257	25.3	30.1 ^{00}	10.0 ^{0}	9.8
Lc 402	28.4***	35.3	10.5	9.8
Lc 403	31.6***	40.1*	10.6	10.1
Lc 404	17.4 ^{000}	32.1	12.1***	10.7*
Lc 406	16.4 ^{000}	30.6 ^{00}	11.4*	11.5***
Lc 407	18.8 ^{00}	35.7	10.3	10.2
W 153R	26.8**	40.0**	10.8	9.6 ^{0}
Lc 3/Dxx	21.4	42.2***	10.0 ^{0}	9.8
Average (control)	23.3	35.7	10.7	10.2

The average production for the genotypes studied is 23.3 q/ha, in comparison with 35.7 q/ha in the favourable year 1999.

The inbred line Lc 406 still remains in 1999 a genotype with a low production potential, but has the highest content of raw protein (11.5 %) of all the genotypes studied.

Lc 3/Dxx has the highest grain yield (42.2 q/ha), but the content of raw protein diminishes in comparison with the drought year from 10.0 to 9.8 %.

If, in conditions of drought and water stress, the average grain yield is diminished by 35%, the content of raw protein in the grain will rise 4% in comparison with the average protein of 1999, a year favourable to maize culture.

Though in stress conditions, the maize plant accumulates a high quantity of protein (probably as a measure of protection), the correlation between the production capacity and the content of raw protein in grain is much better expressed in the circumstances

of a year favourable to maize culture (r=-0.568) in comparison with a drought year (r=-0.456).

It is obvious that, for all the genotypes studied, the quantity of raw protein rises in inverse proportion to the production capacity, so that genotypes such as Lc 404 and Lc 406 can be used in maize improvement programs as germplasm sources for the improvement of the content of raw protein in the grain.

The selection of maize genotypes depending on the intensity of transpiration and the capacity of foliar absorption

--Urechean, V, Bonea, D

During their entire life, plants absorb water from the medium continously, and the water is eliminated mostly in the process of transpiration.

The existence of such a water circuit in the plant's body is an essential condition for the metabolic activity and also for the plant's survival.

In summer heat, a maize plant can eliminate a quantity of water that could exceed the water content of the entire plant in one hour (D. Dorobantu, Plant Physiol. 72, 1977).

These large quantities of water eliminated by transpiration have to be analysed in connection with the other physiological processes. The transpiration participates in the passive absorption of the water, causes the ascending circulation of water and mineral nourishing substances, provides the normal turgidity of all cells, provides the constant maintenance of the vegetable organism's temperature and does not permit the heating of the tissues.

In order to provide this water, the plant absorbs water permanently from the external medium not only through the root (which is the specialised organ for this function), but also through the aeral organs. Leaves absorb water intensely due to their anatomical particularities.

The quantity of water (dew, rainfall) absorbed by leaves is insufficient for the normal activity of plants (5-10% of the necessary quantity) but, when leaves are young and have a thin coat of cuticle, the absorption can attain approximately 50% of the necessary quantity of water (D. Dorobantu, Plant Physiol. 64, 1977).

If every physiological process is determined and genetically controlled and the plant's metabolism on the whole has a genetic determination, the question is:

-Is the selection of genotypes, in all their complexity, possible by analysing distinct physiological aspects that provide the functionality of the plant's body as a whole?

In this work we tried to analyse two physiological aspects: the transpiration and the leaf absorption of 8 inbred lines of maize in different vegetative stages.

As far as these physiological characters can be correlated or not with the production capacity and the index of drought sensibility (characters that have a complex genetic determination),we'll be able to select easier and faster valuable genotypes from the point of view of drought resistance and also of production capacity.

The index of drought sensibility was calculated after the Morizet's formula (J. Morizet et al., Colloque Phisiologie du mais: INRA 493-501, 1990).

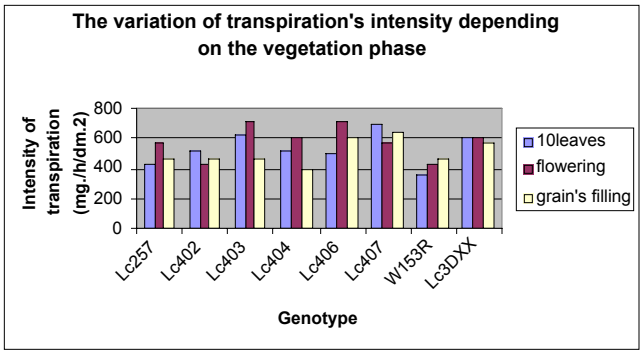
The transpiration's intensity varies between very large limits during the day (Table 1), having a maximum at 12 o'clock a.m. and then decreasing towards 5 o'clock p.m., but also varies from one vegetative stage to another. The most intense transpirations registered in the flowering period (Graph 1).

Lc406, Lc407 and Lc3DXX have maximum values of transpiration in the ten leaf stage at 10 o'clock a.m. After that transpiration continues to decrease towards the evening in Lc406 and Lc407, although in Lc3DXX transpiration intensity increases again after midday.

In the flowering period, the only genotype that makes an exception from the general rule is Lc257, whose lowest value of transpiration intensity is at 12 o'clock a.m.

The genotype's specificity in the determination of the daily and seasonal transpiration intensity becomes obvious.

It is well known that plants that transpire more intensely have a more active photosynthesis and grow more intensely, a fact that is obvious in the genotypes studied until the flowering period.



Graph 1.

Table 1. The intensity of transpiration of maize inbred lines (mg water/h/dm^2)

Vegetative phases	Hour	Genotype																
		Lc257	±x	Lc402	±x	Lc403	±x	Lc404	±x	Lc406	±x	Lc407	±x	W153R	±x	Lc3Dxx	±x	X
10 leaves	10a.m	108		144		198		252		216		270		108		252		
	12a.m	198		198		252		144		144		234		126		162		
	6p.m.	126		180		180		126		144		198		126		198		
Total		432	-103.5	522	-1.5	630	76.5	522	-1.5	504	-49.5	702	148.5	360	-193.5	612	58.5	553.5
Flowering	10a.m	216		108		216		144		108		144		108		144		
	12a.m	144		144		216		288		324		252		144		216		
	6p.m.	216		180		288		180		288		180		180		252		
Total		576	-9.0	432	-153.0	720	135.0	612	27.0	720	135.0	576	-9.0	432	-153.0	612	27.0	585.0
Grain filling	10a.m	144		144		144		144		144		252		144		180		
	12a.m	144		204		180		180		324		288		216		288		
	6p.m.	180		108		144		72		144		108		108		108		
Total		468	-43.5	456	-55.5	468	-43.5	396	-115.5	612	100.5	648	136.5	468	-43.5	576	64.5	511.5

X=average
±x = difference from the average (control)

The production capacity (grain yield), whose elements form and finalize in this vegetation period, seems to be influenced by the transpiration intensity from the period before flowering (correlations between production and transpiration intensity in the ten leaf stage are positive) (Table 3).

In the ten leaf stage and also in the flowering period, Lc 403 and Lc3DXX present a positive difference in the intensity of transpiration (Table 1) in comparison with the average, a fact that might be an explanation for the good production realized by these genotypes. The other genotypes (the rest of them) have either negative values in comparison with the control, or one positive value and the other negative.

Less important is the grain filling phase because the production elements are already finalized.

The difference between the ten leaf stage and the flowering period concerning the (total) intensity of transpiration varies from one genotype to another (from +216 to –90 mg water/h/dm^2).

The great effort of the plant to increase the intensity of transpiration in this period of intense growth and finalization of production, with 216 mg/h/dm^2 (Lc406) and 144 mg/h/dm^2 (Lc 257), can be interpreted as a large consumption of energy and has lots of implications in the lessening of the production capacity (grain yield) (Graph 2).

The capacity of water's foliar absorption is more intense in the first vegetation phases when the leaves are younger and have a thinner cuticle.

It also decreases in the flowering period and rises very easily in the grain filling period (Table 2).

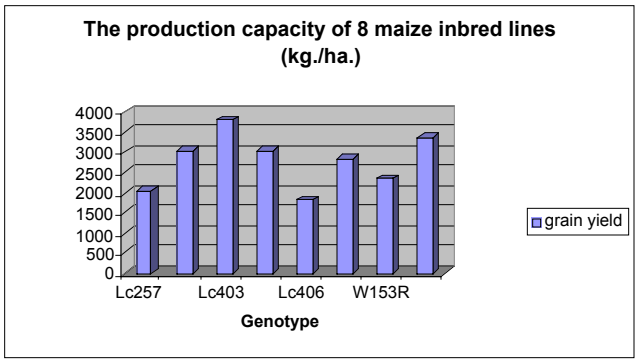
The diminution of the leaves'capacity for absorption is obvious during the vegetation period due to the aging of the leaves and thickening of the cuticle, but also to the reduction of the foliar surface as a result of the basic drying of the leaves.

This is probably the explanation for the increase of the foliar absorption from the flowering period to the grain filling period.

The highest difference between these two periods of development is present in Lc3DXX (1 g/100 g fresh substance) and Lc 403 (0.87 g/100 g fresh substance) which also have the best production (grain yield).

By analysing the correlations between the water's foliar absorption (in three vegetative phases), the intensity of transpiration (in three vegetative phases at different hours of the day), the production capacity (grain yield) and the index of drought sensibility (Table 3), we can observe that:

-There is a negative correlation between the capacity of foliar absorption (in all the vegetation phases) and I.S. (the index of drought sensibility).



Graph 2.

Table 2. The capacity of water's foliar absorption in different vegetation phases (g water/100g fresh substance)

Genotype	10 leaves	flowering	Grain filling
Lc 257	6.08	5.03	5.1
Lc 402	6.1	5.2	5.37
Lc 403	6.42	5.1	5.97
Lc 404	6.89	5.27	6.1
Lc 406	7.5	6.93	7.15
Lc 407	7.52	7.15	7.34
W153R	8.5	6.21	6.92
Lc3DXX	8.71	7.1	8.1

Table 3. The correlation between the capacity of foliar absorption, the transpiration intensity, the grain yield and the index of drought sensibility

Genotype	10 leaf c.a.	flow. c.a.	g. filling c.a.	grain yield	I.S.	10 leaf i.t. (10)	10 leaf i.t. (12)	10 leaf i.t. (6)	flow. i.t. (10)	flow. i.t. (12)	flow. i.t. (6)	g. fill. it. (10)	g. fill. it. (12)	g. fill. it. (6)
Lc 257	6.08	5.03	5.10	2030	0.785	108	198	126	216	144	216	144	144	180
Lc 402	6.10	5.20	5.37	3030	0.767	144	198	180	108	144	180	144	204	108
Lc 403	6.42	5.10	5.97	3810	0.821	198	252	180	216	216	288	144	180	144
Lc 404	6.89	5.27	6.10	3005	0.701	252	144	126	144	288	180	144	180	72
Lc 406	7.50	6.93	7.15	1830	0.739	216	144	144	108	324	288	144	324	144
Lc 407	7.52	7.15	7.34	2820	0.663	270	234	198	144	252	180	252	288	108
W153R	8.50	6.21	6.92	2329	0.720	108	126	126	108	144	180	144	216	108
Lc3DXX	8.71	7.10	8.10	3383	0.763	252	162	198	144	216	252	180	288	108
		0.801	0.911	-0.052	-0.413	0.290	-0.539	0.135	-0.483	0.176	0.033	0.314	0.643	-0.374
			0.930	-0.184	-0.533	0.526	-0.239	0.401	-0.490	0.435	0.147	0.638	0.935	-0.192
				0.065	-0.434	0.599	-0.298	0.406	-0.420	0.443	0.213	0.527	0.843	-0.345
					0.288	0.401	0.495	0.638	0.289	-0.050	0.108	0.143	-0.165	-0.378
						-0.432	0.312	0.053	0.552	-0.388	0.604	-0.607	-0.424	0.606
							0.127	0.513	-0.086	0.790	0.180	0.585	0.563	-0.480
								0.596	0.628	-0.146	0.162	0.395	-0.211	0.346
									0.007	0.041	0.182	0.628	0.443	-0.140
										-0.178	0.327	-0.053	-0.578	0.578
											0.382	0.208	0.568	-0.242
												-0.246	0.295	0.531
													0.500	-0.218

10 leaf c.a.-capacity of foliar absorption at ten leaf stage; flow. c.a.-capacity of foliar absorption at flowering period; g. filling c.a-capacity of foliar absorption at grain filling period; I.S.-the index of drought sensibility; 10 leaf i..t. (10)-intensity of transpiration at ten leaf stage, 10 a.m.; 10 leaf i..t.(12)-intensity of transpiration at ten leaf stage,12 a.m.; 10 leaf i..t.(6)-intensity of transpiration at ten leaf stage, 6 p.m.; flow. i..t.(10)-intensity of transpiration at flowering, 10 a.m.; flow. i..t.(12)-intensity of transpiration at flowering, 12 a.m.; flow. i..t.(6)-intensity of transpiration at flowering, 6 p.m.; g. fill. it.(10)- grain filling, 10 a.m.; g. fill. it. (12)- grain filling, 12 a.m.; g. fill. it. (6)- grain filling, 6 p.m.

-In the ten leaf stage, the lower the capacity of absorption, the higher the intensity of transpiration (r =-0.539, the ten leaf stage, 12 o'clock a.m.).

-There is a positive correlation between the capacity of foliar absorption in all vegetation phases and the intensity of transpiration in the grain filling period at 12 o'clock a.m., and even between the capacity of absorption in the flowering period and the intensity of transpiration in the grain filling stage at 10 o'clock a.m. (r =0.638).

-The production (grain yield) seems to be positively correlated with the intensity of transpiration in the ten leaf phase at 6 o' clock p.m. (r =0.638).

-If the index of drought sensibility can be negatively correlated with the intensity of transpiration in the grain filling period at 10 o'clock a.m. (r =-0.607), things change radically at 6 o' clock p.m. (r =0.606), and the same phenomenon is observed even in the flowering period at 6 o'clock p.m. (r =0.604).

-The higher the intensity of transpiration in the grain filling phase (at 10 o'clock a.m.), the higher it was in the ten leaf phase (at 10 o'clock a.m., r =0.585).

-A correlation of the same intensity, but contrary was observed between the transpiration intensity (at 10 o'clock a.m., flowering stage) and the transpiration intensity in the grain filling period (at 12 o'clock a.m., r =-0.578) and at 6 o'clock p.m. (r =0.578).

The analysis of these results shows that sometimes there are totally unexpected correlations between the physiological processes during the vegetation period, a fact that proves the complexity of the genetic factors implied in the coordination of these processes .

Since the goal of every improvement process is to obtain genotypes with a better production capacity (grain yield), but also with a genetic resistance to stress factors (drought, in our case), it is important to observe the physiological aspects in their interaction, during the vegetation period, in order to determine a genotype that presents the most favourable characters.

The relationship between the genotype, the changes of the suction force in different phases of maize development, and the production capacity

--Urechean, V, Bonea, D

In order to provide themselves with water from the soil, plants need a force to take out the water from the soil's particles. This is the suction force.

The values of the suction force vary depending on the plant's water deficit which, in turn, is determined by the medium where the plant is being cultivated, the species and even by the genotype. In this paper we want to analyse the relationship between the genotype and the suction force at the leaf's level in different vegetation phases as a criterion of fast, early and efficacious selection of the maize genotypes (parental forms) with a good production capacity.

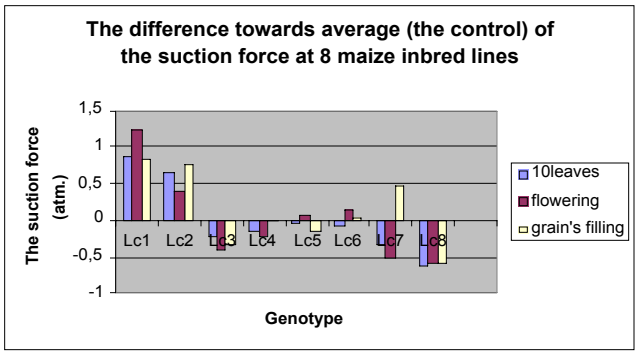
The suction force (S.F.)increases with the age of plants (Table 1), and this increase can be considered as being determined by the increase of the foliar surface and by the aging of the protoplasmic colloids (when the ability to retain water diminishes and the plant loses water more easily).

There are differences toward the average from one genotype to another for all 3 vegetation phases (Graph 1).

For Lc 1, Lc 5 and Lc 6 the increase of the suction force (S.F.)

Table 1. The suction force in different phases of maize vegetation (atm.)

Genotype	10 leaves	Flowering	Grain filling
Lc 1	4.18	4.88	4.90
Lc 2	3.96	4.08	4.81
Lc 3	3.07	3.27	3.74
Lc 4	3.15	3.45	4.06
Lc 5	3.27	3.72	3.91
Lc 6	3.25	3.81	4.1
Lc 7	2.97	3.15	3.61
Lc 8	2.68	3.07	3.48
Average	3.31	3.67	4.07



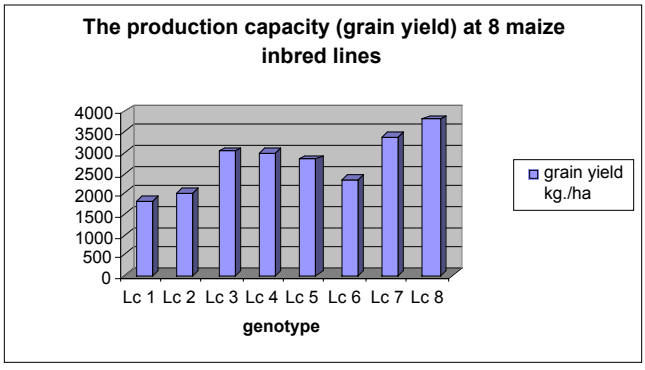
Graph 1.

is higher from the ten leaf phase to the flowering period than from the flowering period to the grain filling phase, when despite the continuing growth of the leaves, drying of the basic leaves occurs, which diminishes the active foliar surface.

The values of the suction force at every phase show that Lc1 and Lc 2 lose water more easily, and as a consequence, present a higher sensitivity to drought and intense heat.

The genotypes that retain water the best are Lc 8, followed by Lc 7 which, even in the flowering period and in the grain filling period when the soil's water deficit is very large due to the very high temperature, still have the lowest values of suction force.

This water retention by the plant could be a sign that the genotype has the capacity to turn to good use water in the metabolic processes, which in the end is found again in the production of grains obtained (Graph 2).



Graph 2.

Before knowing the production capacity of a genotype it is important to know some physiological aspects that are more easily and more rapidly analysed in an early development phase. In the end, this information can be used in the selection work of the improver.

The correlation between the suction force in the 3 vegetation phases and the production capacity (ten leaf-grain yield: r =

-0.403; flowering period-grain yield: r = -0.507; grain's filling period-grain yield: r = -0.311), shows that the production potential of the genotypes studied increases in inverse proportion with suction force.

Once again we have confirmation of the fact that the production elements are being finalized during the flowering period (r = -0.507). A complex study of the plant's metabolism in this vegetation phase could supply us with signs that some characters are genetically controlled and determined, such as the production capacity.

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Screening of herbicide resistance in maize calli in vitro

--Nedev, T, Dimitrov, B, Kruleva, M, Krapchev, B, Nencheva, D

Immature maize embryos from several genotypes were screened for in vitro development and regeneration, and the A619 genotype was reported to have the highest regeneration ability (Todorova, L. et al., MNL 72:76, 1998). This genotype would allow in vitro selection for herbicide resistance. Vigorous weeds have been one of the main causes of crop losses ever since humans started to cultivate plants. Overall, more than one third of all agricultural production is still lost in the same proportion as a century ago (although, of course, the total production is much larger than it was then) (May, R.M., Nature 361:593-594, 1993). Stomp 330 (a product of BASF) is a dinitroanilin herbicide (active substance pendimetalin-N-(1-ethyl-propyl) 3-4 dimethyl-2, 6-dinitroanilin) with a wide range of action, mainly against annual cereals and some dicotyledonous weeds of many crops, vegetables and fruits and vines. A positive effect of this herbicide was observed on the following major crops: maize, wheat, barley, cotton, soy bean, beans, sunflower etc. The mechanism of the action of pendimetalin includes inhibition of the proliferation of root and stem meristemic tissue cells, as well as their elongation. For early selection of herbicide resistance, a laboratory method is highly desirable. The larger number of calli that can be screened, and the limited space that is needed, make the application of in vitro selection an attractive approach. There have been several attempts to create bioassays in which resistance at the tissue culture level can be used as an indicator for resistance of whole plants (Dryanova and Dimitrov, Cytologia 65:17-23, 2000; Kosturkova et al., Proceedings of 4th European Conference on Grain Legumes, pp. 158-159, 2001; Vasic et al., Helia 25(36):145-152, 2002). A correlation between the response of the explants of the same genotypes, when grown on medium to which the herbicide was added, and field resistance of genotypes was found.

In this paper, we describe a method for in vitro screening for resistance to herbicide Stomp 330 by culture of immature maize embryos. Maize inbred genotype A619 was used in our investigations. For phytotoxicity studies, maize control calli were aseptically grown on N6 medium without Stomp 330. Stomp 330 was supplemented to the medium for calli induction after filter sterilization. Treated calli were grown on N6 medium containing different concentrations (0.26%, 0.10%, 0.05% and 0.01%) of Stomp 330. The highest concentration was comparable with that applied in field use. The effect of herbicide on calli development was estimated visually by morphogenetic response after 21 days.

Table 1. Frequency of callus induction and regenerable callus after herbicide treatment.

Genotype	Concentration of Stomp 330 (%)	Total number of embryos inoculated	Undeveloped embryos (%)	Fresh calli (%)	Organogenic calli (%)
A619	0% (Control)	332	12.33±1.48	60.86±1.17	26.77±1.16
	0.01 %	300	72.00±1.48*	28.00±1.70*	0
	0.05 %	324	100.00	0	0
	0.10 %	312	100.00	0	0
	0.26%	340	100.00	0	0

*Significant at P>99.90%.

The experimental materials were separated into three groups: *organogenic calli* – with clear formation of green structures, and leaf-like shoots; *fresh calli* - without evidence of organ - embryogenesis; *undeveloped embryos* - immature embryos without any kind of growth. Each experimental treatment variant included at least 150 embryos and was repeated twice. The statistical significance of differences between the data obtained from the treated embryos and the controls was made by Least Squares analysis (programmes LSML90, Harvey, 1990, Users Guide for LMSLMW Computer Program, PS2 version, Ohio, Modified model for unbalanced data according to Nencheva, D., 2001, Induction of Genetic Variability in *Chrysanthemum marifolium* Ram., Through Radiation Mutagenesis and In Vitro Techniques, Ph. D., Sofia).

Primary choice of Stomp 330 concentrations was made based on the research of Dryanova and Dimitrov (2000) which was done with triticale callus cultures. In our study, concentrations between 0.26%, 0.10% and 0.05% exerted a negative effect on tested genotype parameters. These explants did not grow, and died after 21 days. In the Dryanova and Dimitrov (2000) study, the concentration of 0.01% of Stomp 330 was efficient for some triticale genotypes with high ploidy levels. The high sensitivity of the maize A619 genotype to the above-mentioned concentrations was evidenced by the percentage of callus induction and the reduced in vitro growth rates. The loss of the ability to form regenerative calli can be explained cytologically by a lack of actively proliferating cells, and histologically by a lack of shoot meristems. Our attempt to control these events by different manipulations including treatment with 2, 4-D levels failed.

Maize calli from inbred line A619, resistant to herbicide Stomp 330, were obtained by using the method of in vitro selection of mutant cells. The resistance was proven at a concentration of the herbicide of 0.01%. The present study seems to be applicable as a preliminary step in the production of resistant plants. The results obtained will also be useful for investigations on environmental protection, and for more information about control of weeds.

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***Tripsacum* stage- and ploidy-specific floral cDNA Libraries**

--Goldman, SL[1], Blakey, CA[2], Frutiger, K[1], Dewald, CL[3], Sokolov, VA[4]

Using the pilot project designed at Ball State University (BSU), Muncie, IN, by Blakey et al. (MNL 77), a set of five out of

six possible stage-specific cDNA libraries were constructed at the Univ. of Toledo using the SMART™ PCR cDNA Synthesis Kit (CLONTECH Cat# K1052-1) at the University of Toledo. The original RNA was isolated in 1998 by Blakey et al. (MNL 77) on-site in Woodward, OK, according to the Trizol™ RNA isolation protocol provided by Sigma. The materials were quantitated at BSU and half were shipped to the U. Toledo. Each library was labeled according to the staged tissue from which the RNA was isolated: "E" early diploid (E2) or early tetraploid (E4), "M" middle diploid (M2), and "L" late diploid (L2) or late tetraploid (L4). The only library that was not obtained at this time was the "M" middle tetraploid (M4) library. Twenty-five cDNAs from these libraries were shipped to the DNA Core Facility, Ohio State University, Columbus, OH, for sequencing.

Sequence data analysis of clones from the E2 and M2 libraries indicates that the libraries include genes that function as a serine threonine protein kinase and ribosomal protein S1Sa mRNA respectively. Clones from the E4 and L2 libraries have resulted in chloroplast gene sequences, while a clone from the L4 library was considered novel at the time of this article.

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ZmGrp3 is exclusively expressed in epidermal cells of the root-tip and the columella

--Woll, K, Hochholdinger, F

A full length cDNA of *ZmGrp3* (*Zea mays Glycine rich protein 3*) was isolated in a differential screening of a cDNA-library of maize coleoptilar nodes. Northern-blot analyses showed that *ZmGrp3*-RNA exclusively accumulates in roots (Goddemeier, M. et al., PMB 36:799-802, 1998). Mutants affected in lateral root (*lrt1*) (Hochholdinger, F. et al., Plant J. 848- 855, 1998) or crown root initiation (*rtcs*) (Hetz, W. et al., Plant J. 247-255, 1996) were used to study the root-specific expression of *ZmGrp3* in more detail. For *lrt1* and its homozygous wild-type siblings RNA from consecutive 2 cm sections of the primary root, beginning at the root-tip, was isolated. In wild-type primary roots, hybridization signals were found in all sections along the whole primary root. However, in primary roots of the lateral-rootless mutant, *lrt1*, expression of *ZmGrp3* was restricted to the first section containing the primary root-tip. For *rtcs* and its corresponding wild-type siblings, RNA was isolated from coleoptilar nodes. *ZmGrp3* expression was detected in wild-type coleoptilar nodes, but not in coleoptilar nodes of the mutant *rtcs*, which do not form any crown roots (data not shown). These results indicate that *ZmGrp3* expression is limited to root-tips.

To support this hypothesis in situ hybridization experiments with root-tissues of the maize inbred line B73 were conducted using a DIG-labeled *ZmGrp3*-RNA probe. Hybridization signals were observed in epidermal and columella cells of the root-tips in primary, lateral and crown roots at different developmental stages and in the root-tips of embryos 30 days after pollination (Fig. 1). Analyses on protein level, including western-blot analyses and immunolocalization experiments, are in progress.

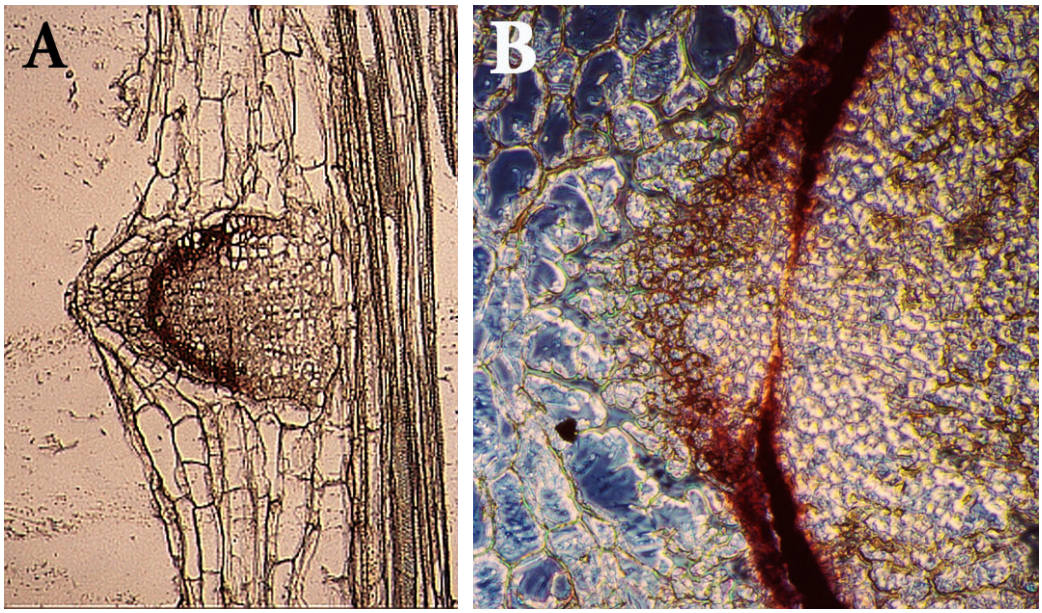

Figure 1. In situ hybridization of B73 roots with a DIG-labeled *ZmGrp3*-RNA-probe
A. Lateral root emerging from a primary root; 6 days after germination; longitudinal section; antisense probe
B. Crown root emerging from a coleoptilar node; 5 days after germination; cross section; antisense probe

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The use of cytoplasmic male-sterility in maize seed production

--Has, V, Has, I, Grecu, C

The use of cytoplasmic male sterility (cms) in maize hybrid seed production is of economic importance and is also advantageous for genetic purity of seeds. Three types of male sterile cytoplasms in maize are used as cms maternal parents to produce hybrids: cms-C, cms-S, cms-T. The concern that in a few years all maize might again be in C or S cytoplasms gave rise to ideas as to how to prevent this narrowing of the cytoplasmic gene base. Thus, a new technique of producing hybrids was proposed, using *multiplasm*, respectively a blend of several kinds of male sterile cytoplasms. The aim of this investigation was: 1) to detect the presence of dominant *Rf* genes in more than 600 inbred lines by crossing with different types of cms: C, ES, M, T; 2) to compare some registered "TURDA" hybrids developed with normal and cms and/or *Rf* parental forms, in different environmental conditions, for three agronomic traits. Restoration reactions of 600 inbreds lines on the cms: C, ES, M and T were scored using Josephson's scale (Josephson et al., 1978). The observations were performed at the Agricultural Research Station-Turda, between 1995-2001. Nine registered "Turda" hybrids carrying both fertile and sterile cytoplasms were grown in two years at five locations.

When using cms in maize breeding programs it is as necessary as it is difficult to identify the inbred lines by their composition of *Rf* genes. Identifying restorers of cms-C and cms-ES becomes much more complicated, due both to the involvement of at least two-three complementary *Rf4*, *Rf5*, *Rf6* genes, and to certain modifying factors, probably quantitative ones which, in some specific environmental conditions, act in the absence of the *Rf* gene, influencing the reactions of lines by the "late-break" phenomenon. The percentage of non-restorer genotypes was 40% both to cms-C and to cms-ES (Table 1).

Table 1. The distribution of inbred lines according to their reaction in crosses to four cms types.

			% inbred lines			
cms types	No. cms tester lines	No. studied lines	Non restorers	Restorers		Different reactions
				partially	fully	
cms-C	5	198	34	4	55	7
cms-ES	3	94	35	5	51	9
cms-M	2	121	20	33	20	27
cms-T	7	223	74	1	16	9
Total-studied lines		636				

121 inbred lines have been tested with cms-M, only 20% of them being identified as *Rf3/Rf3*. The inbred lines which partially restore fertility or have a variable reaction according to the environmental conditions represent 27% of the inbred lines tested with cms-M. Because cms-T is only used in areas less favorable to the disease caused by *Helminthosporium maydis* T-race, research on the use of this cms type is limited. Table 2 presents the synthetic results of the comparison between the cytoplasmic (N or cms) effects on certain agronomic traits of registered hybrids developed at the Agricultural Research Station, Turda, Romania. Trial conditions (years, locations) have emphasized a series of significant differences between the two cytoplasms as far as grain yield is concerned. These differences are greatly determined by nuclear-cytoplasmic interaction or by hybrid x local conditions interaction.

Table 2. Cytoplasmic male sterility effect for some traits in 9 registered "TURDA" hybrids.

Hybrid	Cytoplasms	Grain yield q/ha	Dry matter of grain %	Erect plants at harvest %	Synthetic relative index %
1	2	3	4	5	6
Turda-SU 182	N	98.6	76.6	85.4	100
	cmsC	95.0	77.1	79.3	90
	(%)cms/N	96	101	93	-
Turda-Mold 188	N	101.1	77.7	79.0	100
	cmsC	97.3	77.9	81.8	100
	(%)cms/N	96	100	103	-
Turda Super	N	85.1	75.3	81.6	100
	cmsC	86.7	76.0	78.2	98
	(%)cms/N	102	101	96	-
Saturn	N	78.2	73.2	78.0	100
	cmsC	92.1	75.1	83.2	129
	(%)cms/N	118**	102**	107	-
Turda 215	N	97.5	76.0	73.5	100
	cmsT	86.2	74.4	70.0	82
	(%)cms/N	880	9800	95	-
Turda-SU 210	N	84.9	76.0	73.6	100
	cmsC	89.2	77.0	75.8	110
	(%)cms/N	105	101	103	-
Turda Favorite	N	93.3	75.8	80.7	100
	cmsC	104.5	74.7	74.3	102
	(%)cms/N	112*	99	92	-
Turda 198	N	102.1	76.8	76.1	100
	cmsES	101.2	76.5	75.5	98
	(%)cms/N	99	100	99	-
Turda 160	N	90.0	77.9	78.7	100
	cmsC	87.8	77.1	81.2	97
	(%)cms/N	97	99	100	-
Trial	N	92.3	76.1	78.5	100
mean	cms	93.4	76.1	77.7	100
	(%)cms/N	101	100	99	-

*** Significant at 5% and 1%, respectively
*Si%= {col.3x4x5(cms)/col.3x4x5(N)}. 100

The nine hybrids carrying cms did not differ generally from their counterparts with fertile cytoplasm (N) for yield and for two other traits.

Heritability of some yield components and kernel quality in sweet corn

--Has, V

Ten *sugary1* inbred lines developed at the Agricultural Research Station of Turda were chosen for this study (Table 1). They were crossed using the factorial (m n + n m) mating design with reciprocal combinations in order to estimate GCA and SCA for inheritance of some ear and kernel characteristics and kernel chemical composition (Tables 2, 3, 4), genetic value of parental inbreds, and phenotypic and genotypic correlations among traits. Genotype x year interactions influenced the expression of the most traits, emphasizing the importance of their evaluation in different years. The highly significant GCA mean squares for yield components points to the importance of additive gene action in the genotypes studied here. The significant SCA effects for all traits point to nonadditive gene action as well, although on the basis of comparative mean squares, additive gene action appears the more important. SCA variance was larger than GCA variance only for kernel chemical compositions and pericarp thickness. The predominance of SCA effects indicates that the pattern of

carbohydrate accumulation in a hybrid depended upon the specific interaction of inbred lines involved in the crosses. Reciprocal hybrid differences were detected for all kernel compositions analyzed. These differences should be attributed to an interaction of cytoplasm x nuclear genome. Our sugary parental lines TA 28, TA 22, TA 25 transmitted a large number of positive traits in their crosses. An unfavorable genetic correlation between sucrose - row number, total sugar - ear weight suggest that in breeding programs it's difficult enough to obtain high yield sweet corn hybrids with good quality.

Table 1. Pedigree and genealogy of the sweet inbred lines.

Nr. crt.	Inbred	Pedigree / Origin	Genealogy
1.	SW 87	SUA	-
2.	TA 22 su	Q 206 - Canada	3603-1-1-7-
3.	TA 27 su	Reward - SUA	5103-6-3-5
4.	TA 28 su	Golden Beauty - SUA	7188-1-1-3-
5.	TD 103 su	How Sweet It Is - SUA	7208-1-1-1-
6.	TA 25 su	Reward - SUA	3610-2-4-1-
7.	TA 26 su	Reward - SUA	5093-1-1-1-
8.	TD 101 su	Aux 5651 - SUA	3607-2-1-3-
9.	TD 282 su	Silver Queen - SUA	3870-10-2-1-
10.	TD 102 su	Aromatnaja - R.Moldova	7208-3-1-1-

Table 2. Genetic variances (s^2) involved in the expression of ear and kernel characteristics.

Source of variation	DF	Weight		Ear	Row	Ear	Kernel	Eating
		ear	husk	length	number	shape	depth	quality
TOTAL	547							
YEARS (Y)	1	38250.83**	12229.06**	8.61*	2.36**	8.61**	13.86*	12.66**
REPLICATION	2	262.84	306.42	0.80	0.35	1.02	5.49	5.97
ERROR (a)	2	79.91	220.25	0.43	0.36	1.12	3.81	0.17
GENOTYPES (G)	15	2490.48**	1029.45**	10.09**	17.98**	5.15**	5.76**	2.30**
-Additive actions (Am)	(3)	9672.33**	3114.74**	31.63**	58.47**	16.57**	10.99	3.45
-Additive actions (An)	(1)	6112.29**	3075.17**	41.67**	77.19**	20.53**	19.74**	4.08
-Non-additive actions (NA)	(3)	1854.22**	848.10**	1.35**	3.95**	1.42**	5.08**	2.27**
-Differences m/n	(1)	322.89	111.26	3.05*	2.62	0.38	4.33*	4.13**
-Maternal effects (Mm)	(3)	171.67	268.21**	1.06	1.62	1.13	1.28	2.21
- Maternal effects (Mn)	(1)	541.54**	289.81**	3.75	0.77	0.76	2.04	0.97
Reciprocal effects (R)	(3)	157.55	59.08	1.09**	1.56**	0.54	1.27*	1.05**
GENOTYPES x YEAR (G x Y)	15	1480.66**	333.71**	2.32**	3.26**	0.82**	6.52**	1.75**
- Am x Y	(3)	4611.29**	859.99*	8.20**	8.49**	1.79	17.32	3.08
- An x Y	(1)	3933.88*	485.81	4.71**	8.40**	1.13	9.33	2.55
NA x Y	(3)	1522.78**	339.50**	1.01**	1.37**	0.96**	7.57**	1.02**
- m/n x Y	(1)	239.63	213.12	0.41	1.21	1.24**	4.10	1.20**
- Mm x Y	(3)	84.69	95.95	0.68	2.37	0.52	3.12	1.96
- Mn x Y	(1)	307.73	222.88	0.64	2.07	0.20	3.13	2.29
- R x Y	(3)	154.58	178.74	1.42	1.28**	0.38	2.29**	1.08**
ERROR (b)	60	91.23	133.70	0.36	0.34	0.51	0.80	0.21

Table 3. Genetic variances (s^2) involved in the expression of some kernel and ear characteristics of sweet corn .

Source of variation	DF	Pericarp thickness	Pericarp Weight	Tip fill	Husk length	Flag leaves length	Plant sensitivity to Aphis sp.	Biotest for kernel sensitivity to F.moniliforme
TOTAL	47							
REPLICATION	2	172.40	0.37	0.04	0.07	2.08	114.38	54.87
GENOTYPES	15	3325.52**	6.37**	2.31**	20.61**	34.14**	752.81**	125.03**
-additive actions (Am)	(3)	3122.74	4.70	0.85	6.72**	28.22	1687.72	295.34*
-additive actions (An)	(1)	1354.69	2.43	25.23**	248.21**	376.88**	210.13	463.64*
-non-additive actions (NA)	(3)	2404.69**	18.39**	0.57	0.40	7.57	1661.97**	30.58
-differences m/n	(1)	5742.19**	0.80*	1.84*	1.02*	0.46	512.00*	11.19
-maternal effects (Mm)	(3)	4156.08	3.45	0.55	0.41	2.27	150.30*	26.44
-maternal effects (Mn)	(1)	379.69	5.07	0.48	0.48	2.66	50.00	23.13
-reciprocal effects (R)	(3)	4451.91**	2.54**	0.40	0.28	5.98	6.69	106.80
Error	30	79.06	0.19	0.31	0.21	3.45	106.19	44.80

Table 4. Genetic variances (s^2) involved in the expression of kernel quality of sweet corn .

Source of variation	DF	Kernel contents in:						
		dry matter	total sugar	sucrose	phytoglycogen	starch	protein	fats
TOTAL	179							
REPLICATION	5	1.66	0.10	0.001	0.001	0.25	0.01	0.01
GENOTYPES	87	14.56**	30.31**	2.27**	7.77**	45.56**	2.27**	0.67**
-additive actions (Am)	(11)	25.20	79.65	4.31	7.36	70.94	5.36*	1.47
-additive actions (An)	(10)	25.25	38.74	3.28	22.62	66.11	1.09	0.48
-non-additive actions (NA)	(20)	12.92**	39.31**	3.27**	6.15**	45.21**	2.09**	0.74**
-differences m/n	(5)	11.86**	9.85**	1.16**	3.04**	6.27**	1.37**	0.29**
-maternal effects (Mm)	(11)	11.97	12.72	0.98	2.76	27.98	1.55	0.41
-maternal effects (Mn)	(10)	6.47	5.96	0.83	5.44	26.29	1.54	0.75
-reciprocal effects (R)	(20)	11.13**	16.94**	1.34**	7.29**	50.83**	2.32**	0.44**
Error	87	0.27	0.09	0.001	0.001	0.35	0.001	0.01

Progress in development of maize inbred lines in Turda, Romania

--Has, V, Cabulea, I, Has, I

The maize breeding program at the Agricultural Research Station from Turda, Romania has been developed and finished during the years 1983-2001: 250 normal endosperm inbred lines, 11 *opaque2* endosperm inbred lines, and 20 *sugary1* endosperm inbred lines.

In developing the inbred lines, the following sources have been used: local open-pollinated populations and varieties, synthetic populations (unimproved sources), synthetic based on inbred lines, single and more complex hybrids, initial materials resulting from an improvement program (backcross progenies) of elite inbred lines, and a quality breeding program (Table 1). Some elite inbred lines were improved in a special program (recurrent selection) for resistance to stalk and ear rot, to European corn borer, for cold tolerance or were converted to various male-sterile cytoplasms and/or to restorer of fertility (Table 2).

Table 1. Proportion of the finalized inbred lines related to the origin of initial materials.

Origin of initial material	No.inbred lines	Ratio (%)
Open-pollinated populations, local varieties, synthetics	7	3
Composites	35	14
Backcross progenies	117	47
Hybrids	91	36
Total	250	100

Table 2. "Per se" value of some inbred lines developed at A.R.S.Turda, Romania, during 1983-2001.

							Inbred lines reactions to:	
Inbred line	Kernel type	No.days (sowing-silking) (W153R= 79days)	Stalk lodging (%)	Ear rot (note; 9=very good)	Ear length (cm)	No. kernel rows/ ear	cms C	cms T
Inbred lines developed from: open-pollinated populations, local varieties, synthetics								
TA 23	flint	72	10	3	12.0	12-14	Nrf	Nrf
TA 24	flint	72	10	3	12.5	12	pRf	Nrf
TB 330	flint	83	1	5	14.5	16	-	Nrf
Inbred lines developed from composites								
TD 230	flint	77	6	7	12.5	14-16	Nrf	Nrf
TD 266	dent	75	9	8	17.5	14-16	Rf	Nrf
TD 267	dent	76	6	4	15.5	18	Rf	Nrf
TD 275	dent	74	10	5	17.5	14	Rf	Nrf
TC 350	dent	74	6	4	13.5	18-20	Rf	Nrf
Inbred lines developed from backcross progenities								
TD 270	dent	80	0	5	17.0	12-14	Nrf	Nrf
TD 271	dent	81	0	5	16.0	14	Nrf	Nrf
TB 367	flint	77	11	7	14.0	16	Nrf	Nrf
TC 314	dent	79	3	4	13.5	14	Rf	Nrf
TC 316	dent	77	2	5	14.5	14	Nrf	Rf
TC 317	dent	77	7	6	14.5	14	Nrf	Rf
TC 321	dent	77	7	7	15.5	14	Nrf	Rf
TC 327	dent	77	10	6	16.0	16-18	Rf	Nrf
TC 328	dent	77	2	4	11.5	18	Rf	Nrf
TC 330	flint	88	6	6	13.5	20-22	Rf	Nrf
TC 335	dent	80	2	8	11.0	14-16	Rf	Nrf
TC 357	dent	81	2	4	14.5	14	Rf	Nrf
TC 362	dent	75	2	9	12.0	18-20	Rf	Nrf
TC 365	dent	73	0	7	14.0	18-20	Nrf	Nrf
Inbred lines developed from hybrids								
TC 240	dent	75	3	7	11.0	14-16	Rf	Nrf
TC 241	dent	74	5	8	11.5	16	Rf	Nrf
TD 235	flint	75	4	6	13.5	14	Rf	Nrf
TC 322	dent	79	6	3	14.0	16	Rf	Nrf
TC 344	dent	81	2	5	15.0	18	Nrf	Nrf
TC 373	dent	81	0	5	15.5	16	-	Nrf
TC 386	dent	76	3	7	15.0	14-16	-	Nrf
TC 380	dent	77	4	8	14.5	16	Rf	Nrf
TC 390	dent	78	0	8	15.0	16	-	Nrf
TC 381	dent	77	4	4	14,5	14-16	Rf	Nrf

Nrf = non-restorer; Rf = pollen-fertility restorer; pRf = partial pollen-fertility restorer

The methods used for development of the inbred lines were recurrent selection, pedigree method with early and late testing for general and specific combining ability (Table 3). The three inbred lines used as testers were selected from different heterotic groups. Phenotypic selection at high density (90,000 plants/ha) was at least as effective as testcross selection in screening the elite inbred lines.

Table 3. General combining ability of some elite inbred lines.

Pedigree	No. hybrids	Mean yield		% mean of erect plants		% mean of dry matter		Synthetic index
		q/ha	%/check	%	%/check	%	%/check	%/check
1556-5-1	198	83.7	97	84	91	79.0	104	97
5471-1-1	104	91.5	101	91	99	78.9	104	103
3309-1-4	287	95.8	100	95	103	75.3	100	102
3309-4-2	125	89.0	101	95	102	77.4	102	104
3309-5-1	46	87.1	95	91	1o2	78.3	103	100
2066-1-2	18	94.3	99	88	118	75.7	101	118
1208-2-1	296	91.7	104	89	98	76.0	101	102
4818-1-1	43	101.1	103	96	106	75.5	99	106
5370-2-1	33	101.1	102	97	106	75.5	98	106
4123-2-1	62	93.8	100	92	109	77.0	101	110
4173-3-3	46	100.5	107	89	98	76.6	99	103
4176-2-2	19	103.0	105	86	98	76.9	99	1o3
2075-1-1	25	97.3	102	88	111	76.1	103	116
4256-1-1	36	94.7	101	93	110	76.1	98	109
3363-2-1	44	95.5	102	91	115	79.0	102	118
3123-2-5	244	91.3	103	94	103	76.0	101	106
3244-7-4	43	94.0	108	88	101	75.1	99	108
1148-1-1	239	90.4	104	93	101	76.5	101	106
5743-3-1	22	104.8	107	95	103	77.0	100	109

Use of the improving sources led to finalization of a high ratio of the elite inbred lines. The local populations would be used as initial material only after they were improved in a special program by recurrent or reciprocal-recurrent selection.

The new elite inbred lines are parental forms of the most registered hybrids and new hybrids in official trials, which means real genetic progress in development of inbred lines at the Agricultural Research Station, Turda, Romania, during the years 1983-2001.

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Linkage relationships of *inr2* on 9L: Three-point linkage data for *sh1 wx1 inr2* and *wx1 inr2 wc1*

--Stinard, PS

In MNL 75 (Stinard, P, MNL 75:71-72, 2001), we reported that the *r1* haplotype-specific aleurone color inhibitory locus *inr2* is located on the long arm of chromosome 9. This placement was based on linkage with *wx1* in tests with a series of *wx1* marked A-A translocations, and further refined on the basis of a three-point linkage test with *y1* and *wx1* in crosses involving the translocation T6-9e. The distance between *wx1* and *inr2* varied from about 8 to 30 centiMorgans depending on the translocation used in the crosses, and this variability was attributed to the presence of translocations, which sometimes distort linkage distances. In order to better place *inr2* on 9L and eliminate the distorting effects of the translocations, two separate three-point back cross linkage tests involving the chromosome 9 markers *sh1 wx1 inr2* and *wx1 inr2 wc1* were set up as indicated in Tables 1 and 2. Kernel traits were scored on the test cross ears at maturity. The data in Table 1 represent totals for 4 ears, and the data in Table 2 represent totals for 6 ears. For the *wx1 inr2 wc1* test (Table 2), only the

Table 1. Three-point linkage data for *sh1*, *wx1*, and *inr2*.

Testcross: (*Sh1 Wx1 Inr2-JD R1-Randolph* X *sh1 wx1 inr2 R1-Randolph*) X *sh1 wx1 inr2 R1-Randolph*.

Reg.	Phenotype	No.	Totals
0	Sh Wx Inr	598	
	sh wx inr	610	1208
1	Sh wx inr	170	
	sh Wx Inr	166	336
2	Sh Wx inr	195	
	sh wx Inr	197	392
1 + 2	Sh wx Inr	26	
	sh Wx inr	34	60

map distance *sh1--wx1* = 19.8 ± 0.9 cM
map distance *wx1--inr2* = 22.6 ± 0.9 cM
map distance *sh1--inr2* = 42.5 ± 1.1 cM

Table 2. Partial three-point linkage data for *wx1*, *inr2*, and *wc1*.

Testcross: (*Wx1 Inr2-JD wc1 R1-Randolph* X *wx1 inr2 Wc1 R1-Randolph*) X *wx1 inr2 wc1 R1-Randolph*.

Reg.	Phenotype	No.
0	Wx Inr wc	641
1	wx Inr wc	230
2	Wx Inr Wc	370
1 + 2	wx Inr Wc	70

map distance *wx1--inr2* = 22.9 ± 1.2 cM
map distance *inr2--wc1* = 33.6 ± 1.3 cM
map distance *wx1--wc1* = 56.4 ± 1.4 cM

data for the colorless *Inr* classes are presented due to the difficulty of scoring for *Wc* (white cap) vs. *wc* (yellow endosperm) on full colored *inr* kernels.

The data obtained from these linkage tests agree reasonably well with previously established linkage values based on classical mapping techniques ("1993 map," Neuffer et al., Mutants of Maize, Cold Spring Harbor Laboratory Press, 1997). The *sh1 wx1* distance of about 20 cM obtained in our tests (Table 1) is less than that indicated in Mutants of Maize (27 cM), but agrees well with the two-point summary value presented by Emerson et al. (Cornell Univ. Ag. Exp. Sta. Mem. 180, 1935) of 21 cM. Neither our tests, nor those summarized by Emerson et al., would detect double crossovers between *sh1* and *wx1*. The *wx1 wc1* distance of about 56 cM obtained in our tests (Table 2) agrees well with that presented in Mutants of Maize (51 cM) and takes into account at least some of the double crossovers.

The *wx1 inr2* distances from both tests are nearly identical (about 23 cM) and fall easily within the standard error range. Applying this value to the "1993" chromosome 9 linkage map, one obtains a map coordinate of 79 for the location of *inr2*, placing it in the vicinity of *bk2*, which maps at position 82.

Additional linkage tests involving *wx1*, *inr2*, *bk2*, and *v30* are in progress.

The placement of *inr2* to chromosome 9 raises interesting questions as to whether *inr2* is identical to the *da1* or *da2* dilute aleurone color loci identified by Eyster. *da1* (*dilute aleurone1*) conditions recessively inherited pale aleurone color, and is reported to be on chromosome 9 (Eyster, J. Hered. 22:224-225, 1931). Linkage data presented in Emerson et al. (Cornell Univ. Agric. Exp. Sta. Mem. 180, 1935) indicate that *da1* is located 6 cM from *pg12* and 21 cM from *wx1*. The *pg12 wx1* distance is about 14 cM. Linkage data for *da1* with respect to *sh1* are ambiguous (26 cM and 41 cM in two separate tests). These results indicate that *da1* is probably located on the long arm of chromosome 9, and that the gene order is *wx1 pg12 da1*. This would place *da1* in the vicinity of *inr2*. It is conceivable that *da1* could be a recessive mutant allele of *inr2*, but we have not yet identified such an allele. The Stock Center's *da1* stocks were found to carry a dominant *r1* haplotype-specific aleurone color inhibitor allele at the *inr1* locus (*Inr1-Ref*), but *inr1* is located on the long arm of chromosome 10 (Stinard, MNL 73:89-90, 1999). The *da1* stocks did not appear to carry any recessive mutants affecting aleurone color, and the only factor affecting aleurone color that we managed to isolate from these stocks is located on chromosome 10. For that reason, we feel that Eyster's original *da1* mutant may have been lost from these stocks.

We have found that some lines of maize carry dominant inhibitor alleles at both *inr1* and *inr2* (Stinard, MNL 74:70-71, 2000). If Eyster's original *da1* line carried both factors, then perhaps he mapped one of the factors (*inr2*) to chromosome 9, and other isolates of the stock received by the Stock Center could have carried only the *Inr1-Ref* allele. If the *da1* line that Eyster originally examined carried both of these dominant inhibitory alleles, and if the line were heterozygous for susceptible and nonsusceptible *r1* haplotypes, F2 segregation in such lines would yield a ratio of 49 purple to 15 dilute kernels, which would be confused with a 3:1 ratio. If the inhibitory *inr1* allele is lost and one only considers segregation at *inr2* and *r1*, then the ratio becomes 13:3. Eyster (1931) presents kernel counts for only one self-pollinated ear: 258 purple and 84 dilute. This ratio does not differ significantly from a 3:1 ratio (χ^2 = 0.035), but does differ significantly from a 13:3 ratio (χ^2 = 7.582, $p < 0.01$). Eyster could have mapped a dominant *inr2* allele thinking that it was recessive, but such an alternative would require a set of circumstances that render this possibility unlikely.

The *da2* locus, also reported to be on chromosome 9 (Eyster, Bibliographica Genetica 11:187-392, 1934), has a dominant allele, *Da2*, reported to inhibit aleurone color in the kernel crown. Eyster's linkage data, reported in Emerson et al., indicate that *da2* is located 7 cM from *c1* and 26 cM from *wx1*. Therefore, *da2* is located on the short arm of chromosome 9, perhaps distal to *c1*, and could not be the same locus as *inr2*.

A wide variety of *r1* haplotypes respond to *Fcu*
--Stinard, PS

Fcu was first identified by Gonella and Peterson (Genetics 85:629-645, 1977) as the factor responsible for aleurone color sectoring at the *r1* locus in Cuna tribal maize from Colombia. The *Fcu* system was found to be comprised of two elements: a responsive *r1* haplotype, *r1-cu*, and the controlling element *Fcu*. *r1-cu* produces a variable pale aleurone coloration in the absence of *Fcu*, but produces sectors of full color pigmentation on a pale background in the presence of *Fcu*. Two other *r1* haplotypes, *R1-r(sd2) (spotted dilute2*; also referred to as *R-r#2*; Gonella and Peterson, Molec. Gen. Genet. 167:29-36, 1978) and *R-mo(cu)* (Gonella and Peterson, MNL 50:61-63) were subsequently found to produce sectoring in the presence of *Fcu* as well.

In the course of our studies of the Stock Center's *dilute aleurone1* lines and the green aleurone open-pollinated variety John

Deere, we identified two *r1* haplotype-specific inhibitory loci, *inr1* and *inr2* (Stinard and Sachs, J Hered., in press). Dominant inhibitory alleles at these loci suppress aleurone color in crosses to certain full aleurone color *r1* haplotypes, including *R1-ch(Stadler)*, *R1-d(Catspaw)*, and *R1-Randolph*. We hypothesize that the suppression of aleurone color could be due to interactions of the inhibitors with *Doppia* transposable element sequences (Walker et al., EMBO J 14:2350-2363, 1995) present in the promoter regions of the seed color (*S*) complex of suppressible haplotypes. Because of the possible involvement of tranposable elements in the suppression phenomenon, we decided to cross *Fcu* to these same haplotypes and a few additional ones to see if there was an interaction.

An *r1-g Fcu* source obtained from Peter Peterson (741033-8@) was found to elicit sectoring in the F1 when crossed as males onto the following full aleurone color *r1* haplotypes: *R1-ch(Stadler)*, *R1-d(Catspaw)*, and *R1-Randolph*. This *Fcu* source also induced sectoring in crosses to pale aleurone color derivatives of *R1-r(Venezuela412-PI302347)* and *R1-r(Venezuela559-PI302355)*, as well as in crosses to *R1-Randolph* lines that have pale or colorless aleurone due to the presence of the *r1* haplotype-specific aleurone color inhibitors *Inr1-ref*, *Inr1-JD*, or *Inr2-JD*; and *R1-r(sd2)* in the presence of the aleurone color inhibitor *Dil* (Sastry and Kurmi, MNL 44:101-105, 1970). Control crosses of the *Fcu* line to the *Fcu* reporter haplotype *r1-cu* also elicited sectoring. The pattern of sectoring in all crosses was similar: a relatively small number of dark, irregularly shaped small to medium sized sectors on a pale background (Figure 1).

Figure 1. Cross of *r1-g Fcu* onto *R1-ch:Stadler.*

The sectoring in the crosses to the full aleurone color haplotypes *R1-ch(Stadler)*, *R1-d(Catspaw)*, and *R1-Randolph* appeared on a background of paler aleurone color. It appears that the *Fcu* line either carries aleurone color inhibitors, or that *Fcu* itself is capable of inhibiting aleurone color.

What is the nature of the dark *Fcu*-induced sectors? It is doubtful that the purple sectors in crosses of *Fcu* to responsive *r1* haplotypes are due to somatic excision of a receptor element at *r1*. The responsive haplotypes studied to date most likely have inverted repeat *S* (seed color) complex structures similar to that of *R1-r(standard)*. (*r1* haplotypes with other structures will be subjected to analysis next summer.) What such haplotypes have in common is two coding regions, inverted with respect to each other, flanking a promoter region (called sigma) carrying truncated and inverted *Doppia* transposable element termini. There appear to be no transposable element sequences in the coding regions whose excision would restore or enhance *S* complex function. If excision of *Doppia* sequences from the sigma region were possible, the resulting derivatives would most likely lose *S* complex function rather than gain function, since derivatives of *R1-r(standard)* that have deleted sigma regions are colorless (Walker et al., EMBO J 14:2350-2363, 1995). A second, more circumstantial reason that somatic excision is unlikely to be responsible for *Fcu* sectors is that *Fcu* sectors are relatively large, and large sectors of somatic excision are generally correlated with a high rate of germinal reversion (Peterson, pp. 43-68, in Plant Transposable Elements, Oliver Nelson, ed., 1988). So far, no germinal revertants of *Fcu*-responsive haplotypes have been identified (Gonella and Peterson, Molec Gen Genet 167:29-36, 1978). Finally, the fact that the number of sectors does not vary with the dosage of responsive *r1* haplotypes, but instead varies with the dosage of *Fcu* (Gonella and Peterson, Genetics 85:629-645, 1977), argues that the sectoring is not due to excision of an element from the *r1* locus, but instead is due to some phenomenon at the *Fcu* locus.

Although somatic excision of an element from the *r1* locus cannot be completely ruled out at this time, it seems most likely that the sectoring is due to a change at the *Fcu* locus. Two possibilites arise: (1) *Fcu* could represent a transposable element inserted in an enhancer of *r1* seed color expression. Excision of the transposable element restores the enhancer's function, giving rise to enhanced (full color) expression in the revertant sectors (this possibility was suggested to the author by Jerry Kermicle). Again, the scarcity of full colored germinal revertants would tend to argue against this possibility. (2) *Fcu* is itself a regulator of *r1* seed color expression, and the sectors are due to changes of state in the regulator that occur during endosperm development. Under this model, the initial state of *Fcu* during endosperm development would either be "off," or it would be functioning to suppress *r1* seed color expression. Evidence for a suppressor function comes from the pale background color observed in crosses to responsive full colored *r1* haplotypes. However, the presence of other inhibitors in the *Fcu* line that could be responsible for the observed background suppression has not yet been ruled out. The dark sectors would represent a state in which *r1* seed color expression is enhanced. The enhancement could come about by a direct interaction with the *r1* locus, perhaps transcriptional activation, or it could respresent an interaction with other factors that regulate

r1 seed color expression in a positive or negative way. One intriguing possibility is that *Fcu* might be acting to suppress suppressors of aleurone color in the colored sectors. Evidence for this comes from the presence of colored sectors in crosses of *Fcu* to suppressible *r1* haplotypes carrying inhibitors (*R1-Randolph* with inhibitory alleles of *inr1* or *inr2*; and *R1-r(sd2)* with *Dil*). In these crosses, perhaps the colored sectors are due to inactivation of the inhibitors. Of course, it is also possible that the colored sectors in such crosses are due to an enhancement of *r1* seed color expression that is able to counteract the effect of the inhibitors.

If *Fcu* induces colored sectors due to the suppression of *r1* seed color suppressors, then why are sectors produced in crosses to pale *r1* haplotypes not known to carry suppressors, such as *R1-r(Venezuela412-PI302347)* and *R1-r(Venezuela559-PI302355)*? It could be that the W22 conversions of these haplotypes used in these crosses actually do carry suppressors that had not been previously identified. This past summer, both haplotypes were outcrossed to W22 and W23 *r1-g* conversions. For both haplotypes, the kernels on the W22 outcross ears were lighter in color than the kernels on the W23 outcross ears, suggesting that W22 carries inhibitors of these particular haplotypes relative to W23. Again, these results are very preliminary, and the possibility that the full colored *Fcu* sectors are simply due to enhancement of *r1* seed color expression cannot be ruled out at this time.

Additional linkage tests of *waxy1* marked reciprocal translocations at the MGCSC

--Jackson, JD, Stinard, P, Zimmerman, S

In the collection of A-A translocation stocks maintained at MGCSC is a series of *waxy1*-linked translocations that are used for mapping unplaced mutants. New *wx1*-linked translocations are being introduced into this series and we are in the process of converting each translocation to the inbred backgrounds M14 and W23. These inbred conversions are then crossed together to produce vigorous F1's to fill seed requests. Over the years, pedigree and classification problems arose during the propagation of these stocks. We have been able to sort through the problem ones, and can now supply good sources proven by linkage tests to include the correct translocated chromosomes. Additional pedigree information on bad sources is available should anyone want to check on sources supplied to them previously by the Stock Center.

Previously, we reported the linkage results for some of these stocks (MNL 72:81-82; MNL 73:88-89; MNL 74:67-69; MNL 75:68-71; MNL 76:65-67). Below is a summary of additional translocation stocks we have completed testing. Additional translocation stocks will be tested as time allows.

Table 1. *wx1* T2-9c (2S.49; 9S.33)

A) The M14 source showed linkage of *wx1* with *lg1 gl2*.

3 point linkage data for *lg1 gl2-wx1* T2-9c
Testcross: *lg1 gl2 wx1* N x [*lg1 gl2 Wx1* N x *Lg1 Gl2 wx1* T2-9c]

source:93-480-2 x SIB ^M14

Region	Phenotype	No.	Totals
0	lg gl Wx	103	
	+ + wx	83	186
1	+ gl Wx	28	
	lg + wx	30	58
2	+ + Wx	23	
	lg gl wx	23	46
1+2	lg + Wx	1	
	+ gl wx	2	3

% recombination *lg1-gl2* =20.8±2.4
% recombination *gl2-wx1*=16.7±2.2
% recombination *lg1-wx1* = 37.5±2.8

Table 2. *wx1* T3-9c (3L.09; 9L.12)

A) The M14 source showed linkage of *wx1* with *gl6*.

2 point linkage data for *gl6-wx1* T3-9c
Testcross: [*Gl6 wx1* T3-9c x *gl6 Wx1* N] x *gl6 wx1* N

source:93-481-1 x SIB ^M14

Region	Phenotype	No.	Totals
0	gl Wx	446	
	+ wx	464	910
1	+ Wx	25	
	gl wx	1	26

% recombination *gl6-wx1*=2.8±0.5

B) The W23 source showed linkage of *wx1* with *gl6*.

2 point linkage data for *gl6-wx1* T3-9c
Testcross: [*Gl6 wx1* T3-9c x *gl6 Wx1* N] x *gl6 wx1* N

source:94-1893-2^W23

Region	Phenotype	No.	Totals
0	gl Wx	669	
	+ wx	683	1352
1	+ Wx	29	
	gl wx	3	32

% recombination *gl6-wx1*=2.3±0.4

Table 3. *wx1* T9-10(8630) (9S.28; 10L.37)

A) Another new M14 crossover source showed linkage of *wx1* with *g1*.

2 point linkage data for *g1-wx1* T9-10(8630)
Testcross: [*G1 wx1* T9-10(8630) x *g1 Wx1* N] x *g1 wx1* N

source:99-1351-7c/o^M14

Region	Phenotype	No.	Totals
0	g Wx	2098	
	+ wx	2181	4279
1	+ Wx	71	
	g wx	56	127

% recombination *g1- wx1*=2.9±0.3

Table 4. *wx1* T5-9(8386) (5L.87; 9S.13)

All Coop and Robertson sources showed no linkage with *v2*.

Additional linkage tests of non-waxy (*Waxy1*) reciprocal translocations involving chromosome 9 at the MGCSC

--Jackson, JD, Stinard, P, Zimmerman, S

Approximately 1 acre each year is devoted to the propagation of the large collection of A-A translocation stocks at the Maize Genetics Stock Center. In this collection is a series of *Waxy1*-linked translocations that are used for mapping unplaced mutants. Each translocation is maintained in separate M14 and W23 inbred backgrounds which are crossed together to produce vigorous F1's to fill seed requests. Over the years, pedigree and classification problems arose during the propagation of these stocks. We have been able to sort through the problem ones, and can now supply good sources proven by linkage tests to include the correct translocated chromosomes.

Previously, we reported linkage results for some of these stocks (MNL 72:79-81; MNL 73:86-88; MNL 74:67; MNL 75:67; MNL 76:67-68). Below is a summary of additional translocation stocks we have completed testing.

Table 1. *Wx1* T3-9c (3L.09; 9L.12)

A) The M14 source showed linkage of *wx1* with *gl6*.

2 point linkage data for *gl6-Wx1* T3-9c
Testcross: [*Gl6 Wx1* T3-9c x *gl6 wx1* N] x *gl6 wx1* N

source:82-198-5^M14

Region	Phenotype	No.	Totals
0	+ Wx	1697	
	gl wx	1609	3306
1	gl Wx	18	
	+ wx	27	45

% recombination *gl6-wx1*=1.3±0.2

B) The W23 source showed linkage of *wx1* with *gl6*.

2 point linkage data for *gl6-Wx1* T3-9c
Testcross: [*Gl6 Wx1* T3-9c x *gl6 wx1* N] x *gl6 wx1* N

source:2000-1411-1^W23

Region	Phenotype	No.	Totals
0	+ Wx	1414	
	gl wx	1222	2636
1	gl Wx	16	
	+ wx	21	37

% recombination *gl6-wx1*=1.4±.0.2

Table 2. *Wx1* T6-9(4778) (6S.80; 9L.30)

A) The F1 source showed linkage of *wx1* with *hcf26*.

2 point linkage data for *hcf26-Wx1* T6-9(4778)
Testcross: [*Hcf26 Wx1* T6-9(4778) x *hcf26 wx1* N] x *hcf26 wx1* N

source:87-1023 x 1024^F1

Region	Phenotype	No.	Totals
0	+ Wx	404	
	hcf wx	441	845
1	hcf Wx	40	
	+ wx	31	71

% recombination *hcf26-wx1* =7.8±0.9

Table 3. *Wx1* T5-9(8386) (5L.87; 9S.13)

All Coop and Robertson sources showed no linkage with *v2*.

Table 4. *Wx1* T6-9(8768) (6L.89; 9S..61)

The F1; M14 and W23 sources showed no linkage with *sm1*.

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B chromosome derivatives in maize somatic cells

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Accessory or B chromosomes have been described in hundreds of plant and animal species. They are typically smaller than the members of the regular complement, mostly heterochromatic, transmitted in a non-Mendelian pattern, and not necessary for normal development and reproduction. The maize B chromosome is responsible for its own non-disjunction, due to the induction of late knob replication during mitotic anaphase, when the heterochromatin adjacent to the centromere remains functionally non-divided. The morphology of the B chromosome in the root tip was analyzed. The stock used was the Black Mexican Sweet Corn inbred line with B chromosomes from the Maize Stock Center, at the University of Illinois. Seeds were germinated in Petri dishes containing a film of distilled water, and incubated at 29 C in the dark. Seedlings (1.5 to 2 cm root length) were transferred to a plastic mesh adapted inside 6 cm diameter plastic vessels containing 3 ml of 5 µM amiprophos-methyl (APM) solution. After 2h 30 min, the roots were washed for 15 min in running tap water, fixed in a fresh ice-cold methanol:acetic acid solution (3:1), and kept in a freezer for at least 24 h. Subsequently, root tip meristems were excised, macerated with 200 µL of freshly prepared Flaxzyme (NOVO) enzymatic solution plus 1.6 ml distilled water, and incubated at 34 C for 2h 30 min. The macerated cells were dissociated on a clean slide with a fresh fixative solution, air-dried and stained with a 3% Giemsa solution. Metaphasic figures were digitized directly from a microscope-coupled CCD video camera to a computer. The karyogram was elaborated (Figure 1) and the average length of the homologue A pairs and B set was determined in micrometers (Table 1). Interestingly, the data show that B chromosomes were longer than those measurements reported by other authors. On top of that, figures of the somatic cell-derived B chromosomes have not been widely documented. This makes any kind of comparison with the present results difficult. Besides B chromosomes with standard morphology (B^s), B derivatives (B^d) were observed that were reduced in length (Figure 1). It is possible that the different morphologies observed were due to the highly heterochromatic nature of the maize B chromosome as affected by the arresting agent (APM) used.

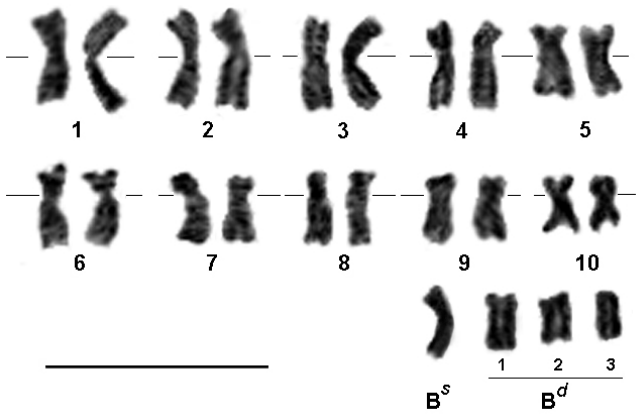

Figure 1. Maize karyogram of the 2n =20A+4B chromosomes. Note the different B chromosome morphologies. Bar = 5 µm.

Table 1. Measurements of maize root tips metaphasic *A* and B chromosomes.

A and **B** Maize chromosomes										
A Pairs	1	2	3	4	5	6	7	8	9	10
Mean Length (μm)	2.22	1.99	1.98	1.86	1.39	1.49	1.41	1.4	1.32	1.11
B Types	B^s	B^{d1}	B^{d2}	B^{d3}						
Length (μm)	1.48	1.20	0.91	0.89						

B^s = Standard B chromosomes
B^d = Derivative B chromosomes

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Structure and sequence analysis of the R region in S-type CMS maize

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The S-type cytoplasmic male sterility (CMS) was reported to be associated with the R region in the mitochondrial genome. A fragment designated as R' was obtained by PCR from the R region. The R' used as a probe was hybridized to *Bam*HI and/or *Pst*I digests of the mitochondrial DNA (mtDNA) from seventeen maize lines, which included N, T, C, and S types of cytoplasms within two nuclear backgrounds of Mo17 and 77. The hybridization pattern of R'/*Bam*HI (Figure 1) demonstrated that there was no fragment of the R region in the C group, while different hybridization bands appeared in the N, T, and S groups. As for the T group, only a fragment of about 0.5kb was found in the hybridization pattern of R'/*Bam*HI+*Pst*I (Figure 2). Maybe there is only a partial R segment in the T group.

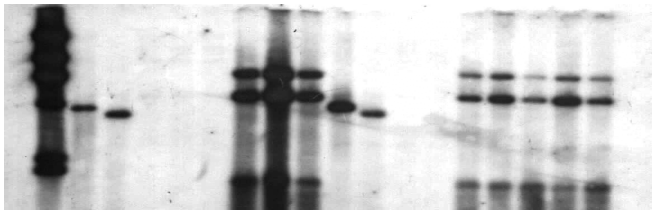

Figure 1. R'/*Bam*HI RFLP pattern. At far left is DNA/*Hin*dIII. From top to bottom are 23.1kb, 9.4kb, 6.6kb, 4.4kb, 2.3kb, 2.0kb. From left to right the others are the 17 types of maize lines: 1.Mo17N; 2.Mo17CMS-T; 3.Mo17CMS-C; 4.Mo17CMS-RB; 5.Mo17CMS-EL; 6.Mo17CMS-TangXu; 7.Mo17CMS-Shung; 8.MO17CMS-J; 9.77N; 10.77CMS-T; 11.77CMS-C; 12.77CMS-EL; 13.77CMS-TangXu; 14.77CMS-Vg; 15.77CMS-Jiang; 16. 77CMS-RJing; 17.77CMS-*S*. These maize lines of No.6, 7, 8, 13, 14, 15, 16, 17 all belong to the S group.

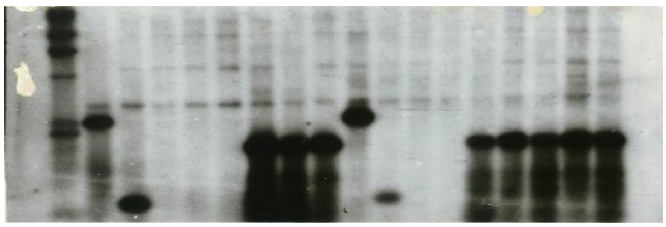

Figure 2. R'/*Bam*HI +PstI RFLP patterns.

Three bands were found in the R'/*Bam*HI hybridizaton pattern of the S group, of which the size was 6.7kb, 4.5kb and 1.8kb respectively. We presumed the DNA fragments of 6.7kb and 4.5kb were in the circular mitochondrial genome. They all contained the R region and recombined with S1 or S2 plasmids through the IR. This leads to linearization of the mitochondrial chromosome, which produced the linear end fragments of 1.8kb. There is a *Pst*I site in the IR region, so only one form of DNA bands appeared in the R'/*Bam*HI+*Pst*I RFLP pattern in the S group (Fig. 2). The structure and recombination model of the R region was shown in Figure 3.

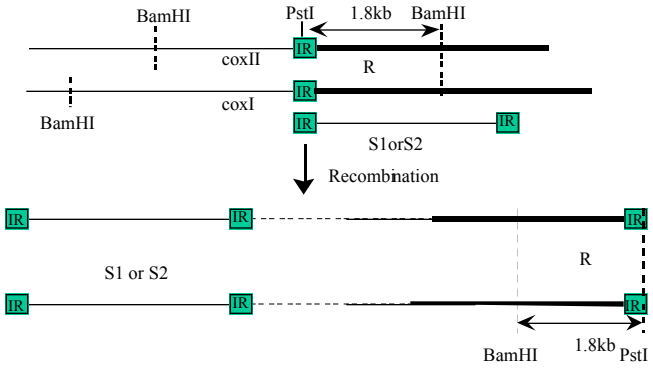

Figure 3. Structure and recombination model of the R region. S1 and S2, which only exist in S cytoplasms, can recombine with the mitochondrial main genome through the IR. This leads to linearization of mitochondrial chromosome. Three types of R can be seen in R'/*Bam*HI, including the linear end 1.8kb fragments. The *coxI* gene was located at 5' upstream of the R region of pV48 and *coxII* was found at the 5' flank region of R of pB39.

Meanwhile, the BAC mitochondrial genome library from Mo17CMS-J was constructed. After screening it with the R' probe, several clones containing the R region were detected. One of these clones, B39, was found to contain the intact 6.7kb fragment. After digestion with *Bam*HI, it was subcloned and named pB39. Another clone, V48, containing the complete 4.8kb fragment, was also subcloned. pB39 and pV48 were sequenced, and the results were submitted to the Gene Bank. The accession numbers are AF545834 and AF542203, respectively. The nucleotide sequence showed that both of them contained orf355 and orf77, which were considered to be the main sequence in the R region. In the clone of pV48, the *coxI* gene was located at the 5' flank region of R, which was coincident with the former report. In the clone of pB39, the first exon of *coxII* was found in the upstream area of the R region. Up to now, this kind of R region has not been reported. Both *cox1* and *coxII* were in the opposite direction of the orf355 and orf77. So the structure of the R region in this study is different from the other types. We did not know the exact relationship between the cytoplasmic male sterility, the R region and its upstream genes. Maybe this unsteady structure is responsible for the unstableness of CMS-S, because obviously the promoter of the R region is easily changed in different nuclear backgrounds (data not shown). In depth research on the transcription and protein products of the R region is underway.

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Identification and molecular tagging of two complementary dominant resistance genes to Maize Dwarf Mosaic Virus

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Maize dwarf mosaic is one of the most devastating and widespread viral diseases in the world. It has become economically important since the late 1980s. The breeding and cultivation of resistant varieties are the basic and most important ways to prevent the yield losses caused by the pathogen. The resistant materials and their inheritance play an important role in the efficiency of resistant breeding. Many reports showed that both major genes and polygenes were involved in the resistance to the virus. It is basic work in resistant breeding to identify new resistant materials and resistance genes. A new elite inbred line, Siyi, from the maize hybrid 78698, was identified that is resistant to maize dwarf mosaic virus strain B at an early and an adult stage. The genetic analysis and mapping of these genes were done by microsatellite markers.

The parents, F1, F2 and backcrosses from the combination Siyi x Mo17 were planted in years 2000 and 2001. Inbred line Siyi is resistant to the virus, while inbred line Mo17 is susceptible to the virus. Resistant plants and susceptible ones of the F2 progeny are easily distinguished, which can be used to map the resistance genes.

DNA extraction was performed on the youngest leaves by the SDS procedure. The sequences of SSR primer sets came from Maize DB. DNA of parents, F1, and F2 plants was analysed by PCR. The main results are as follows:

1) Resistance to maize dwarf virus was investigated. Both parents, Siyi and Mo17, differed significantly in resistance to MDMV over two years (Table 1). Siyi expressed complete resistance at the adult stage. Thirty-one plants in year 2000 and 60 plants in year 2001 of Siyi x Mo17 were symptomless. The (Siyi x Mo17) x Siyi plants in year 2001 were resistant. The progenies of (Siyi x Mo17) x Mo17 segregated into a 1:3 ratio in both year 2000 and 2001, while F2 progenies of (Siyi x Mo17) segregated into a 9:7 ratio in year 2001. The genetic model, the two complementary dominant gene model, was found in the resistant x susceptible combination in two years.

Table 1. Genetic analysis of resistance to maize dwarf mosaic virus.

Year	Materials	No. of plants	No. of resistant plants	No. of susceptible plants	Theoretical ratio	Chi-square test
Summer, 2000	Siyi	19	19			
	Mo17	30		30		
	Siyi x Mo17	31	31			
	(Siyi x Mo17)BC2	66	12	44	1:3	0.214
Summer, 2001	Siyi	50	50			
	Mo17	50		50		
	Siyi x Mo17	60	60			
	(Siyi x Mo17)BC1	150	150			
	(Siyi x Mo17)BC2	193	43	150	1:3	0.106
	(Siyi x Mo17)F2	344	190	154	9:7	0.627

$x^2_{0.05,\,1}=3.84$

2) Microsatellite primers were screened. Based on the genetic analysis, 87 pairs of microsatellite primers distributed randomly on 10 chromosomes were selected (Table 2) to screen parents and different plants from F2 progenies. Only 4 pairs of microsatellite primers on chromosome 3 and 8 pairs of microsatellite primers on chromosome 6 were able to identify the polymorphic fragments which amplified in parents and different plants from F2 progenies. Two genes, one on chromosome 3, the other on chromosome 6, were identified. The genetic analysis on phenotype was confirmed by the molecular analysis. Only 2 pairs of microsatellite primers, *phi029* on chromosome 3 and *phi126* on chromosome 6 link tightly with the two resistance genes.

Table 2. Microsatellites screened.

Chr.	No. of SSR	Chr.	No. of SSR
1	8	6	16
2	7	7	8
3	10	8	7
4	8	9	10
5	7	10	6

Table 3. Microsatellites with polymorphisms between resistant and susceptible parents.

Microsatellite	Bin	Microsatellite	Bin
phi029**	3.04	UMC1023	6.00
mmc0132	3.04	bnlg161	6.00
bnlg1019	3.04	bnlg2191	6.01
bnlg1628	3.04	bnlg1867	6.01
phi126**	6.00	bnlg1433	6.01
UMC1002	6.00	UMC1018	6.01

** Indicate the microsatellite primers linked tightly with the new resistance gene

3) Molecular tagging of the two resistance genes to maize dwarf mosaic virus showed the primers, *phi029* and *phi126*, linked tightly with the two resistance genes, and were amplified successfully on both parents and 100 individuals selected from 344 individuals of the F2 progeny, The linkage distance between *phi029* and the resistance gene on chromosome 3 was 14.5 cM, and the distance between *phi126* and the other resistance gene was 7.2 cM, which confirmed the genetic analysis.

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15,247 seed samples have been supplied in response to 332 requests, for 2002. This includes one large request from a collaborator on the Maize Gene Discovery Project that totaled 9,766 packets. A total of 86 requests were received from 18 foreign countries. Approximately 90% of our requests were received by electronic mail or through our order form on the World Wide Web. Popular stock requests include the IBM RIL mapping populations, Hi-II lines, Stock 6, *ig1* lines, transposable element lines, and B-A translocations. Even without the one large request, we have set a record for both number of requests and samples sent this year.

We have listed more stocks in our Phenotype Only category. These are stocks that have been donated to the Stock Center over the years, and have been classified according to their mutant phenotype. For the most part, these mutants have not as yet been allele tested, nor have they been located to a chromosome arm. While we expect that most of these will represent new alleles of known loci, some will represent unique, as yet undescribed loci. Over the past few years, some mutants in this class have been mapped and/or allele tested and where appropriate, the now characterized mutant stocks have been added to our main catalog. We are now listing all of these mutants to give cooperators that are interested in specific traits, easier access to these mutants.

Approximately 10.5 acres of nursery were grown this summer at the Crop Sciences Research & Education Center located at the University of Illinois. Wetter than normal weather in the early spring delayed the planting of our nurseries. However, growing conditions were excellent, and overall we had a good pollination season. With additional water supplied by irrigation during a dry period, we obtained good increases of most stocks grown this year.

Special plantings were made of several categories of stocks:

1. In the 'Phenotype Only' collection is a series of stocks donated to the Stock Center by Dr. Gerry Neuffer upon his retirement. We have made available an additional 100 stocks in this series.
2. Plantings were also made from donated stocks from the collections of Jack Beckett (B-A translocation lines), Vicki Chandler (*mop1*, *pac1*, and *B1-I* lines), Greg Doyle (inversions), Giuseppe Gavazzi (*lil1* and *Sn1* alleles), Sarah Hake (*Gn1* and *Wab1*), Jerry Kermicle (extensive collection of Brink's *R1* alleles), Rob Martienssen (MTM miniature kernel mutant lines), Don McCarty (*vp14*), Jerald Pataky (*Ht1* lines), Enrico Pé (*bd1* alleles), Tom Peterson (*Ufo1*), Scott Poethig (*epc1* alleles), Paul Scott (*o2* in various inbred backgrounds), Bill Tracy (inbred conversions of *su1* and *sh2*), and others. We expect to receive additional accessions of stocks from maize geneticists within the upcoming year.
3. We conducted allelism tests of several categories of mutants with similar phenotype or chromosome location. We found additional alleles of *pink scutellum1* and *yellow endosperm1.* In this manner, we hope to move stocks from our vast collection of unplaced uncharacterized mutants and integrate them into the main collection.
4. We conducted linkage tests of several mutants that had been placed to chromosome arm using B-A translocations or *waxy*-marked A-A translocations. A more precise location was determined for *inhibitor of r1 aleurone color2*.
5. Two acres were devoted to the propagation of the large collection of cytological variants, including A-A translocation stocks and inversions. In this collection is a series of *waxy1*-marked translocations that are used for mapping unplaced mutants. Over the years, pedigree and classification problems arose during the propagation of these stocks. We were able to sort through the problem ones, and we can now supply good sources proven by linkage tests to include the correct translocated chromosomes. Additional translocation stocks were tested this last year. Results of these tests will be reported in the next issue of the Maize Genetics Cooperation Newsletter.
6. Stocks produced from the NSF project "Maize Gene Discovery, Sequencing and Phenotypic Analysis" (see: http://zmdb.iastate.edu/) were grown this summer. Approximately 30% of these represented plants that originally had to be outcrossed, and needed to be selfed to analyze for mutant segregation. The remaining 70% were seed increases that were planted from those families that originally yielded poorly. These increases help to maintain adequate seed stock to fill future requests. Additionally, we grew 3,184 families of this material to screen for new adult plant mutant traits (see below).

We received 294 IBM (B73 Mo17 intermated population) recombinant inbred lines from Mike Lee and Georgia Davis. We received enough seeds of each line to distribute directly. We are also filling requests directly from seeds of transposed Ac lines provided by Tom Brutnell.

We continue to grow a winter nursery of 0.5 acres at the Illinois Crop Improvement Association's facilities in Juana Díaz, Puerto Rico. We had an excellent winter crop last year, and all indications are that the crop will perform well this year as well. We plan to continue growing our winter nurseries at this location.

The NSF project "Maize Gene Discovery, Sequencing and Phenotypic Analysis" has, to date, generated 31,163 stocks that have been sent to the Stock Center. All of these stocks were screened for ear and kernel mutants at the Stock Center; families with ample seed supplies had two samples removed for additional trait screening. The first sample from each family was sent to UC Berkeley for seedling mutant screening. From the second sample, 3,184 families of the most genetically active grids were planted and screened (by us, other project members and colleagues in the Maize Genetics community) at the University of Illinois for adult plant mutant traits. This was an organized mutant hunt and was very successful in the discovery of novel adult plant mutants. We plan to organize another mutant hunt next summer. The remaining seed generated by this project was placed into cold storage to fulfill requests. Results from the mutant screenings can be found at the ZmDB: Phenotype Database (http://zmfmdb.zool.iastate.edu/). Future work will involve increasing stocks as necessary to maintain seed supply for requests and continue scoring these stocks for kernel and adult plant mutant traits.

We received a budget increase from USDA/ARS and are in the process of hiring a permanent person to handle the new Plant Genome stocks that we are receiving and also an Information Technology Specialist to help us with making our data more accessible to the maize research community.

Marty Sachs Philip Stinard Janet Day Jackson Shane Zimmerman

CHROMOSOME 1 MARKER

101A sr1 zb4 p1-ww
101B sr1 P1-wr
101C sr1 p1-ww
101D sr1 P1-rr
101F sr1 ts2 P1-rr
102A Ws4-N1589
102D Blh1-N1593
102F ms28
102G zb3
102H hcf6-N228B
102I hcf7-N1029D
103D vp5
103DA vp5-DR3076
103DB vp5-86GN4
103DC vp5-86GN3
103DD vp5-86GN6
103DE vp5-86GN11
103DF vp5-Mumm-1
103DG vp5-N81
103E zb4 ms17 p1-ww
104A Ts3
104F ms*-6034
104G ms*-6044
105A zb4 p1-ww
105B zb4 P1-wr
105C zb4 p1-ww br1
105E ms17 P1-wr
105F ms17 p1-ww
106B ts2 P1-rr
106C Glb1-0
106D Glb1-0; Glb2-0
106E ts2-N2409
106F wlu7-N1930
106G v35-N55
106H rgd3-N766B
107A P1-cr
107B P1-rr
107C P1-rw
107D P1-cw
107E P1-mm
107F P1-vv::Ac
107G P1-or
107H p1-ww
109A gs1-PI228173
109B gs1-PI262495
109C gs1-PI267181
109D P1-rr ad1 bm2
109E P1-wr br1 f1
110A P1-wr an1 Kn1 bm2
110D P1-wr an1 bm2
110E P1-wr ad1 bm2
110F P1-wr br1 Vg1
110H P1-wr br1 f1 bm2
110K P1-wr br1
111B hcf3-N846B
111C hcf3-N1242B
111D hcf44-N1278B
111F Les20-N2457
111G rs2
111H Les5-N1449
112B p1-ww br1 f1 bm2
112E as1
112H p1-ww br1
112I p1-ww br1 gs1 bm2
113B rd1
113BA rd1-Wasnok
113C br1 f1
113E br1 f1 Kn1
113K hm1; hm2
113L Hm1; hm2
114C br1 bm2
114D Vg1
114E Vg1; su1
114F br2 hm1; Hm2
114G br2 hm1; hm2
115C v22-8983
115CA v22-055-4
115E bz2-mVW2::Mu1
115F bz2-mVW4::MuDR
115J bz2-m::Ds; A1 A2 C1 C2 Pr1 R1
116A bz2-m::Ds; A1 A2 Ac C1 C2 Pr1 R1
116C an1 bm2
116D def(an1..bz2)-6923; A1 A2 Bz1 C1 C2 Pr1 R1
116G an1
116GA an1-93W1189
116I bz2 gs1 bm2 Ts6; A1 A2 Bz1 C1 C2 R1
117A br2
117D tb1
117DA tb1-8963
117E Kn1
118B Kn1 bm2
118C lw1
118CA lw1-3108
118CB lw1-6474
118J Adh1-3F1124r53
118K Adh1-1S5657; Adh2-33
118L Adh1-3F1124::Mu3
118M Adh1-3F1124r17
118N Adh1-IL14H; su1
118O Adh1-Cm
118P Adh1-FCm
118Q Adh1-Ct
119A Adh1-1S; Adh2-1P
119B vp8
119C gs1
119D gs1 bm2
119E Ts6
119F bm2
119H Adh1-FkF(gamma)25; Adh2-N
119J Adh1-Fm335::Ds1
119K Adh1-Fm335RV1
119L Adh1-2F11::Ds2
119M Adh1-1F725
120A id1
120B nec2-8147
120C ms9
120CA ms9-6032
120CB ms9-6037
120CC ms9-6042
120D ms12
120E v22-055-4 bm2
120F Mpl1-Sisco
120G Mpl1-Freeling
121A ms14
121AA ms14-6005
121B br2-mi8043
121C D8
121D lls1
121DA lls1-N501B
121E ty*-8446
121G ct2
121GA ct2-rd3
124A v*-5688
124B j*-5828
124C w*-8345
124CA w*-013-3
124CB w*-8245
124D v*-5588
124E w*-018-3
124F w20-4791
124G w*-6577
124H w24-8054
124I v32-032-3
124J v*-8943
125A Les2-N845A
125B Mpl1-Jenkins
125C hcf13-N1097B
125D hcf41-N1275C
125E hcf50-N1481
125F hcf2-N506C
125G hcf31-N1268B
126A bz2 gs1 bm2; A1 A2 Bz1 C1 C2 R1
126B id1-N2286A
126C dek1-N928A
126D dek1-N971
126E dek32-N1322A
126F o13
126H P1-vv::Ac bz2-m::Ds
126I P1-vv::Ac
126J P1-ww-1112
126K P1-ovov-1114
126L P1-rr-4B2
126M P1-vv-5145
126N dek1-N1348
126O dek1-N1394
126P dek1-N1401
127A bz2 zb7-N101 bm2
127B dek1-N792
127C dek2-N1315A
127D dek22-N1113A
127E f1
127F Msc1-N791A
127G Tlr1-N1590
127I gt1
128A ij2-N8
128B I16-N515
128C I17-N544
128D pg15-N340B
128E pg16-N219
128G py2-N521A
128H spc2-N262A
129A w18-N495A
129AA w18-571C
129B wlu5-N266A
129C zb7-N101
129D emp1-R
129E ptd1-MS1568
129F dek*-MS2115
129G dek*-MS6214
130A o10-N1356
130B cp3-N888A
130BA cp3-N888A; mn4-N888C
130C id1-NA972
130D dek1-PB388
130E dek1-DR1129
130F ht4
6502A P1-ww-4Co63
6502C P1-ovov-CFS-29
6502D P1-rr(11)-CFS-33
6502E P1-rr(10)-CFS-36
6502F P1-rr(4-5)-CFS-47
6502G P1-rr(9)-CFS-53
6502I P1-rr(8-9)-CFS-75
6502K P1-vv-CFS-96
6502L P1-vv-CFS-110
6502M P1-vv-CFS-116
6502N P1-ovov-CFS-124
6502O P1-vv-CFS-138
6502P P1-rr(7)-CFS-140
6502Q P1-vv-CFS-155
6502R P1-o-grained-red-CFS-167
6502S P1-r pale(8)-CFS-181
6502T P1-rr(9)-CFS-186
6502U P1-vv-CFS-226
6502V P1-vv-CFS-245
6502W P1-vv-CFS-246
6502X P1-vv-CFS-249
6502Y P1-vv-CFS-252
6502Z P1-vv-CFS-255
6502ZA P1-vv-CFS-256
6502ZB P1-vv-CFS-259
6503A P1-rr(11)-CFS-272
6503B P1-vv-CFS-273
6503C P1-vv-CFS-278
6503D P1-vv-CFS-279
6503E P1-vv-CFS-281
6503F P1-vv-CFS-282
6503G P1-vv-CFS-283
6503H P1-vv-CFS-284
6503I P1-r pale(5)-CFS-285
6503J P1-vv-CFS-286 (Brazil)
6503K P1-mm-CFS-286
6503L P1-mm-CFS-287
6503M P1-mm-CFS-289
6503N P1-mm-CFS-290
6503O P1-mm-CFS-291
6503P P1-mm-CFS-292
6503R P1-mm-CFS-294
6503S P1-mm-CFS-297
6503T P1-mm-CFS-301
6503U P1-rw(9)-CFS-302
6503V P1-rr(11)-CFS-303
6503W P1-rr(10)-CFS-305
6503X P1-rr(10)-CFS-315
6503ZA P1-rr(2)-CFS-319
6503ZB P1-rr(8)-CFS-320
6503ZC P1-rr(7)-CFS-321
6504A P1-rw(8)-CFS-324
6504B P1-rw(6-7)-CFS-325
6504C P1-rr(9)-CFS-327
6504D P1-rw(7)-CFS-330
6504E P1-rw(9)-CFS-332
6504F P1-rw(8)-CFS-334
6504G P1-o-grained-red-CFS-335
6504H P1-rw(5-6)-CFS-336
6504I P1-rw(7-9)-CFS-342
6504J P1-rr(5)-CFS-345
6504K P1-rw(7)-CFS-350
6504L P1-rr-CFS-360
6504M P1-rw(5)-CFS-369
6504N P1-ww(1)-CFS-376
6504O P1-vv-CFS-497
6504Q P1-rr(11)-CFS-548

CHROMOSOME 2 MARKER

201A mrl1-IHO
201B hcf106-Mum1::Mu1; hcf106c
201C hcf106-Mum2::Mu1; hcf106c
201D hcf106-Mum3::Mu1; hcf106c
201F ws3 lg1 gl2 b1
201G sm2-Brawn180
201H sm2-Brawn189
201I sm2-Brawn190
201J sm2-Brawn191
201K sm2-Brawn188

202A lg1-PI200299
202B lg1-PI262493
202C lg1-32TaiTaiTaSarga
202D lg1-ZCXGRB
202E lg1-64-4
202F fl1-o8
202G lg1-56-3037-5
202H Gn1-R
202I Gn1-DS
202J lil1-1
203B al1
203BA al1-Brawn
203BB al1-y3
203C al1-1998-2
203D al1 lg1
203G al1-y3 gl2
204A al1-lty3
204B hcf1-N490B
204C Wab1
204D B1'; mop1-1
205A al1 lg1 gl2
205B lg1
205C lg1 gl2
205G al1 gl2 B1
206A lg1 gl2 B1
206C D10-N2428
206D Wrp1-NA1163
206E oro2
207A w3-y11
207B ts1-0174
207C ts1-Anderson
207D ts1-69-Alex-MO17
208B lg1 gl2 B1 sk1
208C lg1 gl2 B1 sk1 v4
208D lg1 gl2 B1 v4
208E lg1 gl2 b1
208H gl2-Salamini
209A gl11-N352A
209E lg1 gl2 b1 sk1
209I gl2-Parker's Flint
210E gl2-3050-3
210F gl2-PI200291
210G gl2-PI239114
210H gl2-PI251009
210I gl2-PI251885
210J gl2-PI251930
210K gl2-PI262474
210L gl2-PI262493
210N gl2-N718
210O gl2-N239
211A lg1 gl2 b1 fl1
211H gl2 wt1
212B lg1 gl2 b1 fl1 v4
212D lg1 gl2 b1 v4
213B lg1 gl2 wt1
213F lg1 B1-v::Bg Ch1
213H lg1 gl2 B1-v::Bg
214A wt1-PI251939
214B lg1 b1 gs2
214C d5
214D gl11 B1
214E B1 ts1
214J sk1
214L lg1 gl2 mn1
215A gl14
215B gl11
215C wt1
215CA wt1-N472A
215CB wt1-N666B
215CC wt1-N178C
215CD wt1-N136A
215D mn1
215E fl1
215EA fl1-o4
215G fl1 v4
215H wt1 gl14
216A fl1 v4 Ch1
216D fl1 w3
216E fl1 v4 w3
216G fl1 v4 w3 Ch1
217A ts1
217B v4
217G v4 Ch1
217H ba2 v4
217I Les10-NA607
217J Les11-N1438
217K Les15-N2007
217L Les18-N2441
217M Les19-N2450
217N cpc1-N2284B
218A w3
218C w3 Ch1
218D Ht1-GE440
218DA Ht1-Ladyfinger
218DB Ht1
218E ba2
218G B1-Peru; A1 A2 C1 C2 r1-r
218GA B1-Peru; A1 A2 C1 C2 R1-r
218H w3-8686
218I w3-86GN12
218J w3-Kermicle-1
219A B1-Peru; A1 A2 C1 C2 r1-g
219B b1; A1 A2 C1 C2 r1-g
219C Ch1
219D Ht1 Ch1
219F B1-Peru; A1 A2 C1 C2 bz2 r1-g
219G B1-Bolivia-706B; A1 A2 C1 C2 r1-g
219H B1-Bolivia; A1 A2 C1 C2 Pl1-Rhoades Pr1 r1-g
219I B1-I; A1 A2 C1 C2 Pl1-Rhoades r1-r
219J B1-I; A1 A2 C1 C2 Pl1-Rhoades r1-g
219K B1-S; R1-g pl1-McClintock
219L B1-S; R1-r pl1-McClintock
220A Les1-N843
220B ws3 lg1 gl2; Alien Addition T2-Tripsacum
220D hcf15-N1253A
220F os1
221A gs2
221AA gs2-0229
221C wlv1-N1860 Ch1
221G wlv1-N1860
224B v*-5537
224H whp1; A1 A2 C1 R1 c2 gl1 in1
224I ws3-7752
224J sr5-7335
224K glnec*-8495
224L ws3-8949
224M ws3-8991
224N ws3-8945
226A ws3-N2357
226B b1-m1::Ds1; A1 A2 C1 C2 r1-g
226C b1-md2::Ds1; A1 A2 C1 C2 r1-g
226D b1-Pm5; A1 A2 C1 C2 r1-g
226E b1-Perum216; A1 A2 C1 C2 r1-g
227A dek3-N1289
227B dek4-N1024A
227C dek16-N1414
227D dek23-N1428
227E Les4-N1375
227I nec4-N516B
227K et2-2352
227L et2-91g6290-26
228A l18-N1940
228B spt1-N464
228C ws3-N453A
228CA ws3-N605A
228E B1-Bh
228F ms33-6019
228G ms33-6024
228H ms33-6029
228I ms33-6038
228J ms33-6041
229A rf3 Ch1
229B v24-N424
229BA v24-N576A
229BB v24-N588A
229BC v24-N350
229C w3 rf3 Ch1
229E emp2-MS1047
229F dek*-MS1365
229G dek*-MS4160
229H dek*-MS2159
229J dek*-PIE

CHROMOSOME 3 MARKER

301A cr1
301B bif2-N2354
301C spc3-N553C
301D Wi2-N1540
301E rd4
301F ns1-R; ns2-R
302A d1-6016
302AA d1-N446
302AB d1-N339
302B d1 rt1
302E d1-tall
303A d1 rt1 Lg3-O
303F g2
303FA g2-pg14::I
303FB g2-v19
303FD g2-56-3040-14
303FE g2-59-2097
303FF g2-94-1478
303G g2 d1
304A d1 ys3
304F d1 Lg3-O ys3
304G Lg3-O Rg1
304I d1 h1
305A d1 Lg3-O
305D d1 Rg1
305K d1 cl1; Clm1-4
306A Rp3-A
306F ref1-MS1185
307A Sdw2-N1991
307C pm1
308B d1 ts4
308E ra2
308F ra2 Rg1
308G ra2-D
309A a1-m3::Ds Sh2
309B a1-m1-5718::dSpm
309C a1-m1-5719A1::dSpm
309D a1-m1-5719A1::dSpm; Mod Pr1
309E a1 Sh2; Spm-w
309F a1-m2-8417::dSpm
309G a1-m2(os)-o1
309H a1-m2-7991A-o2
309I a1-m2-7995::dSpm
309J a1-m2-7977B::dSpm
309K a1-m2-8012A-p1
309L a1 Sh2; Spm-s
309M a1-m1-5719A1::dSpm sh2
309N a1-m2-7995B
309O a1-m1-5996-4::dSpm
309P a1-m1-5719A1::dSpm; Spm-i
309Q a1-m5::Spm-w; Spm-s
309S a1-m2-8411A::Spm-w Sh2
309T a1-m2-7981B6::Spm-w
309U a1-m2-8409::Spm-i
309V a1-m5::Spm-w Sh2
309W a1-m2-8011::Spm-w Sh2
309X a1 Sh2; Spm-w-8745
309Y a1 Sh2; Spm-i
309Z a1-m1-5720-o2
310C ra2 lg2
310D Cg1
311A cl1
311AA cl1-N2
311B cl1; Clm1-2
311BA cl1-7716; Clm1-2
311C cl1; Clm1-3
311D cl1-p; Clm1-4
311E rt1
311F ys3
311G Lg3-O ys3
312A Les14-N2004
312B Les17-N2345
312D Lg3-O
312G brn1-R
312H g2 brn1-R
312I brn1-R cr1
312J brn1-R ra2 lg2
312K brn1-Nelson
312L brn1-3071
312M ms23
313A gl6
313AA gl6-gl7
313AB gl6-N672B
313D ms3
313DA ms3-6008
313DB ms3-6009
313DC ms3-6043
313DD ms3-6020
314A gl6 lg2 A1; A2 C1 C2 R1
314C gl6 lg2 a1-m et1; A2 C1 C2 Dt1 R1
314F Rg1 gl6 lg2
314G gl6 lg2
315B Rg1 gl6
315C Rg1
315D A1-b(P415); A2 C1 C2 R1
315I A1-m2(os)-p1
315J A1-m2(os)-r2
315K a1-m2-7991A-o1
315L a1-m2-7991A-p2
315M a1-m2-7991A-p3
315N a1-m2-7991A-p4
315O a1-m2-7991A-p4b
315P a1-m2-7991A-p5
315Q a1-m2-8010A-o2
315R A1-m3-r1a sh2-m1::Ds
315S a1-m5-o1
315T a1-m5-o2
315U A1-m5-r1
315V A1-m5-r4
315W A1-m5-r5
316A ts4
316B a1-N796
316C dek5-N1339A
316D a1-mt2
316E a1-mt3
316F a1-mt4
316G a1-mt5
316H a1-mt6
316I a1-mt7
316J a1-mt8

316K a1-mt11
316L a1-mt13
316M a1-mt15
316N a1-mt16
316O a1-mt18
316P a1-mt19
317F gl6 ts4 lg2
317I a1-m1-5996-4m::dSpm; Spm
317J a1-m2::Spm-s; Spm-w
317K a1-m2-7991A::Spm-s
317L a1-m2-8004::dSpm
317M a1-m2-8010A::Spm-s
317N a1-m2-8011::Spm-w
317O a1-m2-8012A
317P a1-m2-8147
317Q a1-m2-8167::dSpm
317R a1-m2-8414C
317S a1-m2-8549C
317T a1-m5::Spm-w Sh2
317U a1-m5::Spm-w sh2-1
317W a1-m1-5720::Spm
317X a1-m1-6078::dSpm
317Y a1-m2-8409-2
317Z A1 def-1260
318A ig1
318B ba1
318C y10-7748
318D hcf19-N1257A
318E sh2-N391B
318EA sh2-N2307
318F sh2-N2340
318G na1
318H vp1-Mc
318I y10-8624
319A lg2 A1-b(P415) et1; A2 C1 C2 Dt1 R1
319C lg2 a1-m et1; A2 C1 C2 R1 dt1
319D lg2 a1-m et1; A2 C1 C2 Dt1 R1
319F lg2 a1-st et1; A2 C1 C2 Dt1 R1
319G lg2 a1-st et1; dt1
320A lg2
320B lg2-PI184281
320C lg2 na1
320D lg2-podcorn
320E et1
320F A1 sh2; A2 C1 C2 R1 b1 pl1
320K sh2-94-1001-11
320L sh2-94-1001-58
320M sh2-94-1001-1003
320N a3-Styles; B1-b Pl1-Rhoades r1-g
320O a3-Styles; B1-b Pl1-Rhoades R1-nj
321A A1-d31; A2 C1 C2 R1
321B lg2 a1; A2 C1 C2 R1 dt1
321C lg2 A1-b(P415) et1; A2 C1 C2 R1 dt1
321D a1-m4::Ds; A2 C1 C2 R1
321E a1-rUq; A2 C1 C2 R1
321F a1-Mum1; A2 C1 C2 R1
321H a1-Mum3; A2 C1 C2 R1
321I a1-Mum4; A2 C1 C2 R1
321J a1-Mum5; A2 C1 C2 R1
321K a1-rUq; Uq1
321L a1-rUq(flow); Uq1
322A A1-d31 sh2; A2 C1 C2 R1 dt1
322B A1-d31 sh2; A2 C1 C2 Dt1 R1
322C A1-Mum3-Rev; A2 C1 C2 R1
322F a1-m; A2 C1 R1 b1 dt1 pl1
322I et1-24
322J et1-27
322K et1-34
322L et1-2162
322M et1-2320
322N et1-2424
322O et1-2457
322P et1-3191
322Q et1-3328
322R et1-5079
322S et1-84-6013
322T et1-88g-9733
322U et1-43
323A a1-m; A2 C1 C2 Dt1 R1
323D a1-m sh2; A2 C1 C2 Dt1 R1
323E a1-m et1; A2 C1 C2 Dt1 R1
323G a1-m1::rDt (Neuffer); A2 C1 C2 Dt1 R1
323H a1-st; A2 C1 C2 Mrh R1 dt1
323I a1-m1::rDt (Neuffer); A2 C1 C2 R1 dt1
324A a1-st; A2 C1 C2 Dt1 R1
324B a1-st sh2; A2 C1 C2 Dt1 R1
324E a1-st et1; A2 C1 C2 Dt1 R1
324G a1-st; A2 C1 C2 R1 dt1
324H a1 et1; A2 C1 C2 R1 dt1
324I a1-st et1; A2 C1 C2 R1 dt1
324J A2; C1 C2 R1 a1-sh2-del-Robertson
324K a1-Mus1; A2 C1 C2 R1
324L a1-Mus2; A2 C1 C2 R1
324M a1-Mus3
324N a1-Mus4
325A a1-p et1; A2 C1 C2 R1 dt1
325B a1-p et1; A2 C1 C2 Dt1 R1
325C a1-x1; A2 C1 C2 R1
325D a1-x3; A2 C1 C2 R1
325E A1 ga7; A2 C1 C2 R1
325G a3
325I a1-p; A2 C1 C2 Dt1 R1
325J a1-p; A2 C1 C2 Pr1 R1 dt1
325K a1-m3::Ds sh2-m1::Ds; A2 Ac C1 C2 R1
326A sh2-Elmore
326AA sh2-Garwood
326AB sh2-60-156
326B vp1
326BA vp1-Mum3
326BC vp1-86N6
326BD vp1-86GN14
326BE vp1-86GN18
326BF vp1-86GN19
326BG vp1-Mum2
326BH vp1-Mum1::Mu
326C Rp3
326D te1-1
326DA te1-Forester
326DB te1-Grogan
329A v*-9003
329B v*-8623
329C w21-022-15
329D yd2
329E w*-8336
329F yg*-W23
329G w*-062-3
329H v*-8609
329HA v*-8959
329I pg2
329K yel*-8630
329L yel*-5787
330A h1
330G a1-mrh; A2 C1 C2 Mrh R1
330H A1-b(P415) Ring 3; A2 C1 C2 R1
330I a1-Mum2; A2 C1 C2 MuDR R1
330J a1-Mum2; A2 C1 C2 R1
330K a1 sh2; A2 C1 C2 R1 dt1
330L a1-mrh; A2 C1 C2 R1
332B dek5-N874A
332C dek24-N1283
332D Wrk1-N1020
332F gl19-N169
332G dek6-N627D
332H dek17-N330D
332I Lxm1-N1600
332M Spc1-N1376
332N wlu1-N28
332S Mv1
333A dek5-25
333AA dek5-MS33
333B te1-Galinat
333C dek5-Briggs-1998-1
333D sh2

CHROMOSOME 4 MARKER

401A Rp4-A
401AB Rp4-B
401C Ga1 su1
401D Ga1-S
401E Ga1-S; y1
401I ga1 su1
401J Ga1-M
401K Ga1-S su1
402A st1
402D Ts5
402E ms30-6028
402F hcf23-N1261A
403A Ts5 fl2
403B Ts5 su1
403C su1-F37
403D su1-PI228183
404A su3-5081; su4-5081
404B su3-89-1303-18; su4-89-1303-18
404C su3-94-4079-6; su4-94-4079-6
404D su3-85-3113-11; su4-85-3113-11
404E su3-87-2340-36; su4-87-2340-36
405B la1-PI239110
405BB la1-Funk:2232
405BC la1-N2020
405BD la1-N2276B
405BE la1-PI184284
405D la1-R su1 gl3
405G la1-R su1 gl4
406C fl2
406CA fl2-DR9234
406D fl2 su1
407D su1
407DA su1-N86
407DB su1-N2316
407DC su1-BKG489-13
407DD su1-Pl
407DE su1-R2412
407DF su1-N896A
407DG su1-N1161A
407DH su1-N2313
407DI su1-N2314
407DJ su1-N959
407DK su1-N1968
407DL su1-N1994
407E su1-am
407F su1-am; du1
408B bm3-Burnham su1
408C su1 zb6
408E bm3-91598-3
408J su1 ra3
408K su1; se1
408L su1 zb6 Tu1
409A su1-st
409B su1-66
409C su1-P
409D su1-5051
409F su1-28510
409G su1-28511
409H su1-28512
409I su1-28513
409J su1-28515
409K su1-28516
409L su1-28517
409M su1-28518
409N su1-28519
409O su1-28520
409P su1-30394
409Q su1-30397
409R su1-30398
409S su1-30399
409T su1-30400
409U su1-30401
409V su1-Bn2
410D su1 zb6 gl3
410E su1-A3
410F su1-4582::Mu1
410G su1-8064
410H su1-2401
410I su1-3837
410J su1-7110
410K su1-2857
410L su1-2859
410M su1-90-1101.1
410N su1-83-3383-4
410O su1-87-2046-27
410P su1-85-3217-10
410Q su1-84-5167-6
410R su1-84-5267-18
410S su1-85-3436-29
411A su1-8908
411B su1 gl4 o1
411F gl7 su1 v17
412C su1 gl3
412G su1 gl4 Tu1
413A su1 o1
413B su1 gl4
413D su1 C2-Idf1(Active-1); A1 A2 C1 R1
413F su1 de*-414E
413G v23 Su1 gl3; bm*-COOP
414A bt2
414AA bt2-Williams
414AB bt2-60-158
414AC bt2-9626
414AD bt2-5288
414B gl4
414BA gl4-Stadler
414BB gl4-gl16
414BD gl4-N525A
414C gl4 o1
414E de*-414E
415A j2
415B o1-N1243
415C o1-N1478A
415D bt2-8132
416A Tu1-A158
416B Tu1-l(1st)
416C Tu1-l(2nd)
416D Tu1-d
416E Tu1-md
416F Tu1 gl3
417B v8
417C gl3
417D o1 gl3
417E gl3-N531

418A gl3 dp1
418B c2; A1 A2 C1 R1
418D C2-Idf1(Active-1); A1 A2 C1 R1
418E dp1
418F o1
418G v17
419A v23-8914
419E gl7
419F Dt6 gl3 C2; A2 C1 R1 a1-m
419G Dt6 C2; A2 C1 R1 a1-m
419H c2-m1::Spm; A1 A2 C1 R1
419I c2-m2::dSpm c2-m3::Mpi1
419J c2-Mum1
419K c2-m2::dSpm; Spm-s
419L c2-m881058Y::IRMA; En Med wx1-m8::Spm-I8
419M c2-m3::Mpi1
420A su1 Dt4 C2; A2 C1 R1 a1-m
420C nec*-rd
420CA nec*-016-15
420D yel*-8957
420F dp*-4301-43
420G w*-9005
420H Dt4 C2; A2 C1 R1 a1-m
424C gl3-64-4
424D gl3-56-3120-2
424E gl3-56-3129-27
424F gl3-60-2555
424G gl3-PI183683
424H gl3-PI251928
424I gl3-PI251938
424J gl3-PI254858
424K gl3-PI267180
424L gl3-PI267219
424M gl3-PI311517
424N gl3-15
426A Gl5 Su1; gl20
426B gl3-PI251941
426D cp2-N1324A
427A cp2-o12
427AA cp2-N211C
427AB cp2-N1875A
427AC cp2-MS2608
427AD cp2-N912
427B dek25-N1167A
427C Ysk1-N844
427D orp1-N1186A; orp2-N1186B
427E dek8-N1156
427F dek10-N1176A
427G Ms41-N1995
427H dek31-N1130
427I Sos1-ref
428A gl5 Su1; gl20
428C nec5-N642
428D spt2-N1269A
428E wt2-N10
428F lw4; Lw3
428G bx1
428H gl5 su1; gl20
428L dsc1-MS2058

CHROMOSOME 5 MARKER

501A am1 a2; A1 C1 C2 R1
501B lu1
501D ms13
501E gl17
501F gl17-N260B
501G gl17 a2; A1 C1 C2 R1
501I am1
502B A2 ps1-Sprague pr1; A1 C1 C2 R1
502C D9-N2319
502D A2 bm1 pr1; A1 C1 C2 R1
502E Ms42-N2082
502F Nl2-N1445
502G A2 Bt1 ga10
502H hcf21-N1259A
503A A2 bm1 pr1 ys1; A1 C1 C2 R1
503B hcf43-N1277B
503C a2-mu1::Mu1
503D a2-mu2
503E a2-mu3
503F A2 pac1-ref; A1 C1 C2 R1-r b1
503FA A2 pac1-ref; A1 B1-Peru C1 C2 Pl1-Rhoades r1-r
504A A2 bt1 pr1; A1 C1 C2 R1
504C A2 bm1 pr1 zb1; A1 C1 C2 R1
504E A2 bt1; A1 C1 C2 R1
505B A2 pr1 ys1; A1 C1 C2 R1
505C A2 bt1 pr1 ga*-Rhoades; A1 C1 C2 R1
505D pr1-N1515A
505E pr1-N1527A
506A A2 v3 pr1; A1 C1 C2 R1
506B A2 pr1; A1 C1 C2 R1
506C A2 pr1 v2; A1 C1 C2 R1
506D na2 A2 pr1; A1 C1 C2 R1
506F A2 pr1 v12; A1 C1 C2 R1
506L A2 br3 pr1; A1 C1 C2 R1
507A a2; A1 C1 C2 R1
507AA a2-Mus2; A1 C1 C2 R1
507AB a2-Mus3; A1 C1 C2 R1
507AC a2-Mus1; A1 C1 C2 R1
507F a2 bm1 bt1 ga*-Rhoades; A1 C1 C2 R1
507G a2 bm1 bt1; A1 C1 C2 R1
507H A2 bv1 pr1; A1 C1 C2 R1
507I a2-m4::Ds; wx1-m7::Ac7
508A a2 bm1 bt1 pr1; A1 C1 C2 R1
508C a2 bm1 bt1 bv1 pr1; A1 C1 C2 R1
508F a2 bm1 pr1 ys1; A1 C1 C2 R1
508H a2-Mum1
508I a2-Mum2
508J a2-Mum3
508K a2-Mum4
508L bv1 pr1
509G a2-m1::dSpm Bt1
509H a2-m1(II)::dSpm(class II)
509I pr1-m1
509J pr1-m2
509K a2-m1(ps)
509L a2-m1::dSpm; Spm-s
509M a2-m5::dSpm
509N A2-m1(os)-r1
510A a2 bm1 pr1 v2; A1 C1 C2 R1
510D a2 pr1 gl8; A1 C1 C2 R1
510E a2 ae1 pr1 gl8; A1 C1 C2 R1
510G a2 bm1 pr1 eg1; A1 C1 C2 R1
511C a2 bt1 pr1; A1 C1 C2 R1
511F a2 bt1 Pr1 ga*-Rhoades; A1 C1 C2 R1
511H a2 bt1; A1 C1 C2 R1
512C a2 bt1 pr1 ga*-Rhoades; A1 C1 C2 R1
512D vp2-N1136B
512E Wi4-N2445A
512F pb4
512G gl8-N166A
512H v13
512I lw2-vp12
513A a2 pr1; A1 C1 C2 R1
513C a2 pr1 v2; A1 C1 C2 R1
513D A2 pr1 sh4; A1 C1 C2 R1
513E a2 pr1 v12; A1 C1 C2 R1
514A a2 bm1 pr1; A1 C1 C2 R1
514B ae1-PS1
514C ae1-PS2
514D ae1-PS3
514E ae1-PS4
514F ae1-PS5
514G ae1-PS6
514H ae1-PS7
514I ae1-PS8
514J ae1-PS9
514K ae1-PS10
514L ae1-PS11
514M Ae1-5180-r4
514N bt1-m1::dSpm
514O bt1-m2
514P bt1-m3::dSpm
514Q bt1-m4::Ds
514R Bt1-m1-r1
515A vp2
515AA vp2-DR5180
515AB a2 vp2-green mosaic; A1 C1 C2 R1
515C ps1-Sprague
515CA ps1-8776
515CB ps1-881565-2M
515CC ps1-N80
515CD ps1-8205
515D bm1
515E bt1-N1992
515F bt1-N2308
515G bt1-N2309
516B bt1-R
516BA bt1-Elmore
516BB bt1-C103
516BC bt1-Singleton
516BD bt1-sh3
516BE bt1-sh5
516BF bt1-Eldridge
516BH bt1-6-783-7
516BI bt1-Vineyard
516BJ bt1-T
516BK bt1-W187R
516BL bt1-3040
516BM bt1-N797A
516C ms5
516D td1 ae1
516DA td1-Nickerson
516G A2 bm1 pr1 yg1; A1 C1 C2 R1
517A v3
517AB v3-8982
517B ae1
517BA ae1-EMS
517BB ae1-PS12
517BC ae1-PS13
517BD ae1-PS14
517BE ae1-PS15
517BF ae1-PS16
517BH ae1-Elmore
517E ae1 pr1 gl8
518A sh4
518AA sh4-Rhoades
518AB sh4-o9
518B gl8-Salamini
518BA gl8-R
518BB gl8-6:COOP
518BC gl8-6:Salamini
518BD gl8-10:COOP
518BE gl8-PI180167
518C na2
518D lw2
519AA ys1-W23
519AB ys1-5344
519AC ys1-N755A
519AD ys1-74-1924-1
519B eg1
519C v2
519D yg1
519E A2 pr1 yg1; A1 C1 C2 R1
519F A2 pr1 gl8; A1 C1 C2 R1
519H zb1
519I zb1-2
520A hcf38-N1273
520B v12
520C br3
520F A2 Dap1; A1 C1 C2 R1
520G A2 pr1 Dap1; A1 C1 C2 R1
520H Dap1-2
520I ae1-1979-7
520J ae1-MOEWS
520K ae1-1981-MuT
521A nec3-N409
521B Nec*-3-9c
521C nec*-8624
521D nec*-T5-9(5614)
521E nec*-7476
521F nec*-6853
521G nec*-7281
521H nec*-8376
521I v*-6373
521J yg*-8951
521K lw3; lw4
521L w*-021-7
521N lnec*-5931
521NA lnec*-8549
521P lw3; Lw4
524A v*-PI267226
524B les*-3F-3330
527A dek18-N931A
527B dek9-N1365
527C dek26-N1331
527D dek27-N1380A
527E grt1-N1308B
527F nec7-N756B
527G dek33-N1299
527H Msc2-N1124B
527I ppg1-N199
527J nec6-N493
528A Hsf1-N1595
528B wgs1-N206B
528C anl1-N1634
528CA anl1-330C
528E prg1-MS8186
528F ren1-MS807
528H dek*-MS2146
528I dek*-MS1182
529A anl1-N1643
529B anl1-N1645
529C anl1-N1671
529D anl1-N1685
529E anl1-N1691
529F anl1-N1673

CHROMOSOME 6 MARKER

601C rgd1 y1
601D rgd1-N372B
601F po1-ms6 y1 pl1
601H rhm1 rgd1 y1
601I rhm1 y1 l11
601J Wsm1 Mdm1; Wsm2 Wsm3
601K wsm1 mdm1; wsm2 wsm3
601L Mdm1 y1
602A po1-ms6 wi1 y1
602C y1
602D rhm1 Y1
602H y1-N2236
602J y1-w-mut
602K y1-gbl

602L y1-pb1
602M y1-8549
602N y1-Caspar
602O y1-0317
602P y1-129E
603A y1 l10
603AA y1 l10-1359
603B y1 l11-4120
603C y1 l12-4920
603D w15-8896 y1
603H mn3-1184 y1
604A y1-87-2307-1
604D y1 l15-Brawn1
604F y1 si1-mssi
604FA y1 si1-ts8
604FB y1 si1-Sam
604H y1 ms1
604HA y1 ms1-Robertson
604I Y1 ms1
604IA ms1-6050
605A wi1 y1
605C y1 pg11; Wx1 pg12
605E wi1 Y1 Pl1
605F wi1 Y1 pl1
605G l3
605H pg11-M14; pg12-KYS
605I pg11-Oh43; pg12-KYS
606A Y1 pg11-4484; Wx1 pg12-4484
606AA pg11-8925; pg12-8925
606AB pg11-48-040-8; pg12-48-040-8
606AC pg11-8563; pg12-8563
606AD pg11-8322; pg12-8322
606B y1 pg11; pg12 wx1
606C Y1 pg11; pg12 wx1
606E y1 pl1
606F y1 Pl1
606I y1 pg11 su2; Wx1 pg12
607A y1 Pl1-Bh1; A1 A2 C2 R1 c1 sh1 wx1
607C y1 su2
607E y1 pl1 su2 v7
607H y1 Pl1-Bh1; A1 A2 C2 R1 Wx1 c1 sh1
607I y1 Pl1-Bh1; A1 A2 C2 R1 c1 sh1 skb1 wx1
607J sm1-Brawn168
607K sm1-Brawn178
607L sm1-Brawn184
608A gs3-N268
608C sbd1-N2292
608D Les13-N2003
608F y1 pl1 w1
608G Y1 l11
608H y1-m1301::dSpm
608I Rp8-A
608J Rp8-B
609D Y1 su2
609DA Y1 su2-89-1273
609DB su2-PS1
609DC su2-PS2
609DD su2-1979-5
609DE su2-87-2279-12
609DF su2-1981
609DG su2-1982
609DH su2-0203
609DI su2-PI193430
609DJ su2-1979-1
609F ms1-Albertsen
610B Dt2 Pl1; A2 C1 C2 R1 a1-m
610F Y1 pl1 su2 v7
610G hcf34-N1269C
610H Y1 Dt2 pl1; A2 C1 C2 R1 a1-m
610I hcf36-N1271B
610J hcf48-N1282C
610K hcf26-N1263C
610L hcf323
610M hcf5-N510C
611A Pl1 sm1; P1-rr
611D Pt1
611E Y1 pl1 w1
611EA w1-7366
611I sm1 tan1-py1; P1-rr
611K Y1 Pl1 w1
611L w1; l1
611M afd1
611N sr4-N65A
611O o14-N924
612A w14
612B po1
612BA po1-ms6
612C l*-4923
612D oro1
612DA oro1-6474
612I tan1-py1
612J w14-8657
612K w14-8050
612L w14-6853
612M w14-025-12
612N w14-1-7(4302-31)
612O yel*-1-7(4302-31)
613A 2NOR y1; A1 C1 C2 R1 a2 bm1 pr1 v2 wx1
613D vms*-8522
613F w14-8613
613I tus*-5267
613J gm*-6372
613L w*-8954
613M yel*-039-13
613N yel*-7285
613O l*-4-6(4447)
613P yel*-8631
613T pg11-6656; pg12-6656
627A dek28-N1307A
627B dek19-N1296A
627C vp*-5111
627G dek*-MS1104; l*-1104

CHROMOSOME 7 MARKER

701B In1-D
701D o2
701E o2-Mum1
701F Hs1
702A o2 v5
702B o2 v5 ra1-Ref gl1
702I In1-Brawn
703A o2 v5 gl1
703B De*-B30
703C o2-m(r); Bg
703D o2 ra1-Ref gl1
703E o2-R; Bg
703F o2-m12::Spm
703G o2-m2::Ds; Ac
703H o2-m5::Ac
703J Rs1-O
703JA Rs1-1025::Mu6/7
703K Rs1-Z
704B o2 ra1-Ref gl1 sl1
704C o2-NA696
704D o2-NA697
704E gl1-m8
704F ms22-6036
704H o2-orange
704I gl1-PI267186
705A o2 gl1
705B o2 gl1 sl1
705D o2 bd1
706A o2 sl1
706B vp9-Bot100
707A y8 v5 gl1
707B in1; A1 A2 C1 C2 R1 pr1
707C in1 gl1; A1 A2 C1 C2 R1 pr1
707D v5
707E vp9-R
707EA vp9-3111
707EB vp9-86GN9
707EC vp9-86GN15
707F y8 gl1
707G in1 gl1; A1 A2 C1 C2 Pr1 R1
708A ra1-Ref
708AA ra1-PI262495
708AB ra1-PI184279
708AC ra1-PI239103
708AD ra1-PI267181
708AE ra1-PI267184
708AF ra1-63-3359
708B bd1-N2355
708C o15-N1117
708D y8-lty2
709A gl1
709AA gl1-56-3013-20
709AB gl1-56-3122-7
709AC gl1-PI183644
709AD gl1-PI218043
709AE gl1-PI251652
709AF gl1-PI257507
709AG gl1-Istra
709AH gl1-BMS
709AI gl1-7L
709AJ gl1-9:COOP
709AK gl1-N212
709AL gl1-N269
709AM gl1-N345B
709C gl1-m
710A gl1 Tp1
710B gl1 mn2
710E o5 gl1
710I gl1 Bn1
710J gl1-N271
710K gl1-dy
710L gl1-PI218038
711A Tp1
711B ij1-ref::Ds
711C ij1-60-2454-20
711G ts*-br
712A ms7
712AA ms7-6007
712B ms7 gl1
713A Bn1
713E Bn1 bd1
713H Bn1 ij1
713I bd1 Pn1
714A Pn1
714B o5
714BA o5-PS3038
714BB o5-N76B
714BC o5-N874B
714C o5-N1241
714D va1
715A Dt3; A2 C1 C2 R1 a1-m
715C gl1 Dt3; A2 C1 C2 R1 a1-m
716A v*-8647
716B yel*-7748
716C dlf1-N2389A
716D dlf1-N2461
716F Les9-N2008
727A dek11-N788
727B wlu2-N543A
727D v27-N590A
727DA v27-N53B
727DB v27-N413C
727E gl1-cgl
727F Rs4-N1606
727G Rs1-O o2 v5 ra1-Ref gl1
727H ms34-6004
727I ms34-6010
727J ms34-6013
727K ms34-6014
728A Px3-6
728B ptd2-MS3193
728C mn2-cp1
728D sh6-8601
728E sh6-N1295
728F ren2-NS326
728G dek*-MS2082
728H dek*-MS5153

CHROMOSOME 8 MARKER

801A gl18-g
801B v16
801I yel*-024-5
801K v16 ms8
802A rgh1-N1285
802B emp3-N1386A
802C Ht2
802G ms43
802H gl18-PI262473
802I gl18-PI262490
803A ms8
803B nec1-025-4
803D gl18-g ms8
803F nec1-7748
803G nec1-6697
804A v21-A552
804B dp*-8925
804C tb*-poey1013
805A fl3
805C gl18-g v21-A552
805E el1
805G ms8 j1
808A ct1
808B Lg4-O
808C Htn1
808D epc1-W23
808G Epc1-W23
810A v16 j1; l1
810B j1
810C j1-JSM
827A dek20-N1392A
827B dek29-N1387A
827C Bif1-N1440
827CA Bif1-N2001
827D Sdw1-N1592
827E Clt1-N985
827F pro1-N1058
827G pro1-N1121A
827H pro1-N1528
827I pro1-N1533
827J wlu3-N203A
827K pro1
827L pro1-Tracy
828A ats1
828C pro1-N1154A
828D pro1-NA342
828E pro1-N1530

CHROMOSOME 9 MARKER

901B yg2 C1 sh1 bz1; A1 A2 C2 R1
901C yg2 C1 sh1 bz1 wx1; A1 A2 C2 R1

901E yg2 C1 bz1 wx1; A1 A2 C2 R1
901H yg2 C1 Bz1; A1 A2 C2 R1
902A yg2 c1 sh1 bz1 wx1; A1 A2 C2 R1
902B yg2 c1 sh1 wx1; A1 A2 C2 R1
902C yg2 c1 sh1 wx1 gl15-Hayes; A1 A2 C2 R1
902D yg2 c1 sh1 Bz1 wx1 gl15 K9S-s; A1 A2 C2 R1
902E C1 sh1 Bz1-McC1; A1 A2 C2 R1
902F bz1-m13::dSpm
902G C1 sh1 bz1 wx1; A1 A2 C2 R1 Spm
902H bz1-m13::dSpm; Spm
902I bz1-m13CS1
902J bz1-m13CS3
902K bz1-m13CS4
902L bz1-m13CS5
902M bz1-m13CS6
902N bz1-m13CS7
903A C1 sh1 bz1; A1 A2 C2 R1
903B C1 sh1 bz1 wx1; A1 A2 C2 R1
903D C1-I sh1 bz1 wx1; A1 A2 C2 R1
903E bz1-m13CS8
903F bz1-m13CS10
903G bz1-m13CS11
903H bz1-m13CS12
904B C1 sh1; A1 A2 C2 R1
904C C1 sh1 wx1; A1 A2 C2 R1
904D C1 wx1 ar1; A1 A2 C2 R1
904F C1 sh1 bz1 gl15 bm4; A1 A2 C2 R1
904G rgo1-Sarkar
905A C1 sh1 wx1 K9S-I; A1 A2 C2 R1
905C C1 bz1 Wx1; A1 A2 C2 R1
905D C1 sh1 wx1 K9S-I; A1 A2 C2 K10-I R1
905E C1 sh1 wx1 v1; A1 A2 C2 R1
905G C1 bz1 wx1; A1 A2 C2 R1
905H c1 sh1 wx1; A1 A2 C2 R1-scm2 b1
905I ms45-6040
906A C1 wx1; A1 A2 C2 DsI Pr1 R1 y1
906B C1 wx1; A1 A2 C2 DsI R1 Y1 pr1
906C C1-I Wx1; A1 A2 C2 DsI R1
906D C1-I; A1 A2 C2 R1 y1
906G C1-I Sh1 Bz1 Wx1; DsI
906H C1 Sh1 bz1 wx1; Ac
907A C1 wx1; A1 A2 C2 R1
907E C1-I wx1; A1 A2 C2 R1 y1
907G c1-p; A1 A2 B1-b C2 R1 pl1
907H c1-n; A1 A2 C2 R1 b1 pl1
907I C1-S wx1; A1 A2 C2 R1
908A C1 wx1 da1 ar1; A1 A2 C2 R1
908B C1 wx1 v1; A1 A2 C2 R1
908D C1 wx1 gl15; A1 A2 C2 R1
908F C1 wx1 da1; A1 A2 C2 R1
908H Bf1-99-2070-8
909A C1 wx1 Bf1-ref; A1 A2 C2 R1
909B c1 bz1 wx1; A1 A2 C2 R1
909C c1 sh1 bz1 wx1; A1 A2 C2 R1
909D c1 sh1 wx1; A1 A2 C2 R1
909E c1 sh1 wx1 v1; A1 A2 C2 R1
909F c1 sh1 wx1 gl15; A1 A2 C2 R1
909G hcf42-N1276B
910B c1 sh1 wx1 gl15 Bf1-ref; A1 A2 C2 R1
910D c1; A1 A2 C2 R1
910G C1 sh1-bz1-x2 Wx1; A1 A2 C2 R1
910H C1 sh1-bz1-x3; A1 A2 C2 R1
910I sh1-bb1981 bz1-m4::Ds
910IA sh1-bb1981 bz1-m4::Ds; Ac
910L yg2-str
911A c1 wx1; A1 A2 C2 R1
911B c1 wx1 v1; A1 A2 C2 R1
911C c1 wx1 gl15-Hayes; A1 A2 C2 R1
911D Fas1
911E sem1-1364
911F def(Bf1..bm4)044-4
912A sh1
912AA sh1-1746
912AB sh1-9026-11
912AC sh1-3-6(6349)
912AD sh1-60-155
912AE sh1-EMS
912AF sh1-4020
912AG sh1-9552
912AH sh1-9626
912AI sh1-3017
912AJ sh1-6
912B sh1 wx1 v1
912E lo2
912H lo2 wx1
913C sh1 l7
913D sh1 l6
913E baf1
913F yg2-Mum1
913G yg2-Mum2
913H yg2-Mum3
913I yg2-Mum4
913J yg2-Mum5
913K yg2-Mum6
913L yg2-Mum7
913M yg2-Mum8
913N yg2-Mum9
913O yg2-DR83-106-3
913P yg2-DR83-106-5
914A wx1 d3-COOP
914B dek12-N1054
914K Wc1-Iy; Y1
914L bz1-Mus1
914M bz1-Mus2
914N bz1-Mus3
914O bz1-Mus5
914P bz1-Mus6
914Q bz1-Mus7
914R bz1-Mus10
915A wx1
915B wx1-a
915C w11
915D wx1-N1050A
915F wx1-N1240A
916A wx1 v1
916B wx1 v1-JRL
916C wx1 bk2
916E wx1 v1 gl15
916G Trn1-N1597
916H v31-N828
916I d3-8201
917A wx1 Bf1-ref
917C v1
917D ms2
917DA ms2-6002
917DB ms2-6012
917E gl15-Sprague
917EA gl15-Lambert
917EB gl15-KEW
917F d3-COOP
917FA d3-d2
917FB d3-015-12
917FC d3-072-7
917FD d3-8054
917FF d3-d2-Harberd
917FG d3-d2-Phillips
917FH d3-N660B
918A gl15 Bf1-ref
918B gl15 bm4
918C bk2 Wc1
918D Wc1
918F Wx1 Bf1-ref
918G Wc1 Bf1-ref bm4
918GA Wc1-Wh Bf1-ref bm4
918K bk2 v30
918L wx1 Wc1
919A bm4
919B Bf1-ref bm4
919C l6
919D l7
919G l6; l1
919I Bf1-DR-046-1
919J bz1-Mum9; MuDR
919K bz1-Mum4::Mu1
919L bz1-Mum1
919M bz1-Mum2
919N bz1-Mum3
919O bz1-Mum5
919P bz1-Mum6
919Q bz1-Mum7
919R bz1-Mum8
919S bz1-Mum9
919T bz1-Mum10
919U bz1-Mum11
919V bz1-Mum12
919W bz1-Mum15
919X bz1-Mum16
919Y bz1-Mum18
920A yel*-034-16
920B w*-4889
920C w*-8889
920E w*-8950
920F w*-9000
920G Tp3L-9SRhoades
920L ygzb*-5588
920M wnl*-034-5
920N pyd1
923A wx1-a
923B wx1-B
923C wx1-B1
923D wx1-B2::TouristA
923E wx1-B3::Ac
923F wx1-B4::Ds2
923G wx1-B6
923H wx1-B7
923I wx1-B8
923J wx1-BL2
923K wx1-BL3
923L wx1-C
923M wx1-C1
923N wx1-C2
923O wx1-C3
923P wx1-C4
923Q wx1-C31
923R wx1-C34
923S wx1-F
923T wx1-90
923U wx1-H
923V wx1-H21
923W wx1-I
923X wx1-J
923Y wx1-M
923Z wx1-m1::Ds
923ZA wx1-m6R
923ZB wx1-m6NR
923ZC wx1-m8::Spm-I8
923ZD wx1-P60
923ZE wx1-R
923ZF wx1-Stonor
924A Ring 9S Wd1 C1-I; wd1 C1
924B C1-I Ring 9S; A1 A2 C2 R1
924C yg2
924D wd1
924E wd1 C1 sh1 bz1
924F tiny fragment 9 Sh1 Bz1; C1 sh1 bz1 wx1
924G C1-I Bz1; Ac DsI
924H c1 sh1 bz1 wx1; Ac
925A bz1-m1::Ds wx1-m9::Ac
925B wx1-m9::Ac
925C bz1-m2::Ac
925D Wx1-m9r1
925E bz1-m2(DII)::Ds wx1-m6::Ds
925F C1 sh1 bz1 wx1-m8::Spm-I8
925H bz1-m2(DI)::Ds wx1; R1-sc:124
925I c1-m2::Ds Wx1; Ac
925J c1-m858::dSpm wx1
925K c1-m1::Ds
926A sh1-m5933::Ds
926B Sh1-r3(5933)
926C Sh1-r6(5933)
926D Sh1-r7(5933)
926E Sh1-r8(5933)
926F Sh1-r9(5933)
926G Sh1-r10(5933)
926H Sh1-r11(5933)
926I sh1-m6233::Ds
926J Sh1-r1(6233)
926K Sh1-r2(6233)
926L C1-I sh1-m6258::Ds
926M Sh1-m6258-r1
926N Sh1-r6795-1
926O bz1-m5::Ac
926P Bz1-wm::Ds1
926Q Bz1-m1-p
926R Bz1-m2-r1
926S Bz1-m2(DII)-r1
926T Bz1-m2(DII)-r2
926U Bz1-m2(DII)-r3
926V sh1-bb1981 Bz1-m4-p1
926W sh1-bb1981 Bz1-m4-r6851
926X sh1-bb1981 Bz1-m4-r7840B
926Y sh1-bb1981 Bz1-m4-r8332
926Z Bz1-m5-p1
926ZA Bz1-m5-r1
926ZB Bz1-m5-r2
927A dek12-N873
927B dek13-N744
927C dek30-N1391
927D Les8-N2005
927E Zb8-N1443
927H C1 Dt7; A2 C2 R1 a1-r
927I G6-N1585
927K Rld1-N1990
927L Rld1-N1441
928A yg2-N27
928AA yg2-N585
928AB yg2-N697
928AC yg2-N610
928B wlu4-N41A
928C ms20
928G c1-m5::Spm wx1-m8::Spm-I8; A1 A2 C2 R1
928H wx1-m7::Ac7
928I C1 bz1-mut::rMut; A1 A2 Bz2 C2 Mut R1
928J C1 bz1-(r)d; A1 A2 C2 R1
928K C1 Sh1 bz1-s; A1 A2 C2 Mut R1

928L ms45-6006
928M ms35-6011
928N ms35-6018
928O ms*-6021
928P ms*-6022
928Q ms35-6027
928R ms35-6031
928S ms*-6046
928T ms*-6047
929E Dp9
930A wx1-Mum1
930B wx1-Mum2
930C wx1-Mum3
930D wx1-Mum4
930E wx1-Mum5::Mu
930F wx1-Mum6
930G wx1-Mum7
930H wx1-Mum8
930I wx1-Mum9
930J wx1-Mum10
930K wx1-Mum11
930L wx1-Mus16
930M wx1-Mus181
930N wx1-Mus215
931A Wx1-m5::Ds
931B wx1-m6::Ds
931C wx1-m6-o1
931D Wx1-m7-i1
931E Wx1-m8-r10
931F Wx1-m9-r3
931G Wx1-m9-r4
931H wd1-Mus1
931I wd1-Mus2
931J wd1-Mus3
931K wd1-Mus4
931L wd1-Mus5
931M wd1-Mus6

CHROMOSOME 10 MARKER

X01A oy1-Anderson
X01AA oy1-yg
X01AB oy1-8923
X01B oy1 R1; A1 A2 C1 C2
X01C oy1 bf2
X01E oy1 bf2 R1; A1 A2 C1 C2
X02C oy1 zn1 R1; A1 A2 C1 C2
X02E oy1 du1 r1; A1 A2 C1 C2
X02G oy1 zn1
X02H Oy1-N1459
X02I Oy1-N1538
X02J Oy1-N1583
X02K Oy1-N1588
X02L Oy1-N1989
X03A sr3
X03B Og1
X03D Og1 R1; A1 A2 C1 C2
X03E oy1 y9
X03F Inr1-Ref
X03G Ufo1
X04A Og1 du1 R1; A1 A2 C1 C2
X04B ms11
X04BA ms11-6051
X04D bf2
X04DA bf2-N185A
X04E du1-8501
X04F du1-8802
X05A Og*-0376
X05B Gs4-N1439
X05E bf2 sr2
X05G bf2 g1 R1-r; A1 A2 C1 C2
X05H r1 Sn1-coop; rea1
X05I r1 Sn1-bol1
X05J r1 Sn1-bol2
X05K r1 Sn1-bol3
X06A bf2 r1 sr2; A1 A2 C1 C2
X06C nl1 g1 R1; A1 A2 C1 C2
X06F bf2 R1 sr2; A1 A2 C1 C2
X07A nl1 g1 r1; A1 A2 C1 C2
X07C y9
X07CA y9-y12
X07D nl1
X08A vp10
X08B vp10-86GN5
X08C vp10-TX8552
X08F li1
X08FA li1-ILL90-243Teo
X09B li1 g1 R1; A1 A2 C1 C2
X09EA g1-g4
X09EB g1-56-3005-24
X09EC g1-1-7(X-55-16)
X09ED g1-68-609-13
X09EE g1-ws2
X09EF g1-PI262473
X09F ms10
X09FA ms10-6001
X09FB ms10-6035
X09G li1 g1 r1; A1 A2 C1 C2
X10A du1
X10AA du1-PS1
X10AB du1-PS2
X10AC du1-PS3
X10AD du1-PS6
X10AE du1-PS4
X10AF du1-PS5
X10AG du1-8801
X10AH du1-84-5350-31
X10D du1 g1 r1; A1 A2 C1 C2
X10F zn1
X10FA zn1-N25
X10G du1 v18
X11A zn1 g1
X11D Tp2 g1 r1; A1 A2 C1 C2
X11E g1 R1 sr2; A1 A2 C1 C2
X11F g1 r1; A1 A2 C1 C2
X11H zn1 R1-r; A1 A2 C1 C2
X11I Tp2 g1 sr2
X12A g1 r1 sr2; A1 A2 C1 C2
X12C g1 R1-g sr2; A1 A2 C1 C2
X12E g1 R1; A1 A2 C1 C2
X13D g1 r1-r sr2; A1 A2 C1 C2
X13E g1 r1-ch; A1 A2 C1 C2 wx1
X13G R1-p
X14A r1-r lsr1-Ej; A1 A2 C1 C2
X14E r1; A1 A2 C1 C2 wx1
X14F v18 r1; A1 A2 C1 C2
X14I r1-sc:m3::Ds
X14J R1-nj::Ac
X14K r1-Del902
X14L r1-g; A1 A2 C1 C2
X15B l1 r1 sr2; A1 A2 C1 C2
X15C R1-g; A1 A2 C1 C2
X15D r1-ch; A1 A2 C1 C2
X15F lsr1 R1-g Sr2
X15G isr1 r1-g sr2
X15H isr1 R1-r(Venezuela628-PI302369)
X15HA isr1 R1-r(Venezuela628-PI302369) sr2
X15I isr1 R1-nj Mst1
X16B r1 K10-l; A1 A2 C1 C2
X16C R1-ch; A1 A2 C1 C2 Pl1
X16CA R1-ch(Stadler)
X16D r1 sr2; A1 A2 C1 C2
X16E r1 K10-ll; A1 A2 C1 C2
X16F R1 K10-ll; A1 A2 C1 C2
X17B r1-r; A1 A2 C1 C2
X17C R1-mb; A1 A2 C1 C2
X17D R1-nj; A1 A2 C1 C2
X17E R1-r; A1 A2 C1 C2
X17F R1-scm3
X18A R1-lsk; A1 A2 C1 C2
X18B R1-sk:nc-2; A1 A2 C1 C2
X18C R1-st; A1 A2 C1 C2
X18D R1-sk; A1 A2 C1 C2
X18E R1-st Mst1
X18G R1-scm2; A1 A2 C1 C2 bz2
X18H R1-nj; A1 A2 C1 C2 bz2
X18I r1; A1 A2 C1 C2
X19A R1-sc:124
X19B w2
X19BA w2-Burnham
X19BB w2-2221
X19C l1 w2
X19D o7
X19E R1-r Lc1-Ecuador; b1
X19F r1 w2
X19G r1-n19 Lc1; b1
X19H r1-g:e Lc1; b1
X20B l1
X20C v18
X20I R1-d(Arapaho)
X20J R1-d(Catspaw)
X230A R1-r(Black Beauty Pop)
X230B R1-r(Burnham#2)
X230C R1-r(Cornell)
X230D R1-r(Ecuador1172)
X230E R1-r(Ethiopia-PI193658)
X230F R1-r(India6-PI166163)
X230G R1-r(India6-PI210551)
X230H R1-r(Kansas-PI222629)
X230I R1-r(MacDonald College)
X230J R1-r(Missouri-PI221889)
X230K R1-r(Oklahoma-PI213748)
X230L R1-r(Oklahoma-PI213757)
X230M R1-r(Turkey13-PI174414)
X230N R1-r(Turkey18-PI179131)
X230O R1-r(Turkey22-PI183773)
X230P R1-g(Argentina-PI162573)
X230Q R1-g(Arizona-PI213729)
X230R R1-g(Arizona-PI213738)
X230S R1-g(Arizona-PI218162)
X230T R1-g(Arizona-PI218164)
X231A R1-g(Arizona-PI218175)
X231B R1-g(Arizona-PI218178)
X231C R1-g(Black Mexico)
X231D R1-g(Bolivia1160)
X231E R1-g(Burnham#1)
X231F R1-g(Canada-PI214199)
X231G R1-g(North Dakota-PI213799)
X231H R1-g(North Dakota-PI213807)
X231I R1-g(South Dakota-PI213779)
X231J R1-g(South Dakota-PI213787)
X231K R1-g(Ethiopia32-PI197503)
X231L R1-g(Guatemala5A-Mangelsdorf2837)
X231M R1-g(India6-PI166161)
X231N R1-g(Iowa-PI217411)
X231O R1-d(Acoma)
X231P R1-d(Pony)
X231Q R1-d(Tomi)
X231R R1-d(Valley)
X231S R1-d(Winnebago)
X231T R1-g(Guerrero10)
X232A R1-r(Chiapas70)
X232B R1-g(Ecuador887#6723)
X232C R1-r(Ecuador929-PI302341)
X232D R1-g(Venezuela903-PI302393)
X232E R1-g(Bolivia494)
X232F R1-g(Bolivia705)
X232G R1-g(Argentina216/62-A)
X232H R1-g(BrazilCMI56)
X232I R1-g(BrazilCMI54)
X232J R1-g(Brazil4980)
X232K R1-g(Brazil1963)
X232L R1-g(Brazil3359)
X232M R1-g(Brazil5042)
X232N R1-g(Brazil5011)
X232O R1-g(ParaguayCMI128)
X232P R1-r(Argentina167/62)
X232Q R1-g(Bolivia707#6769)
X232R R1-g(Bolivia716#6759)
X232S R1-g(Bolivia724)
X232T R1-g(Bolivia1004)
X233A R1-g(Bolivia1520)
X233B R1-g(Brawn)
X233C R1-g(Peru San Miguel)
X233D R1-r(Venezuela694#16037)
X233E R1-ch(New Mexico-PI218151) K10-l; Pl1
X233F R1-ch(New Mexico-PI218159) K10-l; Pl1
X233G R1-ch(Pueblo); pl1
X233H R1-r(Venezuela760#16029)
X233I R1-g(New Mexico-PI218150)
X233J R1-g(New Mexico-PI218168)
X233K R1-g(Oklahoma-PI213756)
X233L R1-g(1302-Mangelsdorf2995)
X233M R1-g(Peru1304-Mangelsdorf2993)
X233N R1-g(Peru1595A-Mangelsdorf3013)
X233O R1-g(Turkey8-PI167989)
X233P R1-g(Washington-PI217489)
X233Q R1-nj(North Dakota-CuduD12-PI222285)
X233R R1-nj(New Mexico-PI218170)
X233S R1-st(2-COOP)
X233T R1-g(Bolivia473)
X234A R1-g(Bolivia716)
X234B R1-g(Chile370)
X234C R1-g(Chile406)
X234D R1-g(Ecuador592)
X234E R1-g(Peru568)
X234F R1-g(Peru1182)
X234G R1-g(Peru Corongo-ANC120)
X234H R1-g(Peru Corongo-ANC120#907)
X234I R1-g(Peru Corongo-ANC150)
X234J R1-g(Peru Huarmey)
X234K R1-g(Guerrero23)
X234L R1-r(Ecuador318-PI302308)
X234M R1-r(Ecuador731-PI302327)
X234N R1-r(Venezuela412-PI302347)
X234O R1-r(Venezuela455-PI302348)
X234P R1-r(Venezuela497-PI302351)
X234R R1-r(Venezuela559-PI302355)

X234S R1-r(Venezuela457-PI302356)
X234T R1-r(Venezuela590-PI302362)
X235A R1-r(Venezuela594-PI302363); Arv1
X235B R1-r(Venezuela594-PI302363); arv1-m
X235C R1-r(Venezuela702-PI302370)
X235D R1-g(Venezuela753-PI302381)
X235E R1-r(Venezuela760-PI302383)
X235F R1-r(Colombia1424)
X235G R1-r(Colombia1816)
X235H R1-r(Colombia1817)
X235I R1-r(Colombia1818)
X235J R1-g(Mexico27)
X235K R1-g(Mexico33)
X235L R1-g(Mexico40)
X235M R1-g(Aguas Calientes27)
X235N R1-r(Aguas Calientes39)
X235O R1-g(Aguas Calientes39)
X235P R1-g(Guanajuato97)
X235Q R1-g(San Juan del Rio)
X235R R1-r(Maiz Morado)
X235S R1-g(Bolivia661#7534)
X235T R1-g(Venezuela628#16038)
X236A R1-g(Argentina60/62)
X236B R1-g(Argentina216/62-B)
X236C R1-r(Venezuela628-PI302369)
X236D R1-r(Venezuela1543)
X236E R1-g(New Mexico-PI218143)
X236F R1-g(New Mexico-PI218148)
X236H R1-g(New Mexico-PI218157)
X236I R1-g(New Mexico-PI218169)
X236J R1-g(New Mexico-PI218170)
X236K R1-g(New Mexico-PI218173)
X236L R1-g(Washington-PI217488)
X236M R1-nj(F C Anderson)
X236N R1-nj(Illinois-Emmerling Trisomic)
X236O R1-st(3-COOP)
X236P R1-g(Peru1083)
X236Q R1-g(Guerrero24)
X236R R1-g(Guanajuato31)
X236S R1-g(Colima10)
X236T R1-r(Venezuela459#16039)
X24A cm1
X24B lep*-8691
X24C v*-8574
X25A R1-scm2; A2 C1 C2 a1-st
X25B R1-scm2; A1 A2 C1 c2
X25C R1-sc:122; A1 A2 C1 C2 pr1
X25D R1-scm2; A1 C1 C2 a2
X25E R1-scm2; A1 A2 C2 c1
X26A r1-X1 / R1; A1 A2 C1 C2
X26B R1-scm2; A1 A2 C1 C2
X26C R1-sc:122; A1 A2 C1 C2
X26D R1-sc:5691; A1 A2 C1 C2
X26E R1-scm2; A1 A2 C1 C2 pr1 wx1
X26F R1-scm2; A1 A2 C1 C2 In1-D
X26G R1-scm2; A1 A2 C1 c2-m2::dSpm
X26H R1-scm2; A1 A2 C1 C2 wx1
X27A dek14-N1435
X27B dek15-N1427A
X27C w2-N1330
X27D Les6-N1451
X27E gl21-N478B; gl22-N478C
X27F Vsr1-N1446
X27G Oy1-N700
X27H orp2-N1186B; orp1-N1186A
X27I l19-N425
X27J l13-N59A
X27K v29-N418
X27L Les12-N1453
X28B R1-scm2; a1-m1::rDt (Neuffer)
X28C R1-nj(Cudu); A1 A2 C1 C2
X28D Vsr*-N716
X28E Les3
X28F cr4-6143
X28G R1-nj(Chase); A1 A2 C1 C2
X28I R1-scm2; A2 C1 C2 a1-m1-5719::dSpm
X28J R1-scm2; A1 A2 C1 C2 bz1
X29A ren3-MS1339
X29B dek*-MS2181
X29C cr4-N590C
X29D cr4-N647
X29E cr4-N411
X35A Rp1-A
X35B Rp1-B
X35C Rp1-C
X35D Rp1-D
X35E Rp1-J
X35F Rp1-K
X35G Rp1-M
X35H Rp1-Kr3
X35I Rp1-Kr4
X35J Rp1-Kr1J92
X35K Rp1-Kr1J6
X35L Rp1-G
X35M Rp5
X35N Rp1-D Rp1-J
X35O Rp1-C Rp1-J
X35P Rp1-F Rp1-J
X35Q Rp1-C Rp1-F Rp1-J
X35R Rp1-G Rp1-I
X35S Rp1-F Rp1-G Rp1-J
X35T Rp1-D Rp1-G Rp1-J
X35U Rp5 Rp1-D
X35V Rp5 Rp1-G
X35W Rp5 Rp1-C Rp1-G Rp1-J

UNPLACED GENES

U140A aph1
U140AA Aph1
U140C l4
U140G ms22
U140H ms24
U140I zn2-94-234
U240A Les7-N1461
U240D o11
U240E zn2
U240F zn2-PI251887
U240G zn2-PI236997
U240H zn2-PI239110
U240I zn2-56-3012-10
U340D ws1-COOP ws2-COOP
U340DA ws1-Pawnee ws2-Pawnee
U340H oro4
U340I Mei1-mei025
U440B gl13
U440C hcf49-N1480
U440D ub1-76C
U440E frz1
U440F mg1-Sprague
U540A dv1
U540B dy1
U640A dsy1-Doyle
U640B dsy1-Russian
U640C pam1
U640D pam2
U640E ada1
U640F atn1 Adh1-1S5657
U740A abs1-PI254851
U740C lty1
U740F pi1 pi2
U740G Fbr1-N1602
U740H ad2-N2356A
U740I ba3
U740K Rp7
U840A csp1-NA1173
U840B blc1-Tracy
U840D Les21-N1442
U840F agt1
U840G Wi3-N1614
U840H nld1-N2346
U840I Mc1
U840J hcf16
U940A Ht3
U940B dsy2
U940D hcf11-N1250A
U940E hcf17
U940F hcf73
U940G Glb2-0
U940C v25-N17

MULTIPLE GENES

M141A A1 A2 B1 C1 C2 Pl1 Pr1 R1-g
M141AA A1 A2 B1 C1 C2 Pl1-Rhoades Pr1 R1-g
M141B A1 A2 B1 C1 C2 pl1 Pr1 R1-g
M142A A1 A2 b1 C1 C2 pl1 R1-r
M142B a1 A2 b1 C1 C2 pl1 R1-r
M142C A1 a2 b1 C1 C2 pl1 R1-r
M142D A1 A2 b1 bz1 C1 C2 pl1 R1-r
M142E A1 A2 b1 bz2 C1 C2 pl1 R1-r
M142F A1 A2 b1 c1-p C2 pl1 R1-r
M142G A1 A2 b1 C1-I C2 pl1 R1-r Wx1
M142H A1 A2 b1 C1 c2 pl1 R1-r
M142I A1 A2 b1 C1 C2-Idfm pl1 R1-r
M142J A1 A2 b1 C1 C2-Idf1(Active-1) pl1 R1-r
M142K A1 A2 b1 C1 C2 pl1 pr1 R1-r
M142L A1 A2 b1 C1 C2 gl1 in1 pl1 R1-r
M142M A1 A2 b1 C1 C2 In1-D pl1 R1-r
M142N A1 a2 bt1 C1 C2 pr1 R1
M142O C1 sh1 bz1 wx1; A1 A2 C2 R1-r
M142P c1 sh1 wx1; A1 A2 C2 R1-r
M142Q yg2 c1 sh1 wx1; A1 A2 C2 R1-g
M142R A1 A2 b1 C1-I C2 pl1 R1-r wx1
M142S su1 c2; A1 A2 C1 R1-r
M142T A1 A2 b1 C1 C2 pl1 r1-g
M142U A1 A2 b1 C1 C2 pl1 r1-r
M142V A1 A2 C1 C2 R1-nj
M142W A1 A2 C1 C2 R1-st
M142X A1 A2 b1 C1 C2 Pl1 r1-g
M142Y A1 A2 B1 C1 C2 Pl1 r1-g
M142Z a1-st A2 b1 C1 C2 pl1 R1-scm2
M142ZA A1 a2 b1 C1 C2 pl1 R1-scm2
M142ZB b1 bz1 C1 pl1 R1-scm2 sh1
M142ZC A1 A2 b1 bz2 C1 C2 pl1 R1-scm2
M142ZD A1 A2 b1 c1-n C2 pl1 R1-scm2
M142ZE A1 A2 b1 c1-p C2 pl1 R1-scm2
M241A A1 A2 B1 C1 C2 Pl1 Pr1 r1-g
M241C A1 A2 B1 C1 C2 Pl1 Pr1 R1-r
M241D A1 A2 b1 C1 C2 Pl1-Rhoades r1-g
M242A A1 A2 b1 C1 c2 pl1 R1-scm2
M242B A1 A2 b1 C1 C2 pl1 pr1 R1-scm2
M242C in1 gl1; A1 A2 b1 C1 C2 pl1 R1-scm2
M242D a1 sh2; A2 b1 C1 C2 pl1 R1-scm2
M242E c1 sh1 wx1; A1 A2 b1 C2 pl1 R1-scm2
M242F su1 c2; A1 A2 b1 C1 pl1 R1-scm2
M242G A1 A2 b1 C1 C2 pl1 R1-scm2
M242H A1 A2 b1 C1 C2 pl1 r1-g
M242I A1 A2 b1 C1 C2 pl1 r1-r
M242J c1 sh1 R1-sc
M340A A1 A2 B1 c1 C2 pl1 Pr1 R1-g
M340B A1 A2 B1 c1 C2 Pl1 Pr1 R1-g
M340C A1 A2 b1 c1 C2 pl1 Pr1 R1-g
M341B A1 A2 B1 C1 C2 pl1 Pr1 R1-r
M341C A1 A2 b1 C1 C2 Pl1 Pr1 R1-r
M341CA A1 A2 b1 C1 C2 Pl1-Rhoades Pr1 R1-r
M341D A1 A2 B1 c1 C2 Pl1 Pr1 R1-r
M341F A1 A2 b1 C1 C2 pl1 Pr1 R1-r
M441B A1 A2 B1 C1 C2 pl1 Pr1 R1-r wx1
M441D A1 A2 B1 C1 C2 Pl1 Pr1 r1-r
M441F A1 A2 b1 C1 C2 pl1 Pr1 R1-g wx1
M541B A1 A2 b1 C1 C2 pl1 Pr1 R1-g
M541F a1 A2 C1 C2 R1-nj
M541G A1 a2 C1 C2 R1-nj
M541H A1 A2 c1 C2 R1-nj
M541I A1 A2 C1-I C2 R1-nj
M541J A1 A2 C1 c2 R1-nj
M541K A1 A2 C1 C2-Idf1(Active-1) R1-nj
M541L A1 A2 bz1 C1 C2 Pr1 R1-nj
M541M A1 A2 Bz1 C1 C2 pr1 R1-nj
M541N A1 A2 C1 C2 gl1 in1 R1-nj
M541O A1 A2 C1 C2 In1-D R1-nj
M541P ae1 wx1
M641C A1 A2 b1 C1 C2 pl1 Pr1 R1-r wx1
M641D A1 A2 C1 C2 Pr1 r1 wx1 y1
M641E A1 A2 C1 C2 r1-g wx1 y1

M641F r1-g y1; A1 A2 C1 C2
M641G sm1-Brawn184; sm2-Brawn184
M741A A1 A2 b1 C1 C2 pl1 Pr1 r1-g wx1
M741B Stock 6; A1 A2 B1 C1 C2 Pl1 R1-r
M741C Stock 6; A1 A2 B1 C1 C2 pl1 R1-r
M741F Stock 6; A1 A2 C1 C2 pl1 R1-g y1
M741G Stock 6; A1 A2 C1-I C2 pl1 R1-g wx1 y1
M741H Stock 6; A1 A2 B1 C1 C2 Pl1 R1-nj
M741I Stock 6; A1 A2 C1 C2 R1
M841A A1 A2 C1 C2 pr1 R1 su1
M841B f1 wx1
M841C v4 wx1
M841D v2 wx1
M841F A1 A2 bz2 C1 C2 R1-scm2 wx1
M841G A1 A2 C1 c2 R1-scm2 wx1
M841H gl6 wx1
M841I su1 wx1
M841J v16 wx1
M841K gl4 wx1
M841L gl2 lg1 wx1
M941A A1 A2 c1 C2 Pr1 R1 wx1 y1
M941B Mangelsdorf's tester; a1 bm2 g1 gl1 j1 lg1 pr1 su1 wx1 y1
M941BA Mangelsdorf's tester + R1-nj
M941C a1 Dt1 gl2 lg1 wt1
M941D gl1 wx1 y1
M941E gl8-R wx1 y1
M941F sm1; wx1
MX40A A1 A2 C1 C2 P1-vv::Ac r1-sc:m3::Ds
MX40B A1 A2 Ac2 bz2-m::Ds C1 C2 R1
MX40C A1 A2 C1 C2 r1-sc:m3::Ds Ac8168-9
MX40D P1-vv::Ac r1
MX41A A1 A2 C1 C2 gl1 pr1 R1 wx1 y1
MX41B A1 A2 C1 C2 gl1 pr1 R1 su1 wx1 y1
MX41C a1 a2 bz1 bz2 c1 c2 pr1 r1 wx1 y1
MX41D a1 A2 C1 C2 gl1 pr1 R1 su1 wx1 y1
MX41E a1-m1-n A2 C1 C2 R1 wx1-m8::Spm-I8

B-CHROMOSOME

B542A Black Mexican Sweet; B chromosomes present
B542B Black Mexican Sweet; B chromosomes absent
B542C L289; B chromosomes present
B542D L289; B chromosomes absent

TRISOMIC

123A trisomic 1.
223A trisomic 2
328A trisomic 3
422A trisomic 4
523A trisomic 5
615A trisomic 6
718A trisomic 7
807A trisomic 8
922A trisomic 9
X23A trisomic 10

TETRAPLOID

N102A Autotetraploid; A1 A2 B1 C1 C2 Pl1 Pr1 R1
N102D Autotetraploid; A1 A2 C1 C2 R1
N102E Autotetraploid; B chromosomes present
N102EA Autotetraploid; B chromosomes present
N102F Autotetraploid; A1 a2 C1 C2 R1
N103A Autotetraploid; P1-rr
N103B Autotetraploid; P1-vv::Ac
N103C Autotetraploid; P1-ww
N103D Autotetraploid; P1-wr
N103E Autotetraploid; P1-mm
N104A Autotetraploid; su1
N104B Autotetraploid; A1 A2 C1 C2 pr1 R1
N105B Autotetraploid; wx1 y1
N105D Autotetraploid; A1 a2 bt1 C1 C2 R1
N105E Autotetraploid; bt1
N106C Autotetraploid; wx1
N107B Autotetraploid; W23
N107C Autotetraploid; Synthetic B
N107D Autotetraploid; N6

CYTOPLASMIC STERILE/RESTORER

C736A R213 (N); mito-N Rf1 rf2
C736AB R213 (T) Sterile; cms-T Rf1 rf2
C736B Ky21 (N); mito-N Rf1 Rf2 Rf3 RfC
C736C B37 (N); mito-N rf1 Rf2 rf3 rfC
C736CA B37 (T) Sterile; cms-T rf1 Rf2
C736CB B37 (T) Restored; cms-T Rf1 Rf2
C736E Tr (N); mito-N Rf3 rfC rfT
C736F W23 (N); mito-N rf1 Rf2 rf3 RfC
C736FA W23 (N); mito-N rf1 Rf2 rf3 RfC
C736G B73 (N); mito-N rf1 Rf2 rf3 rfC
C736H L317 (N); mito-N rf3 RfC rfT
C836A Wf9 (T) Sterile; cms-T rf1 rf2
C836B Wf9 (N); mito-N rf1 rf2 rf3 rfC
C836C Wf9 (T) Restored; cms-T Rf1 Rf2 rf3 rfC
C836D Wf9 (S) Sterile; cms-S rf1 rf2 rf3 rfC
C836E Mo17 (T) Sterile; cms-T rf1 Rf2 rf3 rfC
C836F Mo17 (N); mito-N rf1 Rf2 rf3 rfC
C836G Mo17 (C) Sterile; cms-C rf1 Rf2 rf3 rfC
C836H Mo17 (S) Sterile; cms-S rf1 Rf2 rf3 rfC
C936D K55 (N); mito-N Rf1 Rf2 rf3 RfC
C936DA K55 (N); mito-N Rf1 Rf2 rf3 RfC
C936F N6 (N); mito-N rf1 Rf2 rf3 RfC
C936FA N6 (N); mito-N rf1 Rf2 rf3 RfC
C936G N6 (T) Sterile; cms-T rf1 Rf2
C936H N6 (T) Restored; cms-T Rf1 Rf2
C936I SK2 (N); mito-N rf1 Rf2 rf3 rfC
C936J SK2 (T) Sterile; cms-T rf1 Rf2
C936K SK2 (T) Restored; cms-T Rf1 Rf2
C936M 38-11 (N); mito-N rf1 Rf2 rf3 rfC
CX36A N6 (C) Restored; cms-C rf1 Rf2 rf3 RfC
CX36B N6 (S) Sterile; cms-S rf1 Rf2 rf3 RfC
CX36C B37 (C) Sterile; cms-C rf1 Rf2 rf3 rfC
CX36D B37 (S) Sterile; cms-S rf1 Rf2 rf3 rfC

CYTOPLASMIC TRAIT

C337A NCS2
C337B NCS3

TOOLKIT

T0318AA TB-3Ld lg1; ig1 R1-nj
T0318AB cms-L; ig1 R1-nj
T0318AC cms-MY; ig1 R1-nj
T0318AD cms-ME; ig1 R1-nj
T0318AE cms-S; ig1 R1-nj
T0318AF cms-SD; ig1 R1-nj
T0318AG cms-VG; ig1 R1-nj
T0318AH cms-CA; ig1 R1-nj
T0318AI cms-C; ig1 R1-nj
T0318AJ cms-Q; ig1 R1-nj
T0940A Hi-II Parent A (for producing embryogenic callus cultures)
T0940B Hi-II Parent B (for producing embryogenic callus cultures)
T0940C Hi-II A x B (for producing embryogenic callus cultures)
T0940D KYS (for chromosome observations in pachytene microsporocytes)
T0940E Mu off; a1-Mum2 A2 C1 C2 R1
T3301A bti00191::Ac
T3301B bti00194::Ac
T3301C bti00207::Ac
T3301D bti00220::Ac
T3301E bti00225::Ac
T3301F bti00226::Ac
T3301G bti00228::Ac
T3301H bti00245::Ac
T3301I bti00252A::Ac
T3301J bti00257::Ac
T3301K bti9576::Ac
T3301L bti99221::Ac
T3301M mon003073::Ac
T3301N mon003077::Ac
T3301O mon002901::Ac
T3301P mon003068::Ac
T3301R mon00044::Ac
T3301S bti00209::Ac
T3301T bti00230::Ac
T3301W mon00068::Ac
T3301X mon00098::Ac
T3301Y mon00110::Ac
T3301Z mon00126::Ac
T3301ZA mon00212::Ac
T3302A Inv1m; P1-vv::Ac bz2-m::Ds
T3302C T1-2b; P1-vv::Ac bz2-m::Ds
T3302D T1-2(036-7); P1-vv::Ac bz2-m::Ds
T3302E T1-2c; P1-vv::Ac bz2-m::Ds
T3302F T1-3(5883); P1-vv::Ac bz2-m::Ds
T3302G T1-3k; P1-vv::Ac bz2-m::Ds
T3302H T1-3(5597); P1-vv::Ac bz2-m::Ds
T3302I T1-3(5982); P1-vv::Ac bz2-m::Ds
T3302J T1-4i; P1-vv::Ac bz2-m::Ds
T3302K T1-4(064-20); P1-vv::Ac bz2-m::Ds
T3302L T1-4(4308); P1-vv::Ac bz2-m::Ds
T3302M T1-4(8602); P1-vv::Ac bz2-m::Ds
T3302N T1-4b; P1-vv::Ac bz2-m::Ds
T3302O T1-5(5525); P1-vv::Ac bz2-m::Ds
T3303A T1-5(6899); P1-vv::Ac bz2-m::Ds
T3303B T1-5b; P1-vv::Ac bz2-m::Ds
T3303C T1-5(4613); P1-vv::Ac bz2-m::Ds
T3303D T1-5(5045); P1-vv::Ac bz2-m::Ds
T3303E T1-5(043-15); P1-vv::Ac bz2-m::Ds
T3303F T1-5(5512); P1-vv::Ac bz2-m::Ds
T3303G P1-vv::Ac; T1-6(5495) (6S.80; 1.S.25) bz2-m::Ds
T3303H P1-vv::Ac; T1-6(e**) bz2-m::Ds
T3303I T1-6(028-13); P1-vv::Ac bz2-m::Ds
T3303J T1-6(7352); P1-vv::Ac bz2-m::Ds
T3303K T1-6(7097); P1-vv::Ac bz2-m::Ds
T3303L T1-7(4405); P1-vv::Ac bz2-m::Ds
T3303M T1-7i; P1-vv::Ac bz2-m::Ds
T3303N T1-7(4837); P1-vv::Ac bz2-m::Ds
T3303O T1-7(010-12); P1-vv::Ac bz2-m::Ds
T3304A T1-8(6591); P1-vv::Ac bz2-m::Ds
T3304B T1-8(4685); P1-vv::Ac bz2-m::Ds
T3304C T1-8(4307-4); P1-vv::Ac bz2-m::Ds
T3304D T1-9(7535); P1-vv::Ac bz2-m::Ds
T3304E T1-9(8302); P1-vv::Ac

bz2-m::Ds
T3304F T1-9(6762); P1-vv::Ac bz2-m::Ds
T3304G T1-10g; P1-vv::Ac bz2-m::Ds
T3304H T1-10f; P1-vv::Ac bz2-m::Ds
T3304I bz2-m::Ds
T3304J Inv1m; P1-vv::Ac r1-sc:m3::Ds
T3304K Inv1a; P1-vv::Ac r1-sc:m3::Ds
T3304M T1-2c; P1-vv::Ac r1-sc:m3::Ds
T3305A T1-3(5597); P1-vv::Ac r1-sc:m3::Ds
T3305B T1-4i; P1-vv::Ac r1-sc:m3::Ds
T3305C T1-4(064-20); P1-vv::Ac r1-sc:m3::Ds
T3305F T1-4b; P1-vv::Ac r1-sc:m3::Ds
T3305H T1-5(6899); P1-vv::Ac r1-sc:m3::Ds
T3305J T1-5(4613); P1-vv::Ac r1-sc:m3::Ds
T3305M T1-6(5495); P1-vv::Ac r1-sc:m3::Ds
T3305N T1-6e; P1-vv::Ac r1-sc:m3::Ds
T3305O T1-6(028-13); P1-vv::Ac r1-sc:m3::Ds
T3306C T1-7(4444); P1-vv::Ac r1-sc:m3::Ds
T3306D T1-7(4405); P1-vv::Ac r1-sc:m3::Ds
T3306H T1-8(6591); P1-vv::Ac r1-sc:m3::Ds
T3306L T1-9(8302); P1-vv::Ac r1-sc:m3::Ds
T3306M T1-9(6762); P1-vv::Ac r1-sc:m3::Ds
T3306N T1-10g; P1-vv::Ac r1-sc:m3::Ds
T3307A Ac8178-2S
T3307D Ac8163-3S
T3307F Ac8183-3
T3308A Ac8200-4S
T3308B Ac6076-5L
T3308D Ac8175-5S
T3308E Ac8193-5S
T3308F Ac8179-5L
T3308G Ac8181-5L
T3308H Ac8186-5L
T3309A Ac8196-5L
T3309B Ac6062-6L
T3309C Ac6063-6
T3309D Ac8172-6L
T3309E Ac8184-6
T3310A Ac8161-7
T3310B Ac8173-7L
T3310D Ac8190-7
T3310E Ac8194-7
T3310F Ac8185-7L
T3311A Ac8162-8
T3311B Ac8182-8L
T3311D Ac6059-10S
T3311F Ac8180-10
T3312A Ds-1S1 P1-vv::Ac Dek1
T3312B Ds-1S2 P1-vv::Ac Dek1
T3312C Ds-1S3 P1-vv::Ac Dek1
T3312D Ds-1S4 P1-vv::Ac Dek1
T3312E Ds-1L1 P1-vv::Ac Bz2
T3312F Ds-1L3 Bz2; Ac
T3312G Ds-2S1 B1-Peru; P1-vv::Ac
T3312I Ds-2S3 B1-Peru; P1-vv::Ac
T3312J Ds-2S4; P1-vv::Ac
T3312L Ds-3L1 A1 Sh2; P1-vv::Ac
T3312M Ds-3L2 A1 Sh2; P1-vv::Ac
T3312O Ds-4L1 C2; P1-vv::Ac
T3312P Ds-4L3 C2; P1-vv::Ac
T3312Q Ds-4L4 C2; P1-vv::Ac
T3312S Ds-4L6 C2; P1-vv::Ac
T3312T Ds-4L7 C2; P1-vv::Ac
T3312U Ds-5L1 A2 Pr1 Bt1; P1-vv::Ac
T3312V Ds-5S1 A2 Pr1 Bt1; P1-vv::Ac
T3312W Ds-5S2 A2 Pr1 Bt1; P1-vv::Ac
T3312Y Ds-9S1 C1-I wx1; Ac
T3312Z Ds-10L2 R1-sc; P1-vv::Ac

B-A TRANSLOCATIONS (BASIC SET)

122A TB-1La
122B TB-1Sb
222A TB-1Sb-2L4464
222B TB-3La-2S6270
327A TB-3La
327B TB-3Sb
421A TB-4Sa
423E TB-4Lf
522A TB-5La
522C TB-5Sc
614B TB-6Sa
614C TB-6Lc
717A TB-7Lb
719A TB-7Sc
809A TB-8Lc
922B TB-9Lc Wc1
922D TB-9Sd
X21B TB-10L19
X22A TB-10Sc

B-A TRANSLOCATIONS (OTHERS)

122C TB1-Lc
123B TB-1La Bz2; bz2-m
126G TB-1Sb P1-vv::Ac bz2-m::Ds A1 A2 Bz1 C1 C2 R1
221I TB-2Sa B1-Peru
221J TB-2Sb
225A TB-3La-2L7285
225B TB-1Sb-2Lc
320P TB-1La-3Le
320Q TB-5La-3L(1)
320R TB-5La-3L(2)
320S TB-5La-3L(3)
327C TB-3Lc
327D TB-3Ld
329Z T3-B(La); T3-B(Sb)
331A TB-1La-3L5267
331B TB-1La-3L4759-3
331C TB-1La-3L5242
331E TB-3Lf
331F TB-3Lg
331G TB-3Lh
331H TB-3Li
331I TB-3Lj
331J TB-3Lk
331K TB-3Ll
331L TB-3Lm
420B TB-9Sb-4L6504
420I TB-9Sb-4L6222
421B TB-1La-4L4692
421C TB-7Lb-4L4698
421D TB-4Sa Su1; su1
423A TB-4Lb
423B TB-4Lc
423C TB-4Ld
423D TB-4Le
423F TB-1Sb-2L4464-4f
425A TB-4Sg
425B TB-4Lh
425C TB-4Li
428I Dt6 TB-4Sa
522B TB-5Lb
522D TB-5Ld
528D TB-1La-5S8041
614A TB-6Lb
627E TB-6Lc Dt2; A2 C1 C2 R1 a1-m
719B TB-7Sc Vp9; vp9
720A TB-7Lb Dt3; a1-m1::rDt (Neuffer)
806A TB-8La
806B TB-8Lb
921A TB-9La
921B TB-9Sb
921C TB-9Lc
922C TB-9Sb C1-I
929A IsoB9-9 isochromosome Type 1
929B IsoB9-9 isochromosome Type 2
929C T9-B(La); T9-B(Sb)
929D IsoB9-9 isochromosome (original)
929F T9-B (La + Sb)
929G TB-9Sb; T9-8(4453)
929H TB-9Sb; T9-3(6722)
929I TB-9Sb-1866
929J TB-9Sb-1852
929K TB-9Sb-2150
929L TB-9Sb-14
929M TB-9Sb-2010
TX40D TB-1Sb P1-vv::Ac r1-sc:m3::Ds
TX40E TB-3La a1-m Dt1
TX40F TB-8Lc Ac2 bz2-m::Ds
TX40G TB-9Sd a1-m Dt1
TX40H TB-9Lc Ac8168-9 r1-sc:m3::Ds
TX40I TB-10L18 P1-vv::Ac r1-sc:m3::Ds
X21A TB-10La
X21C TB-10Ld
X22B T1La-B-10L18
X22C TB-10Lb
X30A TB-10L1
X30B TB-10L2
X30C TB-10L3
X30D TB-10L4
X30E TB-10L5
X30F TB-10L6
X30G TB-10L7
X31A TB-10L8
X31B TB-10L9
X31C TB-10L10
X31D TB-10L11
X31E TB-10L12
X31G TB-10L14
X31H TB-10L15
X31I TB-10L16
X31J TB-10L17
X32A TB-10L18
X32C TB-10L20
X32D TB-10L21
X32E TB-10L22
X32F TB-10L23
X32G TB-10L24
X32H TB-10L25
X32I TB-10L26
X32J TB-10L27
X32K TB-10L28
X33A TB-10L29
X33B TB-10L30
X33C TB-10L31
X33D TB-10L32
X33F TB-10L34
X33G TB-10L35
X33H TB-10L36
X34A TB-10L37
X34B TB-10L38

INVERSION

I143A Inv1a (1.S.30; 1.L.50)
I143B Inv1c (1.S.30; 1.L.01)
I143C Inv1d (1.L.55; 1.L.92)
I143D Inv1k (1.L.46; 1.L.82)
I243A Inv2b (2S.06; 2L.05)
I243B Inv2h (2L.13; 2L.51)
I444A Inv2a (2S.70; 2L.80)
I343A Inv3a (3L.38; 3L.95)
I343B Inv3b (3L.21; 3L.70)
I343C Inv3c (3L.05; 3L.95)
I343D Inv3(8582) (3S.55; 3L.82)
I443A Inv4b (4S.10; 4L.12)
I443B Inv4c (4S.89; 4L.62)
I443C Inv4a (4L.30; 4L.90)
I443D Inv4d (4L.40; 4L.96)
I443E Inv4f (4L.17; 4L.63)
I543A Inv4e (4L.16; 4L.81)
I543B Inv5a (5S.05; 5L.72)
I743A Inv5(8623) (5S.67; 5L.69)
I743B Inv6d (6S.70; 6L.33)
I743C Inv6(3712) (6S.76; 6L.63)
I743D Inv6a (6S.76; 6L.63)
I843A Inv6e (6S.80; 6L.32)
I943A Inv7f (7L.17; 7L.61)
I943B Inv7(8540) (7L.12; 7L.92)
I943C Inv7(3717) (7S.32; 7L.30)
I943E Inv7a (7L.05; 7L.95)
IX43A Inv8a (8S.30; 8L.15)
I344A Inv9a (9S.70; 9L.90)
IX43B Inv9b (9S.05; 9L.87)

RECIPROCAL TRANSLOCATIONS (wx1 AND Wx1 MARKED)

wx01A T1-9c (9L.22; 1.S.48); wx1
wx01B T1-9(5622) (9L.12; 1.L.10); wx1
wx02A T1-9(4995) (9S.20; 1.L.19); wx1
wx02AA T1-9(4995) (9S.20; 1.L.19); wx1
wx03A T1-9(8389) (9L.13; 1.L.74); wx1
wx04A T2-9c (9S.33; 2S.49); wx1
wx05A T2-9b (9L.22; 2S.18); wx1
wx06A T2-9d (9L.27; 2L.83); wx1
wx07A T3-9(8447) (9L.14; 3S.44); wx1
wx08A T3-9(c**) (9S.20; 3S.15); wx1
wx09A T3-9(8562) (9L.22; 3L.65); wx1
wx10A T4-9e (9L.26; 4S.53); wx1
wx11A T4-9g (9L.27; 4S.27); wx1
wx12A T4-9(5657) (9S.25; 4L.33); wx1
wx13A T4-9b (9L.29; 4L.90); wx1

wx14A T5-9c (9L.10; 5S.07); wx1
wx14B T5-9(022-11) (9L.27; 5S.30); wx1
wx15A T5-9(4817) (9S.07; 5L.06); wx1
wx16A T5-9d (9L.10; 5L.14); wx1
wx17A T5-9a (9S.17; 5L.69); wx1
wx18A T6-9(4778) (9L.30; 6S.80); wx1
wx19A T6-9a (9L.40; 6S.79); wx1
wx19B T6-9e (9L.24; 6L.18); wx1
wx20A T6-9b (9S.37; 6L.10); wx1 y1
wx21A T6-9(4505) (9ctr.00; 6L.13); wx1
wx22A T7-9(4363) (9ctr.00; 7ctr.00); wx1
wx23A T7-9a (9S.07; 7L.63); wx1
wx24A T8-9d (9S.16; 8L.09); wx1
wx25A T8-9(6673) (9S.31; 8L.35); wx1
wx26B T9-10(059-10) (9S.31; 10L.53); wx1
wx27A T9-10b (9S.13; 10S.40); wx1
Wx30A T1-9c (9L.22; 1.S.48); Wx1
Wx30B T1-9(4995) (9S.20; 1.L.19); Wx1
Wx30C T1-9(8389) (9L.13; 1.L.74); Wx1
Wx31A T2-9c (9S.33; 2S.49); Wx1
Wx31B T2-9b (9L.22; 2S.18); Wx1
Wx31C T2-9d (9L.27; 2L.83); Wx1
Wx32A T3-9(8447) (9L.14; 3S.44); Wx1
Wx32B T3-9(8562) (9L.22; 3L.65); Wx1
Wx32C T3-9(c**) (9S.20; 3S.15); Wx1
Wx33A T4-9e (9L.26; 4S.53); Wx1
Wx33B T4-9(5657) (9S.25; 4L.33); Wx1
Wx33C T4-9g (9L.27; 4S.27); Wx1
Wx34A T5-9c (9L.10; 5S.07); Wx1
Wx34B T5-9(4817) (9S.07; 5L.06); Wx1
Wx34C T4-9b (9L.29; 4L.90); Wx1
Wx35A T5-9(8386) (9S.13; 5L.87); Wx1
Wx35B T5-9a (9S.17; 5L.69); Wx1
Wx35C T5-9d (9L.10; 5L.14); Wx1
Wx36A T6-9(4778) (9L.30; 6S.80); Wx1
Wx37A T6-9(8768) (9S.61; 6L.89); Wx1
Wx37B T7-9(4363) (9ctr.00; 7ctr.00); Wx1
Wx37C T6-9(4505) (9ctr.00; 6L.13); Wx1
Wx38A T7-9a (9S.07; 7L.63); Wx1
Wx38B T8-9d (9S.16; 8L.09); Wx1
Wx38C T8-9(6673) (9S.31; 8L.35); Wx1
Wx39A T9-10(8630) (9S.28; 10L.37); Wx1
Wx39B T9-10b (9S.13; 10S.40); Wx1

PHENOTYPE ONLY

Kernel Mutants

blotched aleurone
Bh*-86-1381-1
Bh-Tu*-Mumm

brittle endosperm
bt*-011-11
bt*-1979-14
bt*-1979-16
bt*-1982
bt*-4380
bt*-4539
bt*-4973
bt*-60-151
bt*-8101
bt*-8102
bt*-83-84-3541-1
bt*-84-4
bt*-84-5
bt*-84-5091-9
bt*-84-5257-1
bt*-84-6
bt*-85-3096-6
bt*-85-3098-15
bt*-85-3099-16
bt*-85-3372-27
bt*-87-2132-39
bt*-87-2297-1
bt*-87-88-2630-28
bt*-88-3177-14
bt*-88-3177-2
bt*-88-3177-7
bt*-8804
bt*-8805
bt*-89-1265-18
bt*-90286
bt*-A4109
bt*-Briggs-1998-1
bt*-F-15
bt*-F-23
bt*-F-31
bt*-F-34
bt*-F-36
bt*-F-8
bt*-F10
bt*-Panzio
bt*-PetersonResHy
bt*-PI200197
bt*-PI251887
bt-gm*-84-5045-39
bt-gm*-85-3017-24
bt-sh*-PI251930

brown endosperm
brn*-1981-1
brn*-1981-2
brn*-1981-3
brn*-1981-4
brn*-84-23
brn-bt*-81-F-24

brown kernel
lt-brn-sml*-86-1302-37
bnk*-N747B

brown pericarp
bp*-Coates
bp*-Lima100
bp*-Lima94
bp*-PI183639

collapsed endosperm
cp*-N1076A
cp*-N1078B
cp*-N1092A
cp*-N1104B
cp*-N1229A
cp*-N1255B
cp*-N1275A
cp*-N1293
cp*-N1294
cp*-N1311C
cp*-N1313
cp*-N1318
cp*-N1319A
cp*-N1338
cp*-N1369
cp*-N1379A
cp*-N1385
cp*-N1393A
cp*-N1399A
cp*-N1405A
cp*-N1417
cp*-N1430
cp*-N1436A
cp*-N1527B
cp*-N2356B
cp*-N524E
cp*-N628
cp*-N863A
cp*-N886
cp*-N918A
cp*-N935
cp*-N936A
cp*-N937A
cp*-N968A
cp*-N991
cp*-N992

colored plumule
Pu*-1976-RYDCO

colorless aleurone
cl*-85-86-3559-1
cl*-86-1478-16
cl*-N1333A
cl*-N1345A
cl*-N1346A
cl*-N720E
cl*-N795
cl*-N801
cl*-N818A
cl-crown-pale-base*-85-86-3558-23
r*-86-1590-6

colorless floury
clf*-N2425B

crumpled kernel
crp*-N1429A
crp*-N2207
dnj*-N1534

defective crown
dcr*-N1053A
dcr*-N1158A
dcr*-N1176B
dcr*-N1233A
dcr*-N1409
dcr*-N871A
dcr*-N925A

defective kernel
de*-1276
de*-17
De*-1976-RYDCO
de*-2080
de*-2192
de*-2424
de*-2915
de*-2919
de*-3188
de*-4309
de*-5044Hagie
de*-85-86-3567-35
de*-8505
de*-8507
de*-8508
de*-86-1472-6
de*-8808
de*-8809
de*-8810
de*-8811
de*-8818
de*-N1002A
de*-N1007A
de*-N1057B
de*-N1089
de*-N1101
de*-N1122A
de*-N1136A
de*-N1142
de*-N1149A
de*-N1162
de*-N1166
de*-N1177A
de*-N1196
de*-N1310B
de*-N1329A
de*-N1336B
de*-N1345B
de*-N1390A
de*-N1400
de*-N1403
de*-N1420
de*-N1520B
de*-N1897
de*-N2022
de*-N232B
de*-N260D
de*-N279B
de*-N296C
de*-N307D
de*-N400A
de*-N408D
de*-N513B
de*-N528C
de*-N540A
de*-N573A
de*-N660C
de*-N674A
de*-N748B
de*-N751A
de*-N760B
de*-N877A
de*-N891A
de*-N902A
de*-N903
de*-N929
de*-N932
de*-N939A
de*-N970A
de*-N979A
de*-N981A
de-sml*-8813
de-sml*-8814
de-sml*-8815
de-sml*-8816
de-sml*-8817
def*-8101
def*-8102
def*-8103
def*-8104
def*-8105
def*-8106

def*-8107
def*-8108
def*-8109
def*-8110
def*-8111
def*-8112
def*-8113
def*-8114
def*-8116
def*-8118
def*-8119
def*-8120
def*-8121
def*-8122
def*-8123
def*-8125
def*-8126
def*-8127
def*-8128
def*-8130
def*-8131
def*-8132
def*-8134
def*-8136
def*-8137
def*-8138
def*-8201
def*-84-22
def*-84-28
def*-84-29
def*-84-30
def*-84-31
def*-84-37
def*-84-40
def*-84-41
def*-84-45
def*-84-48
def*-84-49
def*-84-53
def*-84-54
def*-84-58
def*-84-60
dek*-1979-32
dek*-1981-1
dek*-74-0060-4
dek*-84-14
dek*-86-1496-35
dek*-8902
dek*-8903
dek*-8904
dek*-99-6273-1
dek*-F-16
dek*-PS602
wrinkled-de*-86-1473-5
wrinkled-gm*-86-1582-32

dented kernel
dnt*-N1185A
dnt*-N1326
dnt*-N884A

dilute aleurone
dil*-N452D
dil*-N524C
dil*-N743A

discolored kernel
dsc*-N1084
dsc*-N1135A
dsc*-N1302
dsc*-N749
pig*-84-5080-18
pig*-86-1178-6
pig-gm*-1979-51
pig-gm*-1979-52
pig-gm*-1979-9
pig-gm*-1981-A
pig-gm*-1981-B
pig-gm*-1982-3
pig-gm*-5020-14
pig-gm*-84-5078-10
pig-gm*-86-1200-3
pig-gm*-87-2275-15
pig-gm*-87-2305-22
pig-gm*-Briggs 1998-1
pig-gm*-Briggs 1998-2
pig-gm*-PI251930
ptd-dek*-1976-RYDCO
ptd-dek*-1981
ptd-dsc*-87-2490-22
sml-pig-gm*-88-89-3554-44

dull endosperm
du*-Sprague

etched endosperm
et*-3130
et*-3576
et*-5191
et*-6-9321-1
et*-73-766-1
et*-8-M-4
et*-84-5266-26
et*-84-5270-40
et*-85-86-3518-21
et*-86-1493-6
et*-8616
et*-87-2349-13
et*-88-89-3525-22
et*-88-89-3554-33
et*-89-90-1547-19
et*-89-90-1548-13
et*-90-3222-13
et*-Mu1767
et*-Mu2349
et-mutable*-87-2519-31
et*-N1001A
et*-N1078A0
et*-N1332
et*-N1361
et*-N164B
et*-N185B
et*-N357C
et*-N403A
et*-N489A
et*-N509A
et*-N514A
et*-N516C
et*-N518B
et*-N561B
et*-N571A
et*-N586A
et*-N615A
et*-N617
et*-N629F
et*-N643A
et*-N670A
et*-N680C
et*-N701A
et*-N702A
et*-N723A
et*-N724D
et*-N745
et*-N76D
et*-N789
et*-N798A
et*-N818B
et*-N837A
et*-N861
et*-N864A
et*-N868A
Et*-N876A
et*-N953A
et*-N965
et*-Osturana
et-de*-88-89-3526-8
et-gm*-86-1475-34
et-gm*-86-87-1742-38
et-gm*-87-2502-19
granular-o*-84-5274-30
sh*-N972A
sml-et*-85-3522-29
su-sh-et*-98-1887-1

flint kernel
flint*-87-2126-22

floury endosperm
fl*-67-412
fl*-78-513
fl*-83-3386-19
fl*-84-44
fl*-8515
fl*-Mojo
fl*-N1145A
fl*-N1163
fl*-N1208A
fl*-N1287
fl*-N1308A
fl*-N1333B
fl*-N1426
fl*-N7B-65-1294
fl*-N872A
fl*-shoepeg
fl*-sucaxo
fl-cap*-1981
fl-cap*-66-519-1
fl-de*-8905
sml-fl-cap*-1981

germless
brn-gm*-85-3315-6
brn-gm*-85-86-3587-46
brn-gm*-85-86-3595-3
brn-gm*-86-1161-5
emb*-85-3100-32
emb*-85-3378-8
gm*-1387
gm*-1979-11
gm*-1979-53
gm*-5234
gm*-6372
gm*-84-5087-4
gm*-8510
gm*-86-1011-2
gm*-86-1013-4
gm*-86-1097-3
gm*-86-1335-1
gm*-86-1591-7
gm*-86-87-1742-18
gm*-87-2456-9
gm*-N1292
gm*-N1303
gm*-N1311B
gm*-N1312
gm*-N1319B
gm*-N1390C
gm*-N198C
gm*-N869A
gm*-N928B
o-gm*-84-44
o-gm*-98-5733-1
pr-gm*-86-1109-1
sh-gm*-84-5045-32
sh-gm*-88-3082-4
sml-o-gm*-86-1323-4
sml-dsc-gm*-95W-240
w-o-gm*-85-3135-4
w-o-gm*-86-1349-1
w-o-gm*-88-3270-10
y-gm*-85-3288-28

glassy endosperm
ae*-6921
ae*-84-7
ae*-92-1365-3
ae*-96-1449-1
ae*-Briggs 1998-1
ae*-Mu32

lemon white
lw*-1979-45
lw*-1981-10
lw*-1998-1
lw*-73-2548
lw*-82-1
lw*-85-3076-28
lw*-85-3252-5
lw*-86-87-1828-7
lw*-88-3177-2
lw*-89-90-3609-5
lw*-87-2407-36
lw*-B73
lw-y-pg*-1998-4
lw-y-pg*-Funk-81-5
lw-y-pg*-PI200303
pale-y*-83-84-3549-13
pale-y*-84-5082-33
pale-y*-84-5167-48
pale-y*-84-5288-19
pale-y*-85-3005-22
pale-y*-85-3006-30
pale-y*-85-3007-40
pale-y*-85-3010-40
pale-y*-85-3016-15
pale-y*-85-3017-31
pale-y*-85-3065-25
pale-y*-85-3069-6
pale-y*-85-3087-29
pale-y*-85-3377-2
pale-y*-86-1155-3
pale-y*-87-88-2679-1
pale-y*-88-89-3551-35
pale-y*-89-1313-3
pale-y*-89-90-1525-23
pale-y*-90-3220-1
pale-y*-90-3220-26
w*-N677
w*-N70
wh*-BMS-Rhoades
y-pg*-1981-17
y-pg*-84-5275-14
y-pg*-85-3042-7
y-pg*-85-3044-34
y-pg*-85-3078-41
y-pg*-85-3562-31
y-pg*-85-86-3533-9
y-pg*-86-1151-7
y-pg*-86-87-1723-27
y-pg*-87-2160-16

loose pericarp
lsp*-N1045

marbled aleurone
Dap*-3

dap*-86-8126-2
Dap*-89-3177.0
Dap*-89-3177.5
Dap*-89-3178.3
Marbled*-Sprague

miniature kernel
de*-N663C
mn*-1981-51
Mn*-866248U
mn*-87-2215-17
mn*-87-2346-20
mn*-87-2347-36
mn*-87-2422-14
mn*-88-3177-2
mn*-88-89-3509-40
mn*-88-89-3564-25
mn*-N1536
Mn*-N273C
mn*-N378C
mn*-N894
mn*-PI239110
mn*-PI245132
sml-k*-97-4784-1

mosaic aleurone color
msc*-N593A

mottled aleurone
Mt*-2313
Mt*-65-2238
Mt*-N1343A
Mt*-Sprague

multiple aleurone layer
Mal*-Galinat
Mal*-Nelson
Mal*-PI515052

opaque endosperm
lrg-o-crown*-89-1275-17
o*-1979-54
o*-1981-11-Fox-19
o*-1981-3-Fox-7
o*-1981-5-Fox-9
o*-1981-6-Fox-10
o*-1981-8-Fox-15
o*-1982
o*-1982-2-Fox-13
o*-2-Fox-6
o*-3015
o*-73-798-1
o*-76GH-76
o*-8129
o*-82:288-1
o*-83-84-3549-39
o*-84-5025-15
o*-84-5025-17
o*-84-5025-8
o*-84-5044-35
o*-84-5091-13
o*-84-5094-4
o*-84-5095-23
o*-84-5117-16
o*-84-5261-37
o*-84-5270-40
o*-84-5282-27
o*-84-5295-13
o*-84-5321-28
o*-84-5324-29
o*-84-8a
o*-85-3084-8
o*-85-3088-3
o*-85-3335-35
o*-86-87-1767-10
o*-87-2285-33
o*-87-2350-2
o*-88-89-3550-27
o*-97-4784-6
o*-Briggs-1998-1
o*-BS20-Fox-3
o*-Fox-12
o*-N1008A
o*-N1037A
o*-N1039
o*-N1046
o*-N1065A
o*-N1074A
o*-N1119A
o*-N1172A
o*-N1189A
o*-N1195A
o*-N1209
o*-N1218
o*-N1228
o*-N1244A
o*-N1245
o*-N1298
o*-N1301
o*-N1304
o*-N1310A
o*-N1320A
o*-N1355
o*-N1358
o*-N1422
o*-N1433
o*-N436C
o*-N491A
o*-N696A
o*-N829C
o*-N870
o*-N885A
o*-N895
o*-N899
o*-N906A
o*-N908
o*-N910
o*-N915
o*-N930
o*-N938A
o*-N941
o*-N948B
o*-N969A
o*-N973
o*-N989
o*-N995A
o*-N996
o*-N999A
o*-PI195245
o*-PI200285
o-de*-1981-9-Fox-18
o-dek*-6
o-dek*-87-2279-12
o-gm*-83-3398-6
o-gm*-84-33
o-sh*-86-1297-2
o-sh*-F1979-19
os*-2162
pro*-Mu1
sh-o*-87-2455-7
sml-o*-87-88-2692-5
sml-o*-PI195243

pale aleurone
pa*-N893A
pa*-N917A
pale-Cl*-86-1476-14
pale-Cl*-LGC65
pale-Cl-gm*-84-5251-1

pale aleurone, with pigmented sectors
pa-Cl*-m-86-1474-39
pa-Cl*-m-86-1478-4
pa-Cl*-m-87-2224-33

pale crown
pa-crown*-85-86-3558-23

pale yellow endosperm
lw*-8509
lw*-8513
lw*-8514
pale-endo*-73-3
pale-endo*-73-4004
pale-y*-1981
pale-y*-83-3382-16
pale-y*-83-3382-18
pale-y*-83-84-3548-25
pale-y*-84-5103-16
pale-y*-85-3016-30
pale-y*-85-3036-38
pale-y*-85-3134-46
pale-y*-85-3374-13
pale-y*-85-3511-18
pale-y*-86-1155-2
pale-y*-87-2339-10
pale-y*-87-2350-2
pale-y*-87-2350-25
pale-Y*-87-2422-14
pale-y-gm*-Rsssc-77-110
pale-y-o*-84-5288-2
pale-y-o*-86-1296-27
y*-84-5272-12
y*-84-5288-1
y*-85-3041-2
y*-85-3087-12
y*-85-3125-7

pitted kernel
ptd*-N1425A
ptd*-N660E
ptd*-N738B
ptd*-N855A
ptd*-N901A
ptd*-N923

purple pericarp
Pl*-CFS-69

red aleurone
pr*-N707A
pr*-N850

red pericarp
r*-ch-Burbank-CFS-80
r*-ch-PI213730

red silk scar
red-silk-scar*-MTC

rough kernel
rgh*-N1060
rgh*-N1164B
rgh*-N1210
rgh*-N1306A
rgh*-N1524
rgh*-N799A
rgh*-N802
rgh*-N882
rgh*-N974A

shrunken kernel
pale-y-su-sh*-88-3133-28
sh*-1979-10
sh*-1981-14
sh*-1982-2
sh*-2927-Mumm
sh*-2928-Mumm
sh*-83-3328-24
sh*-84-3
sh*-84-5248-20
sh*-84-5317-44
sh*-85-3045-7
sh*-85-3104-27
sh*-85-3112-20
sh*-85-3375-38
sh*-8502
sh*-8503
sh*-8506
sh*-8511
sh*-8517
sh*-86-1565-17
sh*-87-2045-25
sh*-87-2045-6
sh*-87-2050-1
sh*-87-2050-3
sh*-87-2213-19
sh*-87-2215-12
sh*-87-2355-29
sh*-87-2406-3
sh*-87-2496-21
sh*-88-89-3540-1
sh*-8806
sh*-8807
sh*-8906
sh*-8907
sh*-97P-29-5
sh*-F-11
sh*-F-2
sh*-F-25
sh*-KERR
sh*-N1080
sh*-N1105B
sh*-N1147
sh*-N1320B
sh*-N1341
sh*-N1366
sh*-N1519B
sh*-N1969
sh*-N208C
sh*-N252B
sh*-N399A
sh*-N627A
sh*-N689
sh*-N741
sh*-N742
sh*-N750
sh*-N757
sh*-N785A
sh*-N819
sh*-N849
Sh*-N881A
sh*-N887A
sh*-N911
sh*-N961
sh*-PI596356
sh*-RJL
sh-bt*-85-3392-31
sh-crown*-Briggs-1998-1
sh-de*-6607
sh-de*-RSSSC-117
sh-fl*-9180
sh-fl*-9392
sh-o*-87-2410-24
sh-wx*-F-18

su-sh*-F-5

small kernel
smk*-N1003
smk*-N1019
smk*-N1057A
smk*-N1085A
smk*-N1115A
smk*-N1160
smk*-N1165A
smk*-N1168A
smk*-N1203
smk*-N1437
smk*-N1529
smk*-N215D
smk*-N227B
smk*-N320
smk*-N433A
Smk*-N845B
smk*-N890A
smk*-N909A
smk*-N942
smk*-N943
smk*-N994A

spotted aleurone
cl-mut*-85-86-3564-1
cl-mut*-97-4782-9
cl-mut*-99-2170
coarse-mutable*-86-1417-7
Dt*-a; a1-m
Dt*-b; a1-m
Dt*-c; a1-m
Dt*-d; a1-m
Dt*-e; a1-m
Dt*-f; a1-m
Dt*-g; a1-m
Dt*-h; a1-m
Dt*-i; a1-m
fine mut*-86-1283-45
spk*-N551A
spk*-N600Ce
spk*-N687A

sugary kernel
su*-1979-8
su*-83-3383-21
su*-84-5350-2
su*-85-3133-32
su*-8504
su*-8803
su*-89-1279-14
su*-L874261
su*-N1040
su*-N236C
su*-N748A
su*-N817
su-sh*-F-22

viviparous kernel
pale-vp*-87-2286-1
pale-vp*-87-2286-18
pale-vp*-87-2286-2
pale-vp*-87-2286-25
pale-vp*-87-2286-3
pale-y*-84-5027-22
pale-y*-84-5032-21
pale-y-vp*-83-3100-31
pale-y-vp*-83-3124-33
pale-y-vp*-84-5266-5
pale-y-vp*-85-3140-15
pale-y-vp*-85-3240-5
pale-y-vp*-85-3267-6
pale-y-vp*-85-3267-9
pale-y-vp*-85-3385-34
pale-y-vp*-86-1316-27
pale-y-vp*-88-3177-14
ps*-85-3288-28
ps*-85-3492-36
ps*-85-86-3567-1
ps*-86-1105-2
ps*-86-1352-4
ps*-86-1499-3
ps*-86-87-1742-18
ps*-89-90-1588-37
ps*-90-3222-27
ps*-90-91-8549-7
ps*-96-5032-6
ps*-98-5691-5
ps*-99-2157-1
ps*-Mu85-3061-21
ps*-Mu86-1105-1
vp(ps)*-86-1449-3
vp(ps)*-86-1565-17
vp*-0118
vp*-0315
vp*-2-8c
vp*-2000PR-1
vp*-73-30173
vp*-8101
vp*-8104
vp*-8106
vp*-8107
vp*-8108
vp*-8109
vp*-8110
vp*-8111
vp*-8112
vp*-8113
vp*-8114
vp*-8115
vp*-8116
vp*-8117
vp*-8201
vp*-8203
vp*-8204
vp*-8208
vp*-8209
vp*-8210
vp*-8211
vp*-84-5079-29
vp*-84-5279-29
vp*-84-5315-29
vp*-8418
vp*-8420
vp*-85-3011-11
vp*-85-3017-9
vp*-85-3040-29
vp*-85-3042-7
vp*-85-3099-16
vp*-85-3135-4
vp*-85-3182-6
vp*-85-3250-1
vp*-85-3339-25
vp*-85-3422-13
vp*-85-86-3567-20
vp*-86-1109-1
vp*-86-1407-15
vp*-86-1573-27
vp*-87-2146-18
vp*-87-2213-19
vp*-87-2224-3
vp*-87-2274-37
vp*-87-2299-1
vp*-87-2339-1
vp*-88-89-3555-1
vp*-88-89-8625-5
vp*-89-1181-8
vp*-89-1279-14
vp*-89-90-1561-18
vp*-93-1017-2
vp*-95-2086-1
vp*-Funk-8101
vp*-N702C
vp*-PI183642
vp*-PI185847
vp*-PI200204
vp*-PI254854
vp*-PI430482
vp-de*-87-2406-23
vp-Y*-86-1267-31
vp-Y*-86-1361-7
w-vp*-84-5020-4
w-vp*-85-3014-6
w-vp*-85-3304-13
w-vp*-91-1859-8
w-vp*-91-2544-7
w-vp*-92-1408-1
y-vp*-0730
y-vp*-1982-1
y-vp*-1982-2
y-vp*-1999-059-10
y-vp*-2062-Coop
y-vp*-60-153
y-vp*-6961
y-vp*-73-2656
y-vp*-80-6118
y-vp*-81-5
y-vp*-8102
y-vp*-8103
y-vp*-8105
y-vp*-8206
y-vp*-8207
y-vp*-83-1A
y-vp*-83-3101-36
y-vp*-8336
y-vp*-84-13
y-vp*-8419
y-vp*-85-3572-30
y-vp*-8512
Y-vp*-87-2339-10
y-vp*-87-2340-36
y-vp*-8701
y-vp*-88-89-3563-33
y-vp*-88-89-3613-25
y-vp*-99-2226-1

waxy endosperm
wx*-0208
wx*-98-1406-6
wx*-N66C

white cap kernel
Wc*-1982-1
Wc*-Funk-81-22
Wc*-Funk-81-23
Wc*-DC
wc*-N1206A
wc*-N1349
wc*-N897A

white endosperm
y*-1979-46
y*-1981
y*-1981-14
y*-1981-18
y*-1982-3
y*-73-2
y*-73-2262-1
y*-73-2262-2
y*-73-2394
y*-73-324-1
y*-73-4035
y*-73-426
y*-73-6
y*-84-8b
y*-87-2201-3
y*-Funk-81-12
y*-Funk-81-13
y*-Funk-81-2
y*-Funk-81-20
y*-Funk-81-9
y*-Sprague
y*-syn-DOCI
y*-Williams-60-154

wrinkled kernel
wr*-N1075A
wr*-N1389A
wr*-N156C
wr*-N553A
wr*-N612A

Seedling Mutants

aberrant seedling
abbt*-N399B
abbt*-N454C
abbt*-N594B
abbt*-N595B
abbt*-N712B

adherent leaf
ad*-87-2285-18
ad*-N111
ad*-N194
ad*-N1958
ad*-N253
ad*-N273B
ad*-N316
ad*-N377B
ad*-N452E
ad*-N512B
ad*-N551B
ad*-N556D
ad*-N582
ad*-N605B
ad*-N640
ad*-N664
ad*-N682B
ad*-N767
ad*-N877B
ad*-N984B

albino seedling
nlw*-85-3357-17
peach-albino-mutable*-87-2209-30
peach-albino*-N1983B
w*-002-12
w*-005-19
w*-009-6
w*-010-4
w*-011-11
w*-017-14-A
w*-017-14-B
w*-020-9
w*-034-16
w*-037-14
w*-039-15
w*-2065
w*-2246
w*-3858
w*-4670
w*-4873
w*-5201

w*-5255
w*-5267
w*-56-3003-12
w*-5602
w*-5622
w*-5787
w*-5863
w*-6293
w*-6504
w*-6575
w*-7165
w*-7219
w*-7281
w*-74-1674-1
w*-78-297-3
w*-8105W
w*-8129
w*-8147
w*-8201
w*-84-5205-46
w*-84-5222-30
w*-85-3359-11
w*-85-3552-25
w*-85-3559-30
w*-8529
w*-8549
w*-8569
w*-86-1078-6
w*-86-1265-30
w*-86-2222-5
w*-8630
w*-8635
w*-8637
w*-8670
w*-87-2215-8
w*-8925
w*-8963
w*-8970
w*-8977
w*-8992
w*-9235
w*-B-75
w*-BYD
w*-Canario Hembrilla Enano
w*-Fino
w*-MontenegrinFlint
w*-N103
w*-N109
w*-N115
w*-N1158B
w*-N126A
w*-N137D
w*-N145
w*-N147B
w*-N167
w*-N176
w*-N178A
w*-N1834
w*-N1839
w*-N1847
w*-N1849
w*-N1854
w*-N1865
w*-N186
w*-N1890
w*-N1909
w*-N191
w*-N1915
w*-N192
w*-N21A
w*-N22
w*-N220
w*-N224
w*-N23
w*-N24
w*-N278A
w*-N285
w*-N304A
w*-N318
w*-N332
w*-N335
w*-N346A
w*-N355
w*-N364
w*-N367B
w*-N404
w*-N405A
w*-N413B
w*-N42
w*-N428B
w*-N430B
w*-N436A
w*-N456A
w*-N457
w*-N491B
w*-N5
w*-N509B
w*-N516A
w*-N524A
w*-N532
w*-N536A
w*-N540B
w*-N547A
w*-N558B
w*-N563A
w*-N569B
w*-N574
w*-N58
w*-N587C
w*-N593B
w*-N6
w*-N613C
w*-N621B
w*-N627B
w*-N67A
w*-N682A
w*-N704
w*-N708A
w*-N727A
w*-N729A
w*-N736A
w*-N77
w*-N804B
w*-N829B
w*-N883B
w*-N917B
w*-PI184276
w*-PI193438
w*-PI201543
w*-PI213747
w*-PI228176
w*-PI228179
w*-PI228183
w*-PI232961
w*-PI232965
w*-PI232968
w*-PI232972
w*-PI239103
w*-PI239110
w*-PI251009
w*-PI251885
w*-PI251930
w*-PI251932
w*-PI254851
w*-PI267162
w*-PI267179
w*-PI267204
w*-Singleton-16
w*-Singleton-22
w*-Singleton-24
w*-Singleton-25
w*-Singleton-31
w*-Tama
w*-wh-mut
wh*-053-4
wh*-2083
wh*-89-578-6

bilateral coleoptile
blc*-N743C

clasping leaf
clsp*-87-2320-9
clsp*-88-89-3522-1

distorted
dst*-N444A

ectopic coleoptile
ect*-N641B

flecked leaf
flk*-N403C
flk*-N527A
flk*-N564B
flk*-N570A
flk*-N630B
flk*-N653A

glossy leaf
gl*-1-3(5476)
gl*-218-1
gl*-32TaiTaiTaSarga
gl*-4339
gl*-5201
gl*-5249
gl*-56-3023-6
gl*-56-3023-9
gl*-56-3036-7
gl*-6
gl*-60-2484-8
gl*-63-2440-8
gl*-85-3095-12
gl*-8654
gl*-87-2215-8
gl*-87-2215-30
gl*-87-2278-34
gl*-88-3142-4
gl*-97P-261-5
gl*-Bizika
gl*-gl12
gl*-LGC-117
gl*-LGC-27
gl*-Loesch
gl*-Manglesdorf
gl*-Moritsa
gl*-N168
gl*-N203C
gl*-N356
gl*-N546C
gl*-N616A
gl*-N656A
gl*-N681A
gl*-N696E
gl*-PI184286
gl*-PI200203
gl*-PI228177
gl*-PI232974
gl*-PI239101
gl*-PI239110
gl*-PI251885
gl*-PI251933
gl*-PI262474
gl*-PI262476
gl*-PI262494
gl*-PI262500
gl*-PI267203
gl*-PI267209
gl*-PI267212
gl-nec*-N516D
gl*-STL

gravity non-responsive primary root
agt*-N491C

high chlorophyll fluorescence
hcf*-88-3005-3

luteus yellow seedling
l*-009-2
l*-009-6
l*-017-3
l*-025-4
l*-062-3
l*-2215
l*-2673
l*-4356
l*-4545
l*-4871
l*-5-9b[X-7-39]
l*-549-1 Derived Flint
l*-56-3003-12
l*-570-2 Cincantin
l*-5783-straw
l*-62-489-2
l*-6474
l*-6923
l*-6973
l*-7165
l*-7281
l*-73-563
l*-77-564-2
l*-7748
l*-8321
l*-8376
l*-84-5205-13
l*-84-5225-33
l*-8495
l*-85-3215-2
l*-85-3225-4
l*-85-3457-40
l*-85-3513-1
l*-85-3541-20
l*-86-1112-1
l*-86-1354-9
l*-8613
l*-8634
l*-88-89-3555-13
l*-89-90-1552-10
l*-8966
l*-8970
l*-d-8694
l*-leng
l*-LGC-43
l*-LGC-74
l*-Moritza (Bulgaria)
l*-N104
l*-N113
l*-N1145B
l*-N119
l*-N124B
l*-N129
l*-N137B
l*-N140
l*-N171A
l*-N175

l*-N1806B
l*-N1838
l*-N1878
l*-N188A
l*-N1908
l*-N1920
l*-N195
l*-N209
l*-N218
l*-N231
l*-N251
l*-N31
l*-N336
l*-N347
l*-N368B
l*-N392A
l*-N416A
l*-N438A
l*-N496B
l*-N52
l*-N523
l*-N606
l*-N612B
l*-N62
l*-N691A
l*-N703
l*-N730
l*-PI183642
l*-PI183643
l*-PI193433
l*-PI193435
l*-PI193436
l*-PI195245
l*-PI213737
l*-PI213745
l*-PI218038
l*-PI228183
l*-PI239110
l*-PI239114
l*-PI251884
l*-PI254854
l*-PI254856
l*-PI262495
l*-PI267215
l*-PI267226
l*-Rumanian Flint
l*-Tama
l-nec*-2001-519
l*-y wx 6-9b
pyg*-N761
y-l*-85-3234-6
y-l*-8910 Briggs
yd*-87-2278-34
yel*-5344
yel*-8721
yel*-8793
yg*-8962

orobanche
oro*-6577
oro*-69-9291-8
oro*-84-5080-15
oro*-85-3087-3
oro*-85-3106-41
oro*-85-3113-11
oro*-88-3237-31
oro*-88-89-3550-32

pale green seedling
pas*-90-3222-13
pg*-2142
pg*-5619
pg*-6372
pg*-69-5079-2
pg*-6923
pg*-7122
pg*-8129
pg*-84-5234-29
pg*-8412
pg*-8911
pg*-8959
pg*-Caspar
pg*-Fino
pg*-N102
pg*-N11
pg*-N1161B
pg*-N12
pg*-N123C
pg*-N124A
pg*-N127
pg*-N1322B
pg*-N1389B
pg*-N146A
pg*-N147A
pg*-N1476
pg*-N150A
pg*-N155A
pg*-N156B
Pg*-N1604
pg*-N161
pg*-N181
pg*-N1821
pg*-N1822A
pg*-N1824
pg*-N1825
pg*-N1827A
pg*-N1866
pg*-N1881
pg*-N1885
pg*-N1983
pg*-N213
pg*-N215B
pg*-N222
pg*-N247B
pg*-N272C
pg*-N296A
pg*-N338A
pg*-N346B
pg*-N349
pg*-N35
pg*-N357B
pg*-N36A
pg*-N361A
pg*-N362A
pg*-N375B
pg*-N379
pg*-N380
pg*-N381
pg*-N384B
pg*-N40
pg*-N408C
pg*-N417A
pg*-N421
pg*-N429B
pg*-N441
pg*-N445
pg*-N45A
pg*-N450
pg*-N452C
pg*-N459
pg*-N46
pg*-N469
pg*-N478A
pg*-N481
pg*-N484B
pg*-N485
pg*-N506A
pg*-N507A
pg*-N511
pg*-N514B
pg*-N520
pg*-N524B
pg*-N526C
pg*-N535
pg*-N550
pg*-N556B
pg*-N558A
pg*-N570C
pg*-N59B
pg*-N590B
pg*-N596B
pg*-N597B
pg*-N600A
pg*-N603
pg*-N615B
pg*-N618
pg*-N619
pg*-N638
pg*-N639
pg*-N641
pg*-N654B
pg*-N660A
pg*-N663B
pg*-N673A
pg*-N683A
pg*-N686B
pg*-N701B
pg*-N719C
pg*-N71A
pg*-N724B
pg*-N725A
pg*-N73A
pg*-N76A
pg*-N805
pg*-N812C
pg*-N816A
pg*-N836
pg*-N855C
pg*-N884B
pg*-N896B
pg*-N897B
pg*-N906B
pg*-PI183648
pg*-PI193424
pg*-PI251930
pg*-PI262473
pg*-PI262495
pg*-PI267162
pg*-PI267215
pg-nec*-RJL-6527

pale pale green seedling
ppg*-N1474B
ppg*-N1963
ppg*-N393B
ppg*-N406A
ppg*-N427A
ppg*-N449
ppg*-N458B
ppg*-N881B

piebald leaf
pb*-2-7-4400
pb*-87-2442-5
pb*-N1386C

ragged seedling
rgd*-N203E
rgd*-N2290C
rgd*-N261B
rgd*-N378B

red seedling leaf
red-leaf*-86-1569-7

small seedling
d*-N155B
d*-N230A
d*-N254
d*-N266B
d*-N293B
d*-N408A
d*-N429A
d*-N526B
d*-N998B
smp*-N1956
smp*-N276B
smp*-N279A
smp*-N630C
smp*-N751B
sms*-N1221B
sms*-N1964
sms*-N1971
sms*-N204B
sms*-N252A
sms*-N311C
sms*-N369B
sms*-N566
sms*-N570B
sms*-N666C
sms*-N680B

translucent leaf
trans-leaf*-56-3122-7
trans-leaf*-68F-958
trans-leaf*-78-314
trans-leaf*-79-6533
trans-leaf*-PI228176

tube leaf
fused-leaves*-N36B
fused-leaves*-N835B
fused-leaves*-PI228170

virescent seedling
l*-N184
pg*-N1171D
pg*-N39
v*-002-17
v*-007-18
v*-022-17
v*-025-4
v*-037-5
v*-1-2(5376)
v*-1-9(5622)
v*-2-9(5257)
v*-388-Sprague
v*-4308
v*-4698
v*-5-10(5355)
v*-5287
v*-5413
v*-5575
v*-56-3012-10
v*-5828
v*-60-151
v*-60-2397-15
v*-65-1433
v*-7230
v*-7281
v*-7312
v*-74-1690-1
v*-74-1873-1
v*-74-1948-1
v*-77-549-2
v*-8070

v*-8129
v*-8201
v*-8339
v*-8522
v*-8613
v*-8654
v*-8743
v*-8806
v*-8957
v*-8958
v*-9026
v*-Funk-84-13
v*-Funk-84-9
v*-leng
v*-LGC-111
v*-LGC-142
v*-LGC-98
v*-N1007B
v*-N1029B
v*-N1085B
v*-N110
v*-N1133B
v*-N1135B
v*-N1136C
v*-N114A
v*-N1151
v*-N116
v*-N1177B
v*-N1214B
v*-N125
v*-N128
v*-N1268A
v*-N131
v*-N133
v*-N134
v*-N135A
v*-N143B
v*-N153A
v*-N158
v*-N16
v*-N171B
v*-N179
v*-N1799
v*-N1806A
v*-N183A
v*-N1836
v*-N187
v*-N1873
v*-N1886
v*-N19
v*-N1912
v*-N1966
v*-N201
v*-N206A
v*-N2260
v*-N229
v*-N243
v*-N245
v*-N246
v*-N26
v*-N260C
v*-N280
v*-N289
v*-N29
v*-N298
v*-N303
v*-N330B
v*-N34
v*-N341
v*-N352B
v*-N358C
v*-N366
v*-N376
v*-N378A
v*-N395
v*-N397
v*-N398A
v*-N400B
v*-N41B
v*-N414
v*-N422B
v*-N423
v*-N439A
v*-N447B
v*-N463
v*-N467
v*-N470A
v*-N473B
v*-N499
v*-N50
v*-N51B
v*-N517
v*-N526A
v*-N528A
v*-N529B
v*-N53A
v*-N54A
v*-N54B
v*-N560
v*-N587A
v*-N620
v*-N621A
v*-N634A
v*-N64A
v*-N655A
v*-N65B
v*-N660D
v*-N661A
v*-N674B
v*-N678B
v*-N69A
v*-N698B
v*-N699A
v*-N7B
v*-N710B
v*-N713B
v*-N724E
v*-N728
v*-N735
v*-N748C
v*-N75
v*-N756A
v*-N766C
v*-N770
v*-N779A
v*-N806C
v*-N820
v*-N826
v*-N829A
v*-N839
v*-N84B
v*-N840
v*-N878B
v*-N891C
v*-N892B
v*-N909B
v*-N947C
v*-N956C
v*-N970B
v*-N972B
v*-N998D
v*-N999B
v*-pb-3019-16
v*-PI180165
v*-PI180231
v*-PI183640
v*-PI183648
v*-PI185851
v*-PI195244
v*-PI195245
v*-PI200197
v*-PI200201
v*-PI218042
v*-PI228174
v*-PI228176
v*-PI232974
v*-PI236996
v*-PI239105
v*-PI239114
v*-PI239116
v*-PI251883
v*-PI251891
v*-PI251930
v*-PI254856
v*-PI254857
v*-PI262476
v*-PI262487
v*-PI262489
v*-PI267184
v*-PI267209
v*-PI267212
v*-PI270293
v*-Pollacsek
v*-RumanianFlint
v*-Singleton-22
v*-Singleton-34
Vsr*-N1447
wst*-N643B

white luteus seedling
w*-5413
wl*-N1
wl*-N1213B
wl*-N122
wl*-N126B
wl*-N1270A
wl*-N1350B
wl*-N1384B
wl*-N144
wl*-N165A
wl*-N18
wl*-N1803
wl*-N1819
wl*-N1844
wl*-N1848
wl*-N1855
wl*-N1857
wl*-N1863
wl*-N189
wl*-N1928
wl*-N1931
wl*-N1949
wl*-N217A
wl*-N221
wl*-N241
wl*-N255
wl*-N283A
wl*-N290
wl*-N299A
wl*-N311B
wl*-N313
wl*-N315
wl*-N345A
wl*-N358A
wl*-N362B
wl*-N38B
wl*-N4
wl*-N401
wl*-N408B
wl*-N415
wl*-N416B
wl*-N44
wl*-N442
wl*-N448
wl*-N455
wl*-N466
wl*-N47
wl*-N500
wl*-N502B
wl*-N508
wl*-N538A
wl*-N551C
wl*-N554A
wl*-N567
wl*-N575A
wl*-N60
wl*-N629A
wl*-N636
wl*-N637A
wl*-N646
wl*-N648
wl*-N654A
wl*-N663A
wl*-N686A
wl*-N698A
wl*-N709B
wl*-N711A
wl*-N720B
wl*-N758A
wl*-N981B
wl*-N998C

white margins
whm*-N1462
whm*-N1464
whm*-N1465B
whm*-N1470

white striped seedling
ij-mos*-8624
j*-N793
stk*-N359B
str*-2104-4 EBP
str*-2116-1 EBP
str*-5120B-Teo
str*-6-10-4307
str*-78-314-1
str*-78-314-4
str*-78-314-5
str*-84-5222-7
str*-86-1494-27
str*-PI262495
str-et*-PI184276
wst*-N1469
wst*-N173B
wst*-N190A
wst*-N66B

white tipped leaf
wt*-N308
wt*-N432A
wt*-N580B
wt*-N650A

yellow green leaf
l*-N906C
pastel*-1-6-5495
ppg*-N1484
pyg*-N1266A
pyg*-N223
pyg*-N307B
pyg*-N321
pyg*-N460
yg*-0130
yg*-4369
yg*-4889

yg*-5-8(5575)
yg*-56-3021-18
yg*-6697
yg*-68-1429
yg*-6853
yg*-74-1827-1
yg*-77-585
yg*-8105
yg*-8379
yg*-8622
yg*-8631
yg*-8682
yg*-8692
yg*-8946
yg*-910J
yg*-B73
yg*-Caspar
yg*-N1314B
yg*-N1315B
yg*-N157A
yg*-N1800
yg*-N1840
yg*-N1910
yg*-N1948
yg*-N2021
yg*-N2246
Yg*-N2294
yg*-N38A
yg*-N37
yg*-N389B
yg*-N685B
yg*-N706B
yg*-N72
yg*-N769A
yg*-PI180231
yg*-PI228174
yg*-PI239114
yg*-PI267206
yg*-PI267224
yg*-Singleton-127
yg*-Singleton-23
yg*-Singleton-30
yg-nec*-95-5320-7
yg-nec*-Singleton-29
Yg-str*-Mu

zebra striped seedling
zb*-89-3137-5
zb-gl*-2187

Plant Mutants

absence of leaf blade
bladeless*-87-2406-23

adherent tassel
ad*-N613B

albescent
al*-1479
al*-84-5020-32
al*-PI245132
wh top*-Bauman

barren stalk
ba*-1447
ba*-68-679-8
ba*-74-304-12
ba*-74-369-2
ba*-PI200290
ba*-PI218135
ba*-PI239105
ba*-PI251885
ba-ub*-94-4712

bleached leaf
Blh*-N1455
blh*-N203B
blh*-N2302B
blh*-N2359
Blh*-N2421
blh*-N265A
Bh*-SF98-12

blotched leaf
bl*-N1278A
bl*-N43
red leaf blotch*-PI213779
yel-spl*-N152

brachytic plant
br*-2180
br*-78-136KEW
br*-Brawn219-221
br*-Brawn227-229
br*-Brawn230
br*-Brawn231-233
br*-Brawn235-237
br*-Brawn259-260
br*-Brawn261-262
br*-Brawn263-266
br*-Brawn267-268
br*-Brawn269-271
br*-Brawn272-273
br*-Brawn274-275
br*-OSIJEK-Yugoslavia
br*-PI228171
br*-PI239105
br*-Singleton-8
br*-Singleton1969-252
td*-PI262476

brevis plant
bv*-N2283

brittle stalk
bk*-N888D

brown midrib
bm*-N2331B
bm*-PI228174
bm*-PI251009
bm*-PI251893
bm*-PI251930
bm*-PI262480
bm*-PI262485
bm*-PI267186

burned leaf
les*-Funk-4
les*-PI262474

chromosome breaking
Chrom-breaking*-Mu

colored leaf
lc*-PI239110

crinkled leaf
cr*-97P-111
cr*-98-1698
cr*-N769B

crossbanded leaf
cb*-N1620A
Cb*-N2290B
cb*-N696D
cb*-N719A

defective tassel
Tp*-54-55-Jos
Tp*-PI213734
Tp*-Pk41-Jos
Tp*-T8-Jos
Tp*-Tenn61

dwarf plant
d*-018-3
d*-119
d*-136-220
d*-1821
d*-2108
d*-2201
d*-2447-8
d*-3-eared-JC
d*-3047
d*-5312
d*-56-3037-23
d*-60-2428
d*-64-4156-1
d*-74-1701-5
d*-75-6071-1
d*-76-1304-9
d*-76-2186
d*-78-282-3
d*-78-286-1
d*-78-286-5
d*-85-3081-33
d*-87-2198-36
d*-gl11
d*-Brawn254-258
d*-MarovacWhiteDent
d*-N1095B
d*-N1352B
d*-N157B
d*-N1883
d*-N1895
d*-N197A
d*-N203D
d*-N2295
d*-N282
d*-N299B
d*-N403B
d*-N454A
d*-N518A
d*-N549B
d*-N604
d*-N629B
d*-N699B
d*-N994B
d*-PI180231
d*-PI183644
d*-PI184286
d*-PI213769
d*-PI228169
d*-PI228171
d*-PI239110
d*-PI245132
d*-PI251652
d*-PI251656
d*-PI251885
d*-PI254854
d*-PI262495
d*-PI267219
d*-rosette
d*-shlf-9-436-1
d*-su
d*-su2
d*-Teo
d*-ts1

erect leaf
dge*-N2410

faded leaf
fd*-N1938

fine stripe leaf
str*-PI228164

gnarled leaf
Gn*-sgl

gritty leaf
gtl*-N2297

green striped leaf
gs*-98-5700-5
gs*-N359A
gs*-N484A

knotted husks
mwp*-Nelson

lazy plant
la*-N2333B

lesion
les*-2119
les*-74-1873-9
les*-ats
Les*-N1378
Les*-N1450
les*-N2290A
Les*-N2420
Les*-N502C

liguleless
Lg*-64-36
lg*-PI228170

male sterile
Ms*-2471
ms*-6015
ms*-6025
ms*-6026
ms*-6033
ms*-6039
ms*-6045
ms*-6048
ms*-6049
ms*-6052
ms*-6053
ms*-6054
ms*-6055
ms*-6057
ms*-6058
ms*-6059
ms*-6060
ms*-6061
ms*-6062
ms*-6064
ms*-6065
ms*-6066
ms*-N2415
Ms*-N2474
ms*-N2484
ms*-N352C
ms*-N45B
ms*-PI217219
ms-si*-355

many tillers
tlr*-N2243

nana plant
na*-N1519D

narrow leaf
nl*-5688
nl*-N232A
nl*-N410B
nl*-N462B
nl*-N543B
nl*-N622B
nl*-N625
nl*-N727B
nl*-N732A
nl*-N797B
nl*-PI245132
stf*-N601
stk*-N363

necrotic leaf
ll*-N248A
ll*-N264
ll*-N417D
ll*-N623
nec*-011-7
nec*-017-3
nec*-4871
nec*-4889
nec*-5588 early
nec*-5619
nec*-5876
nec*-77-549-2
nec*-77-574-1
nec*-8624
nec*-8737
nec*-fraz
nec*-N1119B
nec*-N1185B
nec*-N1487
nec*-N193
nec*-N200B
nec*-N215F
nec*-N283B
nec*-N419
nec*-N430A
nec*-N465
nec*-N468
nec*-N490A
nec*-N510A
nec*-N541B
nec*-N545B
nec*-N559
nec*-N562
nec*-N581
nec*-N596C
nec*-N599A
nec*-N650D
nec*-N666A
nec*-N669
nec*-N712C
nec*-N811B
nec*-N814
nec*-PI228174
nec*-PI267184
nec*-Vasco
nec-pg*-PI239116
shootless*-99-677-6

oil yellow plant
oy*-N2360A

pale green plant
pg*-56-3012-10
pg*-8321
pg*-Hy2 Nob 7-5
pg*-LGC-61
pg*-N1074B
pg*-N607
pg*-N671

patched leaf
ptc*-N238A
ptc*-N444B
ptc*-N611
ptc*-N904B

pigmy plant
py*-N656B
py*-N714

ragged leaf
rgd*-N2266

ramosa
ra*-412E
ra*-4889

rolled leaf
rld*-N1405B
rld*-N1525
Rld*-N2465
rld*-N556C

small plant
d*-N1074C
d*-N137C
d*-N149
d*-N164A
d*-N188B
D*-N2023
d*-N208B
d*-N210
d*-N2254
d*-N262C
d*-N287B
d*-N305
d*-N328
d*-N394
d*-N524D
d*-N528B
d*-N553D
d*-N707B
D*-N987B
smp*-N121
smp*-N135B
smp*-N153B
smp*-N156A
smp*-N183B
smp*-N1954
smp*-N272A
smp*-N306
smp*-N452B
smp*-N586B
smp*-N600B
smp*-N602
Smp*-N842

speckled leaf
spc*-N112
spc*-N1814
spc*-N198B
spc*-N357A
spc*-N370

spotted leaf
les*-74-1820-6
spt*-N278B
spt*-N412A
spt*-N513A
spt*-N579B
spt*-N939B

stiff leaf
stf*-N1092C
stf*-N235B

streaked leaf
stk*-N1143C
stk*-N351
stk*-N368A
stk*-N433B
stk*-N584A
stk*-N587D
stk*-N589
stk*-N670B
stk*-N769C
stk*-N777B
stk*-N812B
stk*-N835A
stk*-N925B

striate leaf
Sr*-N2430
sr*-N675B

stubby plant
stb*-N938C

tassel seed
Ts*-N1374
ts*-PI251881
ts*-PI267209
ts*-Sprague

tasselless
tls*-Funk
tls*-Va35

tiny plant
ty*-N1975
ty*-N215A
ty*-N236B
ty*-N326C
ty*-N702B

torn leaf
Trn*-N2438

white sheath
ws*-N1979
ws*-N537D

white stripe leaf
ij*-N504A
li*-PI262476
str*-PI262474
str*-X09
ws*-N1815
wst*-N1877
wst*-N248B
wst*-N413A
wst*-N548
wst*-N454B
wst*-N564A
wst*-N696B

yellow stripe leaf
gs*-68-1354
ys*-1479
ys*-5-8(5575)
ys*-67-2403
ys*-68-1354
ys*-8912
ys*-N139B
ys*-N326A
ys*-N71B
ys*-PI228180
ys*-PI262172
ys*-PI262475
ys*-PI267219
ys*-whorled

zebra necrotic leaf
zn*-8637
zn*-BYD
zn*-N230B
zn*-N342A
zn*-N354A
zn*-N372A
zn*-N451
zn*-N571D

Ear Mutants

distichous ear
distichous*-68-1227

distorted segregation
off-ratio*-85-3255-6
off-ratio*-86-1155-1
wx-off-ratio*-86-1110-4

papyrescent glumes
en*-Sprague

polytypic ear
pt*-McClintock
pt*-Mu
pt*-N868B

reduced pollen fertility
ga*-0188
ga*-0213
ga*-0648
ga*-3615
ga*-91-5197-2
ga*-94-764
Ga*-Yugoslavia

silky
si*-0443
si*-0503
si*-8104
si*-N1967A

tunicate
Tu*-5090B

unpaired rows
up*-Shirer

V. MAIZE GENOME DATABASE

Transition to MaizeGDB: http://www.maizegdb.org

MaizeGDB is the next generation Maize Genome Database, with interfaces and all accesses to the data under the guidance of Volker Brendel, Ames, Iowa. It will completely replace the MaizeDB site, www.agron.missouri.edu, September 30, 2003. We welcome Volker's staff: Trent Seigfried, Darwin Campbell, Sanford Baran and Carolyn Lawrence to our community

Some history. In the fall of 2002, the first steering committee for a new Maize Genome Database, MaizeGDB, met to evaluate new interfaces to maize genome data. The Steering Committee for MaizeGDB is chaired by Tom Slezak, and currently includes: Ed Buckler, Vicki Chandler, Mike Freeling, Sarah Hake, Mary Polacco, Marty Sachs, Cari Soderlund, Lincoln Stein, and Virginia Walbot. At that time, a recommendation was made to target September 2003 as a final transition, with full migration of all data in MaizeDB to the new database, contingent on the development of a suite of curation tools. Missouri staff will continue to play a major role in curation of MaizeGDB; stocks will continure to be curated by Marty Sachs and his staff at Illinois. A major effort will be made to engage the community in curation (see below). The MaizeGDB was presented January 2003, at the Plant and Animal Genome Meetings, San Deigo, CA, and as a talk in the first general talks session of the 2003 Maize Meetings held in March at Lake Geneva, WI. It has been available for public review and inputs since Jan 2003 (see announcement on the Jan bionet bulletin board: http://bionet.hgmp.mrc.ac.uk/hypermail/maize/maize.200301/0005.html).

Community Curation of Literature – Coming soon

In May 2003, the MaizeGDB Steering Committee proposed an Editorial Board, whose membership would participate in curation of the literature. The inaugural board, convened by Ginny Walbot, will include: Hugo Dooner, Chief; Lisa Harper, Erich Grotewold, Bill Tracy, and Nathan Springer. This first group will be intimately involved in testing the data curation forms, their utility and friendliness. Once the forms have been vetted, there will be an open invitation to all cooperators to participate. Because the editorial board will curate a limited number of papers, it is highly important that we receive your support in this effort. Your paper could be high-lighted as a 'paper of the week' if comprehensively curated in MaizeGDB.

Community curation of larger research projects

This past year we have successfully developed protocols whereby 2 research projects handled much of the semantic and other checking of data at their site, so that it was consistent with MaizeDB, and supplied in a routine format to MaizeDB. In both cases, the project databases had SQL access to MaizeDB, permitting access to current tables of names and synonyms for loci, probes, and stocks. While the MaizeDB curator still needs to monitor for overall data quality prior to loading, most of the work has been performed by the experts for these data sets. We gratefully acknowledge the support of Marilyn Warburton, Ed Brandon, Carlos Lopez, Juan Alarcon, and Dave Hoisington (CIMMYT); and Mike McMullen, Ed Coe, Hector Sanchez-Villeda, Steve Schroeder and Georgia Davis (Missouri). The current curator of MaizeDB plans to similarly engage other projects in the near future.

Also of note:

- Consensus genetic maps with higher resolution than 'bins'. The current version is presented in this newsletter (pages 137-179). This map, IBM2 neighbors, forms the scaffold for the physical map; note that only loci listed as Backbone have statistically defendable order, being on-frame on the IBM map. We thank the Chromatin (www.chromdb.org) and Maize Mapping (www.maizemap.org) projects for providing new map data for this map. We plan to incorporate other community IBM map data in the near future. In all cases, sources of the data are acknowledged.

- Sorghum genetic maps were entered, courtesy of Andrew Paterson and John Bowers, with links to probes mapped on both the genetic and physical maps of maize. The Paterson BAC probes may be recognized as the 'SOG' markers on the Web FPC presentation at Arizona (http://genome.arizona.edu/fpc/maize).

- Links from maize to Gramene rice physical maps were kindly provided by Doreen Ware and Lenny Teytelman at Gramene. These links are based on sequence similarity of maize Cornsensus and ESTs to rice, and are posted at the Gramene site. These links are also regularly forwarded to Arizona for inclusion in the Web FPC presentation of the physical map of maize.

- A file of the mapped sequences of maize is one of our more requested items by larger projects and currently resides at: www.agron.missouri.edu/files_dl/SequenceMap directory. It lists sequence accessions, map coordinates on bins, IBM and IBM neighbors, and the locus name. A similar file will be maintained at the new site.

Mary Polacco
Curator, Maize Genome Database
July 23, 2003

VI. A CONSENSUS GENETIC MAP
Inter-mated B73 x Mo17 (IBM) Neighbors
5718 Loci July 2003

The IBM neighbors maps are a consensus map representation that is based on the high resolution IBM maps of the Maize Mapping Project (see Web site: www.maizemap.org). Both the IBM and the neighbors maps are used as scaffolding in assembly of the physical map (see also Web site: genome.Arizona.edu/fpc/maize). Note that the inter-mated B73xMo17 or IBM map, based on 4 rounds of random mating, is expanded 3-fold compared to F2 or IF2 (immortal F2) maps and has 15X greater resolving power compared to other public mapping populations (Sharopova et al., Plant Mol Biol 48:463-481, 2002; Lee et al., Plant Mol Biol 48: 453-461, 2002). Maps with loci in common with the IBM can be readily incorporated into IBM neighbors. The algorithm resolves any conflicts in order in favor of map orders with best statistical support. In the current representation, the below maps were included:

- IBM2 Dec 2002; IBM population, 302 individuals
- IBM1 Mar 2002; IBM population, 302 individuals; has a few loci not included on IBM2
- INDEL, April 2003; 302 individuals, subset of markers on IBM2 plus INDEL (insertion deletion polymorphism) and SNP (simple nucleotide polymorphism) markers
- ChromDB; Dec 2002; scored on mini-IBM with 94 individuals, but map computed using IBM 2002 map and all 302 scores. Map provided by Chromatin Mapping Project, see ChromDB Website, www.chromdb.org
- SSR popI, T218xGT119 population of Mike McMullen, 93 individuals
- SSR popII, Tx303xCO159, same population as UMC 98
- UMC 98,Tx303xCO159, immortal F2 population, 54 individuals; see Gardiner et al., Genetics 134:917-930, 1993; Davis et al., Genetics 152:1137-1172, 1999
- BNL 96, combined scores of 2 recombinant inbred mapping populations, T232xCM37 and Tx303xCO159, with 48, and 41 individuals, respectively; map provided by Ben Burr; see Website: acemaz.bnl.gov; see Burr et al., Genetics 118:519-526, 1988
- BNL 2002, population and map source same as BNL 96

Fields in the table:

Locus: Locus symbol.

Contig: C if the locus has a probe associated with a contig; AC if the contig has been anchored unambiguously to this genetic locus.

Coordinate: cM values; estimated for all maps save IBM2. Revisions can be expected as physical mapping progresses.

Backbone: Yes if on frame IBM2, as defined by MapMaker software, otherwise, 'no'.

Bin: Bin location. Bins are stated numerically, as the linkage group or chromosome, followed by a decimal and then a value that defines the bin. Lower values are the distal region of the short arm. Revisions can be expected as physical mapping progresses.

Source Map: The map used to derive map order on IBM neighbors.

Mary Polacco, Hector Sanchez-Villeda, Ed Coe
Columbia, MO

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnl(tas1h)		1.00	-55.80	no	BNL 96
csu804b(dnp)		1.00	-30.50	no	UMC 98
umc1041	C	1.00	-29.00	no	SSR popII
bnl(tas1c)		1.00	-11.70	no	BNL 96
rgpc654		1.00	-11.30	no	UMC 98
umc1619	C	1.00-1.01	-8.00	no	SSR popII
phi056(tub1)	C	1.00-1.01	-2.30	no	IBM2
umc1354	AC	1.00	0.00	yes	IBM2
tub1	AC	1.01	2.50	yes	IBM2
csu738		1.00-1.01	2.50	no	UMC 98
umc1613	C	1.00-1.01	2.50	no	SSR popII
dmt103b	C	1.01	8.30	no	ChromDB
bnlg149		1.00	9.86	no	BNL 2002
umc1177	AC	1.01	10.50	yes	IBM2
umc1566	AC	1.01	16.50	yes	IBM2
bnl5.62a		1.01	22.80	yes	IBM2
fus6		1.01	24.30	no	IBM2
mmp102		1.01	26.10	yes	IBM2
AY110314	C	1.01	31.10	yes	IBM2
umc1292	C	1.01	32.08	no	SSR popII
umc94a		1.01	40.30	yes	IBM2
csu589		1.01	40.40	no	UMC 98
bnl8.05a		1.01	40.40	no	UMC 98
bnlg1124		1.01	41.67	no	BNL 2002
knox1		1.01	42.39	no	UMC 98
umc164c		1.01	43.39	no	UMC 98
lim179		1.01	48.70	yes	IBM2
csu680a	C	1.01	52.59	no	UMC 98
mmp49		1.01	57.80	yes	IBM2
cdo1081a		1.01	59.50	yes	IBM2
bnlg1179		1.01	64.14	no	BNL 2002
asg31	C	1.01	66.90	yes	IBM2
npi415		1.01	67.70	yes	IBM2
AY110401	C	1.01	68.30	no	IBM2
cdo507a(ant)		1.01	68.52	no	UMC 98
umc1106		1.00	68.71	no	SSR popII
umc1305	C	1.00	69.70	no	SSR popI
umc1281	C	1.05-1.06	69.70	no	SSR popI
std20b(uce)		1.01	70.62	no	UMC 98
uaz104		1.01	70.96	no	BNL 96
asg59a		1.01	71.10	no	UMC 98
php20537b		1.01	71.10	yes	IBM2
ufg31		1.01	73.30	yes	IBM2
ufg33		1.01	73.70	yes	IBM2
ufg32	C	1.01	74.50	yes	IBM2
ufg34		1.01	76.10	yes	IBM2
PCO072650	C	1.01	79.25	no	INDEL
umn857b		1.01	80.20	no	UMC 98
uaz260b(rpL5)		1.01	80.20	no	UMC 98
rgpc385a(rpL5)		1.01	80.20	no	UMC 98
bnlg1014	C	1.01	82.80	yes	IBM2
umc1363	C	1.01	83.70	yes	IBM2
umc1071	C	1.01	85.20	yes	IBM2
umc1269	C	1.01	86.30	yes	IBM2
umc2012	C	1.01	87.40	no	IBM2
tda47		1.01	88.18	no	UMC 98
csu454(gst)		1.01	88.18	no	UMC 98
umc1977	C	1.01	89.20	yes	IBM2
PCO132874	C	1.01-1.02	90.85	no	INDEL
umc1948	AC	1.01	91.50	no	IBM2
php20603		1.01	91.70	yes	IBM2
npi97a		1.01	92.74	no	UMC 98
umc266b(ptk)		1.01	92.74	no	UMC 98
dpg12b		1.02	93.06	no	BNL 2002
umc2215		1.01	93.88	no	SSR popI
smt2		1.01	94.18	no	SSR popII
cdo20a		1.01-1.02	95.28	no	BNL 2002
prc3	AC	1.01	97.97	no	SSR popII
rz444c	C	1.01	98.29	no	IBM1
umc1484		1.01	98.39	no	SSR popII
php20689		1.01	101.10	yes	IBM2
umc1685	AC	1.01	103.00	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mmp93		1.01	103.20	yes	IBM2
uaz182		1.01	103.37	no	BNL 2002
bnlg1112		1.01	104.48	no	BNL 2002
npi406		1.02	105.64	no	BNL 2002
pbs11		1.01	107.44	no	BNL 2002
cat2		1.01	107.97	no	BNL 2002
umc1160	AC	1.01	108.30	yes	IBM2
umc2224	AC	1.01-1.02	110.90	yes	IBM2
npi579b		1.01	112.20	yes	IBM2
csic(rab30)		1.02	112.20	no	BNL 2002
bnlg1130		1.01-1.02	114.33	no	BNL 2002
umc157(chn)	AC	1.02	114.40	yes	IBM2
umc1222	C	1.01-1.02	114.40	no	SSR popII
pmcb1		1.02	115.20	yes	IBM2
uaz2a		1.02	123.57	no	BNL 2002
mmp68		1.02	123.60	yes	IBM2
umc2225	AC	1.01-1.02	124.70	yes	IBM2
uaz146b(rps28)		1.01-1.02	125.60	no	BNL 2002
csu1171		1.02	127.30	yes	IBM2
umc115		1.02	127.30	no	UMC 98
umc194a(gpr)		1.02	127.30	no	UMC 98
csu1190		1.02	127.39	no	UMC 98
tda50		1.02	129.30	no	UMC 98
csu680c	C	1.02	129.30	no	UMC 98
std2c(dba)		1.02	129.30	no	UMC 98
rgpc1122c(rpL15)		1.02	129.30	no	UMC 98
mmp171b		1.02	131.80	no	IBM2
umc1166	AC	1.02	133.60	yes	IBM2
PCO128140	C	1.02	139.41	no	INDEL
umc1568	AC	1.02	141.80	yes	IBM2
bnlg1429	AC	1.02	143.50	yes	IBM2
umc1467	AC	1.02	143.50	no	SSR popI
pds1	C	1.02	144.28	no	BNL 96
dnap9705(Ac)		1.02	144.28	no	BNL 2002
ensl001		1.02	144.39	no	BNL 2002
ifbf33		1.02	145.74	no	BNL 2002
php20640		1.02	146.90	yes	IBM2
npi411b		1.02	149.13	no	BNL 2002
lim504		1.02	151.60	yes	IBM2
npi423		1.02	152.62	no	BNL 2002
csu691		1.02	156.85	no	UMC 98
bnlg1614		1.02	159.11	no	BNL 2002
npi209b		1.02	160.06	no	BNL 2002
bnlg1627		1.02	160.06	no	BNL 2002
npi109a		1.02	160.06	no	BNL 96
umc1976	AC	1.02	160.60	yes	IBM2
bnlg176		1.03	161.19	no	BNL 2002
csu860b		1.02	161.82	no	UMC 98
umc2226	AC	1.02	165.80	no	IBM2
mmp135		1.02	166.00	yes	IBM2
bnlg1127		1.02	167.50	yes	IBM2
bnlg1953	AC	1.02	170.00	yes	IBM2
bnlg1178		1.02	171.40	no	BNL 2002
bnlg1007		1.02	173.10	no	BNL 2002
umc2204	C	1.02	175.52	no	SSR popI
umc1711		1.02	176.69	no	SSR popII
npi403b		1.02	183.80	yes	IBM2
csu320a		1.02	183.95	no	UMC 98
bnl9.13		1.02	188.22	no	BNL 2002
bnlg109		1.02	188.58	no	BNL 2002
umc2383	C	1.02-1.03	188.67	no	SSR popII
uaz1		1.02	193.14	no	BNL 2002
bnl5.21c		1.03	194.13	no	BNL 2002
bnlg1803		1.02	198.32	no	BNL 2002
umc76	C	1.03	198.40	yes	IBM2
gln6	AC	1.02-1.03	198.40	no	UMC 98
umc243b		1.02-1.03	198.40	no	UMC 98
uaz120		1.03	199.17	no	BNL 2002
isu2117c		1.03	199.17	no	BNL 2002
ufg78		1.02-1.03	199.70	no	IBM2
uaz267		1.03	200.03	no	BNL 2002
uox(bru1)		1.02-1.03	200.56	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi241b		1.03	200.61	no	BNL 2002
bnl35d(blr)		1.03	200.75	no	BNL 2002
mpik33h		1.02-1.03	200.75	no	BNL 2002
bnlg1083		1.02	201.32	no	BNL 2002
cdo1387b(emp70)		1.03	201.50	yes	IBM2
bnlg147		1.02	201.97	no	BNL 2002
lim122		1.03	205.00	yes	IBM2
umc1073		1.03	208.50	yes	IBM2
umc1403	C	1.03	210.60	yes	IBM2
npi439a		1.03	216.80	yes	IBM2
umc230		1.03	218.40	yes	IBM2
umc11a		1.03	218.80	yes	IBM2
npi425c		1.03	218.80	no	UMC 98
npi234a		1.03	219.00	no	IBM2
bnlg1484	AC	1.03	219.00	no	IBM2
bnl10.38a		1.03	223.18	no	BNL 2002
mmp66		1.03	224.40	yes	IBM2
umc2397		1.03	224.76	no	SSR poplI
AY109929	AC	1.03	225.40	no	IBM2
csu315c		1.03	225.80	no	UMC 98
umc1397	AC	1.03	226.40	yes	IBM2
AY110052	C	1.03	229.60	yes	IBM2
csu859(gol)		1.03	242.15	no	UMC 98
AY110028	C	1.03	246.30	yes	IBM2
PCO074335	C	1.03	252.19	no	INDEL
npi448		1.03	254.28	no	BNL 96
ifbf91		1.03	254.35	no	BNL 2002
ias8		1.03	254.77	no	BNL 2002
bnlg2204		1.03	254.86	no	BNL 2002
dgg9b		1.03	255.13	no	BNL 2002
npi242b		1.03	255.20	yes	IBM2
bnl1.326a		1.06	255.31	no	BNL 2002
ts2		1.03	255.50	no	BNL 2002
ncr(sod4a)		1.03	255.55	no	BNL 2002
mpik36		1.03	255.57	no	BNL 2002
csu181a		1.03	256.62	no	UMC 98
csu254b		1.03	256.62	no	UMC 98
csu214b(grp)		1.03	256.62	no	UMC 98
csu179a(hsp70)		1.03	256.62	no	UMC 98
umc1479	AC	1.03	257.40	yes	IBM2
umc8a		1.03	257.47	no	UMC 98
csu238a(apx)		1.03	257.47	no	UMC 98
csu710a(apx)		1.03	257.55	no	UMC 98
asg26	C	1.03	257.90	no	IBM2
lim51		1.03	258.70	no	IBM2
bnlg439	AC	1.03	259.10	no	IBM2
bnlg1203	AC	1.03	259.30	yes	IBM2
fad8	AC	1.03	260.70	yes	IBM2
uaz139		1.03	261.74	no	BNL 2002
pbs16b		1.03	262.46	no	BNL 2002
wusl1032		1.03	262.46	no	BNL 2002
AY110640		1.03	264.40	yes	IBM2
npi427b		1.03	268.16	no	BNL 96
bnlg1458	C	1.03	268.90	no	IBM2
umc13		1.03	270.60	yes	IBM2
pdc3		1.03	270.60	no	BNL 2002
ibp2		1.03	271.37	no	BNL 2002
bnlg2180		1.03	272.53	no	BNL 2002
asg35b		1.03	273.90	yes	IBM2
csu215b(grp)		1.03	275.27	no	UMC 98
umc266a(ptk)		1.03	275.39	no	UMC 98
dpg4		1.03	275.94	no	BNL 2002
dpg10		1.03	275.94	no	BNL 2002
uaz264b		1.03	277.51	no	BNL 2002
dpg8		1.03	277.95	no	BNL 2002
AY110632	AC	1.03	278.10	no	IBM2
umc1701		1.03	279.13	no	SSR poplI
npi589		1.03-1.04	279.41	no	BNL 2002
p1	C	1.03	279.96	no	SSR popI
csu814b		1.03	279.96	no	UMC 98
ndp2		1.03	282.60	yes	IBM2
csu745d(rpPo)	C	1.03	285.65	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mmp23		1.03	286.20	yes	IBM2
AW400087	C	1.03	287.20	no	IBM2
npi286		1.03	288.50	no	UMC 98
ndp1		1.03	288.60	yes	IBM2
hcf3		1.03	290.10	no	BNL 2002
ynh21		1.03	290.10	no	BNL 2002
bnlg1866	C	1.03	290.10	yes	IBM2
bnlg182		1.03	290.10	no	BNL 2002
pge(phyB1)		1.03	290.10	no	BNL 2002
umc1880	C	1.03	290.30	no	IBM2
phi109275	C	1.03	290.40	no	IBM2
umc1598		1.03	290.70	yes	IBM2
dpg11		1.03	290.73	no	BNL 2002
chs5054		1.03	290.82	no	BNL 2002
csu753		1.03	291.10	no	UMC 98
csu392b		1.03	291.10	no	UMC 98
dpg9		1.03	291.25	no	BNL 2002
lim432		1.03	292.40	yes	IBM2
bnl12.06a		1.03	293.00	no	IBM2
fmi1(pki)		1.04	293.00	no	UMC 98
csu924(wsi)		1.04	293.00	no	UMC 98
mmp151a		1.03	297.20	yes	IBM2
umc1514		1.03	301.37	no	SSR poplI
AY110393	C	1.03	302.80	no	IBM2
mmp100		1.03	311.40	yes	IBM2
umc2145		1.03	319.00	no	IBM2
uaz146a(rps28)		1.03-1.04	320.56	no	BNL 2002
mmp56		1.04	320.90	yes	IBM2
cdo938a		1.04	323.10	yes	IBM2
asg69	C	1.04	323.61	no	UMC 98
csu633		1.04	323.61	no	UMC 98
csu941		1.04	323.61	no	UMC 98
umc227		1.04	323.61	no	UMC 98
csu632a		1.04	323.61	no	UMC 98
asg45(ptk)	C	1.04	323.61	no	SSR poplI
umc1452		1.03-1.04	323.80	no	SSR popI
npi(sod4)		1.03	325.24	no	BNL 2002
les22		1.04	325.30	no	UMC 98
bnlg2238	AC	1.04	326.70	yes	IBM2
bnlg1016		1.04	326.70	no	BNL 2002
umc2124	AC	1.04	328.50	no	IBM2
uaz266a(nad)		1.03	328.69	no	BNL 2002
csu1082		1.04	329.37	no	UMC 98
cdo38a(ntp)	C	1.03	330.43	no	BNL 2002
umc1849		1.04	335.00	yes	IBM2
asg75		1.04	336.50	yes	IBM2
umc1169	C	1.04	337.50	yes	IBM2
chr125b		1.04	339.60	no	ChromDB
asg30b		1.04	340.70	yes	IBM2
rgpr44a		1.04	340.70	no	UMC 98
csu737(npc)		1.04	340.70	no	UMC 98
rgpc361(ppi)		1.04	340.70	no	UMC 98
PCO099415	C	1.04	344.42	no	INDEL
umc1472	C	1.04	345.85	no	SSR poplI
uaz3		1.03-1.04	348.99	no	BNL 96
csu389		1.04	349.88	no	UMC 98
rz672a(cgs)		1.04	349.88	no	UMC 98
AY110330	AC	1.04	350.60	yes	IBM2
umc29a		1.05	351.00	no	BNL 2002
sod4		1.04	351.10	no	UMC 98
rgpc198a(sik)		1.04	351.10	no	UMC 98
bnl2.323		1.04	353.12	no	BNL 2002
csu207		1.04	356.00	yes	IBM2
csu452		1.04	356.00	no	UMC 98
rz251a		1.04	356.00	no	UMC 98
csu649(scp)	AC	1.04	356.00	no	UMC 98
umc2217	C	1.03-1.04	358.40	no	SSR popI
uaz248a(his3)		1.04	359.70	no	IBM2
umc2227	AC	1.04	360.90	yes	IBM2
bnlg652		1.05	365.51	no	BNL 2002
umc1144	AC	1.04	368.97	no	SSR poplI
ufg13b		1.04	369.20	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
ufg77		1.04	373.20	yes	IBM2
umc1917	AC	1.04	374.80	no	IBM2
umc2390		1.04	376.98	no	SSR popII
isu041b		1.04	377.20	yes	IBM2
csu323		1.04	378.52	no	UMC 98
csu887		1.04	378.52	no	UMC 98
isu61a		1.04	379.06	no	IBM1
ufg43		1.04	383.60	yes	IBM2
npi262		1.04	383.71	no	UMC 98
bcd450e		1.04	383.71	no	UMC 98
uaz198d(rpL10)		1.04	383.71	no	UMC 98
bnlg1811	AC	1.04	386.40	yes	IBM2
bnl7.21a		1.05-1.07	388.85	no	BNL 2002
umc275		1.04	389.56	no	BNL 2002
bnl9.11b(lts)	C	1.04	390.80	yes	IBM2
umc2228	AC	1.04	391.80	no	IBM2
umc1770	AC	1.04	392.10	no	SSR popII
bnlg1886		1.05	396.77	no	BNL 2002
umc2229	AC	1.04	397.30	no	IBM2
bnlg2295	AC	1.04	398.20	yes	IBM2
dpg12a		1.04	399.20	no	BNL 2002
bnlg2086	AC	1.04	401.20	no	IBM2
umc2112	AC	1.04	401.30	no	IBM2
asg3		1.04	401.90	yes	IBM2
csu3	C	1.05	405.00	yes	IBM2
umc1243	AC	1.04-1.05	405.00	no	SSR popI
csu694b(uce)	C	1.05	408.21	no	UMC 98
CL34571_2	C	1.05	411.48	no	INDEL
mmp61		1.05	412.60	yes	IBM2
PCO099462	C	1.05	413.06	no	INDEL
lim497		1.05	413.70	yes	IBM2
rz500(stp)	AC	1.05	415.58	no	UMC 98
umc2025	C	1.05	417.00	yes	IBM2
umc1558		1.05	417.00	no	SSR popI
bnlg1832		1.05	422.81	no	BNL 2002
npi453		1.04	422.81	no	BNL 96
umc1734	AC	1.05	423.00	no	SSR popII
mmp39		1.05	425.20	yes	IBM2
umc1244	C	1.05	427.60	no	SSR popI
pop1		1.05	429.38	no	UMC 98
csu822		1.05	429.38	no	UMC 98
csu263b		1.05	429.38	no	UMC 98
csu781b	C	1.05	429.38	no	UMC 98
rgpc316	C	1.05	429.38	no	UMC 98
csu653(fbn)		1.05	429.38	no	UMC 98
csu1041a(ptk)		1.05	429.38	no	UMC 98
umc1515	AC	1.05	430.60	yes	IBM2
AY109646	AC	1.05	431.20	no	IBM2
nfd104c		1.05	432.04	no	ChromDB
umc2230	AC	1.05	432.40	yes	IBM2
AY111680	AC	1.05	433.60	yes	IBM2
umc1297	C	1.05	434.69	no	SSR popII
umc1469	AC	1.05	435.09	no	SSR popI
rz421		1.05	435.47	no	UMC 98
uaz246c(mbf)	C	1.05	436.40	yes	IBM2
csu793		1.05	437.08	no	UMC 98
AY109678	C	1.05	437.30	no	IBM2
mmp143		1.05	437.90	yes	IBM2
umc1461	AC	1.05	438.80	no	IBM2
csu1138		1.05	439.00	yes	IBM2
umc260		1.05	439.00	no	UMC 98
umc167a		1.05	439.00	no	UMC 98
csu781c	C	1.05	439.00	no	UMC 98
uaz198c(rpL10)		1.05	439.00	no	UMC 98
rz323a		1.05	439.30	no	IBM2
umc1493		1.05	439.30	no	IBM2
umc1076	AC	1.05	440.00	yes	IBM2
mmp101		1.05	441.20	yes	IBM2
umc1689		1.05	445.10	no	SSR popII
AY110396	AC	1.05	445.50	yes	IBM2
umc1676	AC	1.05	450.80	yes	IBM2
umc2231	AC	1.05	453.50	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1703		1.05	453.90	yes	IBM2
rs2		1.05	457.00	yes	IBM2
umc1611	AC	1.05	458.40	no	SSR popII
eno2		1.05	460.60	no	BNL 2002
uaz9		1.05	460.60	no	BNL 2002
pbs9b		1.05	460.60	no	BNL 2002
uaz7a		1.05	460.60	no	BNL 2002
npi214		1.05	460.60	no	BNL 2002
cdo344c(rga)		1.05	460.60	yes	IBM2
mpik41d(mem1)		1.05	460.60	no	UMC 98
rz892a(alt)		1.05	461.50	no	UMC 98
umc1626		1.05	464.08	no	SSR popI
AI855190	AC	1.05	464.70	no	IBM2
CL14065_1	C	1.05	465.03	no	INDEL
umc1906	AC	1.05	467.00	yes	IBM2
umc1903	AC	1.05	467.90	no	IBM2
mmp124		1.05	469.40	yes	IBM2
umc2232		1.05	470.90	yes	IBM2
umc1395	AC	1.05	471.70	yes	IBM2
umc1321	AC	1.05	473.20	yes	IBM2
umc1601		1.05	473.80	yes	IBM2
umc2233	AC	1.05	474.50	yes	IBM2
csu710f(apx)		1.05	475.60	no	UMC 98
umc1603	AC	1.05	475.90	yes	IBM2
hac101b		1.05	481.90	yes	IBM2
npi304		1.05	483.75	no	BNL 2002
rz296a		1.05	483.75	no	BNL 2002
npi598		1.05	483.75	no	BNL 96
umc1323	AC	1.05	483.83	no	SSR popI
uaz13		1.05	484.68	no	BNL 2002
mmp95		1.05	484.70	no	IBM2
uaz4		1.05	484.75	no	BNL 2002
uaz5		1.05	484.75	no	BNL 2002
uaz6		1.05	484.75	no	BNL 2002
pbs6d		1.05	484.75	no	BNL 2002
npi401		1.05	484.75	no	BNL 2002
bnl1.556		1.05	484.75	no	BNL 2002
uaz276		1.05	485.90	yes	IBM2
uaz203		1.05	486.16	no	BNL 2002
npi279		1.06	486.77	no	BNL 2002
uaz17a		1.06	486.93	no	BNL 2002
uaz273		1.05-1.06	487.00	no	IBM2
uaz11		1.04	488.19	no	BNL 2002
ucsd61g		1.00-1.05	489.17	no	BNL 2002
uaz253		1.05	489.41	no	BNL 2002
npi272		1.06	491.10	no	BNL 2002
umc67a		1.06	496.60	yes	IBM2
csu881(cys)		1.06	496.60	no	UMC 98
mbd106	C	1.06	496.60	no	ChromDB
csu574b(eif2B)	C	1.06	496.60	no	UMC 98
isu146		1.06	501.20	yes	IBM2
umc1972		1.06	503.30	yes	IBM2
umc1988		1.06	504.93	no	SSR popII
umc1754	AC	1.06	506.83	no	SSR popII
umc1812	AC	1.06	508.20	no	IBM2
myb6		1.06	514.70	yes	IBM2
asg11	C	1.06	516.33	no	UMC 98
umc196		1.06	516.33	no	UMC 98
umc1590	AC	1.06	517.00	yes	IBM2
AY109499	C	1.06	517.70	no	IBM2
AY110566		1.06	518.90	no	IBM2
bnl5.59		1.06	520.40	yes	IBM2
csu92	AC	1.06	520.40	no	UMC 98
umc1508	AC	1.06	521.41	no	SSR popII
php20654		1.06	523.30	yes	IBM2
AY110296		1.06	523.90	yes	IBM2
php20682		1.06	524.50	no	IBM2
asg58		1.06	525.70	yes	IBM2
umc1811	AC	1.06	526.40	yes	IBM2
csu675a(prh)	C	1.06	527.06	no	SSR popI
bnlg2057	C	1.06	527.60	yes	IBM2
csu194(mthr)		1.06	528.05	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu503(met)		1.06	528.21	no	UMC 98
rgpc356		1.06	528.71	no	UMC 98
umc177a		1.06	528.71	no	UMC 98
umc2234	AC	1.06	529.00	no	IBM2
csu256(hsp90)		1.06	532.18	no	UMC 98
bnlg1598	AC	1.06	532.80	yes	IBM2
umc1123	AC	1.06	535.10	yes	IBM2
npi429		1.05-1.06	535.27	no	BNL 96
umc1398		1.06	540.91	no	SSR popII
AY104360	C	1.06	541.30	yes	IBM2
npi258		1.06	542.31	no	BNL 2002
ptk3		1.06	543.99	no	UMC 98
mmp156		1.06	544.20	yes	IBM2
uaz15		1.06	547.66	no	BNL 2002
bnl23b		1.06	547.66	no	BNL 2002
csu60b		1.06	547.66	no	BNL 2002
csu91b		1.06	547.66	no	BNL 2002
dup382		1.06	547.66	no	BNL 2002
uaz14a		1.06	547.66	no	BNL 2002
bnl34		1.06	547.66	no	BNL 96
bnlg1273		1.06	547.70	no	BNL 2002
bnlg1908b		1.06	547.96	no	BNL 2002
cdo464a		1.06	547.97	no	BNL 2002
ucsd61a		1.06	548.17	no	BNL 2002
bnlg1057	AC	1.06	548.30	no	IBM2
isu2191i		1.06	548.30	no	BNL 2002
umc1396	AC	1.06	548.40	yes	IBM2
umc2235	AC	1.06	550.00	yes	IBM2
umc1748		1.06	553.60	yes	IBM2
umc1919	AC	1.06	555.80	yes	IBM2
PCO116807	C	1.06	556.80	no	INDEL
bnlg1615	C	1.06	557.60	yes	IBM2
csu805	AC	1.06	558.50	no	IBM2
csu899b(ant)		1.06	558.50	no	UMC 98
psr152a		1.06	559.80	yes	IBM2
uwo2		1.06	560.05	no	BNL 96
AY111153	C	1.06	561.00	no	IBM2
umc2151		1.06	563.90	yes	IBM2
cdo595		1.06	565.55	no	BNL 2002
cdo475b		1.06	565.55	no	BNL 2002
umc1664		1.06	566.63	no	SSR popI
umc1668		1.06	566.63	no	SSR popI
uaz249a(ubf9)		1.06	567.08	no	BNL 2002
ntf1	C	1.06	570.80	yes	IBM2
csu590(rpL17)		1.06	570.80	no	UMC 98
csu505(rpL7)		1.06	573.18	no	UMC 98
umc58	C	1.06	575.90	yes	IBM2
umc119		1.06	575.90	no	UMC 98
rz28a		1.06	576.75	no	BNL 2002
cdo116a		1.06	576.75	no	BNL 2002
zmm6		1.06	577.19	no	BNL 2002
mpik34		1.06	577.19	no	BNL 2002
ucsd72a		1.06	577.19	no	BNL 2002
asg16b		1.06	578.20	yes	IBM2
umc82b		1.06	581.27	no	BNL 2002
mmp123		1.06	583.30	yes	IBM2
umc1035	AC	1.06	587.00	no	IBM2
umc1709	AC	1.06	588.20	no	IBM2
php20644		1.06	589.60	yes	IBM2
bnlg421		1.06	591.69	no	BNL 2002
umc1122	C	1.06	593.04	no	SSR popII
umc1924	AC	1.06	593.80	yes	IBM2
umc2396		1.06-1.07	594.96	no	SSR popII
csu1150		1.06	596.34	no	UMC 98
ufg50	C	1.06	597.50	yes	IBM2
umc1254	AC	1.06	598.60	no	SSR popI
uaz147b		1.06	600.00	yes	IBM2
uaz18d		1.07	603.21	no	BNL 2002
csu1132		1.06	603.80	yes	IBM2
umc2236	AC	1.06	604.80	yes	IBM2
hm1	C	1.06	605.95	no	UMC 98
umc1925	AC	1.06	606.50	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
dpg7b		1.06-1.07	607.27	no	BNL 2002
asg62	AC	1.07	607.30	yes	IBM2
umc1499	C	1.07	607.30	no	SSR popII
npi224g		1.07	610.23	no	BNL 2002
wsu(nia4)		1.07	610.23	no	BNL 96
isu2117h		1.07	611.22	no	BNL 2002
ncr(nrA)		1.07	611.37	no	BNL 2002
isu2117a		1.07	615.35	no	BNL 2002
umc274		1.06-1.07	615.89	no	BNL 2002
cuny21		1.06-1.07	616.02	no	BNL 2002
uaz20a		1.07	617.33	no	BNL 2002
umc2237	AC	1.06	618.50	yes	IBM2
npi566		1.07	619.06	no	BNL 2002
bnlg615		1.07	626.63	no	SSR popII
csh11		1.07	626.86	no	UMC 98
umc1374	AC	1.06-1.07	627.10	no	SSR popI
umc2239	AC	1.06	630.60	yes	IBM2
umc1486		1.07	636.08	no	SSR popII
umc2238	AC	1.06	638.30	no	IBM2
csu374b		1.07	642.30	yes	IBM2
php20855		1.07	647.40	yes	IBM2
csh12		1.07	647.73	no	UMC 98
bcd450d		1.07	649.50	no	UMC 98
bcd98a	AC	1.07	649.50	yes	IBM2
csu614a		1.07	649.50	no	UMC 98
uaz19c		1.07	649.50	no	BNL 2002
umc1278	C	1.07	652.40	no	SSR popII
umc1356		1.07	652.65	no	SSR popI
umc1661	AC	1.07	652.65	no	SSR popI
umc1358	AC	1.07	653.40	yes	IBM2
npi605a		1.07	655.63	no	BNL 96
AY111834	AC	1.07	656.70	yes	IBM2
bnlg1556	AC	1.07	658.60	yes	IBM2
bnl7.08b		1.07	659.74	no	BNL 2002
umc1833		1.07	662.18	no	SSR popI
umc33a		1.07	664.17	no	UMC 98
agrp83b		1.07	664.17	no	UMC 98
std1b(his2B1)		1.07	664.17	no	UMC 98
dmt103c	C	1.07	669.39	no	ChromDB
umc23a		1.07	670.20	yes	IBM2
umc1706	AC	1.07	671.29	no	SSR popII
uaz151(sar)		1.07	672.57	no	BNL 2002
uaz2b		1.07	674.08	no	BNL 2002
npi236		1.07	677.45	no	BNL 96
uaz228d(his2b)		1.07	677.81	no	BNL 2002
umc2064		1.07	678.49	no	SSR popI
rz698a(ppy)		1.07	679.85	no	UMC 98
csu921b(ppp)		1.07	679.85	no	UMC 98
csu542		1.07	682.27	no	UMC 98
hon105		1.07	683.56	no	ChromDB
lim442		1.07	685.20	yes	IBM2
med63b		1.07	685.88	no	UMC 98
csu660a	C	1.07	688.54	no	UMC 98
bcd98g		1.07	689.71	no	BNL 96
mmp189		1.07	690.50	yes	IBM2
uaz205b(hsp70)		1.07	692.64	no	UMC 98
mmp173		1.07	693.60	yes	IBM2
umc2387	C	1.07	697.22	no	SSR popII
php20661		1.07	699.90	yes	IBM2
php20713b		1.07	700.50	no	IBM2
bnlg1025	C	1.07	700.50	yes	IBM2
bnl17.15b(bt2)	C	1.07	700.55	no	BNL 2002
dpg7c		1.07	700.58	no	BNL 2002
bcd207a		1.07	703.50	yes	IBM2
bcd98m		1.08	704.57	no	BNL 2002
AY110356	C	1.07	706.40	yes	IBM2
umc1128	C	1.07	711.50	yes	IBM2
bsd2		1.05	712.12	no	BNL 2002
umc1147	AC	1.07	714.40	yes	IBM2
bcd386a		1.07	717.80	yes	IBM2
umc1848		1.07	717.80	no	SSR popI
bnlg1564		1.07	718.50	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi447a		1.07	720.30	yes	IBM2
phi002	C	1.07-1.08	720.90	yes	IBM2
umc1245	C	1.07	721.90	yes	IBM2
AY110159	C	1.07-1.08	722.30	no	IBM2
umc128	C	1.08	722.40	yes	IBM2
mwg645f		1.08	722.40	no	BNL 2002
rz583a(msb)		1.08	722.40	no	UMC 98
umc37b		1.02	723.74	no	BNL 2002
bnlg1629		1.08	723.82	no	BNL 2002
rny(pcr)a		1.08	724.87	no	BNL 2002
umc37a		1.08	726.10	yes	IBM2
npi224f		1.05-1.12	727.83	no	BNL 2002
bnl17.06		1.08	728.23	no	BNL 2002
cdo94b		1.07-1.08	730.48	no	BNL 2002
mdh4		1.08	734.42	no	UMC 98
AY110313	C	1.08	735.20	yes	IBM2
AY110191	C	1.08	740.40	no	IBM2
cdo98b	C	1.08	744.70	yes	IBM2
umc1998	C	1.08	747.90	no	IBM2
npi614		1.08	748.92	no	BNL 2002
npi573		1.08	748.92	no	BNL 96
mmp99		1.08	750.00	yes	IBM2
csu12b(cin4)		1.08	750.23	no	UMC 98
csu580a(mdh)		1.08	750.23	no	UMC 98
bnlg2228	AC	1.08	755.20	yes	IBM2
csu1007(eif4F)		1.08	756.19	no	UMC 98
umc83a	AC	1.08	756.50	yes	IBM2
dup135a		1.08	756.50	no	BNL 2002
umc1085	AC	1.08	757.22	no	SSR popI
umc2029		1.08	760.13	no	SSR popII
lim254		1.08	760.30	yes	IBM2
chr124		1.08	765.10	no	ChromDB
npi120		1.08	765.90	yes	IBM2
umc2080	C	1.08	769.40	no	IBM2
umc1955	C	1.08	770.40	yes	IBM2
uce1		1.08	770.92	no	UMC 98
bnlg1044		1.08	772.50	no	BNL 2002
umc2181	AC	1.08	774.50	yes	IBM2
npi255		1.08	775.20	yes	IBM2
npi569a		1.08	775.41	no	BNL 2002
id1		1.08	775.57	no	BNL 2002
rz561a		1.08	776.90	no	UMC 98
umc1838	C	1.08	777.40	yes	IBM2
csh4(id1)		1.08	779.20	yes	IBM2
umc1446	C	1.08	781.60	yes	IBM2
mpik37		1.08	781.90	no	BNL 96
umc1928		1.08	783.20	yes	IBM2
mmp22		1.08	784.70	no	IBM2
an1	C	1.08	785.30	yes	IBM2
mmc0041	C	1.08	787.49	no	SSR popII
sdg123	C	1.08	789.30	no	ChromDB
csu982(goa)		1.08	790.84	no	UMC 98
bz2	C	1.08	792.42	no	UMC 98
AY110349	C	1.08	793.40	yes	IBM2
csu531		1.08	798.74	no	UMC 98
vp14	AC	1.08	798.74	no	UMC 98
csu780b		1.08	798.74	no	UMC 98
rgps10558a		1.08	798.74	no	UMC 98
csu66a(lhcb)		1.08	798.74	no	UMC 98
csu889b(lhcb)		1.08	798.74	no	UMC 98
umc1991	C	1.08	800.70	yes	IBM2
bnlg1643		1.08	802.89	no	BNL 2002
dup103		1.08	803.08	no	BNL 2002
umc2385	C	1.08-1.09	803.99	no	SSR popII
umc1383	AC	1.08	805.30	yes	IBM2
umc1843		1.08	805.30	no	SSR popII
bnl29d(pds)		1.08	805.83	no	BNL 2002
bnlg100		1.09-1.10	805.95	no	BNL 2002
umc2240	AC	1.08-1.09	806.50	no	IBM2
ufg(vp2274a)		1.08	807.63	no	BNL 2002
umc1914	AC	1.08-1.09	809.90	no	IBM2
lim247		1.08-1.09	811.00	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY109506	AC	1.08-1.09	811.00	no	IBM2
cdj2	AC	1.09	812.30	yes	IBM2
csu1174		1.09	812.30	no	UMC 98
rgpr250		1.09	812.30	no	UMC 98
csu21a(ago)		1.09	812.30	no	UMC 98
umc24b(lhcb)		1.09	812.30	no	UMC 98
umc1512	AC	1.08-1.09	813.30	no	IBM2
csu745e(rpPo)	C	1.09	813.60	no	UMC 98
rz474b(dnaj)		1.08-1.09	813.60	no	IBM2
ufg53		1.09	815.20	yes	IBM2
bnl8.10a		1.09	815.76	no	BNL 96
ufg10	C	1.08-1.09	817.30	no	IBM2
uaz268c		1.09	817.60	no	BNL 2002
dup218b		1.09	818.52	no	BNL 2002
nfc103a	C	1.08	819.03	no	ChromDB
csu696		1.09	821.50	yes	IBM2
rth1		1.09	824.40	no	UMC 98
cdo795a		1.09	824.40	no	UMC 98
umc27b	C	1.09	825.14	no	BNL 2002
rz403		1.09	825.80	yes	IBM2
umc1715		1.09	828.29	no	SSR popII
npi615		1.09	828.36	no	BNL 2002
csu1097c		1.09	828.75	no	UMC 98
chrom7		1.09	833.00	yes	IBM2
asg63b		1.09	833.71	no	UMC 98
csu511a		1.09	833.71	no	UMC 98
umc252b		1.09	836.51	no	UMC 98
ias7		1.09	836.70	no	BNL 96
glb1	AC	1.09	839.30	yes	IBM2
umc2047	AC	1.09	842.30	yes	IBM2
umc140a		1.09	846.10	yes	IBM2
umc129(geb)		1.09	846.10	no	UMC 98
bnlg1331	AC	1.09	847.00	yes	IBM2
csu222a(wsi)		1.09	847.30	yes	IBM2
umc1298	AC	1.09	850.27	no	SSR popII
rgpc746(rnp)		1.09	854.70	no	UMC 98
AY110452		1.09	855.40	yes	IBM2
tbp1		1.09	857.65	no	BNL 96
bnlg1041		1.06	858.18	no	BNL 2002
bnlg1720		1.09-1.10	858.39	no	BNL 2002
csu200b		1.09	858.91	no	UMC 98
bnl17.04(tua)		1.09-1.10	860.73	no	BNL 2002
msu2(iaglu)		1.09	862.10	yes	IBM2
umc1411	AC	1.09	863.92	no	SSR popII
rpa6b		1.09	864.60	no	UMC 98
uat1(lox)		1.09	864.60	no	UMC 98
umc197a(rip)		1.09	864.60	yes	IBM2
bcd1072c(hsp70)		1.09	864.60	no	UMC 98
ucsd61e		1.08	869.20	no	BNL 2002
umc2411		1.09	869.42	no	SSR popI
lpe1		1.03	871.90	no	BNL 96
ole4	AC	1.09	873.50	no	SSR popI
csu110b		1.09	874.30	no	UMC 98
csu554a(rnh)		1.09	874.30	yes	IBM2
csu921a(ppp)		1.09	874.30	no	UMC 98
ucsd113d		1.09	875.17	no	BNL 2002
umc2028		1.09	875.58	no	SSR popII
bnlg1502		1.09-1.10	875.60	no	BNL 2002
mmp195d		1.09	879.70	no	IBM2
umc1306		1.09	881.24	no	SSR popII
umc1082	AC	1.09	882.70	yes	IBM2
umc1431	AC	1.09	886.10	yes	IBM2
umc107a(croc)	AC	1.10	886.90	yes	IBM2
gln2	C	1.10	887.30	no	UMC 98
cdo122a(nad)		1.10	887.50	yes	IBM2
AI665421	AC	1.10	889.90	yes	IBM2
bnlg400		1.09	890.69	no	BNL 2002
bnlg1597a		1.09-1.10	890.87	no	BNL 2002
AY110019	C	1.10	890.90	no	IBM2
rz912a(phy)		1.10	891.48	no	UMC 98
bcd808a		1.10	891.70	yes	IBM2
nfa103a		1.10	892.10	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2189	AC	1.10	892.20	no	IBM2
chb101b		1.10	892.20	no	ChromDB
chr106a		1.10	892.20	no	ChromDB
umc1290	AC	1.09	892.77	no	SSR popII
PCO087393	C	1.10	892.91	no	INDEL
mmp141		1.10	893.70	yes	IBM2
tua2		1.10	898.44	no	UMC 98
knox3		1.10	898.44	no	UMC 98
tua1	C	1.10	898.44	no	UMC 98
csu248		1.10	898.44	no	UMC 98
csu947		1.10	898.44	no	UMC 98
bnl15.18		1.10	898.44	no	UMC 98
csu272a(tua)		1.10	898.44	no	UMC 98
umc2149	AC	1.10	898.70	yes	IBM2
mmp83		1.10	899.20	yes	IBM2
phyA1		1.10	900.00	no	BNL 96
bnl17.21(tua)		1.10	900.00	no	BNL 2002
AY111936	AC	1.10	902.10	yes	IBM2
kn1		1.10	903.86	no	BNL 2002
BE639426	AC	1.10	907.10	yes	IBM2
umc2223		1.10	907.14	no	SSR popI
uaz167a		1.10	910.39	no	BNL 2002
adh1		1.10	910.77	no	SSR popII
umc1885		1.10	910.77	no	SSR popII
pge19		1.10	912.51	no	BNL 2002
umc72b		1.10	912.51	no	BNL 2002
bnlg1268		1.09	912.51	no	BNL 2002
bnlg1671	AC	1.10	913.40	yes	IBM2
hxa102b		1.10	913.40	no	ChromDB
bnlg1116		1.09-1.10	913.57	no	BNL 2002
mmp172		1.10	915.20	yes	IBM2
npi407		1.10	916.70	yes	IBM2
umc1534		1.10	918.21	no	SSR popII
npi98a		1.10	920.10	no	UMC 98
rz632c		1.10	920.10	no	UMC 98
umc106a		1.10	920.10	no	UMC 98
rz630a(sat)		1.10	920.10	yes	IBM2
umc1774	C	1.10	923.01	no	SSR popI
vef101b	C	1.10	923.99	no	ChromDB
ucsd64c		1.10	925.07	no	BNL 2002
ucsd104b(zag6)		1.10	925.29	no	BNL 2002
lim99a		1.10	926.30	yes	IBM2
bcd450b		1.10	926.83	no	UMC 98
phi308707	C	1.10	927.40	no	IBM2
npi282b		1.10	927.90	yes	IBM2
PCO095183	C	1.10	929.52	no	INDEL
lim78		1.10	930.50	yes	IBM2
mta1		1.10	932.92	no	UMC 98
uat4a		1.10	932.92	no	UMC 98
csu261		1.10	932.92	no	UMC 98
csu137b(ap)		1.10	932.92	no	UMC 98
bnlg1347		1.10	933.09	no	BNL 2002
mpik22a(zmm4)		1.10	934.49	no	BNL 2002
uaz130a(tlk)	C	1.10	934.50	yes	IBM2
asg54a		1.10	936.13	no	UMC 98
mmp165		1.10	939.70	no	IBM2
mmp87		1.10	942.40	yes	IBM2
knox8		1.10	944.47	no	UMC 98
npi581a		1.10	948.17	no	BNL 96
ucsd106d		1.10	949.67	no	BNL 2002
lim39		1.10	950.20	yes	IBM2
bnl7.25a		1.10	951.20	no	IBM2
csu954		1.10	951.20	no	UMC 98
umc147b		1.10	952.19	no	BNL 2002
bnl17.18b		1.10	952.19	no	BNL 96
umc257	C	1.10	963.20	no	IBM2
phi1		1.11	963.60	no	UMC 98
rpa7a		1.11	963.60	no	UMC 98
umc264		1.11	963.60	no	UMC 98
umc161a	C	1.11	963.60	yes	IBM2
csu1169b		1.11	963.60	no	UMC 98
uaz21a		1.10	963.60	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY109834	C	1.11	970.00	yes	IBM2
phi265454	AC	1.11	973.00	yes	IBM2
npi75b		1.10	973.80	no	BNL 2002
csu63a(cdj)		1.11	973.97	no	UMC 98
csu570b(mtl)		1.11	973.97	no	UMC 98
umc1500	AC	1.11	985.11	no	SSR popII
ias13a		1.11	985.24	no	BNL 2002
AY110426	C	1.11	987.30	yes	IBM2
uaz166a		1.10	992.50	no	BNL 2002
ufg14		1.11	995.00	no	IBM2
mmp195g		1.11	1000.90	yes	IBM2
bnl8.08a		1.11	1001.46	no	BNL 2002
bnlg1023b		1.06	1002.02	no	BNL 2002
npi238		1.11	1006.10	yes	IBM2
asg68b		1.11	1006.10	no	UMC 98
jpsb239b		1.11	1006.60	no	IBM2
usu1a(fnr)		1.11	1006.90	no	UMC 98
cdo87b(ptk)	C	1.11	1006.90	yes	IBM2
umc1553	C	1.11	1007.60	yes	IBM2
gdh1		1.11	1008.46	no	BNL 2002
umc1421		1.11	1010.20	yes	IBM2
umc1681	AC	1.11	1014.90	yes	IBM2
bnlg2331		1.11	1016.21	no	BNL 2002
uaz10		1.05	1018.62	no	BNL 2002
uaz12		1.04-1.05	1018.62	no	BNL 2002
csu868(trp)		1.11	1019.06	no	UMC 98
umc1129	AC	1.11	1019.10	yes	IBM2
bnl8.29a		1.11	1021.40	yes	IBM2
ohp1	AC	1.11	1021.40	no	BNL 2002
tum5		1.07-1.12	1021.40	no	BNL 2002
csu604a(trh)	AC	1.11	1021.40	no	UMC 98
umc1111	C	1.11	1022.60	yes	IBM2
umc1862		1.11	1023.30	no	SSR popII
npi241a		1.11	1025.70	yes	IBM2
uaz240c		1.11	1026.12	no	BNL 2002
hon110		1.11	1027.30	no	ChromDB
umc1737	AC	1.11	1029.96	no	SSR popI
csu33b	AC	1.11	1030.14	no	UMC 98
umc2241	AC	1.11	1031.00	yes	IBM2
umc2242	AC	1.11	1031.80	no	IBM2
bnlg1055		1.11	1033.99	no	BNL 2002
umc1118	AC	1.11	1034.30	yes	IBM2
ccr1		1.11	1037.79	no	UMC 98
csu381		1.11	1037.79	no	UMC 98
csu755		1.11	1037.79	no	UMC 98
csu536(ccr)		1.11	1037.79	no	UMC 98
csu663b(psaD)		1.11	1037.79	no	UMC 98
bnlg667a	AC	1.11	1039.42	no	SSR popI
AY110479	C	1.11	1039.70	yes	IBM2
umc1538		1.11	1040.93	no	SSR popII
umc1744	C	1.11	1051.10	yes	IBM2
umc84a	AC	1.11	1054.20	yes	IBM2
umc86a		1.11	1054.70	yes	IBM2
csu134a(thf)		1.11	1054.73	no	UMC 98
umc1630	C	1.11	1055.90	yes	IBM2
ids1		1.11	1057.19	no	SSR popII
php15058		1.11	1057.80	no	IBM2
PCO063726	C	1.11	1060.61	no	INDEL
mpik9		1.12	1062.19	no	BNL 2002
AY110160	C	1.11	1063.80	yes	IBM2
bnlg504		1.11	1065.42	no	BNL 2002
bnlg131	C	1.11	1065.62	no	SSR popI
csu175e(eif5A)		1.11	1065.66	no	UMC 98
chi1		1.11	1070.58	no	UMC 98
bnlg2123	C	1.11	1073.46	no	SSR popII
dpg1a		1.11	1084.42	no	BNL 2002
bnlg257		1.07	1091.35	no	BNL 2002
cdo457b		1.11	1091.89	no	UMC 98
lim228		1.11	1092.40	yes	IBM2
csu266		1.11	1095.02	no	UMC 98
umc1725	AC	1.12	1096.05	no	SSR popII
CL62610_1	C	1.11	1096.12	no	INDEL

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1331	AC	1.11	1096.50	yes	IBM2
phi227562	AC	1.11	1097.40	no	IBM2
csu1089		1.11	1098.00	yes	IBM2
rz614(fdx)		1.12	1098.00	no	UMC 98
fdx3	AC	1.11	1098.40	no	IBM2
umc2243	AC	1.11	1098.40	no	IBM2
umc2045	C	1.11	1099.30	yes	IBM2
phi064	AC	1.11	1103.00	yes	IBM2
uaz22		1.12	1103.73	no	BNL 2002
tum4		1.07-1.12	1110.28	no	BNL 2002
bnl6.32		1.12	1113.20	yes	IBM2
rgpr3239a		1.11-1.12	1113.20	no	UMC 98
csu865(phb)		1.11-1.12	1113.20	no	UMC 98
umc1605	AC	1.12	1117.10	yes	IBM2
umc1797		1.12	1119.09	no	SSR popII
umc1819	AC	1.12	1119.20	no	IBM2
umc2244	AC	1.11	1120.30	yes	IBM2
AY110983		1.12	1121.19	no	INDEL
mmp31		1.12	1121.90	no	IBM1
lim331		1.12	1121.90	no	IBM1
ufg35b		1.12	1121.90	no	IBM1
ufg75a		1.12	1121.90	no	IBM1
tufm1	AC	1.12	1121.90	yes	IBM2
csu1084		1.12	1122.42	no	UMC 98
csu1146		1.12	1122.42	no	UMC 98
csu1154		1.12	1122.42	no	UMC 98
npi294i		1.12	1122.42	no	UMC 98
acp4		1.12	1122.42	no	BNL 96
csu1114		1.12	1128.24	no	UMC 98
csu1193		1.12	1132.60	no	UMC 98
AY109916	AC	1.12	1137.90	yes	IBM2
sdg119		1.12	1272.50	no	ChromDB
PCO091677	C	2.00-2.01	-47.10	no	INDEL
AY110535	AC	2.00	0.00	yes	IBM2
crr1		2.00-2.01	2.60	no	SSR popII
umc2246	AC	2.03	3.10	no	IBM2
isu53a		2.00-2.01	3.80	yes	IBM2
bnl(tas1a)		2.00	6.80	no	BNL 96
pgs1		2.00	13.10	no	BNL 96
umc1419	AC	2.00-2.01	15.20	no	SSR popI
bnl8.45a	C	2.01	18.80	no	SSR popI
npi239		2.00-2.01	18.80	no	UMC 98
umc2Stelo-1		2.00-2.01	18.80	no	UMC 98
umc2Stelo-2		2.00-2.01	18.80	no	UMC 98
csu1192(apx)		2.00-2.01	18.80	no	UMC 98
rny(pcr)c		2.00	20.83	no	BNL 96
csu326		2.01	21.13	no	UMC 98
bnl10.38b		2.01	21.39	no	UMC 98
npi417a		2.00	22.51	no	BNL 2002
agrc805		2.01	23.72	no	UMC 98
uaz21b		2.00	24.55	no	BNL 2002
AY109692	C	2.01	25.30	no	IBM2
isu144a		2.01	27.40	yes	IBM2
phi96100	AC	2.01	28.10	no	IBM2
umc2245	AC	2.01	30.90	yes	IBM2
php20568b		2.01	34.30	yes	IBM2
bnlg1092		2.01	36.78	no	BNL 2002
csu29a	AC	2.01	37.96	no	UMC 98
umc2363	C	2.01 - 2.02	40.20	no	SSR popII
jpsb485b		2.01	43.30	yes	IBM2
umc1227		2.01	45.55	no	SSR popII
umc1165	AC	2.01	47.40	yes	IBM2
csu300a		2.01	48.31	no	UMC 98
umc53a		2.02	50.90	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu1053		2.02	50.90	no	UMC 98
csu642	AC	2.02	52.02	no	UMC 98
mir3b(thp)		2.02	53.23	no	UMC 98
fht1		2.01 - 2.02	53.39	no	BNL 96
rz590a		2.02	54.54	no	UMC 98
bnlg1302		2.02	55.11	no	BNL 2002
cdo524		2.02	55.57	no	UMC 98
csu552		2.02	55.57	no	UMC 98
csu12d(cin4)		2.02	55.57	no	UMC 98
npi254a		2.02	55.60	yes	IBM2
csu1148		2.02	57.53	no	UMC 98
umc1542	AC	2.02	57.60	yes	IBM2
umc1552		2.01 - 2.02	59.51	no	SSR popII
bnlg1297		2.02	59.90	yes	IBM2
cdo244b(crp)		2.02	60.42	no	UMC 98
bnlg1017		2.02	65.70	yes	IBM2
npi577a		2.02	73.44	no	BNL 96
umc1980		2.02	75.60	yes	IBM2
bcd98x		2.02	76.96	no	BNL 2002
umc2403		2.02	77.44	no	SSR popII
umc1265		2.02	77.70	yes	IBM2
uaz24b		2.02	79.14	no	BNL 2002
AY109603		2.02	82.30	yes	IBM2
bnlg1338		2.01	85.65	no	BNL 2002
CL52019_1	C	2.01 - 2.02	87.02	no	INDEL
BE640649	C	2.02	87.80	yes	IBM2
npi208c		2.02	90.30	yes	IBM2
npi421a		2.02	90.30	yes	IBM2
pbs5		2.02	90.30	no	BNL 2002
umc1961	C	2.02	92.00	no	IBM2
umc1824a	C	2.02	92.60	yes	IBM2
umc1823	C	2.02	92.80	no	IBM2
sgb101	C	2.02	92.90	no	ChromDB
mmc0111	C	2.02	93.30	yes	IBM2
AY109516	AC	2.02	94.40	yes	IBM2
uaz25b		2.02	94.55	no	BNL 2002
uaz26a		2.02	94.55	no	BNL 2002
uaz251b(rpS11)		2.02	109.65	no	BNL 2002
dmt102b	C	2.02	113.79	no	ChromDB
cpx1		2.02	118.28	no	BNL 2002
npi290b		2.02	118.28	no	BNL 96
eks1	C	2.02	122.40	yes	IBM2
agrc539a		2.02	122.40	no	UMC 98
umc1756	C	2.02	141.60	no	IBM2
bnlg2277	C	2.02	143.10	yes	IBM2
csu1091		2.02	144.67	no	UMC 98
ucsd(lfyB)		2.02	145.87	no	BNL 96
CL12768_1	C	2.02-2.03	146.85	no	INDEL
ias6a		2.02	148.10	no	BNL 2002
bnlg1327	AC	2.02	148.10	yes	IBM2
myb5		2.02	149.20	yes	IBM2
mpik4b		2.03	150.00	no	BNL 2002
csu1113		2.02	150.40	no	UMC 98
umc2193	C	2.03	152.77	no	SSR popI
umc1262	C	2.02	153.10	yes	IBM2
umc1261	C	2.02	154.60	yes	IBM2
umc1518		2.02	155.72	no	SSR popII
csu425(gct)		2.02	156.12	no	UMC 98
umc1422	AC	2.02	156.60	yes	IBM2
csu348a		2.02	158.88	no	UMC 98
AY106040	C	2.03	163.50	yes	IBM2
bnlg125	C	2.03	164.33	no	SSR popI
umc6	C	2.03	164.80	yes	IBM2
csu1058		2.03	165.03	no	UMC 98
umc6a	C	2.03	165.03	no	INDEL
si605074C02	C	2.03	168.64	no	INDEL
lim328		2.03	171.50	yes	IBM2
mmc0231		2.03	179.40	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc44b	C	2.03	182.30	yes	IBM2
nfd102	C	2.03	186.20	no	ChromDB
bnlg1537		2.03	186.30	no	BNL 2002
inra1(tmp)		2.03	189.79	no	UMC 98
bnlg1393		2.02	190.24	no	BNL 2002
npi287a		2.03	191.50	yes	IBM2
umc61		2.03	193.30	yes	IBM2
bcd855a(ext)	C	2.03	193.30	no	UMC 98
csh6		2.03	193.38	no	UMC 98
csh7		2.03	193.46	no	UMC 98
csu176		2.03	195.38	no	UMC 98
csu498		2.03	195.38	no	UMC 98
b1	AC	2.03	197.20	yes	IBM2
npi402		2.03	197.60	no	BNL 96
umc1845		2.03	197.89	no	SSR popII
bnlg1621b		2.03	200.33	no	BNL 2002
mmp33		2.03	203.10	yes	IBM2
bnlg2248		2.03	207.74	no	BNL 2002
agrr113a		2.03	207.76	no	UMC 98
uaz27b		2.03	207.76	no	BNL 2002
ufg3a(ivr)		2.03	207.76	no	UMC 98
csu761		2.03	211.35	no	UMC 98
psr901		2.03	212.20	yes	IBM2
npi269a		2.03	212.90	no	BNL 96
csu1167		2.03	212.95	no	UMC 98
ufg28b		2.03	216.00	no	IBM2
bnl(plB)		2.04	216.48	no	BNL 2002
ole1	AC	2.03	216.50	yes	IBM2
sdg104	C	2.03	216.50	no	ChromDB
npi587		2.03	216.80	no	IBM2
mmp42		2.03	218.70	yes	IBM2
npi583		2.03	220.36	no	BNL 96
csu571a(ipp)		2.03	221.34	no	UMC 98
AI920398	AC	2.03	221.40	yes	IBM2
agrr167a		2.03	223.33	no	UMC 98
bnl10.42a		2.03	223.33	no	UMC 98
umc1555	AC	2.03	225.38	no	SSR popII
bnl12.36a		2.03-2.04	225.70	no	BNL 96
bnlg1064	AC	2.03	227.10	yes	IBM2
bnl17.23b(pal)		2.03	227.30	no	BNL 2002
sdg107		2.03	228.40	no	ChromDB
AY104214	AC	2.03	236.40	yes	IBM2
csu861		2.03	236.51	no	UMC 98
csu821		2.03	238.51	no	UMC 98
si606023F08	C	2.03-2.04	242.86	no	INDEL
umc34	AC	2.04	243.30	yes	IBM2
csu40(grx)		2.03-2.04	243.30	no	UMC 98
phi109642	AC	2.03-2.04	244.00	no	IBM2
bnlg381	AC	2.04	244.70	yes	IBM2
npi607		2.04	247.20	yes	IBM2
bnl1.45b		2.04	247.20	no	BNL 2002
npi248		2.04	248.54	no	BNL 96
umc1024	AC	2.04	250.10	yes	IBM2
umc1769	C	2.04	250.94	no	SSR popI
umc2247	AC	2.04	251.10	yes	IBM2
bnl8.04		2.04	252.27	no	UMC 98
umc1026		2.04	256.05	no	SSR popII
mpik35b		2.04	258.34	no	BNL 2002
bnlg2287		2.04	258.96	no	BNL 2002
isu2117b		2.04	262.54	no	BNL 2002
AY110266	C	2.04	262.60	yes	IBM2
PCO098412	C	2.04	263.84	no	INDEL
csu348b		2.04	266.76	no	UMC 98
csu350(gpdh)		2.04	266.76	no	UMC 98
umc1326	C	2.04	266.80	yes	IBM2
cta1	C	2.04	267.21	no	SSR popII
isu58a		2.04	267.50	no	IBM2
umc2248	AC	2.04	267.80	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc259b	C	2.04	268.40	yes	IBM2
csu735(geb)		2.04	269.52	no	UMC 98
umc1448	C	2.04	269.60	yes	IBM2
PCO140184	C	2.04	269.87	no	INDEL
umc234		2.04	271.59	no	UMC 98
hag103a	C	2.04	273.60	no	ChromDB
umc1465	AC	2.04	273.70	yes	IBM2
umc1541	AC	2.04	274.90	yes	IBM2
npi242c		2.04	274.95	no	BNL 96
mmp122		2.04	275.60	no	IBM2
CL58207_1	C	2.04	276.17	no	INDEL
umc135		2.04	277.80	no	UMC 98
npi220d	C	2.04	277.80	no	UMC 98
mmp167		2.04	281.30	yes	IBM2
umc1579		2.04	284.40	no	SSR popI
prp2	AC	2.04	284.70	yes	IBM2
CL10221_1	C	2.04	285.89	no	INDEL
bnl12.09		2.04	287.11	no	BNL 2002
pbs12		2.04	288.13	no	BNL 2002
dpg6a		2.04	288.53	no	BNL 2002
umc134b		2.04	288.80	yes	IBM2
AY110485	AC	2.04	292.50	yes	IBM2
csu56c(ohp)	C	2.04	292.87	no	UMC 98
lim86		2.04	293.80	no	IBM2
umc1580	AC	2.04	294.20	yes	IBM2
bnlg1018	AC	2.04	294.20	yes	IBM2
bnlg1175	AC	2.04	295.10	yes	IBM2
csu334		2.04	295.39	no	UMC 98
csu762		2.04	295.39	no	UMC 98
csu393(fbn)	C	2.04	295.39	no	UMC 98
bnlg166		2.04	295.74	no	BNL 2002
umc2251	AC	2.04	295.80	yes	IBM2
umc2249	AC	2.04	296.30	yes	IBM2
bnlg1909		2.05	297.40	no	BNL 2002
bnl35e(blr)		2.04	297.48	no	BNL 2002
mmp91		2.04	302.60	yes	IBM2
accA		2.05	305.51	no	BNL 96
bnlg108	C	2.04	306.30	yes	IBM2
bnlg1861a		2.04	307.02	no	BNL 2002
bnlg1818		2.04	307.69	no	BNL 2002
pic3		2.04	307.78	no	BNL 2002
bnlg1914		2.05	307.86	no	BNL 2002
csh(prl1)		2.04	308.13	no	BNL 2002
uaz234		2.05	308.45	no	BNL 2002
uaz235(px)		2.05	308.45	no	BNL 2002
npi271a		2.05	308.66	no	BNL 2002
bnlg1085a		2.04	308.98	no	BNL 2002
hcf106		2.05	309.37	no	BNL 2002
bnlg1063b	C	2.05	309.37	no	BNL 2002
dupssr21		2.05	309.40	no	BNL 2002
bnlg1140		2.08	309.69	no	BNL 2002
msu1		2.04	309.84	no	BNL 2002
bnl29(pds3)		2.05	309.84	no	BNL 2002
uaz25c		2.05	309.96	no	BNL 2002
bnlg1613		2.04	309.96	no	BNL 2002
bnlg2328a		2.05	309.96	no	BNL 2002
pbs15		2.05	309.96	no	BNL 96
umc1259	C	2.04	310.20	yes	IBM2
umc2030	AC	2.04	313.50	yes	IBM2
umc1861	AC	2.04	314.40	yes	IBM2
npi242a		2.04	315.00	yes	IBM2
umc8b		2.04	315.50	no	IBM2
sdg102a		2.04	315.50	no	ChromDB
umc2088	AC	2.04	316.70	yes	IBM2
csu1117b		2.04	316.84	no	UMC 98
bnlg121		2.04	319.30	yes	IBM2
tug4		2.04	319.30	no	BNL 2002
umc2079	AC	2.04	320.70	yes	IBM2
php10012		2.04	321.00	yes	IBM2
hda102	C	2.04	322.20	no	ChromDB
hrg1	C	2.04	323.30	no	IBM2
rgpg271	C	2.04	328.79	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2250	C	2.04	329.00	yes	IBM2
umc1485	AC	2.04	329.60	no	SSR popI
mmp89		2.04	331.40	yes	IBM2
bcd450f		2.04	331.93	no	UMC 98
umc184b(glb)		2.04	331.93	no	UMC 98
umc2125	AC	2.04	332.20	no	IBM2
umc2007		2.04	334.20	yes	IBM2
csu255a		2.04	335.34	no	UMC 98
uaz262		2.05	336.40	no	IBM2
umc1455	AC	2.04-2.05	338.13	no	SSR popI
csu148b(clx)		2.04	338.21	no	UMC 98
umc1454	AC	2.04	339.30	yes	IBM2
umc1235	AC	2.04	339.82	no	SSR popII
umc1007		2.04-2.05	340.54	no	SSR popII
umc131		2.05	342.40	yes	IBM2
umc1410	AC	2.04-2.05	342.40	no	SSR popII
psr922b		2.04-2.05	342.90	no	IBM2
isu89		2.05	343.00	yes	IBM2
psr666		2.05	344.20	yes	IBM2
umng2		2.05	344.26	no	UMC 98
umc1581	C	2.05	344.40	no	IBM2
csu1060		2.05	344.42	no	UMC 98
umng1		2.05	344.50	no	UMC 98
csu143		2.05	344.50	no	UMC 98
umc1635	AC	2.05	344.80	no	IBM2
csu4a		2.05	344.90	no	UMC 98
csu833		2.05	344.90	no	UMC 98
csu842		2.05	344.90	no	UMC 98
csu1066		2.05	344.90	no	UMC 98
csu1163		2.05	344.90	no	UMC 98
umn1(acc)		2.05	344.90	no	UMC 98
zpu1	AC	2.05	345.00	yes	IBM2
umc1922		2.05	345.20	no	IBM2
agrp173		2.05	345.71	no	UMC 98
csu671a		2.05	345.71	no	UMC 98
PCO096835	C	2.05	346.24	no	INDEL
mmp119		2.05	346.50	yes	IBM2
asg29b		2.05	346.52	no	UMC 98
csu1059		2.05	346.84	no	UMC 98
bnlg1184		2.06	347.11	no	BNL 2002
bnlg1887		2.06	347.11	no	BNL 2002
uaz179		2.05	347.60	no	BNL 2002
uaz28b		2.05	347.60	no	BNL 2002
umc1884		2.05	347.96	no	SSR popI
ucsd1.8c		2.05	348.28	no	BNL 2002
uaz135		2.05	348.74	no	BNL 2002
uaz181		2.05	348.74	no	BNL 2002
AY109687	AC	2.05	349.00	yes	IBM2
csu2a		2.05	349.67	no	UMC 98
uaz236b(ser)		2.05	349.69	no	BNL 2002
ssu2		2.05	350.00	no	BNL 2002
bnl20		2.05	350.00	no	BNL 2002
umc8c		2.05	350.00	no	BNL 2002
psr109a		2.05	350.00	no	BNL 2002
bnl17.25		2.05	350.00	no	BNL 2002
bnlg2039		2.05	350.00	no	BNL 2002
mwg645i		2.05-2.06	350.00	no	BNL 2002
hsbp1		2.05	350.86	no	SSR popII
csu850		2.05	351.13	no	UMC 98
csu851a		2.05	351.13	no	UMC 98
umc8g		2.05	352.18	no	UMC 98
AW681281	C	2.05	352.40	no	IBM2
csu1073a		2.05	353.23	no	UMC 98
umc1459	AC	2.05	353.81	no	SSR popII
csu1080b		2.05	354.60	yes	IBM2
csu337		2.05	355.97	no	UMC 98
npi123c		2.05	357.10	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2110	AC	2.05	357.50	no	IBM2
umc255a	AC	2.06	358.32	no	SSR popII
mmc0401	AC	2.05	358.60	yes	IBM2
umc2252	C	2.05	359.10	no	IBM2
umc112a		2.06	360.76	no	UMC 98
umc1028	AC	2.06	361.20	yes	IBM2
tda217b		2.06	364.27	no	UMC 98
AY110336	AC	2.06	364.50	no	IBM2
npi297		2.06	367.20	yes	IBM2
rz509b(mip)		2.06	367.33	no	UMC 98
umc176	C	2.06	368.00	no	SSR popI
pbf1	AC	2.06	368.10	no	IBM2
umc1156	AC	2.06	368.57	no	SSR popII
bnlg1831	AC	2.06	368.80	no	IBM2
bnlg180		2.05	369.18	no	BNL 2002
uaz18b		2.05	369.24	no	BNL 2002
umc1079	AC	2.06	369.30	yes	IBM2
uaz265a(sbe1)		2.05-2.06	369.51	no	BNL 2002
ici99		2.06	369.53	no	BNL 2002
umc2b	C	2.06	369.53	no	BNL 2002
uaz194b(ugu)		2.06	369.53	no	BNL 2002
uaz29		2.05	369.54	no	BNL 2002
bcd249a		2.06	369.83	no	BNL 2002
bnlg371		2.05	369.90	no	BNL 2002
mpik33i		2.05-2.06	369.91	no	BNL 2002
npi356a		2.06	370.31	no	BNL 96
umc267(kapp)		2.06	370.47	no	UMC 98
csu281b		2.06	370.74	no	UMC 98
klp1d		2.06	372.06	no	UMC 98
dia1		2.06	372.77	no	BNL 96
bnlg1036	AC	2.06	373.50	yes	IBM2
bnlg1225		2.06	373.68	no	BNL 2002
csu747a(arf)	C	2.06	373.74	no	UMC 98
umc55a		2.06	373.90	no	UMC 98
pbs13b		2.06	373.90	no	BNL 2002
ucsd141b		2.06	373.92	no	BNL 2002
bnl35c(blr)		2.06	373.94	no	BNL 2002
bnlg1396		2.06	373.95	no	BNL 2002
bnlg2313b		2.06	373.96	no	BNL 2002
uaz352b		2.06	374.05	no	UMC 98
umc139a		2.06-2.08	375.12	no	UMC 98
umc1658	AC	2.06	375.30	yes	IBM2
umc2253	C	2.05	376.10	yes	IBM2
ufg2(agp2)		2.06	376.31	no	BNL 96
umc2178	C	2.06	377.40	yes	IBM2
umc2254	AC	2.05	378.70	no	IBM2
AY105915	C	2.06	378.90	yes	IBM2
tug3		2.06	379.20	no	BNL 2002
umc1875	C	2.06	379.20	no	IBM2
bnlg1138	AC	2.06	379.20	yes	IBM2
umc1763		2.06	379.20	no	SSR popI
umc1923	AC	2.06	379.40	no	IBM2
bcd1087a		2.06	379.85	no	UMC 98
umc2192	C	2.06	379.97	no	SSR popI
umc1080	AC	2.06	380.00	yes	IBM2
jpsb365b		2.06	380.50	yes	IBM2
umc2194	C	2.06	380.58	no	SSR popI
umc1755	AC	2.06	380.60	no	IBM2
AY109981	AC	2.06	380.80	no	IBM2
ucsd1.8b		2.06	380.99	no	BNL 2002
umc1004	AC	2.06	381.80	yes	IBM2
csu270		2.06	382.30	no	UMC 98
npi456		2.06	382.52	no	BNL 96
PCO063114	C	2.06-2.07	383.38	no	INDEL
uky1(P450)		2.06	383.98	no	UMC 98
npi565b		2.05-2.06	384.60	no	BNL 2002
bnlg1047c		2.05	384.76	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnl17.24		2.06	385.07	no	BNL 2002
npi221b		2.06	386.59	no	BNL 2002
umc1806		2.06	386.59	no	SSR popII
npi277a		2.06-2.07	386.59	no	BNL 96
umc2372		2.06	389.03	no	SSR popII
uaz30c		2.06-2.07	389.79	no	BNL 2002
csu1051		2.06	391.16	no	UMC 98
umc1749		2.06	391.25	no	SSR popII
umc2023		2.06	391.41	no	SSR popII
bnlg1329	AC	2.08	391.62	no	BNL 2002
bnlg1413		2.07	393.38	no	BNL 2002
bnlg2103		2.06	394.48	no	BNL 2002
npi47a		2.07	394.52	no	UMC 98
umc98a		2.07	394.52	no	UMC 98
bnl27		2.07	394.52	no	BNL 2002
umc5a	C	2.07	394.52	no	SSR popI
umc29b		2.06-2.07	394.52	no	UMC 98
tjp1(thp)		2.06-2.07	394.52	no	UMC 98
umc1946		2.06-2.07	394.52	no	SSR popII
umc2019	AC	2.07	394.97	no	SSR popII
bnlg1258		2.08	395.59	no	BNL 2002
npi613		2.07	396.04	no	BNL 2002
uaz228a(his2b)		2.06	396.32	no	BNL 2002
amy3	AC	2.07	399.43	no	UMC 98
umc1637		2.07	399.72	no	SSR popI
umc1108	AC	2.07	401.50	yes	IBM2
umc2402		2.07-2.08	406.80	no	SSR popII
bcd926b	C	2.07	409.30	yes	IBM2
asg72a		2.07	411.40	no	UMC 98
php20005		2.07	411.40	yes	IBM2
umc1497		2.07	411.98	no	SSR popI
umc2129	AC	2.07	414.10	yes	IBM2
ucsd64i		2.07	415.88	no	BNL 96
mmp177b		2.07	416.60	no	IBM2
umc2220		2.07	416.73	no	SSR popI
umc1554	C	2.07	417.98	no	SSR popII
umc2205		2.07	420.56	no	SSR popI
umc1890	AC	2.07	422.70	yes	IBM2
umc2032	AC	2.04	424.49	no	SSR popII
csu1103		2.07	424.60	no	UMC 98
umc1285	C	2.04	425.23	no	SSR popII
AY110410	AC	2.07	427.90	yes	IBM2
php20569b		2.07	428.45	no	BNL 96
uaz269b(kri)		2.07	433.88	no	BNL 2002
mmc0271		2.07	438.30	no	SSR popI
nfc104b		2.07	443.41	no	ChromDB
rz474c(dnaj)		2.07	446.90	yes	IBM2
uaz194a(ugu)		2.07	450.40	yes	IBM2
ugp1		2.07	450.99	no	UMC 98
asg84a		2.07	450.99	no	UMC 98
csu635		2.07	450.99	no	UMC 98
umc22a		2.07	450.99	no	UMC 98
mpik27a(zmm7)		2.07	450.99	no	UMC 98
AY109917	C	2.07	452.20	no	IBM2
nfd101b		2.07	452.20	no	ChromDB
sdg106		2.07	452.40	no	ChromDB
phi251315	C	2.07	453.80	yes	IBM2
umc2380	C	2.07-2.08	459.13	no	SSR popII
AY109722		2.07	461.70	yes	IBM2
umc1042		2.07	466.65	no	SSR popI
csu54a		2.07	467.16	no	BNL 96
bnlg1633		2.07	468.70	no	BNL 2002
umc88(P450)		2.07	469.10	no	BNL 2002
bnlg1267	AC	2.08	470.73	no	BNL 2002
bnlg1045		2.07	470.99	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg2144		2.08	471.22	no	BNL 2002
sdg116b		2.07	471.40	no	ChromDB
umc36b		2.07	472.90	yes	IBM2
php20017a		2.07	474.40	yes	IBM2
chr119		2.07	474.40	no	ChromDB
bnlg2077	AC	2.07-2.08	474.80	no	IBM2
umc1560	AC	2.07	475.10	yes	IBM2
psr135b		2.07-2.08	477.90	no	IBM2
asg20	AC	2.08	478.70	yes	IBM2
umc4a	C	2.08	478.70	no	UMC 98
agrr85a		2.08	478.70	no	UMC 98
umc1536		2.08	478.70	no	SSR popII
csu658(mam)		2.08	478.70	no	UMC 98
csu657(atpd)		2.08	478.70	no	UMC 98
csu800(lhca)		2.08	478.70	no	UMC 98
csu847a(lhcb)		2.08	478.70	no	UMC 98
csu154a(eif5A)	C	2.08	478.70	no	UMC 98
umc1049	AC	2.08	480.70	yes	IBM2
mmp116		2.08	482.20	yes	IBM2
umc1745		2.08	485.58	no	SSR popI
mmc0191		2.07-2.08	486.45	no	SSR popII
tua5		2.08	490.00	no	UMC 98
csu749b		2.08	490.00	no	UMC 98
umc125a		2.08	490.00	no	UMC 98
mmc0143		2.07-2.08	491.43	no	SSR popII
umc2374	C	2.07-2.08	492.54	no	SSR popII
csu17b(rnp)		2.08	494.53	no	UMC 98
umc122a		2.08	496.03	no	UMC 98
csu203b(eif5A)	AC	2.08	496.03	no	UMC 98
bcd808c		2.08	496.10	no	IBM2
rgpg99		2.08	496.79	no	UMC 98
mmp84		2.08	498.30	yes	IBM2
umc116b		2.08	501.31	no	UMC 98
umc1126	C	2.08	503.61	no	SSR popII
AY109583	AC	2.08	507.40	yes	IBM2
bnlg1233	AC	2.08	509.20	no	IBM2
asg23		2.08	509.60	no	UMC 98
umc137a		2.08	509.60	yes	IBM2
rgpc74c		2.08	509.60	no	UMC 98
bnl5.21b		2.08	509.60	no	UMC 98
csu175a(eif5A)		2.08	509.60	no	UMC 98
umc2005		2.08	511.48	no	SSR popI
AI668346	AC	2.08	515.80	yes	IBM2
umc1526		2.08	516.90	no	SSR popII
hda109	C	2.08	519.60	no	ChromDB
chr122	C	2.08	520.00	no	ChromDB
phi435417	C	2.08	520.50	yes	IBM2
bnl8.21b		2.07	521.71	no	BNL 96
umc1947	C	2.08	522.40	yes	IBM2
bnlg1335		2.08	522.84	no	BNL 2002
umc1604	C	2.08	523.50	yes	IBM2
csu894a		2.08	524.73	no	UMC 98
csu920a		2.08	524.73	no	UMC 98
umc1618		2.08	528.53	no	SSR popII
bnlg1316	C	2.08	529.20	no	IBM2
bnlg198		2.08	529.50	no	BNL 2002
ucsd106f		2.08	529.50	no	BNL 2002
bnl17.30b		2.08	529.50	no	BNL 2002
rgpc1122a(rpL15)		2.07	529.50	no	UMC 98
csh1b(chi)		2.07-2.08	529.50	no	BNL 96
bnlg1141		2.08	529.52	no	BNL 2002
bnlg1908a		2.08	529.56	no	BNL 2002
bnlg1721		2.08	529.57	no	BNL 2002
uaz31b		2.08	529.59	no	BNL 2002
bnlg1662		2.08	529.59	no	BNL 2002
bnlg1767		2.08	529.59	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz32		2.08	529.61	no	BNL 2002
npi591		2.08	529.61	no	BNL 2002
uaz23b		2.08	529.61	no	BNL 2002
bnl6.20		2.08	529.80	yes	IBM2
hag105		2.08	532.00	no	ChromDB
csu909		2.08	535.99	no	UMC 98
npi210		2.08	536.50	yes	IBM2
dup1390		2.06	536.79	no	BNL 2002
bnlg1169		2.08	536.79	no	BNL 2002
dupssr24		2.08	536.79	no	BNL 2002
ast(amyBS2)b		2.08	536.79	no	BNL 96
mmp137		2.08	537.10	no	IBM2
chc101b	C	2.08	537.20	no	ChromDB
umc1464	C	2.08	538.49	no	SSR popII
AY109645	C	2.08	538.80	yes	IBM2
bnl5.61b		2.08	539.05	no	BNL 96
uaz241b		2.08	539.58	no	BNL 2002
asg28c		2.08	539.95	no	UMC 98
csu1097b		2.08	539.95	no	UMC 98
rgpc643c		2.08	539.95	no	UMC 98
uaz140		2.07	540.36	no	BNL 2002
npi274		2.08	541.11	no	BNL 2002
bnlg1109		2.06	541.56	no	BNL 2002
ias4a		2.08	543.32	no	BNL 2002
PCO102097	C	2.08	544.27	no	INDEL
umc2085	C	2.08	544.40	yes	IBM2
npi413a		2.08	546.59	no	BNL 2002
npi113b		2.08	548.10	no	IBM2
npi298	C	2.08	548.30	yes	IBM2
npi452		2.08	548.30	no	BNL 2002
umc1633	C	2.08	548.50	no	IBM2
npi45a		2.06-2.07	550.00	no	BNL 2002
bnl8.44b		2.08	551.09	no	UMC 98
umc1798		2.08	551.13	no	SSR popI
umc2202	C	2.08	551.13	no	SSR popI
AY109575	C	2.08	552.70	yes	IBM2
umc1992	C	2.08	556.21	no	SSR popII
mmp34		2.08	562.50	yes	IBM2
umc31b	C	2.08	564.30	no	BNL 96
mmp138		2.08	565.90	no	IBM2
psr119b		2.08	566.00	no	IBM2
npi610		2.08	567.40	yes	IBM2
bcd249h		2.08	567.61	no	BNL 2002
pur1		2.08	570.10	no	UMC 98
uaz239b		2.08	570.73	no	BNL 2002
mmc0381	C	2.08	572.40	yes	IBM2
dpg6d		2.08	573.15	no	BNL 2002
mmp188		2.08	573.30	yes	IBM2
cdo38c(ntp)	C	2.08	573.30	no	IBM2
bnlg1746	C	2.08	573.60	yes	IBM2
bnlg1606		2.08	573.95	no	BNL 2002
bcd98l		2.09	575.19	no	BNL 2002
isu115		2.08	575.20	no	IBM2
isu91b		2.08	575.40	yes	IBM2
bnlg1940	AC	2.08	577.60	yes	IBM2
psr144a		2.08	579.50	yes	IBM2
psr144c		2.08	581.10	yes	IBM2
rDNA5S		2.08	582.60	no	BNL 96
umc1516	AC	2.08	584.30	yes	IBM2
mpik(chs1b)		2.09	589.98	no	BNL 2002
umc171b(oec23)		2.09	589.98	no	UMC 98
umc49a	AC	2.09	591.50	yes	IBM2
umc1230		2.08-2.09	593.56	no	SSR popII
umc1551	C	2.09	597.97	no	SSR popII
umc1256	C	2.09	600.70	yes	IBM2
umc1252	C	2.09	600.90	yes	IBM2
AY109592	C	2.09	601.60	no	IBM2
csu304a		2.09	601.78	no	UMC 98
csu728b	C	2.09	601.78	no	UMC 98
npi47c		2.09	603.73	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
whp1		2.09	603.73	no	SSR popI
mpik26		2.09	605.83	no	BNL 2002
bnlg1520		2.09	605.83	no	BNL 2002
npi294d		2.09	605.83	no	BNL 96
csu64a(grf)		2.09	606.13	no	UMC 98
betl1		2.09	606.40	no	UMC 98
umc1525		2.09	612.29	no	SSR popII
mpik38		2.09	618.93	no	BNL 2002
uaz33a		2.09	622.05	no	BNL 96
csu622		2.09	622.94	no	UMC 98
agrc39b		2.09	622.94	no	UMC 98
csu315d		2.09	622.94	no	UMC 98
fco1b(pex)		2.09	622.94	no	UMC 98
fco1a(pex)		2.09	627.01	no	UMC 98
umc1736		2.09	627.98	no	SSR popII
bnl(tas1g)		2.10	631.06	no	BNL 2002
csu200a		2.09	634.74	no	UMC 98
mmp195e		2.09	636.80	yes	IBM2
srk1		2.09	642.88	no	UMC 98
bnlg469b	C	2.09	650.10	yes	IBM2
bnlg2042		2.02	650.17	no	BNL 2002
bcd98k		2.09	650.26	no	BNL 2002
bnlg1893	C	2.09	654.80	yes	IBM2
csu109a	C	2.09	660.38	no	SSR popI
umc36a		2.10	661.10	yes	IBM2
npi294a		2.09	661.10	no	BNL 2002
pbs10		2.09	665.81	no	BNL 2002
mha1		2.09	665.81	no	BNL 96
ucsd61c		2.10	669.92	no	BNL 2002
csu611a(grp)		2.09	669.98	no	UMC 98
csu665a(adt)		2.09	674.42	no	UMC 98
AY110389	C	2.10	681.80	yes	IBM2
csu810a		2.10	688.69	no	UMC 98
umc1704		2.08-2.10	689.93	no	SSR popII
umc2184	C	2.10	692.40	yes	IBM2
mmp183		2.10	694.60	yes	IBM2
php20581b(tb)		2.10	695.99	no	SSR popI
bnl17.14		2.10	702.50	yes	IBM2
csu251b		2.10	702.50	no	UMC 98
npi400b		2.10	702.50	no	BNL 2002
lim104		2.10	706.50	yes	IBM2
nfa103b		2.10	708.10	yes	IBM2
chr106b		2.10	708.10	no	ChromDB
umc2Ltelo		2.10	708.33	no	UMC 98
ufg55		2.10	711.00	yes	IBM2
bnl17.19b		2.10	711.07	no	BNL 96
phi101049	AC	2.10	712.10	yes	IBM2
AY109586	AC	2.10	713.10	no	IBM2
cdo938c		2.10	716.30	no	IBM1
umc1696		2.10	716.30	yes	IBM2
knox4		2.10	716.30	no	BNL 2002
bcd98n		2.10	718.24	no	BNL 2002
rgpc12b		2.10	721.36	no	UMC 98
ucsd113b		2.10	724.27	no	BNL 2002
bnl(tas1p)		2.10	724.27	no	BNL 2002
ucsd106a		2.10	724.27	no	BNL 96
AY111236	AC	2.10	725.30	yes	IBM2
umc2214		2.10	728.36	no	SSR popI
ucsd113c		2.10	768.59	no	BNL 96
uaz109		3.00	-21.30	no	BNL 96
bnl(tas4l)		3.00	-1.20	no	BNL 96
umc32a	C	3.01	-1.10	no	SSR popI
umc2118	AC	3.00	0.00	yes	IBM2
g2	C	3.00	2.00	yes	IBM2
umc1931	AC	3.00	5.60	yes	IBM2
umc1746	C	3.00	7.10	no	IBM2
phi453121	AC	3.00	7.50	yes	IBM2
umc2255	C	3.01	9.50	yes	IBM2
phi404206	C	3.01	11.00	yes	IBM2
umc1780	C	3.01	11.20	yes	IBM2
bnl8.15	C	3.01	11.40	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc3Stelo		3.00-3.01	14.68	no	UMC 98
umc1394	C	3.01	21.80	yes	IBM2
umc2256	C	3.01	23.40	yes	IBM2
umc1970	C	3.01	28.20	yes	IBM2
umc2071	C	3.01	29.20	yes	IBM2
asg64		3.01	29.60	yes	IBM2
umc2257	C	3.01 - 3.02	30.50	no	IBM2
mmp158a		3.01	31.80	yes	IBM2
umc1892	C	3.01	35.50	yes	IBM2
php20905		3.01	37.20	yes	IBM2
phi104127	C	3.01	38.00	yes	IBM2
umc2049	C	3.01	38.70	yes	IBM2
mmp38		3.01	42.60	yes	IBM2
e8		3.01	44.22	no	UMC 98
csu628		3.01	44.22	no	UMC 98
umc249		3.01	44.22	no	UMC 98
umc1793		3.00	45.17	no	SSR popII
umc2376	C	3.01	45.37	no	SSR popII
umc2377	C	3.01	47.91	no	SSR popII
umc121		3.01	54.30	no	IBM2
asg30c		3.01	58.00	yes	IBM2
csu32a	C	3.02	60.00	yes	IBM2
bnl44		3.01	61.47	no	BNL 2002
csu1062		3.02	64.85	no	UMC 98
umc1458	AC	3.02	67.20	yes	IBM2
mpik24b(zmm2)		3.02	74.10	no	UMC 98
zem1		3.02	75.04	no	BNL 2002
zpia		3.02	75.04	no	BNL 2002
bnlg1144	AC	3.02	77.00	yes	IBM2
umc1886	AC	3.02	78.50	yes	IBM2
bnlg1523		3.03	81.50	no	BNL 2002
uaz210(hsp18)		3.03	82.86	no	BNL 2002
csu230		3.02	83.56	no	UMC 98
umc1814		3.02	86.84	no	SSR popII
hsp18f		3.03	91.22	no	BNL 2002
AY109549	AC	3.02	95.40	yes	IBM2
cko1	AC	3.02	97.60	yes	IBM2
csu75a		3.02	98.91	no	UMC 98
asg16a	C	3.02	100.80	no	UMC 98
me3	AC	3.02	101.02	no	UMC 98
csu199b		3.02	101.30	no	UMC 98
php20042a		3.02	101.30	yes	IBM2
bnlg1647	AC	3.02	103.30	yes	IBM2
csu324b(cts)		3.02	107.90	yes	IBM2
csu728c	C	3.03	109.00	no	UMC 98
asg24a(gts)	AC	3.03	109.00	yes	IBM2
csu56b(ohp)	C	3.03	109.00	no	UMC 98
zag4		3.02	115.93	no	BNL 96
umc2369	C	3.03	117.03	no	SSR popII
bnlg1325		3.03	117.76	no	BNL 2002
lim66		3.03	124.80	yes	IBM2
umc2258	AC	3.02-3.03	127.80	yes	IBM2
bnlg1447	C	3.03	129.40	yes	IBM2
mus2		3.02-3.03	130.73	no	BNL 2002
umc2259	AC	3.02-3.03	131.70	no	IBM2
mmp79		3.03	139.30	yes	IBM2
mmp186		3.03	145.30	yes	IBM2
asg48	AC	3.04	152.70	yes	IBM2
umc2024		3.03-3.04	152.70	no	SSR popII
csu242		3.04	153.40	no	UMC 98
bnl8.35a		3.04	153.40	yes	IBM2
bcd98j		3.04	153.64	no	BNL 2002
chs566		3.04	153.70	no	BNL 2002
npi249a		3.04	153.86	no	BNL 2002
isu91a		3.04	153.97	no	BNL 2002
npi276a		3.04	154.00	yes	IBM2
uaz164d		3.03-3.04	154.06	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csh(prl2)		3.04	154.42	no	BNL 2002
uaz159b		3.04	157.30	no	IBM2
umc1030		3.04	159.00	yes	IBM2
umc59e	AC	3.04	159.00	yes	IBM2
me1		3.02-3.03	160.45	no	BNL 96
std1d(his2B1)		3.04	162.05	no	UMC 98
phi234966		3.04	163.50	no	IBM1
umc1772	AC	3.04	163.50	no	IBM2
npi446		3.04	163.80	yes	IBM2
phi243966	C	3.02	163.80	no	IBM2
umc1425	C	3.04	165.00	yes	IBM2
umc2000	AC	3.04	166.90	yes	IBM2
umc1729		3.04	167.36	no	SSR popI
umc1608	AC	3.04	168.00	yes	IBM2
umc154		3.04	172.87	no	UMC 98
csu949a		3.04	172.87	no	UMC 98
bnlg2136		3.04	174.67	no	BNL 2002
umc2158	AC	3.04	176.60	yes	IBM2
umc1495	AC	3.04	177.40	yes	IBM2
nfc104c		3.04	179.44	no	ChromDB
umc1392	AC	3.04	181.10	yes	IBM2
rgpc601b		3.04	181.52	no	UMC 98
umc2033	AC	3.04	181.70	yes	IBM2
haf101	C	3.04	183.65	no	ChromDB
rgpc131a	AC	3.04	184.77	no	UMC 98
psr754b		3.04	186.00	yes	IBM2
umc1742	AC	3.04	189.00	yes	IBM2
umc2117	C	3.04	190.20	yes	IBM2
bnlg1019a	AC	3.04	190.60	no	IBM2
umc1717	AC	3.04	190.80	no	IBM2
bnlg1113	AC	3.04	190.80	yes	IBM2
bnlg1452	AC	3.04	190.80	yes	IBM2
umc1655	AC	3.04	191.10	no	IBM2
tpi4	AC	3.04	192.34	no	UMC 98
ucsd201		3.04	192.35	no	BNL 2002
umc1025		3.04	192.54	no	SSR popII
bnlg1638		3.04	193.10	yes	IBM2
pbs14e		3.04	193.10	no	BNL 2002
uaz34a		3.04	193.10	no	BNL 2002
umc42b		3.04	193.10	no	BNL 2002
dup183b		3.04	193.10	no	BNL 2002
bnlg1628		3.04	193.10	no	BNL 2002
bnlg2047		3.04	193.10	no	BNL 2002
isu1719h		3.04	193.10	no	BNL 2002
mpik32e(zag2)		3.04	193.10	no	BNL 2002
uaz249b(ubf9)		3.04	193.10	no	BNL 2002
npi(tpi)		3.04	193.33	no	BNL 2002
isu2117i		3.04	193.71	no	BNL 2002
rz543a	C	3.04	193.96	no	UMC 98
pbs14a		3.04	194.27	no	BNL 2002
bnlg1085b		3.04	195.01	no	BNL 2002
bnlg1957		3.05	195.13	no	BNL 2002
bet1		3.04	195.22	no	BNL 2002
dup104		3.04	195.22	no	BNL 2002
uaz34b		3.04	195.22	no	BNL 2002
dup287a		3.04	195.22	no	BNL 2002
dup53		3.04	195.63	no	BNL 2002
isu2191c		3.04	195.63	no	BNL 2002
klp1a		3.04	196.12	no	UMC 98
umc92a		3.04	196.12	no	UMC 98
asg46a	C	3.04	196.12	no	UMC 98
ttu1(hsp18)		3.04	196.12	no	UMC 98
mmp144		3.04	196.90	yes	IBM2
npi398a		3.04	197.54	no	BNL 2002
isu1719b		3.04	197.68	no	BNL 2002
ucla(obf6)		3.04	197.87	no	BNL 2002
tis903.6a		3.04	198.08	no	BNL 2002
umc1351	C	3.04	199.97	no	SSR popII
umc1965		3.04	200.65	no	SSR popII
e4		3.04	200.71	no	UMC 98
umc1721		3.04	202.67	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mmp36		3.04	203.40	yes	IBM2
mmc0132	AC	3.04	208.60	yes	IBM2
cdo244d(crp)		3.04	208.60	yes	IBM2
umc2261	AC	3.04	210.40	yes	IBM2
mmc0312	AC	3.04	212.70	yes	IBM2
umc1908	AC	3.04	213.60	yes	IBM2
npi247		3.04	213.80	yes	IBM2
npi114b		3.04	213.80	no	BNL 2002
dup162		3.04	213.96	no	BNL 2002
isu76a		3.04	214.16	no	BNL 2002
php20509		3.04	214.70	no	IBM2
php20576		3.04	214.70	no	IBM2
umc2262	AC	3.04	214.70	no	IBM2
ens1004		3.04	214.89	no	BNL 2002
umc161b	C	3.04	214.89	no	BNL 2002
ufg44		3.04	214.90	no	IBM2
bnl43		3.04	215.26	no	BNL 2002
isu157		3.03-3.04	215.26	no	BNL 2002
isu148		3.04	215.44	no	BNL 2002
mmp69		3.04	215.60	yes	IBM2
uaz255		3.04	215.60	no	BNL 2002
ici273c		3.04	215.82	no	BNL 2002
AY109870	C	3.04	219.50	yes	IBM2
PCO107756	C	3.04	220.24	no	INDEL
csu621		3.04	223.64	no	UMC 98
rz382a		3.04	224.10	yes	IBM2
csu2b		3.04	224.46	no	UMC 98
bnlg1816		3.04	226.90	yes	IBM2
umc2263	AC	3.04	227.80	yes	IBM2
umc1504	AC	3.04	228.20	no	IBM2
umc1347	AC	3.04	228.34	no	SSR popII
mmp29		3.04	228.50	no	IBM2
rz244b(dia)		3.04	230.10	yes	IBM2
chr110a		3.04	230.70	no	ChromDB
php10016c		3.04	231.50	yes	IBM2
umc50a		3.04	232.16	no	BNL 96
umc1900		3.04	232.40	no	IBM2
umc1223		3.04	234.40	yes	IBM2
csu29b	C	3.04	236.69	no	UMC 98
PCO068796	C	3.04	237.40	no	INDEL
AY110403	C	3.04	238.10	no	IBM2
csu1070		3.04	241.55	no	UMC 98
csh10b(cycII)		3.04	241.55	no	UMC 98
PCO141323	C	3.04	242.64	no	INDEL
AY110297	C	3.04	244.70	yes	IBM2
tha1		3.04	246.96	no	UMC 98
rps25		3.04	246.96	no	UMC 98
umc97		3.04	246.96	no	UMC 98
csu795		3.04	246.96	no	UMC 98
umc175		3.04	246.96	no	UMC 98
bnl5.33e		3.04	246.96	no	UMC 98
umc1968	C	3.04	250.40	no	IBM2
csu212b		3.04	254.53	no	UMC 98
AY110151	AC	3.04	254.60	yes	IBM2
umc1920		3.04	258.40	yes	IBM2
umc10a	C	3.04	259.40	yes	IBM2
chr126b		3.04	259.40	no	ChromDB
php20558a		3.04	260.10	yes	IBM2
mbd105		3.04	260.10	no	ChromDB
php20511		3.04	260.30	no	IBM2
umc2264	AC	3.04	261.10	yes	IBM2
rz995b(fbp)		3.04	261.22	no	UMC 98
npi220b	C	3.04	261.22	no	BNL 96
mmp9		3.04	262.90	yes	IBM2
csu851b		3.04	264.81	no	UMC 98
csu408(grp)		3.04	264.81	no	UMC 98
umc1683	C	3.04	266.00	no	IBM2
bnl13.05b		3.04	266.85	no	BNL 96
csu404b		3.04	266.97	no	UMC 98
umc1449	AC	3.04	269.40	yes	IBM2
umc1835		3.04	270.88	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg602	C	3.04	270.88	no	SSR popII
csu290		3.04	275.62	no	UMC 98
cdo1160b(kri)	C	3.04	275.62	no	UMC 98
hac101a		3.04	276.60	yes	IBM2
lg3		3.04	276.61	no	BNL 2002
uaz35		3.04	276.77	no	BNL 2002
umc1527	AC	3.04	279.30	yes	IBM2
umc1773	C	3.04	280.40	yes	IBM2
psr628		3.04	280.60	yes	IBM2
ici286b		3.04	283.72	no	BNL 96
jpsb527a		3.04	283.90	yes	IBM2
umc1386	AC	3.04	284.39	no	SSR popII
umc2002	AC	3.04	290.60	yes	IBM2
bnlg1399		3.05	291.50	no	BNL 2002
mpik35d		3.04	292.06	no	BNL 2002
cdo459		3.04	294.50	no	BNL 2002
cdo344a(rga)		3.04	294.50	yes	IBM2
bnlg1022b		3.04	296.00	no	BNL 2002
umc102	C	3.05	296.10	yes	IBM2
mpik35e		3.04	296.63	no	BNL 2002
bnlg1246b		3.05	297.57	no	BNL 2002
bnlg1456		3.05	298.57	no	BNL 2002
uaz19a		3.04	298.62	no	BNL 2002
bnl31b		3.05	298.64	no	BNL 2002
nabr1		3.04	298.89	no	BNL 2002
umc1174	AC	3.05	299.20	yes	IBM2
umc1600	AC	3.05	301.00	yes	IBM2
umc1300		3.05	301.44	no	SSR popII
tda30		3.05	301.78	no	UMC 98
rgpc529		3.05	301.78	no	UMC 98
mmp80		3.05	303.70	yes	IBM2
rgpc6(rpS9)	C	3.05	304.80	no	UMC 98
uaz288a(ppi)		3.05	305.30	yes	IBM2
umc1693	AC	3.05	305.80	no	IBM2
umc1907		3.05	306.10	no	IBM2
bnlg1601	AC	3.05	306.10	no	IBM2
umc1874		3.05	306.10	no	SSR popI
umc1616		3.05	306.71	no	SSR popI
phys2	C	3.05	307.00	yes	IBM2
rz261b(sad)		3.05	307.39	no	UMC 98
npi612		3.05	307.69	no	BNL 2002
npi609		3.05	307.69	no	BNL 96
cdo250		3.05	308.00	no	BNL 96
rz296b		3.05	309.50	yes	IBM2
tda64		3.05	310.84	no	UMC 98
umc1750		3.05	310.97	no	SSR popI
umc1102	AC	3.05	312.80	yes	IBM2
chr109b	C	3.05	313.10	no	ChromDB
bnlg1035	AC	3.05	313.40	yes	IBM2
AY110352	AC	3.05	315.40	yes	IBM2
csu229b(oec)		3.05	316.88	no	UMC 98
mmc0022	AC	3.05	318.20	yes	IBM2
umc2020	AC	3.05	318.20	yes	IBM2
php20508		3.05	318.40	no	IBM2
cyp7		3.05	319.04	no	UMC 98
umc1167	AC	3.05	319.20	yes	IBM2
atp1	C	3.05	319.47	no	UMC 98
bnl8.08g		3.05	319.56	no	BNL 2002
rz390c(cyb5)		3.05	319.80	no	IBM2
pgd2		3.05	323.35	no	UMC 98
csu561a		3.05	323.35	no	UMC 98
npi611b		3.05	323.35	no	UMC 98
umc252a		3.05	323.35	no	UMC 98
bnl6.06a		3.05	323.35	no	UMC 98
csu234a(gbp)		3.05	323.35	no	UMC 98
umc1501		3.05	325.40	yes	IBM2
AY112215	AC	3.05	326.20	no	IBM2
psr119a		3.05	327.90	yes	IBM2
cdo105		3.05	330.60	yes	IBM2
AY111507	AC	3.05	331.30	yes	IBM2
bnl(tas1l)		3.05	332.94	no	BNL 2002
uaz37		3.06	333.04	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
isu68		3.04	333.30	no	BNL 2002
bnlg1904		3.04	334.22	no	BNL 2002
AY111541	AC	3.05	334.60	yes	IBM2
isu52		3.05	336.49	no	BNL 2002
isu118b		3.04	336.75	no	BNL 2002
umc1307		3.05	339.61	no	SSR popI
vp1		3.05	340.35	no	BNL 96
asg52b		3.05	341.04	no	UMC 98
asg67b		3.05	341.04	no	UMC 98
umc1954	AC	3.05	341.05	no	SSR popII
ldp1	C	3.05	344.20	no	UMC 98
umc26a		3.05	344.20	yes	IBM2
umc268		3.05	344.20	no	UMC 98
uiu8(geb)		3.05	344.20	no	UMC 98
csu44(gst)		3.05	344.20	no	UMC 98
csu961(fnr)		3.05	344.20	no	UMC 98
umc18a(psaN)		3.05	344.20	no	UMC 98
csu237b(psaN)		3.05	344.20	no	UMC 98
csu439(trm)	AC	3.05	344.20	no	UMC 98
rz141a(emp70)		3.05	344.20	no	UMC 98
bnlg420		3.05	345.99	no	BNL 2002
klp3		3.05	346.80	no	UMC 98
myb2	C	3.05	346.80	no	ChromDB
umc1839		3.05	346.92	no	SSR popII
csu382c(cld)	C	3.05	349.67	no	UMC 98
si618046E03	C	3.05	352.15	no	INDEL
umc2265	AC	3.05-3.06	354.00	no	IBM2
asg1b		3.05	358.30	no	UMC 98
sps2	AC	3.05	358.30	yes	IBM2
umn41		3.05	358.30	no	UMC 98
csu362		3.05	358.30	no	UMC 98
mwg645c		3.05	358.30	no	BNL 2002
csu636		3.05	361.10	yes	IBM2
rz14	C	3.05	362.51	no	UMC 98
uaz189(rpL5)		3.05	365.94	no	BNL 2002
csu268		3.05	366.03	no	UMC 98
umc1973	AC	3.05	371.40	yes	IBM2
ici98		3.06	374.87	no	BNL 96
umn857a		3.05	375.17	no	UMC 98
AY106230	C	3.05	377.90	yes	IBM2
AY111296	AC	3.05	384.90	yes	IBM2
rgpc385b(rpL5)		3.05	386.86	no	UMC 98
AI770873	AC	3.05	388.10	yes	IBM2
mmp184		3.05	389.10	no	IBM2
npi296		3.05	389.70	yes	IBM2
umc1539	AC	3.05-3.06	390.30	yes	IBM2
bnl5.37b		3.05-3.06	390.80	yes	IBM2
bnl5.37a		3.06	391.40	no	IBM2
npi108a		3.05-3.06	391.40	no	UMC 98
umc1400	AC	3.05-3.06	391.40	no	SSR popII
uaz260a(rpL5)		3.05-3.06	391.40	no	UMC 98
umc1311	C	3.06	394.80	yes	IBM2
umc1593b		3.06	394.80	no	SSR popII
umc1730	AC	3.06	398.40	yes	IBM2
ucsd72d		3.06	400.17	no	BNL 2002
uaz8b(spr1)		3.06	400.89	no	BNL 2002
umc1027	AC	3.06	401.20	yes	IBM2
asg61a		3.06	401.80	no	UMC 98
bnl5.14		3.06	401.80	no	UMC 98
bnl10.24a		3.06	401.80	yes	IBM2
lim486		3.06	405.30	yes	IBM2
rz538b		3.06	411.10	yes	IBM2
csu1029		3.06	411.10	no	UMC 98
npi268b	C	3.06	411.10	no	UMC 98
umc1266	AC	3.06	411.60	no	IBM2
umc1876		3.06	414.69	no	SSR popI

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
asg39		3.06	416.10	yes	IBM2
asg15		3.06	416.10	no	UMC 98
asg34b(msd)	C	3.06	416.10	no	UMC 98
umc165a		3.06	423.29	no	UMC 98
bnl8.01		3.06	423.29	no	BNL 96
rz630d(sat)		3.06	423.54	no	BNL 2002
BE639846		3.06	423.60	yes	IBM2
bnl47g		3.04	425.35	no	BNL 2002
PCO089398	C	3.06	428.85	no	INDEL
umc2266	AC	3.06	434.30	yes	IBM2
umc164b		3.06	435.65	no	BNL 96
isu166b		3.04	436.83	no	BNL 2002
bnlg1047a		3.06	438.02	no	BNL 2002
bnlg1063a	C	3.06	441.26	no	BNL 2002
bnlg1350a		3.08	443.99	no	BNL 2002
phi102228	AC	3.06	445.00	yes	IBM2
ksu1a		3.06	447.70	no	UMC 98
csu776b		3.06	447.70	no	UMC 98
csu38a(taf)		3.06	447.70	no	UMC 98
lg2		3.06	449.04	no	BNL 2002
AY110055		3.06	450.30	yes	IBM2
bnlg1449		3.06	450.38	no	BNL 2002
npi328b		3.06	450.59	no	BNL 96
mmp27		3.06	451.40	no	IBM2
mmp88		3.06	451.40	no	IBM2
jpsb79		3.06	451.50	yes	IBM2
umc60	AC	3.06	452.70	yes	IBM2
zag2		3.05	453.36	no	BNL 2002
mpik2		3.05	453.36	no	BNL 2002
uaz36		3.05	453.36	no	BNL 2002
abp1	AC	3.05	453.36	no	BNL 2002
bnlg1505		3.05	453.36	no	BNL 2002
gst4		3.05	453.41	no	BNL 2002
isu131		3.04	454.16	no	BNL 2002
bnlg1117		3.05	454.24	no	BNL 2002
mpik30a		3.05	454.31	no	BNL 2002
bnlg2241		3.06	454.31	no	BNL 2002
umc1951	AC	3.06	456.70	no	SSR popI
psr754a		3.06	459.90	yes	IBM2
umc2268	AC	3.06	461.10	yes	IBM2
umc2408		3.06	467.36	no	SSR popII
umc1644		3.06	473.10	yes	IBM2
bnlg2243		3.08	474.75	no	BNL 2002
mmp5		3.06	477.50	yes	IBM2
umc1674		3.06	479.31	no	SSR popII
csu1183		3.06	480.10	yes	IBM2
bnlg1951	AC	3.06	481.60	yes	IBM2
rz444b	C	3.06	481.72	no	UMC 98
csu351	AC	3.06	481.72	no	UMC 98
cdo251a		3.06	481.92	no	BNL 2002
mpik39b(myb)		3.04	482.06	no	BNL 2002
umc82c		3.06	482.30	yes	IBM2
umc2269	AC	3.06	482.30	no	IBM2
pho2		3.04	482.67	no	BNL 2002
bnlg1798		3.06	482.73	no	BNL 2002
csu215a(grp)		3.06	482.73	no	UMC 98
ufg42	C	3.06	486.20	yes	IBM2
tub6		3.06	488.00	no	UMC 98
csu264		3.06	488.00	no	UMC 98
csu191	AC	3.06	488.00	yes	IBM2
umc252c		3.06	488.00	no	UMC 98
csu223b(psei)		3.06	488.00	no	UMC 98
sdg113		3.06	489.85	no	ChromDB
bnlg1160	AC	3.06	491.40	yes	IBM2
umc2271	AC	3.06	494.00	yes	IBM2
umc2270	AC	3.06-3.07	494.00	yes	IBM2
csu96a(psei)		3.06	495.36	no	UMC 98
umc1985		3.06	495.69	no	SSR popII
csu180		3.06	496.18	no	UMC 98
CL13054_1	C	3.06	499.82	no	INDEL
lim424		3.06	503.00	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
lim269		3.06	504.70	no	IBM2
umc2381	C	3.06-3.07	505.18	no	SSR popII
php20026		3.07	505.19	no	BNL 96
ucla(obf3A)		3.07	506.11	no	BNL 2002
bnlg1931		3.07	506.96	no	BNL 2002
AY111125	AC	3.06	507.20	yes	IBM2
umc39a		3.06	510.07	no	UMC 98
php15033		3.06	511.10	yes	IBM2
bnlg197	AC	3.06	511.50	yes	IBM2
chs13d		3.04	511.50	no	BNL 2002
bnlg1796		3.06	511.51	no	BNL 2002
bnl3.18		3.07	511.71	no	UMC 98
bnlg1779		3.07	512.00	no	BNL 2002
csu690		3.06	512.53	no	UMC 98
AI770795	AC	3.06	512.70	yes	IBM2
uaz38a		3.07	515.53	no	BNL 2002
asg7b		3.06	517.00	yes	IBM2
dupssr17	AC	3.06-3.07	517.95	no	SSR popI
bnl6.16a		3.07	520.70	yes	IBM2
cdo241a		3.06-3.07	520.70	no	UMC 98
bcd738b(pgk)	C	3.06-3.07	520.70	no	UMC 98
umc1949		3.06-3.07	527.06	no	SSR popI
umc3b		3.06-3.07	529.40	no	IBM2
si618016E09	C	3.07	529.90	no	INDEL
bnl15.20		3.06-3.07	535.82	no	BNL 96
umc2050	AC	3.07	538.20	yes	IBM2
ici273a		3.07	538.47	no	BNL 2002
si605077F08	C	3.07	539.74	no	INDEL
umc1135	AC	3.07	540.20	yes	IBM2
umc1767		3.07	542.00	yes	IBM2
umc2272	C	3.07	544.20	yes	IBM2
umc1528	AC	3.07	544.40	yes	IBM2
PCO142509	C	3.07	544.56	no	INDEL
umc1399	C	3.07	544.60	yes	IBM2
bnlg1605	AC	3.07	544.60	yes	IBM2
umc1690	AC	3.07	544.60	no	SSR popII
bnl54		3.04	544.81	no	BNL 2002
ufg21		3.07	544.97	no	BNL 2002
npi212b		3.07	545.00	yes	IBM2
bnl45c		3.04	545.09	no	BNL 2002
hox3		3.07	547.05	no	UMC 98
umc1148		3.07	552.14	no	SSR popII
umc1659		3.07	552.14	no	SSR popII
csu567(ces)		3.07	552.67	no	UMC 98
cdo1395d		3.07	554.22	no	UMC 98
csu680b	C	3.07	554.22	no	UMC 98
csu706	AC	3.07	554.22	no	UMC 98
asg4		3.07	554.39	no	UMC 98
bcd805		3.07	554.39	no	UMC 98
bnl1.297a		3.07	554.39	no	UMC 98
bnl1.326b		3.07	554.39	no	UMC 98
bnl5.33b		3.07	554.39	no	BNL 96
AY104511	AC	3.07	562.10	yes	IBM2
umc1286	C	3.07	566.23	no	SSR popI
AY109828		3.07	566.50	yes	IBM2
asg10		3.07	567.40	no	IBM2
gps4		3.04	567.56	no	BNL 2002
umc1489	AC	3.07	567.60	yes	IBM2
umc2273	AC	3.07	568.00	no	IBM2
umc1404	C	3.07	568.30	yes	IBM2
csu1130		3.07	571.61	no	UMC 98
rgpc643b		3.07	571.61	no	UMC 98
php20521		3.07	572.70	yes	IBM2
sdg117a	C	3.07	573.96	no	ChromDB
umc15b		3.08	574.65	no	BNL 96

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
hon108	C	3.07	576.47	no	ChromDB
umc1825	C	3.07	579.50	yes	IBM2
dhn6		3.08	585.50	no	BNL 2002
umc16a		3.08	585.50	no	UMC 98
umc17a	AC	3.08	585.50	yes	IBM2
umc228b		3.08	585.50	no	UMC 98
umc103b		3.08	585.50	no	BNL 2002
csu189(thr)		3.08	585.50	no	UMC 98
rny(atpb)		3.08	585.50	no	BNL 2002
bcd828a(atpb)		3.08	585.50	no	BNL 2002
uaz243a(atpb)		3.08	585.50	no	BNL 2002
csu240		3.08	589.16	no	UMC 98
umc231		3.08	591.16	no	UMC 98
bcd1127a		3.08	594.72	no	BNL 2002
csu772a		3.08	596.49	no	UMC 98
npi432	C	3.08	596.49	no	UMC 98
umc226a		3.08	596.49	no	UMC 98
uaz176b		3.08	596.49	no	BNL 2002
cdo345b	C	3.08	596.53	no	BNL 2002
bnl17.27		3.08	597.38	no	BNL 2002
dgc13		3.08	597.51	no	BNL 2002
AY105849	C	3.08	597.60	yes	IBM2
npi201a		3.08	597.64	no	BNL 2002
rz527a		3.08	598.16	no	BNL 2002
uaz251e(rpS11)		3.08	599.30	no	BNL 96
bnl24b		3.08	599.38	no	BNL 2002
csu1117a		3.08	599.82	no	UMC 98
bnlg1861b		3.08	604.12	no	BNL 2002
umc1844		3.08	605.81	no	SSR popII
umc2274		3.07-3.08	608.60	no	IBM2
umc1140	C	3.08	609.20	yes	IBM2
umc2275	C	3.07-3.08	610.20	yes	IBM2
mmc0251		3.08	611.40	yes	IBM2
cdo118		3.08	611.80	no	IBM2
npi91a		3.08	612.04	no	BNL 2002
npi257a		3.08	612.04	no	BNL 2002
cdo1160c(kri)	C	3.07	612.22	no	BNL 2002
uaz18c		3.08	612.27	no	BNL 2002
umc1915	AC	3.08	617.50	yes	IBM2
bnlg1108	AC	3.08	618.60	yes	IBM2
umc2081		3.08	627.10	yes	IBM2
umc1521		3.08	627.13	no	SSR popII
csu744	C	3.08	629.36	no	UMC 98
csu456(uce)		3.08	629.36	no	UMC 98
sdg115	C	3.08	630.00	no	ChromDB
mdh3		3.08	632.40	no	UMC 98
php10080		3.08	632.40	yes	IBM2
isu158		3.08-3.08	632.40	no	BNL 2002
umc1320	AC	3.08	633.80	yes	IBM2
umc1273	AC	3.08	634.80	yes	IBM2
AY109934	AC	3.08	638.30	yes	IBM2
si946021A07	C	3.08-3.09	640.58	no	INDEL
umc2276	AC	3.08-3.09	652.40	yes	IBM2
uaz164c		3.08	681.62	no	BNL 2002
umc2174		3.08	683.60	yes	IBM2
csu703		3.08	688.71	no	UMC 98
AY110540		3.08	691.20	yes	IBM2
a1		3.09	697.20	no	UMC 98
umc63a	C	3.09	697.20	yes	IBM2
csu869(cah)		3.09	697.20	no	UMC 98
csu125a(cah)		3.09	697.20	no	UMC 98
csu397(cah)	C	3.09	697.20	no	UMC 98
umc184d(glb)		3.09	697.20	no	UMC 98
bnl47f		3.08-3.09	697.20	no	BNL 2002
csu303		3.09	699.20	yes	IBM2
med68		3.09	699.87	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnl1.67		3.09	699.87	no	UMC 98
csu845		3.09	702.20	yes	IBM2
sh2	AC	3.09	702.20	no	UMC 98
bnl1.123		3.09	702.20	no	BNL 2002
bnl12.30b		3.09	702.20	no	BNL 2002
pge25c		3.09	703.99	no	BNL 2002
bcd134b		3.09	712.91	no	UMC 98
cdo920b(egl)		3.09	712.91	no	UMC 98
CL29988_-2	C	3.09	713.08	no	INDEL
jpsb107c		3.09	728.10	yes	IBM2
cdo962b		3.09	728.49	no	BNL 96
csu305b		3.09	728.70	no	UMC 98
dupssr33		3.09	731.26	no	BNL 2002
jpsb41		3.09	732.50	yes	IBM2
jpsb443		3.09	732.50	yes	IBM2
sho38		3.09	732.60	no	IBM2
jpsb106		3.09	732.60	no	IBM2
sho89		3.09	732.70	yes	IBM2
umc2152	AC	3.09	738.70	yes	IBM2
lim182		3.09	743.00	yes	IBM2
csu768		3.09	745.05	no	UMC 98
etm3		3.09	746.54	no	BNL 2002
umc2008	AC	3.09	747.00	no	IBM2
umc2277	AC	3.08-3.09	747.50	no	IBM2
umc1813	AC	3.09	748.50	yes	IBM2
csu780a		3.09	750.69	no	UMC 98
csu919a		3.09	750.69	no	UMC 98
cdo455b	C	3.09	750.69	no	UMC 98
dup214		3.09	750.69	no	BNL 2002
rgps10558b		3.09	750.69	no	UMC 98
ici94		3.09	751.67	no	BNL 2002
bnlg1536		3.09	752.10	yes	IBM2
bnlg1182		3.09	752.10	no	BNL 2002
isu102c		3.09	753.02	no	BNL 2002
pic6a		3.09	754.15	no	BNL 2002
lhcb1		3.09	755.76	no	UMC 98
csu1086		3.09	755.76	no	UMC 98
csu1142		3.09	755.76	no	UMC 98
bnlg1754		3.09	757.00	yes	IBM2
ias21		3.09	757.10	no	BNL 2002
bnlg1257		3.09	757.18	no	BNL 2002
uiu1a(pog)		3.09	757.31	no	BNL 2002
uaz110		3.09	757.34	no	BNL 2002
bnlg2118		3.09	757.41	no	BNL 2002
uaz114		3.10	757.48	no	BNL 2002
uaz133		3.09	757.54	no	BNL 2002
dup216		3.09	757.71	no	BNL 2002
uaz213b		3.09	757.98	no	BNL 2002
csu58a	C	3.09	758.02	no	UMC 98
ias22a		3.09	758.02	no	BNL 2002
uaz117a		3.10	758.02	no	BNL 2002
csu21b(ago)		3.09	758.02	no	UMC 98
csu899a(ant)		3.09	758.02	no	UMC 98
npi457		3.09	758.20	yes	IBM2
umc1578	AC	3.09	758.41	no	SSR popII
npi425a	AC	3.09	759.90	yes	IBM2
bnlg1496	AC	3.09	760.90	no	IBM2
umc96		3.09	764.78	no	UMC 98
csu289		3.09	764.78	no	UMC 98
umc187		3.09	764.78	no	UMC 98
php20726		3.09	764.78	no	UMC 98
isu57a		3.09	766.61	no	BNL 2002
AY110567	AC	3.09	769.00	yes	IBM2
mmc0001	C	3.09	772.43	no	SSR popII
isu1410h		3.09	773.24	no	BNL 2002
mwg645j		3.09	774.37	no	BNL 2002
uaz39		3.09	774.81	no	BNL 2002
bnl7.26		3.09	780.57	no	UMC 98
umc1361	C	3.09	786.39	no	SSR popII
pbs13f		3.10	790.20	no	BNL 2002
npi420		3.09	791.60	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu36c(rpL19)		3.09	791.99	no	BNL 2002
bnlg1098		3.10	792.16	no	BNL 2002
umc2a	C	3.10	801.50	no	BNL 96
umc1052	C	3.09	806.39	no	SSR popI
umc1641	AC	3.09	806.90	yes	IBM2
nph1	AC	3.09	807.64	no	SSR popII
lim444		3.09	817.00	yes	IBM2
lim96		3.09	823.50	yes	IBM2
lim82		3.09	824.70	yes	IBM2
umc1639		3.09	825.24	no	SSR popII
csu320b		3.09	827.33	no	IBM1
plt2	AC	3.09	827.40	no	IBM2
mmp191		3.09	828.90	no	IBM1
mmp193		3.09	828.90	no	IBM1
umc1594	AC	3.09	828.90	yes	IBM2
umc1136	AC	3.10	830.70	no	SSR popII
cyp1	AC	3.10	831.31	no	SSR popII
umc2048	AC	3.10	858.62	no	SSR popI
tda117		3.10	870.84	no	UMC 98
csu728a	AC	3.10	870.84	no	UMC 98
csu1061a		3.10	870.84	no	SSR popI
chr126a		3.09	913.40	no	ChromDB
agrr43b		3.10	914.76	no	UMC 98
uaz198a(rpL10)		3.10	914.76	no	UMC 98
bnlg372		4.00	-149.20	no	BNL 96
umc1232		4.00	-116.50	no	SSR popI
agrr115	C	4.01	-105.40	no	INDEL
bnlg1318		4.01	-50.03	no	BNL 2002
bnlg1370	C	4.00	-43.98	no	BNL 2002
bnlg1241		4.01	-36.04	no	BNL 2002
npi294j		4.01	-19.74	no	UMC 98
cyp1710		4.01	-11.63	no	UMC 98
cyp2707		4.01	-11.63	no	UMC 98
csu618(P450)		4.01	-11.63	no	UMC 98
cyp3	C	4.01	-6.83	no	SSR popII
umc1276	C	4.01	-6.83	no	SSR popII
AY109715	AC	4.00	-4.10	no	IBM2
umc2278	AC	4.00	0.00	yes	IBM2
ufg26		4.01	1.80	yes	IBM2
mtl1	AC	4.00-4.01	2.90	no	IBM2
bnlg1434	AC	4.01	4.30	yes	IBM2
ufg52	C	4.01	7.00	yes	IBM2
rca1	AC	4.01	9.90	yes	IBM2
umc4Stelo		4.00-4.01	10.67	no	UMC 98
mmp192		4.01	13.70	no	IBM2
msf1	C	4.01	15.80	yes	IBM2
uaz103a		4.01	17.03	no	BNL 2002
csu221		4.01	18.70	yes	IBM2
umc2279	C	4.01	22.90	no	IBM2
umc1228	C	4.01	23.40	yes	IBM2
bx1		4.01	23.48	no	SSR popI
bx5		4.01	23.55	no	BNL 2002
bnl(tas1e)		4.00	23.82	no	BNL 2002
uaz59		4.00-4.05	24.14	no	BNL 2002
umc123	C	4.01	24.60	yes	IBM2
umc1561		4.00-4.01	25.93	no	SSR popII
uaz58a		4.01	29.77	no	BNL 2002
mmp174		4.01	30.40	yes	IBM2
uaz53a		4.01	37.30	no	BNL 2002
bx4	C	4.01	37.50	yes	IBM2
bx3		4.01	37.50	no	BNL 2002
bx2		4.01	38.96	no	BNL 2002
uaz41d		4.01	42.31	no	BNL 2002
cyp5	AC	4.01	47.60	yes	IBM2
umc1669		4.01	57.50	yes	IBM2
rz329b(bga)		4.01	64.12	no	UMC 98
umc2409		4.01	70.05	no	SSR popII
uaz43b		4.01	73.44	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1855		4.01	74.18	no	SSR popII
uaz54		4.01	75.74	no	BNL 2002
uaz47b		4.01	75.74	no	BNL 2002
uaz129		4.02	77.62	no	BNL 2002
uaz51		4.01	78.04	no	BNL 2002
zpl1d		4.02	78.04	no	BNL 2002
npi604a		4.01	79.74	no	BNL 96
umc1757	AC	4.01	81.00	no	IBM2
umc1759	AC	4.01	81.00	yes	IBM2
phi295450	AC	4.01	81.00	yes	IBM2
umc1758		4.01 - 4.02	81.93	no	SSR popI
uaz30a		4.02	83.05	no	BNL 2002
ias10		4.01 - 4.02	83.05	no	BNL 2002
php20725a		4.02	83.05	no	INDEL
uaz184(hfi)		4.02	86.90	no	BNL 2002
uaz61a		4.01 - 4.02	87.64	no	BNL 2002
uaz60		4.01 - 4.02	87.97	no	BNL 2002
uaz185(zp22)		4.02	88.32	no	BNL 2002
uaz55		4.01	89.53	no	BNL 2002
uaz43d		4.01	89.53	no	BNL 2002
uaz52a		4.01	89.53	no	BNL 2002
uaz50		4.01	90.57	no	BNL 2002
uaz14b		4.01	90.57	no	BNL 2002
uaz26b		4.01	90.57	no	BNL 2002
uaz42b		4.01	90.57	no	BNL 2002
uaz45b		4.01	90.57	no	BNL 2002
uaz46a		4.01	90.57	no	BNL 2002
uaz48a		4.01	90.57	no	BNL 2002
uaz49b		4.01	90.57	no	BNL 2002
uaz44b(zp19)		4.01	90.57	no	BNL 2002
cdo520(ser)	C	4.02	90.60	no	UMC 98
umc2410		4.02	91.57	no	SSR popII
uaz57a		4.01	91.72	no	BNL 2002
uaz38b		4.02	92.14	no	BNL 2002
uaz149(zp19)		4.02	92.14	no	BNL 2002
uaz70c		4.02	92.49	no	BNL 2002
zpl1b		4.02	92.87	no	BNL 2002
zpl1c		4.02	92.87	no	BNL 2002
zpl1a		4.01 - 4.02	92.87	no	BNL 2002
umc277		4.02	94.20	no	UMC 98
uaz17b		4.02	97.22	no	BNL 2002
uaz64b		4.02	97.22	no	BNL 2002
zpl1f		4.02	97.54	no	BNL 2002
umc1509		4.02	100.08	no	SSR popII
umc1943	AC	4.02	101.10	yes	IBM2
uaz67		4.02	101.81	no	BNL 2002
uaz65b		4.02	101.81	no	BNL 2002
uaz66a		4.02	101.81	no	BNL 2002
uaz69a		4.02	101.81	no	BNL 2002
uaz68b(zp19)		4.02	101.81	no	BNL 2002
bnl17.13b		4.02	101.81	no	BNL 96
uaz41c		4.02	105.09	no	BNL 2002
uaz103b		4.02	105.95	no	BNL 2002
inra2(prp)		4.02	106.42	no	UMC 98
umc1288	C	4.02	107.04	no	SSR popI
umc1294	C	4.02	108.43	no	SSR popII
PCO146629	C	4.02-4.03	110.44	no	INDEL
uaz40a		4.02-4.03	113.26	no	BNL 2002
dnap3		4.01	114.81	no	BNL 2002
chs556		4.03	126.23	no	BNL 2002
umc55b		4.03	126.28	no	BNL 2002
uaz63a		4.02	129.64	no	BNL 2002
php20713a		4.01	129.64	no	BNL 2002
zpl1e		4.01 - 4.02	129.64	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz62a		4.01 - 4.02	129.64	no	BNL 2002
psr144b		4.02	130.10	yes	IBM2
umc171a(oec23)		4.02-4.03	130.86	no	UMC 98
umc87a	C	4.02	134.10	yes	IBM2
chr117c		4.02	134.10	no	ChromDB
umc31a	AC	4.03	135.10	no	IBM2
bnlg1126		4.03	135.30	no	IBM2
AY110398	AC	4.03	135.70	no	IBM2
umc1926		4.03	140.90	yes	IBM2
umc2082		4.03	141.60	no	IBM2
csu235		4.03	143.40	yes	IBM2
csu63b(cdj)		4.03	143.40	no	UMC 98
csu583		4.03	143.82	no	UMC 98
csu585		4.03	143.82	no	UMC 98
rgpc496b(adh)		4.03	143.82	no	UMC 98
adh2	AC	4.03	147.10	no	IBM2
rz53b		4.03	147.20	no	IBM2
AY110253	C	4.03	152.90	yes	IBM2
isu144b		4.03	157.60	yes	IBM2
umc2281	AC	4.03	158.60	yes	IBM2
umc2280	AC	4.03	158.80	no	IBM2
AY110573		4.03	163.90	yes	IBM2
uaz180		4.03	164.49	no	BNL 2002
bnlg1162		4.03	168.17	no	BNL 2002
umc2176		4.03	174.60	yes	IBM2
bnl5.46a		4.03	177.34	no	UMC 98
uaz298(PDsI)		4.03	177.34	no	UMC 98
uaz239a		4.03	181.34	no	BNL 96
umc1902	AC	4.03	181.40	yes	IBM2
dpg2		4.03	186.63	no	BNL 2002
pdi1	C	4.03	187.61	no	SSR popII
mmp111		4.03	189.10	yes	IBM2
uaz46b		4.05	189.63	no	BNL 2002
uaz48b		4.05	189.63	no	BNL 2002
dpg14		4.02-4.03	192.15	no	BNL 2002
rz630b(sat)		4.03	192.49	no	UMC 98
agrr109		4.03	195.71	no	UMC 98
umc2039	AC	4.03	196.40	yes	IBM2
pgd3	C	4.03	200.30	yes	IBM2
fl2		4.00-4.04	200.30	no	UMC 98
csu449		4.03-4.04	200.30	no	UMC 98
agrc39a		4.03-4.04	200.30	no	UMC 98
csu1135		4.03-4.04	200.30	no	UMC 98
uaz57b		4.04	201.89	no	BNL 2002
uaz145(ahh)		4.04	201.89	no	BNL 96
umc2211		4.03	203.68	no	SSR popI
wip2		4.03	205.00	yes	IBM2
uaz62b		4.04	211.40	no	BNL 2002
uaz63b		4.04	211.40	no	BNL 2002
csu855		4.03-4.04	211.40	no	UMC 98
med63c		4.03-4.04	211.40	no	UMC 98
bnl8.45c	C	4.03-4.04	211.40	no	IBM1
csu1185		4.03-4.04	211.40	no	UMC 98
csu298a		4.03-4.04	211.40	no	UMC 98
npi386(eks)	AC	4.04	211.40	yes	IBM2
rz900a(ahh)		4.03-4.04	211.40	no	UMC 98
uaz53b		4.04	213.86	no	BNL 2002
umc49e	C	4.04	213.91	no	IBM1
umc1821	C	4.04	214.47	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz30b		4.03-4.04	216.89	no	BNL 2002
umc1117	AC	4.04	218.50	yes	IBM2
csu12c(cin4)		4.04-4.05	219.81	no	BNL 2002
lim415		4.04	223.60	yes	IBM2
umc1963	AC	4.04	225.70	yes	IBM2
bnlg1741		4.06	226.91	no	BNL 2002
umc1652	AC	4.04	228.40	yes	IBM2
jpsb527b		4.04	230.40	yes	IBM2
zp1	AC	4.04	232.20	no	IBM2
mmc0471	AC	4.04	232.20	yes	IBM2
sdg108a	C	4.04	232.20	no	ChromDB
umc2206	C	4.04	234.85	no	SSR popI
bnlg490	AC	4.04	237.80	yes	IBM2
psb3	C	4.04	239.38	no	UMC 98
uaz69b		4.05	239.42	no	BNL 2002
rgps2470		4.04	239.79	no	UMC 98
agrr37b	C	4.05	244.53	no	SSR popII
aco1		4.04-4.05	245.47	no	BNL 2002
bnl17.13c		4.05	245.47	no	BNL 2002
npi574a		4.05	245.47	no	BNL 96
bm3	C	4.05	245.50	no	UMC 98
agrr301		4.05	245.50	yes	IBM2
agrr321		4.05	245.50	no	UMC 98
csu599a		4.05	245.50	no	UMC 98
bap2		4.05	246.97	no	UMC 98
agrp67		4.05	246.97	no	UMC 98
agrp54b		4.05	247.79	no	UMC 98
umc1969		4.05	248.60	yes	IBM2
uaz42c		4.05	248.79	no	BNL 2002
uaz48c		4.05	248.79	no	BNL 2002
umc2061	AC	4.05	250.80	yes	IBM2
orp1		4.05	253.02	no	UMC 98
gpc1	AC	4.05	254.00	yes	IBM2
csu294		4.05	254.00	no	UMC 98
csu1098		4.05	254.00	no	UMC 98
csu1125		4.05	254.00	no	UMC 98
rz143b(gpc)		4.05	254.00	no	IBM2
csu565(rpPo)		4.05	254.00	no	UMC 98
csu474(rpS14)	AC	4.05	254.00	no	UMC 98
bnlg1937		4.05-4.06	254.11	no	BNL 2002
uaz49A		4.05	254.20	no	BNL 2002
umc2282	AC	4.05	254.90	no	IBM2
bnlg1217		4.05	255.32	no	BNL 2002
uaz61b		4.05	256.24	no	BNL 2002
uaz212		4.05	256.83	no	BNL 2002
bnl17.10		4.05	256.83	no	BNL 2002
npi289		4.05	257.70	no	BNL 2002
npi95a		4.05	257.70	no	BNL 96
umc191(gpc1)	C	4.05	258.60	yes	IBM2
uaz216		4.05	261.77	no	BNL 2002
uaz230a		4.05	261.77	no	BNL 2002
uaz157(rpL19)		4.05	261.77	no	BNL 2002
uaz265c(sbe)		4.05	261.77	no	BNL 96
agrc567		4.05	263.58	no	UMC 98
bnlg1265	AC	4.05	268.40	yes	IBM2
uaz218a(gss)		4.05	268.81	no	BNL 2002
agrr89		4.05	269.06	no	UMC 98
umc193d(orp)		4.05	269.06	no	UMC 98
umc1303	AC	4.05	270.30	yes	IBM2
umc1382	C	4.05	270.30	no	SSR popII
uaz41b		4.05	270.36	no	BNL 2002
uaz42a		4.05	270.36	no	BNL 2002
uaz45a		4.05	270.36	no	BNL 2002
uaz46c		4.05	270.36	no	BNL 2002
zpl2a		4.04-4.05	270.36	no	BNL 2002
uaz44a(zp19)		4.05	270.36	no	BNL 2002
uaz43a		4.05	270.78	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1964	AC	4.05	271.40	no	IBM2
bnl17.23c(pal)		4.05	272.44	no	BNL 2002
AY110290	C	4.05	274.70	yes	IBM2
uaz56		4.05	274.77	no	BNL 2002
uaz246a(mbf)	C	4.05	274.77	no	BNL 2002
bnlg2209		4.05	276.54	no	BNL 2002
dnap4		4.05	276.59	no	BNL 96
umc1390		4.05	277.57	no	SSR popI
psr152b		4.05	277.80	yes	IBM2
csu509	AC	4.05	279.90	yes	IBM2
umc1662		4.05	282.04	no	SSR popII
mmp125		4.05	283.30	yes	IBM2
umc1031	AC	4.05	286.00	yes	IBM2
chr112a	C	4.05	287.20	no	ChromDB
umc1175	AC	4.05	287.30	no	IBM2
hda108		4.05	287.70	no	ChromDB
umc1896		4.05	288.09	no	SSR popII
umc1362	C	4.05	288.09	no	SSR popII
umc1451	C	4.05	288.09	no	SSR popII
umc42a		4.05	288.40	yes	IBM2
bnlg252		4.06	288.42	no	BNL 2002
pic1b		4.05	288.60	no	BNL 2002
zpl3a		4.04-4.05	288.62	no	BNL 2002
bnlg1729		4.05	288.67	no	BNL 2002
uaz72		4.05	288.71	no	BNL 2002
mpik11f		4.05	288.71	no	BNL 2002
mpik15b		4.05	288.71	no	BNL 2002
uaz261b		4.05	288.71	no	BNL 2002
ucsd72l		4.05	288.71	no	BNL 2002
umc(orp1)		4.05	288.71	no	BNL 2002
ucsd62j(zag4)		4.05	288.71	no	BNL 2002
bnl(tas3a)		4.05	289.92	no	BNL 96
isu61d		4.05	291.30	yes	IBM2
jpsb67		4.05	292.40	no	IBM2
bt2	C	4.05	292.90	no	UMC 98
bet2		4.05	292.90	no	BNL 2002
csu902		4.05	292.90	no	UMC 98
med63a		4.05	292.90	no	UMC 98
agrr286		4.05	292.90	no	UMC 98
agrr62b		4.05	292.90	no	UMC 98
bnl15.45		4.05	292.90	yes	IBM2
csu1026		4.05	292.90	no	UMC 98
dpg7a		4.05	292.90	no	BNL 2002
umc242	C	4.05	292.90	no	UMC 98
umc263	C	4.05	292.90	no	UMC 98
umc47a	C	4.05	292.90	no	UMC 98
npi367b		4.05	292.90	no	BNL 2002
bnlg1168		4.05	292.90	no	BNL 2002
bnlg1790		4.05	292.90	no	BNL 2002
bnlg667b		4.05	292.90	no	BNL 2002
bnl12.06b		4.05	292.90	no	BNL 2002
bnl15.27a		4.05	292.90	no	BNL 2002
std1a(his2B1)		4.05	292.90	no	UMC 98
csu19(colp)		4.04-4.05	293.14	no	BNL 2002
umc1953	AC	4.05	294.30	no	IBM2
umc2283	AC	4.05	294.40	no	IBM2
bnlg1159a	AC	4.05	294.86	no	BNL 2002
umc1511	AC	4.05	295.20	yes	IBM2
wsu(nia2)		4.05	296.55	no	BNL 2002
pbs13a		4.05	296.88	no	BNL 2002
bnl17.09		4.05	296.88	no	BNL 2002
umc2054		4.05	296.99	no	SSR popII
csu74(fdx)		4.05	297.06	no	UMC 98
psr128		4.05	297.40	yes	IBM2
uaz195(ms)		4.05	297.49	no	BNL 2002
umc33b		4.05	297.53	no	UMC 98
csu716	C	4.05	297.53	no	UMC 98
cdo395a(ypt)		4.05	297.53	no	UMC 98
umc1791	AC	4.05	298.10	no	IBM2
mmp190		4.05	298.40	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mmp140		4.05	298.90	yes	IBM2
umc1895		4.05	298.93	no	SSR popI
ncr(nrB)		4.05	299.39	no	BNL 2002
uaz71a		4.05	299.48	no	BNL 2002
bnlg1755	AC	4.05	299.90	yes	IBM2
mmp45		4.05	300.20	no	IBM2
umc1851		4.05	302.33	no	SSR popII
umc1142	AC	4.05	302.50	yes	IBM2
uaz73		4.05	302.94	no	BNL 2002
bnl35b(blr)		4.05	302.97	no	BNL 2002
csu81b(ank)		4.05	303.33	no	BNL 2002
dup(als1)		4.05	303.76	no	BNL 2002
agrp83a		4.05	304.00	no	UMC 98
csu93c	C	4.05	304.00	no	UMC 98
bnl5.71b		4.05	304.00	no	UMC 98
umc1346	C	4.05	304.30	yes	IBM2
mpik19b		4.05	304.51	no	BNL 2002
ucsd72g		4.05	304.64	no	BNL 2002
mpik11d		4.05	304.90	no	BNL 2002
nfd104e		4.05	304.97	no	ChromDB
umc1702	AC	4.05	305.20	no	IBM2
mmp155		4.05	305.50	no	IBM2
mmp149		4.05	306.40	yes	IBM2
npi284		4.05	306.96	no	BNL 96
mmp86		4.05	307.40	no	IBM2
cdo497		4.05	308.63	no	UMC 98
tda62b		4.05	308.63	no	UMC 98
cdo116b		4.05	308.63	no	UMC 98
bnl5.33a		4.05	308.63	no	UMC 98
std16a(blr)		4.05	308.63	no	UMC 98
mmp78		4.05	310.70	yes	IBM2
ias12		4.05	311.36	no	BNL 2002
CL65845_1	C	4.05-4.06	312.07	no	INDEL
umc1317	C	4.05	313.00	no	SSR popI
ucsd64f		4.05	313.15	no	BNL 2002
csu84		4.05	313.25	no	UMC 98
npi267		4.05	313.25	no	UMC 98
bnl7.20		4.05	313.25	no	UMC 98
npi594b		4.05	313.25	no	UMC 98
umc273b		4.05	313.25	no	UMC 98
npi259a		4.05	313.25	no	BNL 2002
csu100(ptk)		4.05	313.25	no	UMC 98
csu693(lrr)		4.05	313.25	no	UMC 98
csu742b(rpS7)		4.05	313.25	no	UMC 98
nfa104		4.05	314.90	no	IBM2
csu1063		4.05	317.42	no	UMC 98
csu358b(pal)	C	4.05	317.42	no	UMC 98
umc1548		4.05	318.73	no	SSR popI
umc1891		4.05	318.73	no	SSR popI
AY110562	AC	4.05	320.40	yes	IBM2
bnlg1930		4.05-4.06	324.68	no	BNL 2002
umc23b		4.05	324.80	no	BNL 2002
AY110355	AC	4.05	326.50	yes	IBM2
uaz170		4.06	327.59	no	BNL 2002
umc156a	C	4.06	327.59	no	SSR popI
php20597a		4.06	329.60	yes	IBM2
npi340b		4.06	329.89	no	BNL 96
uaz47a		4.06	331.26	no	BNL 2002
mmc0371	AC	4.06	331.30	yes	IBM2
umc2284	AC	4.05	332.40	no	IBM2
csu638		4.06	332.50	no	UMC 98
umc1945	AC	4.06	333.20	yes	IBM2
mmp74		4.06	335.20	no	IBM2
ucsd61i(zag4)		4.05-4.06	336.12	no	BNL 96
npi396		4.06	338.41	no	BNL 2002
umc2391		4.06	345.35	no	SSR popII
nfd105		4.06	346.72	no	ChromDB
csu661	AC	4.06	349.68	no	UMC 98
umc2027		4.06	349.80	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mmp97		4.06	354.50	yes	IBM2
csu640		4.06	355.20	no	UMC 98
mmp176		4.06	355.40	yes	IBM2
AY110310	AC	4.06	362.40	yes	IBM2
rgpr663a		4.06	366.25	no	UMC 98
mpik3		4.06	367.20	yes	IBM2
uaz144a		4.06	367.29	no	BNL 96
bnl8.08h		4.06	371.62	no	BNL 2002
dupssr16		4.06	371.71	no	BNL 2002
csu816		4.06	371.77	no	UMC 98
csu587a		4.06	371.77	no	UMC 98
umc1299	AC	4.06	372.84	no	SSR popII
uaz228c(his2b)		4.06	372.84	no	BNL 2002
rz567b(klc)	AC	4.06	373.30	yes	IBM2
npi584		4.06	375.04	no	BNL 2002
uaz257		4.06	375.04	no	BNL 2002
bnlg1023a		4.06	378.95	no	BNL 2002
rz273a(ant)		4.06	379.30	yes	IBM2
uaz130b(tlk)	C	4.05	379.99	no	BNL 2002
umc1869		4.06	380.19	no	SSR popII
umc2070	AC	4.06	380.58	no	SSR popII
ias11		4.06	382.26	no	BNL 2002
dge18		4.06	383.37	no	BNL 2002
csu643b		4.06	384.04	no	UMC 98
csu907a		4.06	384.04	no	UMC 98
umc1329	C	4.06	384.91	no	SSR popI
mpik11e		4.05	385.55	no	BNL 2002
mpik15a		4.05	385.55	no	BNL 2002
mpik16e		4.05	385.55	no	BNL 2002
rgpc601a		4.06	388.03	no	UMC 98
trg1		4.06	389.92	no	BNL 96
bnlg2291	AC	4.06	392.20	no	IBM2
bnlg1137	AC	4.06	392.40	yes	IBM2
gln5		4.06	393.24	no	UMC 98
ucsd64g		4.06	393.64	no	BNL 2002
bnlg1784		4.07	395.80	no	BNL 2002
dupssr34		4.07	395.81	no	BNL 2002
uaz263		4.07	396.73	no	BNL 2002
uaz74		4.07	397.13	no	BNL 2002
umc66	C	4.07	397.40	yes	IBM2
pbs13c		4.07	397.73	no	BNL 2002
prh1		4.07	399.69	no	UMC 98
csu525(rpL17)		4.07	399.69	no	UMC 98
umc66a(lcr)	C	4.07	399.69	no	INDEL
rz446a		4.07	402.95	no	UMC 98
klp1e		4.07	405.49	no	UMC 98
umc104a		4.07	408.70	yes	IBM2
bnlg1621a		4.06	409.59	no	BNL 2002
pbs16c		4.07	410.74	no	BNL 2002
mmp147		4.07	410.80	yes	IBM2
umc2038	AC	4.07	411.30	yes	IBM2
umc1651		4.07	412.12	no	SSR popII
umc19	C	4.07	414.20	yes	IBM2
umc229a		4.07	414.20	no	UMC 98
uaz66b		4.07	414.20	no	BNL 2002
bnl8.08i		4.07	414.20	no	BNL 2002
umc1994	AC	4.07	414.40	no	SSR popII
agrp168c		4.07	415.30	no	UMC 98
bnl5.67a		4.07	415.30	no	UMC 98
umc1847		4.07	418.20	no	SSR popII
umc244a		4.07	418.66	no	UMC 98
mmp115		4.07	420.60	yes	IBM2
zag3		4.05-4.06	421.23	no	BNL 2002
umc1620		4.07	421.25	no	SSR popII
umc126b	C	4.06	425.54	no	BNL 2002
umc1194		4.07	427.56	no	SSR popI
bnlg1189	AC	4.07	428.00	no	IBM2
uaz222		4.07	428.21	no	BNL 2002
bnl5.24b		4.07	430.20	yes	IBM2
wsu(nia3)		4.07	432.69	no	BNL 96
umc127c		4.08	436.72	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
PCO119336	C	4.07-4.08	436.95	no	INDEL
asg33	C	4.07	437.50	yes	IBM2
csu672b	C	4.07	437.50	no	UMC 98
csu597d(dah)	C	4.07	437.50	no	UMC 98
asg9a		4.07	440.88	no	UMC 98
uaz171		4.08	441.91	no	BNL 2002
mmc0341	AC	4.07	443.19	no	SSR popI
umc1775	C	4.08	443.20	yes	IBM2
asg74b		4.08	443.92	no	UMC 98
umc2009		4.08	446.76	no	SSR popI
npi292		4.07	448.98	no	BNL 96
umc1667		4.08	449.40	yes	IBM2
asg85a		4.08	451.01	no	UMC 98
AY109534	AC	4.08	452.10	no	IBM2
umc1808		4.08	452.90	yes	IBM2
mmp3		4.08	455.90	yes	IBM2
asg27a		4.08	458.10	yes	IBM2
npi253b		4.08	458.92	no	BNL 96
umc1476	C	4.08	462.10	no	IBM2
bnlg1444		4.08	462.50	yes	IBM2
dupssr28		4.08	462.58	no	BNL 2002
bnlg1927	AC	4.07	462.58	no	BNL 2002
bnl22		4.08	462.61	no	BNL 2002
npi208a		4.08	462.66	no	BNL 2002
fer1		4.08	463.30	no	UMC 98
gol1	C	4.08	463.30	yes	IBM2
csu91a		4.08	463.30	no	UMC 98
umc1871		4.08	464.39	no	SSR popII
bnl7.65		4.08	464.80	no	IBM2
rgpg24		4.08	464.80	no	UMC 98
umc133a		4.08	464.80	no	UMC 98
rgpg124a	C	4.08	464.80	no	UMC 98
bnl10.05		4.08	466.10	yes	IBM2
bnlg2244	AC	4.08	467.10	yes	IBM2
bnl8.45b	C	4.08	468.75	no	SSR popI
umc2384		4.08	468.77	no	SSR popII
umc1899	AC	4.08	470.60	yes	IBM2
pdh1	AC	4.08	471.86	no	SSR popII
umc2404		4.08	471.86	no	SSR popII
umc158		4.08	473.90	yes	IBM2
umc14a		4.05-4.06	473.90	no	UMC 98
csu720b		4.05-4.06	473.90	no	UMC 98
uaz252a(ptk)		4.08	473.90	no	BNL 2002
csu428(cyb561)		4.05-4.06	473.90	no	UMC 98
umc1418	AC	4.08	475.60	no	SSR popII
bnlg2162	AC	4.08	475.70	no	IBM2
mmp70		4.08	476.00	no	IBM2
umc2405		4.08	476.46	no	SSR popII
umc2635		4.08	477.90	no	SSR popII
PCO129009	C	4.08	478.89	no	INDEL
npi570		4.08	480.70	yes	IBM2
umc2041		4.08	483.93	no	SSR popI
AY112127	AC	4.08	487.70	yes	IBM2
ufg23		4.08	499.90	yes	IBM2
umc1086	C	4.08	500.59	no	SSR popII
AY110631		4.08	510.00	yes	IBM2
umc2285	AC	4.08	514.90	yes	IBM2
npi270		4.08	516.60	yes	IBM2
npi300c		4.08	516.69	no	BNL 2002
php20071		4.08	518.10	yes	IBM2
rgpl102		4.08	518.10	no	UMC 98
cdo127a(pyk)	C	4.08	518.10	no	UMC 98
mmc0321	AC	4.08	518.34	no	SSR popI
uaz122		4.08	519.55	no	BNL 2002
bnl17.05(ssu)		4.08	520.12	no	BNL 96
ssu1	AC	4.08	522.10	yes	IBM2
CL12681_1	C	4.08	523.23	no	INDEL
umc1612	AC	4.08	523.40	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi444		4.08	524.10	yes	IBM2
umc15a		4.08	525.80	yes	IBM2
umn433		4.08	525.80	no	UMC 98
csu166a		4.08	525.80	no	UMC 98
rgpg111		4.08	525.80	no	UMC 98
csu1038b		4.08	525.80	no	UMC 98
csu1073b		4.08	525.80	no	UMC 98
cdo365(pet)	AC	4.08	525.80	no	UMC 98
csu597a(dah)	C	4.08	525.80	no	UMC 98
php20562		4.08	526.00	no	UMC 98
c2	C	4.08	526.57	no	SSR popI
tda44		4.08	526.57	no	UMC 98
csu178a		4.08	526.57	no	UMC 98
npi910		4.08	526.57	no	BNL 2002
umc1051	AC	4.08	526.57	no	SSR popI
csu202(rpL7)		4.08	526.57	no	UMC 98
PCO136722	C	4.08	530.42	no	INDEL
umc2187	C	4.08	531.70	yes	IBM2
npi410		4.08	533.87	no	BNL 2002
psr109b		4.08	533.87	no	BNL 2002
umc1842		4.08	534.80	yes	IBM2
umc1856		4.08	534.80	no	SSR popII
umc1371	C	4.08	534.80	no	SSR popII
AY109980	C	4.06	535.40	no	IBM2
umc1132	AC	4.08	535.50	no	IBM2
nfd106	C	4.08	535.55	no	ChromDB
AY105971	AC	4.08	536.30	yes	IBM2
AY110989	AC	4.08	536.90	yes	IBM2
ensl002a		4.08	537.11	no	BNL 2002
rz596b		4.08	539.00	yes	IBM2
bnl23a		4.08	542.87	no	BNL 2002
bnl29(pds2)		4.08	542.87	no	BNL 2002
umc2200	C	4.08	543.44	no	SSR popI
umc2135		4.08	544.10	yes	IBM2
uaz33b		4.09	548.95	no	BNL 2002
mmp178		4.08	551.00	yes	IBM2
umc1834		4.08	551.21	no	SSR popII
csu704	C	4.08	553.34	no	UMC 98
umc2286	AC	4.08	553.70	no	IBM2
mpik(chs1a)		4.08	553.81	no	BNL 2002
umc2188	AC	4.08	554.10	yes	IBM2
umc2360	C	4.08-4.09	554.90	no	SSR popII
uaz142		4.08	558.11	no	BNL 2002
umc52	C	4.09	559.00	yes	IBM2
csu39	C	4.08-4.09	559.00	no	UMC 98
csu50a	C	4.08-4.09	559.00	no	UMC 98
umc1559		4.08-4.09	559.00	no	SSR popII
AY110170	C	4.09	561.50	no	IBM2
umc1313	C	4.08-4.09	562.75	no	SSR popI
lim446		4.09	565.40	yes	IBM2
csu201		4.09	567.32	no	UMC 98
mwg645e		4.09	570.61	no	BNL 96
csu241b		4.09	570.64	no	UMC 98
rgpc643a		4.09	570.64	no	UMC 98
uaz115		4.09	570.99	no	BNL 2002
csu304b		4.09	571.47	no	UMC 98
uaz41a		4.09	571.95	no	BNL 2002
cuny9		4.09	572.37	no	BNL 2002
bnlg1019b	C	4.09-4.10	573.11	no	BNL 2002
bnlg2148		4.09	573.69	no	BNL 2002
bnlg292b	C	4.08-4.09	573.71	no	SSR popI
umc2139	AC	4.09	574.80	yes	IBM2
csu674(gts)		4.09	578.13	no	UMC 98
php10025		4.09	579.80	yes	IBM2
ensl002b		4.09	580.08	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
PCO104784	C	4.09	580.31	no	INDEL
umc1939		4.09	580.69	no	SSR popII
umc1940	AC	4.09	581.80	no	IBM2
umc1999	AC	4.09	581.80	yes	IBM2
ris2		4.09	583.12	no	BNL 96
uaz137		4.08	584.64	no	BNL 2002
mgs2	C	4.09	589.37	no	BNL 2002
umc1854		4.09	595.70	yes	IBM2
rgpr3235b	C	4.09	597.00	no	UMC 98
csu862b(rpL11)		4.09	597.00	no	UMC 98
mmp24		4.09	598.60	no	IBM2
umc1989		4.09	599.40	no	SSR popII
mmp134		4.09	599.50	yes	IBM2
rz476a		4.09	601.40	no	IBM2
rz599b	C	4.09	601.40	no	IBM2
npi449b		4.09	601.60	yes	IBM2
umc1650		4.09	602.10	no	IBM2
umc1803		4.09	602.20	no	IBM2
asg22		4.09	603.30	yes	IBM2
csu745b(rpPo)	C	4.09	603.30	no	UMC 98
mmp94		4.09	605.50	yes	IBM2
umc1740	AC	4.09	611.90	no	SSR popI
AY109933	AC	4.09	613.00	yes	IBM2
CL2227_3	C	4.09	613.42	no	INDEL
AY110064	C	4.09	616.70	no	IBM2
umc1328	AC	4.09	618.10	yes	IBM2
umc1631		4.09	618.10	no	SSR popII
umc2287	AC	4.09	619.40	yes	IBM2
rpd3	AC	4.09	621.42	no	SSR popII
umc1643		4.09	621.61	no	SSR popI
umc1820		4.09	622.93	no	SSR popII
cdo534a(cts)		4.09	623.20	yes	IBM2
csu324a(cts)		4.09	623.20	no	UMC 98
csu34b(rpS8)	C	4.09	623.20	no	UMC 98
cdo534c(cts)		4.09	623.40	no	IBM2
umc2382	C	4.09	624.36	no	SSR popII
npi333		4.09-4.10	625.99	no	BNL 96
AY110231	AC	4.09	635.20	yes	IBM2
cdo1395c		4.09	635.91	no	UMC 98
csu1107		4.09	637.21	no	UMC 98
csu719(lox)		4.09	637.21	no	UMC 98
umc1284		4.09	641.02	no	SSR popI
csu631		4.09	643.08	no	UMC 98
sbp2	AC	4.09	644.30	yes	IBM2
bnlg1565		4.09	645.70	no	IBM2
bnlg572b		4.09	647.82	no	BNL 2002
uaz65a		4.09	648.81	no	BNL 2002
bnlg2299		4.09	650.44	no	BNL 2002
knox7		4.09-4.10	650.48	no	BNL 2002
npi116a		4.09	651.61	no	BNL 2002
npi593a		4.09	651.70	yes	IBM2
npi294g		4.09	652.20	no	UMC 98
uaz123b		4.09-4.10	652.92	no	BNL 2002
PCO088312	C	4.09-4.10	654.70	no	INDEL
umc1101	C	4.09	655.00	yes	IBM2
umc2046	AC	4.09	657.00	yes	IBM2
bnlg2186		4.11	657.66	no	BNL 2002
uaz279(cbp)		4.09	658.07	no	UMC 98
csu848a(vpp)		4.09	658.07	no	UMC 98
ici281		4.10	659.03	no	BNL 2002
uwo3		4.10	666.64	no	BNL 96
csu283a		4.10	669.80	no	UMC 98
csu758	AC	4.10	669.80	no	UMC 98
csu330(ubi)		4.10	669.80	no	UMC 98
csu377a(ubi)		4.10	669.80	no	UMC 98
php20608a	AC	4.09-4.10	669.80	yes	IBM2
uwo8		4.11	670.20	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg589	AC	4.10	670.20	yes	IBM2
isu2191a		4.10	670.20	no	BNL 2002
umc1503	AC	4.09-4.10	671.48	no	SSR popI
umc1532		4.10	671.90	yes	IBM2
umc124b(chk)		4.10	672.40	yes	IBM2
pge17		4.11	678.18	no	BNL 2002
uaz247(ubi)		4.10	679.17	no	BNL 2002
dpg15a		4.10	680.28	no	BNL 2002
agrr169		4.10	682.59	no	INDEL
bnl32		4.11	685.82	no	BNL 2002
umc1109	AC	4.10	687.80	yes	IBM2
umc1720		4.10	688.03	no	SSR popII
lim471		4.10	688.70	yes	IBM2
npi451		4.11	688.91	no	BNL 2002
bnl(tas1o)		4.11	689.21	no	BNL 2002
umc2011		4.10	689.25	no	SSR popI
dba1		4.10	691.20	no	UMC 98
bnl15.07a		4.10	691.20	yes	IBM2
umc2288	AC	4.10	692.10	yes	IBM2
umc1699		4.10	692.94	no	SSR popI
asg41		4.10	695.50	yes	IBM2
umc2044		4.10	696.05	no	SSR popII
umc1180	AC	4.10	698.90	yes	IBM2
csu36a(rpL19)		4.10	699.17	no	UMC 98
PCO109372	C	4.10	699.66	no	INDEL
cas1		4.10	701.86	no	UMC 98
AY109668	C	4.10	702.20	yes	IBM2
bnlg1917		4.10	703.52	no	BNL 2002
csh2a(cdc2)		4.10	704.21	no	BNL 96
bnlg1337		4.11	707.24	no	BNL 2002
umc2289	AC	4.10	707.80	yes	IBM2
AY109859	AC	4.11	708.50	yes	IBM2
AY109611	AC	4.11	715.50	yes	IBM2
umc1738	AC	4.10	720.48	no	SSR popII
bnl8.23a		4.10-4.11	726.30	no	UMC 98
ncr(cat3)		4.10	727.63	no	BNL 96
csu380		4.11	728.50	no	UMC 98
umc169	AC	4.11	728.50	yes	IBM2
umc111a(psy)		4.11	728.50	no	UMC 98
cpn10		4.10-4.11	728.50	no	SSR popII
umc1719	AC	4.10-4.11	730.75	no	SSR popI
umc1716	AC	4.11	732.99	no	SSR popI
umc112c		4.11	733.63	no	UMC 98
umc2290	AC	4.11	736.70	no	IBM2
bip2	AC	4.11	737.80	yes	IBM2
umc1649	AC	4.11	739.30	no	IBM2
mmp182		4.11	740.70	yes	IBM2
csu710b(apx)		4.11	742.68	no	UMC 98
csu315b		4.11	743.41	no	UMC 98
cat3	AC	4.11	744.10	yes	IBM2
umc1707	C	4.11	748.30	yes	IBM2
bnlg1890		4.11	750.20	yes	IBM2
ncr(b70b)		4.10	752.97	no	BNL 2002
isu61b		4.11	753.50	no	IBM1
ufg(ivr2a)		4.10	804.83	no	BNL 96
umc1491	AC	5.00	-32.40	no	SSR popI
bnl(tas1n)		5.00	-13.30	no	BNL 96
bnl(tas2g)		5.00	-9.34	no	BNL 2002
bnl(tas2b)		5.00	-3.07	no	BNL 2002
AI676903	AC	5.00	0.00	yes	IBM2
umc1308	AC	5.00	6.30	no	SSR popI
AY110625	AC	5.00	10.70	yes	IBM2
CL21419_1	C	5.00	13.70	no	INDEL
tum3		5.00-5.03	14.66	no	BNL 2002
umc1240	C	5.00	16.30	no	SSR popII
AY109758	C	5.00	17.10	yes	IBM2
uaz75		5.00	17.21	no	BNL 2002
ufg36	C	5.00	20.80	yes	IBM2
mmc0151	AC	5.00	22.60	no	SSR popII
umc1253	AC	5.00	22.70	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2292	AC	5.00	22.70	yes	IBM2
umc2291	AC	5.00	23.30	yes	IBM2
csu1087		5.00	24.50	yes	IBM2
uaz214		5.00	29.69	no	BNL 2002
umc1423	AC	5.00	30.00	yes	IBM2
csu277		5.00	31.50	no	UMC 98
csu527(crm)	C	5.00	31.50	no	UMC 98
uaz259		5.00	31.52	no	BNL 2002
PCO062666	C	5.00	34.14	no	INDEL
umc1445	AC	5.00	37.60	yes	IBM2
umc1496	AC	5.00	38.52	no	SSR popI
csh1c(chi)		5.00	39.20	no	BNL 96
umc2022	AC	5.00	39.40	no	IBM2
umc1097	AC	5.00	40.80	yes	IBM2
npi890		5.00	42.25	no	BNL 2002
mmp6		5.00	42.40	yes	IBM2
bnl8.33	C	5.00	46.80	yes	IBM2
cdo457a		5.00	46.80	no	UMC 98
bnlg1006	AC	5.00	47.50	no	IBM2
umc1901	AC	5.00	50.10	yes	IBM2
umc86b		5.00	52.80	yes	IBM2
uaz76a		5.00	54.13	no	BNL 2002
umc1325	AC	5.00	54.60	yes	IBM2
asg60		5.00	57.48	no	UMC 98
rgpg164	AC	5.00	61.16	no	UMC 98
umc1260	AC	5.00	68.10	yes	IBM2
sca1	C	5.00	68.50	yes	IBM2
npi409	AC	5.01	69.50	yes	IBM2
bnl6.25a		5.01	69.50	no	UMC 98
csu33a	AC	5.01	69.50	no	UMC 98
csu663a(psaD)		5.01	69.50	no	UMC 98
umc1679	AC	5.01	71.50	no	IBM2
umc1523	AC	5.01	71.90	yes	IBM2
csu604b(trh)	C	5.01	73.04	no	UMC 98
mmp43		5.01	73.30	no	IBM2
bnl7.21c		5.01	74.40	yes	IBM2
ohp2	AC	5.01	75.66	no	BNL 2002
umc1478		5.01	79.17	no	SSR popII
cdo87a(ptk)	C	5.01	83.67	no	UMC 98
jpsb239a		5.01	83.70	yes	IBM2
bnl8.29b		5.01	83.92	no	BNL 96
lim407		5.01	85.10	yes	IBM2
tua3		5.01	90.17	no	UMC 98
rpa7b		5.01	90.17	no	UMC 98
umc144a		5.01	90.17	no	UMC 98
csu1169a		5.01	90.17	no	UMC 98
csu570a(mtl)		5.01	90.17	no	UMC 98
AY109733	C	5.01	90.20	yes	IBM2
umc1365	AC	5.01	97.95	no	SSR popII
umc147a		5.01	99.03	no	UMC 98
umc240	C	5.01	99.03	no	UMC 98
bnl17.18a		5.01	99.03	no	UMC 98
npi75a		5.01	99.05	no	BNL 2002
npi579a		5.01	99.05	no	BNL 96
uaz134		5.02	103.23	no	BNL 2002
bnl7.24b		5.01	103.69	no	BNL 2002
uaz201(tua)		5.01	104.40	no	BNL 2002
csu707		5.01	104.93	no	UMC 98
bnlg1836		5.01	106.08	no	BNL 2002
asg54b		5.01	107.88	no	UMC 98
umc1766		5.01	111.76	no	SSR popI
bnlg143		5.01	114.17	no	BNL 96
uat4b		5.01	116.45	no	UMC 98
uaz163		5.01	122.34	no	BNL 2002
bcd450a		5.01	123.24	no	UMC 98
csu137a(ap)		5.01	123.24	no	UMC 98
umc2036	AC	5.01	124.70	yes	IBM2
umc1781	AC	5.01	124.70	no	SSR popI
npi282a		5.01	129.30	yes	IBM2
cuny7		5.01	129.30	no	BNL 2002
npi581b		5.01	129.30	no	BNL 2002
ucsd104a(zag6)		5.01	129.30	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
hxa102a		5.01	130.00	no	ChromDB
ucsd64a		5.01	133.17	no	BNL 96
mpik22b(zmm4)		5.01	133.17	no	BNL 2002
rgpc975(rpS27)		5.01	134.46	no	UMC 98
npi305a		5.01	137.04	no	BNL 2002
ucsd72j		5.01	137.04	no	BNL 96
uaz166b		5.01	137.50	no	BNL 2002
rz630f(sat)		5.01	138.00	yes	IBM2
hcf108		5.01	141.18	no	BNL 2002
csu318		5.01	141.25	no	UMC 98
umc72a		5.01 - 5.02	141.25	no	UMC 98
umc90	AC	5.02	142.43	no	SSR popI
ucsd106c		5.01	144.67	no	BNL 2002
tua4	C	5.02	147.50	yes	IBM2
bnlg1382		5.01	148.43	no	BNL 2002
asg73		5.02	149.70	yes	IBM2
umc144b		5.01 - 5.02	149.70	no	UMC 98
bnlg565	AC	5.02	150.90	yes	IBM2
ole3	AC	5.03- 5.04	151.75	no	BNL 2002
bcd808d		5.02	152.00	no	IBM2
psr922a		5.02	153.80	yes	IBM2
chb101a		5.02	153.80	no	ChromDB
umc1587	AC	5.02	156.90	yes	IBM2
rz632a		5.02	158.15	no	UMC 98
umc107b(croc)	AC	5.02	160.20	yes	IBM2
csu554b(rnh)		5.02	161.60	no	IBM2
umc1894		5.01 - 5.02	164.59	no	SSR popI
cdo122b(nad)		5.02	164.60	yes	IBM2
uaz167b		5.02	165.17	no	BNL 2002
pgm2		5.02	165.17	no	BNL 96
umc106b		5.02	173.44	no	BNL 2002
phyA2		5.02	177.16	no	BNL 2002
ufg27	C	5.02	179.30	no	IBM2
mmp130		5.02	179.60	yes	IBM2
csu10a		5.02	181.70	no	UMC 98
bcd1072a(hsp70)		5.02	181.70	yes	IBM2
uaz211		5.02	182.23	no	BNL 2002
uaz219(hsp)		5.02	182.91	no	BNL 2002
uaz215b(odo)		5.02	183.23	no	BNL 2002
uaz205a(hsp70)		5.03	184.27	no	BNL 2002
uwm2(rnp)		5.02	185.09	no	UMC 98
bnlg105	AC	5.02	185.09	no	SSR popI
csu108(gbp)	C	5.02	185.09	no	UMC 98
bnlg1879	AC	5.03	189.80	yes	IBM2
ufg25	C	5.03	190.90	no	IBM2
umc2293	C	5.03	196.90	yes	IBM2
tub4	C	5.03	200.46	no	SSR popII
mbd109		5.03	203.20	no	ChromDB
csu164b	C	5.03	203.30	yes	IBM2
csu511b		5.03	204.10	no	UMC 98
rz474a(dnaj)		5.03	204.10	yes	IBM2
csu222b(wsi)		5.03	204.10	no	UMC 98
csu574a(eif2B)	C	5.03	204.10	no	UMC 98
umc2388	C	5.02- 5.03	206.86	no	SSR popII
bnlg1660		5.03	207.75	no	BNL 2002
knox10		5.02- 5.03	207.75	no	BNL 2002
csic(mah9)		5.03	207.75	no	BNL 96
csu150b		5.03	208.66	no	BNL 2002
nfc103b	C	5.03	208.78	no	ChromDB
csy1		5.03	209.19	no	BNL 2002
uaz25d		5.03	209.38	no	BNL 2002
umc1686		5.03	210.30	yes	IBM2
tbp2	AC	5.03	211.74	no	UMC 98
rpa6a		5.02	211.90	no	UMC 98
niu2::Bs1		5.03	212.30	no	BNL 2002
mmp112		5.03	212.70	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg557		5.03	213.46	no	BNL 2002
mpik33e		5.03	213.46	no	BNL 2002
umc1852		5.03	213.91	no	SSR popII
cdo795b		5.03	214.50	yes	IBM2
bnlg1046	AC	5.03	216.30	yes	IBM2
dnap2		5.03	216.41	no	BNL 2002
npi434		5.03	216.41	no	BNL 2002
umc1597	AC	5.03	217.80	yes	IBM2
umc27a	C	5.03	217.85	no	BNL 96
ici97		5.03	218.35	no	BNL 2002
bnl7.56		5.03	219.20	yes	IBM2
umc2060		5.03	220.70	no	SSR popI
rps15	AC	5.03	220.95	no	SSR popII
csu340		5.03	222.50	yes	IBM2
rgpc643d		5.03	222.50	no	UMC 98
rgpr440a(gap)		5.03	222.50	no	UMC 98
csu175c(eif5A)		5.03	222.50	no	UMC 98
uaz159a		5.03	223.44	no	BNL 2002
psr544		5.03	227.20	yes	IBM2
umc1468		5.03	227.35	no	SSR popII
bcd207b		5.03	229.00	yes	IBM2
mmp180		5.03	229.90	no	IBM2
mmc0351	AC	5.03	230.40	yes	IBM2
umc2035	AC	5.03	231.00	yes	IBM2
PCO135705	C	5.03	232.17	no	INDEL
rny(pcr)b		5.03	235.25	no	BNL 96
AY111142	C	5.03	235.60	yes	IBM2
cdo98a	C	5.03	239.60	yes	IBM2
umc1705		5.03	240.80	no	IBM2
mdh5		5.03	241.20	no	UMC 98
bnl5.02a		5.03	241.20	yes	IBM2
umc166a		5.03	241.20	no	UMC 98
umc83b	C	5.03	241.20	no	UMC 98
csu580b(mdh)		5.03	241.20	no	UMC 98
bnlg2309		5.03	241.25	no	BNL 2002
umc1048	AC	5.03	242.60	yes	IBM2
umc1557	C	5.03	245.10	no	IBM2
umc2294	AC	5.03	245.50	no	IBM2
umc1447	AC	5.03	247.60	yes	IBM2
AY109995		5.03	250.30	no	IBM2
AY109606	C	5.03	250.30	no	IBM2
cpn1	C	5.03	251.24	no	UMC 98
rz561b		5.03	251.24	no	UMC 98
cdo475d		5.03	251.24	no	UMC 98
uky2(P450)		5.03	251.24	no	UMC 98
px13	AC	5.03	251.59	no	SSR popI
lim175		5.03	254.00	yes	IBM2
bnlg1700		5.03	255.13	no	BNL 2002
hag101		5.03	256.10	no	ChromDB
std2b(dba)		5.03	256.76	no	UMC 98
rz892b(alt)		5.03	256.76	no	UMC 98
umc2295	C	5.03	257.80	yes	IBM2
umc1315	AC	5.03	260.20	yes	IBM2
umc1274	C	5.03	263.13	no	SSR popII
umc1151	AC	5.03	263.82	no	SSR popI
ufg49		5.03	265.10	yes	IBM2
bnl5.27		5.03	265.80	no	BNL 2002
umc43		5.03	266.30	yes	IBM2
umc1830		5.03	266.30	no	IBM2
bnl6.10		5.03	266.30	yes	IBM2
rgpc1122e(rpL15)		5.03	266.30	no	UMC 98
umc2296	AC	5.03	267.50	no	IBM2
umc1935	AC	5.03	267.70	yes	IBM2
mmp8		5.03	269.10	no	IBM2
umc1850		5.03	270.10	no	SSR popII
npi256		5.03	270.23	no	BNL 96
rz242b		5.03	270.50	yes	IBM2
umc1692	AC	5.03	271.50	no	IBM2
umc1475	AC	5.03	271.50	no	SSR popII
csu419		5.03	273.55	no	UMC 98
ucr1b(eif)		5.03	273.55	no	UMC 98
xet1		5.03	273.70	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1609	AC	5.03	275.90	yes	IBM2
uaz77		5.03	277.27	no	BNL 2002
umc1373		5.03	277.34	no	SSR popI
isu2192a		5.03	277.90	no	BNL 2002
umc2297	AC	5.03	279.10	yes	IBM2
umc1		5.03	280.80	yes	IBM2
cat1	C	5.03	280.80	no	UMC 98
csu338		5.03	280.80	no	UMC 98
npi275		5.03	280.80	no	BNL 2002
umc1784		5.03	281.00	no	SSR popII
umc1355	C	5.03	281.20	yes	IBM2
csu168a		5.03	281.54	no	BNL 2002
php20557b		5.03	281.90	no	IBM2
isu45b		5.03	282.00	no	IBM2
bnl1.380		5.03	283.22	no	BNL 2002
bnl7.43		5.03	283.44	no	BNL 2002
bnl6.22a		5.03	283.51	no	BNL 2002
mmp108a		5.03	284.30	yes	IBM2
umc1870	AC	5.03	285.50	no	IBM2
umc1731	AC	5.03	285.50	no	SSR popII
phi109188	AC	5.03	285.70	no	IBM2
bnl10.06		5.03	285.93	no	BNL 2002
ici287		5.03	285.93	no	BNL 96
ncr200b(rip)		5.03	286.28	no	UMC 98
umc1389	AC	5.03	286.50	yes	IBM2
umc1429	AC	5.03	286.60	no	IBM2
psr167		5.03	286.70	yes	IBM2
uaz186		5.04	287.94	no	BNL 2002
ncr(b70a)		5.03	288.49	no	BNL 2002
isu61e		5.03	288.70	no	IBM2
isu61c		5.03	288.90	no	IBM2
php15018		5.03	288.90	no	IBM2
php15024		5.03	289.30	yes	IBM2
ivr2		5.03	289.76	no	BNL 2002
npi213		5.03-5.04	290.08	no	BNL 2002
mmp154		5.03	290.20	no	IBM2
ufg60		5.03	291.20	yes	IBM2
uaz226(cat1)		5.04	291.83	no	BNL 2002
umc2063		5.03	292.60	no	SSR popII
AY104079	C	5.03	292.90	no	IBM2
umc1226	AC	5.03	292.96	no	SSR popI
gtc101		5.03	293.80	no	ChromDB
gtc102	C	5.03	293.80	no	ChromDB
uaz213a		5.04	294.85	no	BNL 2002
mmp58	C	5.03	295.00	yes	IBM2
bnlg150		5.04	297.40	no	BNL 2002
bnlg1902	AC	5.03	297.50	yes	IBM2
csu252a(cdc2)		5.03	297.73	no	UMC 98
knox6		5.04	298.03	no	BNL 2002
umc1110	AC	5.03	298.10	no	SSR popII
uwo4		5.04	299.25	no	BNL 2002
ncr(cat1)		5.03	299.25	no	BNL 96
csu720c		5.03	299.67	no	UMC 98
csu652(rpL27)	C	5.03	299.67	no	UMC 98
uaz275		5.04	301.60	no	UMC 98
umn388		5.04	301.60	no	UMC 98
bnl4.36	C	5.04	301.60	yes	IBM2
csu283b		5.04	301.60	no	UMC 98
csu305a		5.04	301.60	no	UMC 98
csu315a		5.04	301.60	no	UMC 98
csu670	C	5.04	301.60	no	UMC 98
csu660b	C	5.04	301.60	no	UMC 98
csu377b(ubi)		5.04	301.60	no	UMC 98
uaz132a(dts)		5.04	301.60	no	UMC 98
csu36b(rpL19)		5.04	301.60	no	UMC 98
csu774(lhcb)	AC	5.04	301.60	no	UMC 98
sbp1		5.04	306.62	no	SSR popII
umc2066		5.04	306.62	no	SSR popII
umc2373		5.04	306.62	no	SSR popII
umc2400		5.04	306.62	no	SSR popII
umc1815	C	5.04	306.62	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2298	AC	5.04	307.00	yes	IBM2
umc40		5.04	308.20	yes	IBM2
umc250		5.04	309.60	no	UMC 98
csu562b(ubi)		5.04	309.60	no	UMC 98
umc2299	AC	5.04	310.00	no	IBM2
mmp60		5.04	310.20	yes	IBM2
umc1563	C	5.04	311.30	no	SSR popII
umc2406	C	5.04	311.30	no	SSR popII
asg51a		5.04	312.80	no	UMC 98
bnlg1829c		5.04	312.80	no	IBM1
rz87(clp)		5.04	312.80	yes	IBM2
umc1283	AC	5.04	313.28	no	SSR popI
bnlg1892c	C	5.04	313.30	no	IBM2
umc1629		5.04	313.98	no	SSR popII
umc1860		5.04	313.98	no	SSR popII
umc1591	AC	5.04	314.10	yes	IBM2
umc1224		5.04	314.64	no	SSR popII
umc2300	AC	5.04	315.20	no	IBM2
umc2301	AC	5.04	315.30	no	IBM2
umc2302	AC	5.04	316.80	yes	IBM2
umc1060	AC	5.04	317.60	yes	IBM2
umc1162	AC	5.04	317.66	no	SSR popI
umc2407		5.04	317.99	no	SSR popII
umc1990		5.04	318.90	yes	IBM2
BE639933	C	5.04	320.10	no	IBM2
umc1747	C	5.04	321.00	yes	IBM2
bnlg603	AC	5.04	321.00	no	SSR popI
uwo7		5.04	321.39	no	BNL 2002
uwo6		5.04	321.39	no	BNL 96
a2	C	5.04	321.61	no	BNL 2002
isu2191j		5.04	321.62	no	BNL 2002
dupssr1		5.02	321.63	no	BNL 2002
bnl17.30a		5.04	321.90	no	BNL 2002
bnlg1287		5.04	321.94	no	BNL 2002
rny2(rita)		5.03-5.04	322.10	no	BNL 2002
bnlg1208	AC	5.04	323.10	yes	IBM2
php20589		5.04	323.70	no	IBM2
lim4		5.04	324.30	yes	IBM2
mip1		5.04	324.62	no	UMC 98
asg43	C	5.04	324.62	no	UMC 98
bnl7.71		5.04	324.62	no	UMC 98
csu241a		5.04	324.62	no	UMC 98
dupssr10	AC	5.04	324.62	no	UMC 98
csu862a(rpL11)		5.04	324.62	no	UMC 98
bnlg2323		5.04	328.50	yes	IBM2
bt1		5.04	328.99	no	BNL 2002
npi408		5.04	328.99	no	BNL 2002
npi424		5.04	328.99	no	BNL 2002
npi571		5.04	328.99	no	BNL 2002
npi449a		5.04	331.40	yes	IBM2
rz476b		5.04	331.80	no	IBM2
mmp19		5.04	332.70	no	IBM2
AY110906	C	5.04	336.50	yes	IBM2
ris1		5.04	336.77	no	BNL 96
npi(pmr15)		5.04	336.77	no	BNL 2002
AY105029	AC	5.04	338.00	no	IBM2
csu302		5.04	339.40	yes	IBM2
dpg15b		5.03-5.04	339.62	no	BNL 2002
chs572		5.04	339.68	no	BNL 2002
npi53b		5.04	339.68	no	BNL 2002
bnlg653		5.04	340.99	no	BNL 2002
npi104a		5.04	342.24	no	BNL 2002
uaz70a		5.04	342.67	no	BNL 2002
umc1092	C	5.04	342.70	no	SSR popII
umc1192	AC	5.04	342.70	no	SSR popII
bnl31a		5.04	342.90	no	BNL 2002
PCO103687	C	5.04	344.20	no	INDEL
umc1349	C	5.04	346.50	yes	IBM2
bnlg1063c	C	5.03	346.92	no	BNL 2002
AY109532	AC	5.04	351.20	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
mpik33a		5.04	352.45	no	BNL 2002
amp3		5.04	354.81	no	BNL 96
koln2a(hox)		5.04	357.72	no	BNL 2002
myb3		5.04	358.90	yes	IBM2
ici273b		5.04	358.99	no	BNL 2002
uaz131		5.04	363.14	no	BNL 2002
koln10a(hox2)		5.04	365.17	no	BNL 2002
umc1332		5.04	366.60	no	SSR popI
umc1221	AC	5.04	368.40	yes	IBM2
umc1975		5.04	370.79	no	SSR popII
csu308		5.04	371.20	yes	IBM2
csu765		5.04	371.20	no	UMC 98
dup(als2)		5.04	374.29	no	BNL 2002
uaz238(ppi)		5.04	374.29	no	BNL 96
uaz248b(his3)		5.05	375.52	no	BNL 2002
incw1	AC	5.04	376.40	yes	IBM2
csu600	AC	5.04	377.00	no	IBM2
umc1966	AC	5.04	377.90	no	IBM2
ucsd64h		5.04-5.05	379.13	no	BNL 2002
umc1482		5.05	383.80	yes	IBM2
npi295a		5.04	383.88	no	BNL 2002
bnl5.71a		5.05	387.00	yes	IBM2
mmc0081	AC	5.05	389.90	yes	IBM2
mpik14(Cin4)		5.05	390.91	no	BNL 2002
AY109682	AC	5.05	392.70	no	IBM2
phi333597	AC	5.05	394.40	yes	IBM2
bnl35a(blr)		5.04	394.61	no	BNL 2002
umc1348		5.04-5.05	396.10	no	SSR popI
umc1937		5.04-5.05	396.10	no	SSR popI
umc1822		5.05	396.60	yes	IBM2
umc2026	AC	5.05	397.00	yes	IBM2
PCO060271	C	5.05	400.89	no	INDEL
mmp47	AC	5.05	402.20	yes	IBM2
ufg18	C	5.05	404.00	no	IBM2
bnl10.12		5.05	404.34	no	BNL 96
umc1264	AC	5.05	404.90	yes	IBM2
csu1080a		5.05	406.20	no	UMC 98
csu93b	C	5.05	406.20	no	SSR popII
PCO078116	C	5.05	408.36	no	INDEL
rz166(nac)		5.05	408.44	no	UMC 98
umc2303	AC	5.05	408.80	yes	IBM2
tda62a		5.05	410.01	no	UMC 98
std16b(blr)		5.05	410.01	no	UMC 98
umc1155	AC	5.05	410.80	yes	IBM2
csu713		5.05	412.18	no	UMC 98
csu95b	C	5.05	412.18	no	UMC 98
CL11475_1	C	5.05	413.29	no	INDEL
csu173	C	5.05	413.60	no	IBM2
gl8	AC	5.05	413.80	no	UMC 98
nbp35	C	5.05	413.80	yes	IBM2
rgpc174a		5.05	413.80	no	UMC 98
gte102		5.05	414.07	no	ChromDB
uaz79		5.05	414.13	no	BNL 2002
mmp90		5.05	414.70	yes	IBM2
PCO099796	C	5.05-5.06	415.78	no	INDEL
umc1800		5.05	415.95	no	SSR popII
CL16923_1	C	5.05-5.06	419.02	no	INDEL
mmc0282	AC	5.05	419.09	no	SSR popII
npi237		5.05	419.26	no	BNL 2002
umc2386	C	5.05	423.27	no	SSR popII
uaz261a		5.05	425.07	no	BNL 2002
uaz190(gpc)		5.05	425.07	no	BNL 96
bnlg1847		5.06	425.21	no	BNL 2002
serk2	C	5.05	428.30	yes	IBM2
umc1687	AC	5.05	429.19	no	SSR popII
pal1		5.05	436.68	no	UMC 98
asg71		5.05	436.68	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu1105		5.05	436.68	no	UMC 98
umc1502		5.05	439.29	no	SSR popII
bnlg278		5.05	441.69	no	SSR popI
umc1853		5.05	449.40	no	SSR popII
uaz164a		5.05-5.06	450.22	no	BNL 96
csu550		5.05	453.42	no	UMC 98
bnlg1237		5.05-5.06	454.01	no	BNL 2002
umc1722	AC	5.05	456.01	no	SSR popII
mmp104		5.05	457.40	yes	IBM2
bnl5.40		5.06	458.44	no	UMC 98
rpl19		5.05	461.79	no	UMC 98
AY110063	C	5.05	467.20	yes	IBM2
umc126a	C	5.06	469.60	yes	IBM2
AY109938	C	5.06	470.10	yes	IBM2
mmc0481	AC	5.06	476.60	yes	IBM2
umc2305	AC	5.06	479.70	no	IBM2
umc54	C	5.06	481.20	yes	IBM2
csu777		5.06	481.20	no	UMC 98
umc14c		5.06	481.20	no	UMC 98
umc156b	C	5.06	481.20	no	BNL 2002
cdo395b(ypt)		5.06	481.20	no	UMC 98
nfd104a		5.06	483.73	no	ChromDB
umc1752	AC	5.06	488.40	yes	IBM2
uaz78		5.05	489.59	no	BNL 2002
npi562		5.06	491.49	no	BNL 2002
umc1941	AC	5.06	492.60	no	IBM2
umc141		5.06	493.26	no	UMC 98
umc1524	AC	5.06	493.50	yes	IBM2
umc1680	AC	5.06	493.50	yes	IBM2
umc51a	AC	5.06	493.70	no	IBM2
csu434		5.06	493.96	no	UMC 98
csu440	C	5.06	493.96	no	UMC 98
php20531		5.06	494.20	yes	IBM2
bnlg1246a		5.05	495.77	no	BNL 2002
csh10a(cycII)		5.06	496.87	no	UMC 98
uaz138c		5.06	497.13	no	BNL 2002
csu26c(ant)		5.05	498.71	no	BNL 2002
npi458a		5.06	499.70	yes	IBM2
zag5		5.06	499.95	no	BNL 2002
umc2306	AC	5.06	500.10	yes	IBM2
rgpg57		5.06	500.57	no	UMC 98
umc262		5.06	500.57	no	UMC 98
umc253a		5.06	500.57	no	UMC 98
bnlg609	AC	5.06	500.70	yes	IBM2
uaz215a(odo)		5.06	500.70	no	BNL 2002
asg81a		5.06	504.54	no	UMC 98
csu587b		5.06	504.54	no	UMC 98
csu615a	AC	5.06	504.54	no	UMC 98
uaz204		5.06	510.88	no	BNL 2002
PCO111982	C	5.06-5.07	511.07	no	INDEL
rz567a(klc)	C	5.06	511.30	yes	IBM2
ici229		5.06	511.87	no	BNL 96
php20566		5.06	512.00	yes	IBM2
sdg117b	C	5.06	512.00	no	ChromDB
uaz254a		5.06	515.75	no	BNL 2002
mmp169		5.06	516.30	yes	IBM2
umc2216		5.06	518.37	no	SSR popI
csu1164		5.06	520.10	no	UMC 98
csu643a		5.06	520.10	no	UMC 98
csu907b		5.06	520.10	no	UMC 98
rz273b(ant)		5.06	520.10	yes	IBM2
cdo507b(ant)		5.06	520.10	yes	IBM2
csu26a(ant)		5.06	520.10	no	UMC 98
uaz144b		5.06	524.40	no	BNL 2002
gln4	AC	5.06	528.70	yes	IBM2
npi442		5.06	530.00	yes	IBM2
umc108	AC	5.07	536.60	yes	IBM2
bnl9.07b		5.07	536.60	no	BNL 2002
psr3b		5.07	537.57	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2201	C	5.07	542.05	no	SSR popI
bnlg1346		5.07	544.64	no	BNL 2002
npi253c		5.07	550.21	no	BNL 2002
umc1537	AC	5.07	553.61	no	SSR popII
umc2198	C	5.07	554.92	no	SSR popI
klp5		5.07	555.46	no	UMC 98
asg84b		5.07	555.46	no	UMC 98
mpik10		5.07	557.09	no	BNL 2002
bnlg1306		5.07	557.09	no	BNL 2002
bnlg2305		5.07	557.09	no	BNL 2002
umc68a		5.07	557.09	no	BNL 96
umc241		5.07	559.61	no	UMC 98
umc1646		5.07	566.30	no	SSR popI
umc1375		5.07	571.66	no	SSR popI
umc2013		5.07	571.66	no	SSR popI
csu288		5.07	574.70	no	UMC 98
asg9b		5.07	578.47	no	UMC 98
lhcb4		5.07	578.47	no	UMC 98
ppp1	C	5.07	578.47	no	UMC 98
asg74a		5.07	578.47	no	UMC 98
cdo516a		5.07	578.47	no	UMC 98
csu1074		5.07	578.47	no	UMC 98
ucsd106e		5.05	583.55	no	BNL 2002
agrc563a		5.07	586.39	no	UMC 98
csu672a	C	5.07	586.39	no	UMC 98
wsu(nia5)		5.07	588.07	no	BNL 96
bnlg1118	AC	5.07	590.40	yes	IBM2
pbs6a		5.07	590.95	no	BNL 2002
bnlg1416		5.07	592.07	no	BNL 2002
nnr2		5.07	599.50	yes	IBM2
umc1072	AC	5.07	600.00	yes	IBM2
AY110369	AC	5.07	600.40	no	IBM2
mmp118		5.07	601.30	yes	IBM2
bnl5.24a		5.08	609.40	yes	IBM2
bnlg118	AC	5.08	609.40	yes	IBM2
bnlg1597c		5.08	613.80	yes	IBM2
ias13b		5.09	615.76	no	BNL 2002
mmp170		5.08	619.70	yes	IBM2
umc1792	AC	5.08	625.80	yes	IBM2
uaz71b		5.08	628.30	no	BNL 2002
AY110413		5.08	630.80	yes	IBM2
npi288a		5.08	632.60	yes	IBM2
umc57d		5.08	638.50	no	IBM2
php20523b		5.08	638.80	yes	IBM2
umc1225	AC	5.08	641.40	yes	IBM2
uaz240a		5.08	641.75	no	BNL 2002
AY110182	AC	5.08	643.60	no	IBM2
mmp175		5.08	645.40	yes	IBM2
got2		5.08	648.23	no	BNL 96
csu834(mss)		5.08	649.24	no	UMC 98
csu799(rpCL9)		5.08	656.15	no	UMC 98
AY105910	AC	5.08	656.70	yes	IBM2
bnlg1695		5.07	657.08	no	BNL 2002
bnlg1885		5.07	657.08	no	BNL 2002
csu695(rpL9)		5.08	657.14	no	UMC 98
umc104b		5.08	660.10	yes	IBM2
bnlg389		5.09	661.56	no	BNL 2002
rz446b		5.08	661.80	yes	IBM2
bnlg386		5.09	661.94	no	BNL 2002
AW065811		5.08	664.30	yes	IBM2
bnlg1711		5.07	666.54	no	BNL 2002
php10017	AC	5.09	669.40	yes	IBM2
umc1829		5.09	671.53	no	SSR popII
umc2307		5.09	672.60	yes	IBM2
umc2308	C	5.09	672.60	no	IBM2
mmp109		5.09	676.70	no	IBM1
umc1153	AC	5.09	676.70	yes	IBM2
umc2209	C	5.09	678.29	no	SSR popI
umc49f	C	6.00	0.00	yes	IBM2
csu150a		6.00	4.57	no	BNL 96
fdx2		6.00	9.10	no	SSR popI
isu139		6.00	17.30	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc2208		6.00	17.39	no	SSR popI
umc1143	AC	6.00	17.50	yes	IBM2
bnlg238		6.00	23.20	yes	IBM2
bnlg161b		6.00	23.20	yes	IBM2
csu926(frk)		6.00	25.75	no	UMC 98
umc2310	AC	6.00	27.60	yes	IBM2
umc2309	AC	6.00	27.80	no	IBM2
PCO069699	C	6.00-6.01	39.27	no	INDEL
umc2068		6.00	47.80	no	SSR popII
agrp144		6.00	49.00	no	IBM2
uaz18a		6.00	51.97	no	BNL 2002
npi340a		6.00	51.97	no	BNL 96
rz143a(gpc)		6.00	56.70	yes	IBM2
rgpc174b		6.00	60.32	no	UMC 98
bnlg1433		6.01	60.64	no	BNL 2002
bnlg1246d		6.01	61.69	no	BNL 2002
bnlg1139		6.01	61.72	no	BNL 2002
csu178b		6.00	63.34	no	UMC 98
csu710d(apx)		6.00	63.34	no	UMC 98
AY110100	AC	6.00	63.60	yes	IBM2
umc1883		6.00	63.70	no	SSR popII
umc1996	C	6.00	63.70	no	SSR popII
mpik11b		6.01	64.87	no	BNL 2002
nor		6.01	64.87	no	BNL 96
mpik(DH7)		6.01	64.87	no	BNL 2002
uiu1b(pog)		6.01	64.87	no	BNL 2002
isu2232h		6.01	64.90	no	BNL 2002
bnlg2097		6.01	64.95	no	BNL 2002
csu70		6.01	66.40	no	UMC 98
umc159a		6.00	66.40	no	UMC 98
umc85a	AC	6.01	66.40	yes	IBM2
gpc2	AC	6.00-6.01	66.40	no	SSR popII
isu85a		6.01	67.70	yes	IBM2
pic7b		6.05	68.50	no	BNL 2002
uaz102		6.01	68.83	no	BNL 2002
bnl17.28		6.01	68.83	no	BNL 2002
umc1606	AC	6.01	69.20	yes	IBM2
sdg102b		6.01	69.20	no	ChromDB
hon104b	C	6.01	69.20	no	ChromDB
uaz269c(kri)		6.01	69.61	no	BNL 2002
umc1753	C	6.00-6.01	70.37	no	SSR popI
cdo1173c		6.01	71.10	yes	IBM2
uaz258a		6.01	71.20	no	BNL 2002
umc2311	AC	6.01	71.50	no	IBM2
mmp163		6.01	71.80	no	IBM2
bnlg1600		6.00	71.89	no	BNL 2002
bnlg1371	AC	6.01	72.70	yes	IBM2
bnl6.29a		6.01	73.30	yes	IBM2
bnlg1165		6.01	73.87	no	BNL 2002
npi235a		6.01	73.87	no	BNL 96
bnlg1043		6.00	73.94	no	BNL 2002
uaz150		6.01	74.80	no	BNL 2002
uaz197b(cdpk)		6.01	74.80	no	BNL 2002
isu1410b		6.01	75.39	no	BNL 2002
umc2312	AC	6.01	75.80	yes	IBM2
bnlg1867	AC	6.01	78.30	yes	IBM2
mmp13		6.01	79.60	no	IBM2
pge23		6.01	80.17	no	UMC 98
csu699		6.01	80.17	no	UMC 98
csu700		6.01	80.17	no	UMC 98
bnl7.28		6.01	80.17	no	UMC 98
bnlg426	AC	6.01	80.17	no	UMC 98
cdo580b(ivd)		6.01	80.17	no	UMC 98
umc1229	AC	6.01	80.70	yes	IBM2
umc1625		6.01	81.72	no	SSR popI
csu680e	C	6.01	83.27	no	UMC 98
uaz80(iron)		6.01	84.32	no	BNL 2002
bnlg1432		6.01	84.61	no	BNL 2002
tug2		6.01	84.61	no	BNL 96

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
php20528		6.01	85.50	yes	IBM2
rz390d(cyb5)		6.01	86.30	no	IBM2
isu1410j		6.01	86.50	no	BNL 2002
pic7a		6.01	86.54	no	BNL 2002
umc2196	C	6.01	86.83	no	SSR popI
cdo545		6.01	86.90	yes	IBM2
csu243		6.01	87.05	no	UMC 98
csu809		6.01	87.05	no	UMC 98
agrr221		6.01	87.05	no	UMC 98
csu1120		6.01	87.05	no	UMC 98
psr160a		6.01	87.70	no	IBM2
php20854		6.01	87.70	yes	IBM2
uaz197a(cdpk)		6.01	87.74	no	BNL 2002
npi594a		6.01	88.11	no	BNL 2002
umc2313	AC	6.01	91.90	yes	IBM2
pgd1		6.01	96.00	no	UMC 98
uck1	C	6.01	96.00	yes	IBM2
csu1187		6.01	96.00	no	UMC 98
csu1196		6.01	96.00	no	UMC 98
csu94a		6.01	97.38	no	UMC 98
umc36c		6.01	97.38	no	UMC 98
umc1832		6.01	97.80	no	IBM2
umc2074	AC	6.01	98.00	no	IBM2
umc1444	C	6.01	98.40	no	IBM2
AY110213	AC	6.01	98.40	no	IBM2
bnlg1641	AC	6.01	98.40	no	IBM2
umc1133	AC	6.01	98.60	yes	IBM2
umc2315		6.01	98.80	no	IBM2
umc2056	AC	6.01	99.00	no	IBM2
umc2314	AC	6.01	99.30	yes	IBM2
nfa101		6.01	99.30	no	ChromDB
uaz232b(sci)		6.01	100.30	yes	IBM2
zp15		6.01	100.91	no	BNL 2002
uaz23a		6.01	100.91	no	BNL 2002
bnlg249		6.01	100.91	no	BNL 2002
isu1774a		6.01	100.91	no	BNL 2002
npi606		6.01	100.91	no	BNL 96
mmp160		6.01	101.90	yes	IBM2
mmp76		6.01	103.80	yes	IBM2
umc1498	AC	6.01	104.45	no	SSR popI
ufg69	C	6.01	104.80	yes	IBM2
mmp20		6.01	105.90	yes	IBM2
bnl6.22b		6.02	107.37	no	UMC 98
csu56a(ohp)	C	6.02	107.37	no	UMC 98
csu146a(cdc48)		6.02	107.37	no	UMC 98
mmp10		6.01	110.40	yes	IBM2
cyc3	AC	6.01	114.25	no	SSR popII
mmp4		6.01	116.20	yes	IBM2
mmp108b		6.01	118.30	yes	IBM2
umc1517		6.01	119.19	no	SSR popII
umc1195		6.01	120.41	no	SSR popII
y1	AC	6.01	120.50	yes	IBM2
mpik33d		6.01	120.50	no	BNL 2002
si1		6.02	120.57	no	BNL 2002
bnlg1188		6.01	120.66	no	BNL 2002
rz444e	C	6.02	123.70	yes	IBM2
umc59a	AC	6.02	124.12	no	SSR popII
umc1376		6.01 - 6.02	124.12	no	SSR popII
enp1		6.02	124.50	no	UMC 98
agrr189		6.02	124.50	no	IBM2
csu548		6.02	124.50	no	UMC 98
oec33		6.02	124.60	no	UMC 98
csu395a	C	6.02	124.60	no	UMC 98
umc51b		6.02	124.64	no	UMC 98
umn361		6.02	124.64	no	UMC 98
bnlg1047b		6.01	124.77	no	BNL 2002
bnlg1422		6.01	124.81	no	BNL 2002
mpik1		6.02	124.87	no	BNL 2002
bnlg107		6.01	124.87	no	BNL 2002
bnl28(sbe1)		6.02	124.87	no	BNL 2002
umc1006	AC	6.02	125.00	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu183a(cdc48)		6.02	125.58	no	SSR popI
mir2	AC	6.02	126.46	no	SSR popII
bnlg1538		6.01	127.02	no	BNL 2002
npi373		6.02	127.02	no	BNL 96
mir1		6.02	127.10	yes	IBM2
mir4(thp)		6.02	127.10	no	UMC 98
uiu5(chn)		6.02	127.10	no	UMC 98
uiu6(chn)		6.02	127.10	no	UMC 98
ucr1a(eif)		6.02	127.10	no	UMC 98
rz242a		6.02	127.80	yes	IBM2
agrr87a		6.02	127.80	no	UMC 98
umc1083	AC	6.02	127.80	no	IBM2
psu1a(spe)		6.02	128.18	no	UMC 98
csu309(atpc)		6.02	128.57	no	UMC 98
pbs8		6.01	128.97	no	BNL 2002
phi077		6.01	129.05	no	BNL 2002
saur1		6.02	129.06	no	SSR popII
npi377		6.02	129.57	no	BNL 2002
bnlg2151		6.02	129.71	no	BNL 2002
mpik18		6.02	129.77	no	BNL 2002
uaz162		6.02	129.96	no	BNL 2002
umc1656	AC	6.02	133.40	yes	IBM2
mmp117		6.02	139.50	yes	IBM2
php20045a		6.02	142.12	no	BNL 96
mmp51		6.02	143.20	yes	IBM2
sdg102c		6.02	145.10	no	ChromDB
umc1257	C	6.02	145.70	yes	IBM2
umc1628		6.02	147.60	no	SSR popI
psr129b		6.02	147.90	yes	IBM2
bnlg2191	AC	6.02	148.70	no	IBM2
bnlg1753		6.01	148.86	no	BNL 2002
bnlg391		6.01	148.93	no	BNL 2002
uaz237b(prc)		6.01	148.95	no	BNL 2002
mwg645b		6.01	148.96	no	BNL 2002
uaz169		6.01	149.29	no	BNL 2002
bcd98f		6.01	149.32	no	BNL 2002
uaz233b(act)		6.01	149.32	no	BNL 2002
uaz233d(act)		6.01	149.32	no	BNL 2002
jpsb108		6.02	151.10	yes	IBM2
csu605		6.02	151.27	no	UMC 98
php06007		6.02	151.27	no	UMC 98
csu747b(arf)	C	6.02	151.27	no	UMC 98
mmp65		6.02	152.60	no	IBM2
sbp3	C	6.02	153.70	yes	IBM2
uaz227(end)		6.01	153.78	no	BNL 2002
npi100		6.00-6.01	154.86	no	BNL 2002
csu923(sec61)		6.02	158.70	yes	IBM2
npi393		6.03	161.87	no	SSR popI
umc2316	AC	6.02-6.03	166.60	no	IBM2
umc1887	AC	6.03-6.04	166.80	no	IBM2
AY104775	AC	6.04	167.60	yes	IBM2
uaz106a		6.03	169.35	no	BNL 96
csu226b(elf1A)		6.03	170.96	no	UMC 98
AY111964	AC	6.04	171.20	yes	IBM2
csu199a		6.03	172.41	no	UMC 98
bnl(tas1i)		6.04	173.71	no	BNL 2002
npi98b		6.03	175.68	no	BNL 96
umc65a	AC	6.04	181.90	yes	IBM2
std6b(dba)		6.03-6.04	181.90	no	UMC 98
umc1796		6.04	189.50	yes	IBM2
umc1918	AC	6.04	189.90	no	IBM2
rz476d		6.04	191.30	yes	IBM2
bnlg480		6.04	196.12	no	BNL 2002
npi223a		6.04	196.30	yes	IBM2
uaz160		6.04	196.66	no	BNL 2002
umc1105	AC	6.04	199.00	yes	IBM2
umc1979	AC	6.04	200.30	yes	IBM2
uaz161a(elf)		6.04	202.74	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1857	AC	6.04	203.20	yes	IBM2
PCO075489	C	6.04	204.62	no	INDEL
rgpc74b		6.04	207.68	no	UMC 98
si606044D05	C	6.04	208.86	no	INDEL
umc113b		6.04	209.63	no	BNL 2002
pl1	C	6.04	211.50	yes	IBM2
gta105		6.04	212.56	no	ChromDB
mmc0523		6.04	219.51	no	SSR popII
tug8		6.04	223.54	no	BNL 96
umc2006	AC	6.04	228.90	yes	IBM2
pic2a		6.04	229.71	no	BNL 2002
umc248b		6.04	230.01	no	UMC 98
agrr118a		6.04	232.64	no	UMC 98
npi253d		6.04	235.26	no	UMC 98
rz144b	AC	6.04	235.26	no	UMC 98
umc2317	C	6.04	235.80	yes	IBM2
dzs23		6.04	235.98	no	BNL 96
dup1375		6.04	236.12	no	BNL 2002
umc1614		6.04	236.94	no	SSR popII
tda51		6.04	238.18	no	UMC 98
rgpc643e		6.04	238.18	no	UMC 98
uat2(noi)		6.04	238.18	no	UMC 98
isu61f		6.04	238.70	yes	IBM2
hex2		6.04	239.60	no	BNL 96
umc21		6.05	240.80	yes	IBM2
tug6		6.04	240.80	no	BNL 2002
npi617		6.04	240.80	no	BNL 2002
bnlg1617		6.05	240.80	no	BNL 2002
bnlg1922		6.05	240.80	no	BNL 2002
PCO152525	C	6.04-6.05	241.23	no	INDEL
isu111a		6.05	243.30	no	IBM2
csu578a		6.05	243.79	no	UMC 98
csu1083a		6.05	243.79	no	UMC 98
umc2318	C	6.05	244.70	no	IBM2
umc2319	AC	6.05	244.90	yes	IBM2
umc1795	C	6.05	245.29	no	SSR popII
chr117d		6.05	246.60	no	ChromDB
ufg11	C	6.05	248.10	yes	IBM2
umc2055		6.04-6.05	248.62	no	SSR popI
uaz280c(ppp)		6.05	251.70	yes	IBM2
asg52c		6.05	252.44	no	UMC 98
csu835		6.05	252.44	no	UMC 98
csu382a(cld)	AC	6.05	252.44	no	UMC 98
bnlg1154	AC	6.05	253.00	no	IBM2
npi265		6.05	253.00	no	BNL 2002
umc1250	AC	6.05	254.50	yes	IBM2
umc1751		6.05	254.50	no	SSR popII
ucsd78a(zag1)		6.05	255.65	no	BNL 2002
psr108		6.04	255.89	no	BNL 2002
tug7		6.04	256.39	no	BNL 2002
uaz244a(prh)		6.04	258.61	no	BNL 2002
ici96		6.04	258.87	no	BNL 2002
csu481		6.05	261.10	yes	IBM2
csu310(ptk)		6.05	262.11	no	UMC 98
PCO146525	C	6.05	262.46	no	INDEL
csu225		6.05	262.79	no	UMC 98
umc265(ptk)		6.05	263.97	no	UMC 98
bnl3.03		6.05	263.97	no	BNL 96
umc1826	C	6.05	267.70	yes	IBM2
zag1	AC	6.05	269.80	yes	IBM2
csu259		6.05	269.80	no	UMC 98
umc1352	C	6.05	271.50	yes	IBM2
npi224i		6.04	272.10	no	BNL 2002
AI665560	AC	6.05	273.20	no	IBM2
umc1413	AC	6.05	277.10	yes	IBM2
uaz220(elf)		6.05	277.33	no	BNL 2002
bnlg2249	AC	6.05	278.00	no	IBM2
bnl15.37a		6.05	279.83	no	BNL 2002
csu360(elf1A)	C	6.05	281.45	no	UMC 98
umc1114		6.05	281.70	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
pge20		6.05	282.07	no	BNL 2002
umc137b		6.05	283.65	no	BNL 2002
umc1314	AC	6.05	284.30	no	IBM2
csu1065		6.05	286.14	no	UMC 98
csu782	C	6.05	286.14	no	UMC 98
rgpc74a		6.05	286.14	no	UMC 98
csu1189		6.05	286.67	no	UMC 98
AY110542	AC	6.05	290.60	yes	IBM2
PCO134814	C	6.05	291.08	no	INDEL
dhn1	C	6.05	291.88	no	UMC 98
uky3b(P450)		6.05	291.88	no	UMC 98
csu116a(elf1)		6.05	291.88	no	UMC 98
ynh(me2)		6.05	293.69	no	BNL 96
umc2141	AC	6.05	295.40	yes	IBM2
AY110435	AC	6.05	296.30	no	IBM2
umc1379	C	6.05	297.10	yes	IBM2
npi560		6.05	299.20	yes	IBM2
ncr(sod3a)		6.05	299.24	no	BNL 2002
umc2040	C	6.05	299.26	no	SSR popII
csu71a		6.01	299.34	no	BNL 2002
csu236		6.05	301.80	no	UMC 98
csu60a		6.05	301.80	no	UMC 98
csu807b		6.05	301.80	no	UMC 98
npi294c		6.05	301.80	no	UMC 98
umc1388	C	6.05	302.00	yes	IBM2
mmp62		6.05	304.10	yes	IBM2
mmc0241	C	6.05	306.59	no	SSR popII
npi616a		6.05	308.30	yes	IBM2
AY110260	AC	6.05	310.70	yes	IBM2
npi252	AC	6.05	312.00	yes	IBM2
csu760a		6.05	312.07	no	UMC 98
umc46		6.05	312.07	no	BNL 96
bcd855b(ext)	C	6.05	312.07	no	UMC 98
csu666(his2A1)		6.05	312.07	no	UMC 98
dup400(pac)		6.05	313.32	no	BNL 96
jpsb107b		6.05	314.00	yes	IBM2
AY109873	C	6.05	314.80	no	IBM2
ufg16		6.05	315.40	no	IBM1
bnlg1174	AC	6.05	315.40	yes	IBM2
chs562		6.05	317.40	no	BNL 96
bnl17.26		6.05	317.44	no	BNL 2002
AY110050	AC	6.05	318.60	no	IBM2
umc2321	AC	6.05	319.00	no	IBM2
chr116a		6.05	319.50	no	ChromDB
bnlg1702		6.05	320.70	yes	IBM2
AY110873	AC	6.05	321.90	no	IBM2
csu812		6.05	322.67	no	UMC 98
umc2320	AC	6.05	322.90	yes	IBM2
csu1095		6.05	323.36	no	UMC 98
csu1101a		6.05	323.36	no	UMC 98
mbd101b	C	6.05	323.36	no	ChromDB
pdk1	AC	6.05	323.50	yes	IBM2
umc1462		6.06	325.10	no	SSR popI
pmg1	AC	6.05	325.90	yes	IBM2
rgpc43b		6.05	330.59	no	UMC 98
csu581b(tua)		6.05	330.59	no	UMC 98
umc2065	AC	6.05	335.71	no	SSR popII
npi608		6.05	342.70	yes	IBM2
npi63b		6.05	342.70	no	BNL 2002
bnl5.47a		6.05	344.42	no	BNL 96
umc1805		6.05	346.22	no	SSR popII
umc1474	AC	6.06	356.72	no	SSR popII
bnl8.06b		6.05	359.57	no	BNL 96
uaz400		6.05	362.00	no	IBM2
uaz121a		6.05	362.40	yes	IBM2
mmp145		6.05	367.40	yes	IBM2
bnl17.22		6.05	371.76	no	BNL 96
bnlg1732	C	6.05	373.80	yes	IBM2
rz444d	C	6.05	375.80	yes	IBM2
isu1410i		6.05	376.98	no	BNL 2002
mmp150		6.05	378.40	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
si606039C09	C	6.05-6.06	378.99	no	INDEL
uaz209		6.05	379.02	no	BNL 2002
umc152c		6.05	380.12	no	UMC 98
bnlg345		6.06	381.41	no	BNL 2002
umc38a	C	6.06	385.80	yes	IBM2
bnlg1443		6.05	385.80	no	BNL 2002
cdo89(aat)		6.05-6.06	385.80	no	UMC 98
bnl8.08c		6.06	387.24	no	BNL 2002
umc1912	AC	6.06	388.70	yes	IBM2
umc1859	AC	6.06	391.40	yes	IBM2
roa2	C	6.05-6.06	393.76	no	SSR popI
umc1463	C	6.06	393.90	yes	IBM2
uaz256		6.06	393.96	no	BNL 96
umc160a		6.06	393.96	no	BNL 96
umc1762	C	6.06	394.10	yes	IBM2
umc1424		6.06	396.06	no	SSR popI
CL10251_1	C	6.06	396.78	no	INDEL
dup1373		6.06	398.17	no	BNL 2002
umc2162	C	6.06	398.50	yes	IBM2
gtb101		6.06	399.20	no	ChromDB
sdg111a		6.06	399.20	no	ChromDB
asg50a		6.06	400.30	no	UMC 98
umc138a		6.06	400.30	no	UMC 98
ufr1(cal)		6.06	400.30	no	UMC 98
bcd738a(pgk)	C	6.06	400.30	yes	IBM2
mmp1		6.06	401.70	no	IBM2
umc2389	C	6.06	404.12	no	SSR popII
umc2322	C	6.06	404.40	yes	IBM2
AY104923	C	6.06	410.30	yes	IBM2
bnl8.08j		6.06	413.43	no	BNL 2002
npi280		6.06	413.43	no	BNL 96
umc1520		6.06	414.48	no	SSR popII
uaz19d		6.06	419.46	no	BNL 2002
csu727(trh)		6.06	419.46	no	UMC 98
lim379		6.06	420.40	yes	IBM2
php20904		6.06	421.90	no	UMC 98
lim151		6.06	423.00	yes	IBM2
gte101	C	6.06	423.70	no	ChromDB
uaz243b(atpb)		6.06	424.37	no	BNL 2002
uaz43e		6.06	426.38	no	BNL 2002
AY105728	AC	6.06	426.40	yes	IBM2
AY105785	C	6.06	427.20	yes	IBM2
psr162		6.06	428.40	yes	IBM2
umc2375	C	6.06-6.07	431.04	no	SSR popII
csu841a		6.06	433.05	no	UMC 98
umc2170	AC	6.06	435.10	yes	IBM2
bnl17.12		6.06	437.14	no	BNL 96
asg6a		6.06	441.80	yes	IBM2
hox2		6.06-6.07	444.20	no	UMC 98
umc237		6.06-6.07	444.20	no	UMC 98
umc132a(chk)	AC	6.07	444.20	yes	IBM2
umc1296		6.06-6.07	444.20	no	SSR popII
csu238b(apx)		6.06-6.07	444.20	no	UMC 98
hdt103	C	6.07	444.70	no	ChromDB
nfa102		6.07	447.90	yes	IBM2
mmp50		6.07	448.50	no	IBM2
umc266c(ptk)		6.07	450.13	no	UMC 98
phi299852	AC	6.07	450.70	yes	IBM2
mlg3	AC	6.07	452.70	yes	IBM2
bcd828b(atpb)		6.07	456.07	no	UMC 98
asg18		6.07	462.00	no	UMC 98
umc1490	AC	6.07	466.50	yes	IBM2
asg47		6.07	469.33	no	UMC 98
umc1897		6.07	471.61	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY110400	C	6.07	472.30	yes	IBM2
npi419a		6.07	481.00	yes	IBM2
csu928		6.07	482.25	no	UMC 98
umc2323	C	6.07	483.50	no	IBM2
umc1779	C	6.07	484.29	no	SSR popII
umc246		6.07	490.63	no	UMC 98
umc238a		6.07	490.63	no	UMC 98
umc1248		6.07	491.24	no	SSR popII
mmp113		6.07	491.80	yes	IBM2
AY109797	AC	6.07	498.70	yes	IBM2
AY104289	AC	6.07	501.20	yes	IBM2
umc2165	AC	6.07	502.90	yes	IBM2
bnlg1759a	AC	6.07	503.40	yes	IBM2
uaz81		6.06	503.87	no	BNL 2002
uaz269d(kri)		6.07	504.46	no	BNL 2002
idh2		6.07	504.59	no	UMC 98
npi597a		6.07	504.59	no	BNL 2002
umc1350	C	6.07	504.80	yes	IBM2
bnlg1740	C	6.07	510.60	yes	IBM2
csu291		6.07	511.22	no	UMC 98
csu293		6.07	511.22	no	UMC 98
umc62	C	6.07	513.80	yes	IBM2
ufg(vp2274b)		6.06	513.80	no	BNL 2002
AY109996		6.07	521.90	yes	IBM2
mdh2		6.07	524.83	no	UMC 98
umc1621	C	6.07	526.01	no	SSR popII
npi561		6.07	526.80	yes	IBM2
bnlg1136	C	6.07	531.80	yes	IBM2
php20599		6.07	532.80	yes	IBM2
umc133b		6.08	532.80	no	BNL 2002
mmp105		6.07	534.60	yes	IBM2
umc1653	C	6.07	534.60	no	IBM2
agp2	C	6.07	536.40	yes	IBM2
bnlg1521		6.07-6.08	537.12	no	BNL 2002
umc28		6.08	538.45	no	UMC 98
asg7a		6.08	538.45	no	SSR popII
uaz229		6.08	538.45	no	BNL 2002
ufg(agp1)		6.08	538.45	no	BNL 2002
uaz123c		6.07-6.08	538.45	no	BNL 2002
PCO068526	C	6.08	540.18	no	INDEL
umc1127		6.07-6.08	540.47	no	SSR popII
chr121		6.07	541.00	no	ChromDB
umc2059	AC	6.08	542.70	yes	IBM2
umc2324	AC	6.08	544.50	yes	IBM2
cdo345c	C	6.08	545.80	yes	IBM2
csu68a(mcf)		6.08	548.57	no	UMC 98
cdo202a(mcf)	C	6.08	548.70	yes	IBM2
umc134a		6.08	549.33	no	UMC 98
uaz240b		6.08	559.39	no	BNL 96
uor1a(rpS12)		6.08	579.29	no	UMC 98
bnlg1642		7.00-7.01	-27.20	no	BNL 2002
umc7Stelo		7.00	-7.10	no	UMC 98
ucsd106b		7.00	-3.80	no	BNL 96
bnlg1686		7.00	-1.40	no	BNL 2002
bnlg1367	AC	7.00	-0.05	no	BNL 2002
umc2177		7.00	0.00	yes	IBM2
csu582		7.00	2.70	yes	IBM2
hsp3	AC	7.00	5.10	no	IBM2
bnl25		7.00	6.76	no	BNL 2002
npi576a		7.00	10.45	no	BNL 2002
umc1241	AC	7.00	13.80	yes	IBM2
npi567		7.00	14.80	no	BNL 96
umc1788	AC	7.00	19.90	no	SSR popII
umc1642	AC	7.00	27.20	no	IBM2
umc1378	AC	7.00	27.40	yes	IBM2
rs1		7.00	30.40	no	BNL 96
umc1672	AC	7.00	43.80	yes	IBM2
umc1694	C	7.00	45.00	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1695	AC	7.00	45.60	no	IBM2
umc1426	AC	7.00	47.80	yes	IBM2
bnlg2132	AC	7.00	53.30	yes	IBM2
knox8b		7.00	55.07	no	UMC 98
rgpg124b	C	7.00	56.77	no	UMC 98
asg8(myb)		7.01	61.30	yes	IBM2
csu251a		7.00-7.01	61.30	no	UMC 98
mmc0171		7.00-7.01	66.28	no	SSR popII
usu1b(fnr)		7.01	67.63	no	UMC 98
si945036H05	C	7.01	68.06	no	INDEL
AY104465	AC	7.01	69.10	yes	IBM2
umc1840		7.00-7.01	70.67	no	SSR popI
php20581a(tb)		7.01	74.20	yes	IBM2
PCO143084	C	7.01	75.45	no	INDEL
bnlg1292		7.01	79.52	no	BNL 2002
cuny12		7.01	79.70	no	BNL 2002
AW308691	AC	7.01	86.30	yes	IBM2
hda110	C	7.01	89.96	no	ChromDB
umc1159	AC	7.01	92.00	yes	IBM2
isu84c		7.01	93.30	no	IBM2
uaz20b		7.01	96.92	no	BNL 96
csu486b		7.01	103.86	no	UMC 98
uaz83		7.01	106.73	no	BNL 2002
umc2364	C	7.01	107.65	no	SSR popII
mdh6		7.01	109.56	no	UMC 98
csu810b		7.01	109.56	no	UMC 98
npi400a		7.01	109.56	no	UMC 98
csu129	AC	7.01	109.56	no	UMC 98
rgpc1122b(rpL15)		7.01	109.56	no	UMC 98
umc1409	C	7.01	110.59	no	SSR popII
mmp18		7.01	113.40	yes	IBM2
umc2392		7.01	114.68	no	SSR popII
mmp81	AC	7.01	115.80	yes	IBM2
umc235		7.01	118.69	no	UMC 98
o2	AC	7.01	122.40	yes	IBM2
umc1270	C	7.01	123.50	yes	IBM2
his1a	C	7.01	125.20	yes	IBM2
umc1632	C	7.01	126.30	no	IBM2
csu611b(grp)		7.01	127.46	no	UMC 98
umc2325	AC	7.01	127.60	yes	IBM2
csu794		7.01	129.60	no	UMC 98
zds1		7.02	130.98	no	BNL 2002
hon102	C	7.01	131.10	no	ChromDB
asg34a(msd)	C	7.02	132.00	yes	IBM2
umc1428	AC	7.01 - 7.02	132.00	no	SSR popII
bnlg2160		7.01	132.76	no	BNL 2002
npi294b		7.02	140.01	no	BNL 2002
isu1410c		7.02	140.01	no	BNL 2002
ast(dcm1)		7.02	140.01	no	BNL 96
gta101a		7.02	148.50	yes	IBM2
AY109536	AC	7.02	151.50	yes	IBM2
ufg1		7.02	152.72	no	BNL 2002
uaz85		7.02	152.72	no	BNL 2002
uaz86		7.02	152.72	no	BNL 2002
uaz87		7.02	152.72	no	BNL 2002
uaz88		7.02	152.72	no	BNL 2002
in1		7.02	152.72	no	BNL 96
bnlg1003		7.02	152.72	no	BNL 2002
ucsd141a		7.02	152.72	no	BNL 2002
rny(pcr)d		7.02	152.72	no	BNL 2002
bnl17.13a		7.01 - 7.02	152.72	no	BNL 2002
csu93d		7.01	152.93	no	BNL 2002
umc1401	AC	7.02	153.00	yes	IBM2
umc1986	AC	7.02	153.30	no	IBM2
umc1036	AC	7.02	153.95	no	SSR popI
umc2326	AC	7.02	154.80	yes	IBM2
mmp75		7.02	155.20	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
sdg101	C	7.02	155.20	no	ChromDB
mmc0162		7.02	155.50	no	IBM2
kpp1	C	7.02	155.80	yes	IBM2
umc1978	AC	7.02	156.90	yes	IBM2
bnlg398		7.02	157.38	no	BNL 2002
umc2327	AC	7.02	158.00	yes	IBM2
AY105589	AC	7.02	162.40	yes	IBM2
psu2(bZip)		7.02	164.66	no	UMC 98
csu4b		7.02	165.01	no	BNL 96
tug9		7.02	165.39	no	BNL 2002
npi600		7.02	167.40	yes	IBM2
zpl2b		7.02	167.40	no	BNL 2002
uaz64a		7.02	167.40	no	BNL 2002
uaz68a(zp19)		7.02	167.40	no	BNL 2002
umc1927		7.02	168.50	no	IBM2
umc1549		7.02	169.48	no	SSR popI
crt2	C	7.02	170.80	yes	IBM2
uaz7b		7.01	171.40	no	BNL 2002
tug5		7.02	171.70	no	BNL 2002
bcd98i		7.02	171.70	no	BNL 2002
uaz173		7.02	174.11	no	BNL 2002
npi568		7.02	175.17	no	BNL 96
uaz89		7.02	176.23	no	BNL 2002
AY110576	AC	7.02	176.80	yes	IBM2
npi367a		7.02	177.72	no	BNL 2002
uaz268b		7.02	177.72	no	BNL 2002
umc(nabp1)		7.02	177.72	no	BNL 2002
php20690b		7.01 - 7.02	177.72	no	BNL 96
AY110473	AC	7.02	178.00	no	IBM2
cyp6		7.02	179.90	yes	IBM2
tda45		7.02	179.90	no	UMC 98
npi294e		7.02	179.90	no	UMC 98
uaz352a		7.02	179.90	no	UMC 98
bcd1087b		7.02	179.90	no	UMC 98
bnl5.33g		7.02	179.90	no	UMC 98
csu848b(vpp)		7.02	179.90	no	UMC 98
bnlg1759b	AC	7.02	179.93	no	BNL 2002
ucsd81c(zag2)		7.02	180.26	no	BNL 2002
bnlg1094	AC	7.02	180.50	yes	IBM2
mmp187		7.02	181.30	no	IBM2
umc1433	AC	7.02	181.79	no	SSR popI
rz509a(mip)		7.02	181.96	no	UMC 98
psr371b		7.02	182.60	yes	IBM2
ufg121		7.02	183.10	no	IBM2
umc1879	AC	7.02	183.40	no	IBM2
umc1666		7.02	183.40	no	SSR popII
uaz187		7.02	183.70	yes	IBM2
mmp26		7.02	184.40	no	IBM2
umc270		7.02	184.70	no	UMC 98
rz698e(ppy)		7.02	185.00	no	IBM2
umc112b		7.02	185.16	no	UMC 98
uor1c(rpS12)		7.02	185.39	no	UMC 98
rz698d(ppy)		7.02	185.60	yes	IBM2
umc193c(orp)		7.02	185.62	no	UMC 98
bnlg1247	AC	7.02	186.30	yes	IBM2
epl101		7.02	186.30	no	ChromDB
vef101a	C	7.02	186.30	no	ChromDB
bnlg2233		7.02	186.50	yes	IBM2
bnlg1380	C	7.02	188.10	yes	IBM2
csu7a		7.02	188.73	no	BNL 96
zpc2		7.02	189.97	no	BNL 2002
ciw(S10)		7.02	190.16	no	BNL 2002
zp50		7.00-7.01	190.19	no	BNL 2002
bnlg1792	AC	7.02	190.40	no	IBM2
bnlg2203	AC	7.02	190.60	yes	IBM2
hag102	C	7.02	190.60	no	ChromDB
sdg110		7.02	190.70	no	ChromDB
mpik4a		7.02	190.78	no	BNL 2002
uaz19b		7.02	190.78	no	BNL 2002
npi596		7.02	190.90	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg1200		7.01	190.98	no	BNL 2002
AY109809	C	7.02	192.50	yes	IBM2
lim333		7.02	195.60	yes	IBM2
npi224a		7.02	197.63	no	BNL 96
uaz143		7.02	199.79	no	BNL 2002
umc1932	AC	7.02	204.80	yes	IBM2
CL4745_2	C	7.02	207.60	no	INDEL
ucsd107b		7.02	212.37	no	BNL 2002
chs606		7.02	212.84	no	BNL 2002
psr3a		7.02	212.88	no	BNL 2002
npi111		7.02	212.88	no	BNL 2002
npi221a		7.02	212.88	no	BNL 2002
bnl15.40		7.02	212.88	no	BNL 96
umc1339		7.02	214.12	no	SSR popII
uaz351a(rpS12)		7.02	215.06	no	UMC 98
bcd450c		7.02	215.54	no	UMC 98
gl1		7.02	217.75	no	BNL 2002
csu11		7.02	217.96	no	UMC 98
csu233		7.02	217.96	no	UMC 98
csu936		7.02	217.96	no	UMC 98
csu241c		7.02	217.96	no	UMC 98
csu281a		7.02	217.96	no	UMC 98
csu919b		7.02	217.96	no	UMC 98
uaz84		7.02	217.96	no	BNL 2002
csu81a(ank)		7.02	217.96	no	UMC 98
bnlg1579		7.03	220.72	no	BNL 2002
zpb36		7.02	227.28	no	BNL 96
AY109968	AC	7.02	228.70	yes	IBM2
umc1983	AC	7.02	244.30	yes	IBM2
umc2142	AC	7.02	246.30	yes	IBM2
umc1138	C	7.02	247.70	yes	IBM2
umc1929	AC	7.02	249.10	yes	IBM2
umc2057		7.02	249.87	no	SSR popI
npi112a		7.02	251.86	no	BNL 96
umc1787	AC	7.02	252.40	yes	IBM2
umc2092	AC	7.02	252.90	yes	IBM2
PCO115023	C	7.02	254.02	no	INDEL
umc1393	AC	7.02	258.40	yes	IBM2
umc258	C	7.02	259.00	no	IBM2
umc98b		7.02	259.00	no	UMC 98
bnlg1164		7.02	260.11	no	BNL 2002
umc1585	AC	7.02	261.03	no	SSR popII
npi47b		7.02	261.39	no	BNL 2002
umc5b	C	7.02	261.50	yes	IBM2
isu86		7.02	262.50	yes	IBM2
mmp21		7.02	265.30	no	IBM2
bnlg657		7.02	276.79	no	BNL 2002
bnlg1022a		7.02	277.98	no	SSR popII
umc1881		7.02	280.19	no	SSR popII
ufg54		7.02	280.50	yes	IBM2
ufg65	C	7.02	280.70	no	IBM2
cdo412b		7.02	285.40	yes	IBM2
bnlg1808		7.02	286.30	yes	IBM2
asg49	AC	7.03	286.57	no	SSR popII
uaz205c(hsp70)		7.02-7.03	286.57	no	UMC 98
dupssr11		7.02-7.03	287.70	no	BNL 2002
dupssr9		7.02-7.03	288.18	no	BNL 2002
umc116a		7.03	288.90	yes	IBM2
mmp127		7.03	290.20	yes	IBM2
mmc0411		7.03	292.70	yes	IBM2
umc1713	AC	7.03	298.40	yes	IBM2
php20569a	AC	7.03	300.00	yes	IBM2
umc1567		7.03	300.00	no	SSR popII
bcd926a	C	7.03	307.40	yes	IBM2
bnl15.21		7.03	309.90	yes	IBM2
bnl15.37b		7.03	310.09	no	UMC 98
bnl5.46c		7.03	310.60	no	IBM2
csu274(hsp90)		7.03	311.43	no	UMC 98
mmp177c		7.03	314.70	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
tda37b		7.03	314.87	no	UMC 98
csu395c	C	7.03	314.87	no	UMC 98
umc1450	C	7.03	315.90	yes	IBM2
umc1987	AC	7.03	318.00	yes	IBM2
mmp46		7.03	319.60	yes	IBM2
bnlg1070	AC	7.03	322.70	yes	IBM2
bnlg1305		7.03	322.77	no	BNL 2002
npi122		7.03	322.83	no	BNL 2002
bnlg434	AC	7.03	323.30	yes	IBM2
ij1	AC	7.03	324.42	no	UMC 98
umc222(fgh)		7.03	324.42	no	UMC 98
umc1333		7.03	325.00	no	SSR popII
csu296		7.03	327.48	no	UMC 98
umc1456		7.03	329.65	no	SSR popII
npi394	AC	7.03	330.60	yes	IBM2
mpik27b(zmm7)		7.03	333.28	no	UMC 98
uaz123d		7.03	334.64	no	BNL 2002
uaz118b		7.03	335.59	no	BNL 2002
csu253		7.03	336.64	no	UMC 98
bnlg339	AC	7.03	336.64	no	SSR popI
umc1718	C	7.03	338.66	no	SSR popII
PCO071075	C	7.03	342.21	no	INDEL
umc1275	C	7.03	344.76	no	SSR popII
brd103		7.03	344.80	no	ChromDB
mmp152		7.03	345.40	yes	IBM2
AY110374	AC	7.03	347.20	yes	IBM2
umc1660	C	7.03	351.40	yes	IBM2
sdg116a		7.03	353.60	no	ChromDB
rz596c		7.03	354.02	no	IBM1
npi389		7.03	354.90	yes	IBM2
npi455a		7.03	354.90	no	BNL 2002
umc1481		7.03	356.97	no	SSR popII
ucsd106g		7.03	358.39	no	BNL 2002
umc56	C	7.03	361.90	yes	IBM2
umc110a		7.03	364.80	yes	IBM2
umc1408	C	7.03	365.40	no	IBM2
umc1837	AC	7.03	368.90	yes	IBM2
csu820		7.03	369.88	no	UMC 98
csu1124		7.03	371.46	no	UMC 98
umc149a		7.03	372.10	no	UMC 98
rz404(ccp)	C	7.03	374.00	yes	IBM2
si614054G01	C	7.03	375.11	no	INDEL
bnl6.27		7.03	375.61	no	BNL 96
bnlg155		7.03	376.90	yes	IBM2
PCO101826	C	7.03	377.90	no	INDEL
umc111b(psy)		7.03	379.00	yes	IBM2
umc1865	AC	7.03	380.60	no	IBM2
umc1841		7.03	380.60	no	SSR popI
umc1134	AC	7.03	381.20	yes	IBM2
isu84a		7.03	381.50	no	IBM2
mmp194		7.03	381.50	no	IBM2
umc2328	AC	7.03	381.50	no	IBM2
AY109644	AC	7.03	381.50	no	IBM2
nfd101a		7.03	381.60	no	ChromDB
psr371a		7.03	381.80	yes	IBM2
ndk1		7.03	382.60	yes	IBM2
bnlg2271	C	7.03	383.80	yes	IBM2
npi283a		7.04	383.84	no	BNL 2002
umc2329	AC	7.03	384.40	no	IBM2
umc1112	AC	7.03	385.10	yes	IBM2
uaz91(ndk)		7.04	385.50	no	BNL 2002
uaz31c		7.04	385.74	no	BNL 2002
tum2		7.02-7.06	385.97	no	BNL 2002
csh2b(cdc2)		7.03	385.97	no	BNL 2002
bnl13.24		7.04	386.44	no	BNL 2002
umc1324	AC	7.03	387.50	yes	IBM2
umc1888	AC	7.03	390.50	yes	IBM2
oec6	AC	7.03	391.00	no	SSR popI
bnlg1805	AC	7.03	392.10	yes	IBM2
bnlg572		7.03	392.19	no	BNL 2002
uaz28a		7.04	392.46	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi435		7.04	392.71	no	BNL 96
isu150		7.03	393.10	yes	IBM2
uaz221(his2a)		7.03	393.61	no	BNL 2002
bcd249i		7.04	394.42	no	BNL 2002
uaz224(eif2)		7.02	394.42	no	BNL 2002
rz596a		7.03	395.26	no	IBM1
ias5		7.04	395.32	no	BNL 2002
tif1		7.03	399.30	yes	IBM2
ast(amyBS2)a		7.04	401.26	no	BNL 96
psr135a		7.03	403.40	yes	IBM2
umc1301	AC	7.03	405.50	yes	IBM2
umc1936	AC	7.03	405.50	yes	IBM2
umc1001		7.03	407.23	no	SSR popII
PCO102751	C	7.03-7.04	407.78	no	INDEL
umc254		7.04	408.10	yes	IBM2
asg5		7.03-7.04	408.10	no	UMC 98
bas1		7.03-7.04	408.10	no	UMC 98
csh14		7.03-7.04	408.10	no	UMC 98
rgpg20		7.03-7.04	408.10	no	UMC 98
bnl4.24		7.03-7.04	408.10	no	UMC 98
uor2(crp)		7.03-7.04	408.10	no	UMC 98
rz753(cdpk)		7.03-7.04	408.10	no	UMC 98
csu229a(oec)		7.03-7.04	408.10	no	UMC 98
cdo59a(gos2)	C	7.03-7.04	408.10	no	UMC 98
umc2330	C	7.04	408.40	no	IBM2
umc2331	C	7.04	408.40	no	IBM2
uaz90		7.04	409.99	no	BNL 2002
umc1710	C	7.04	410.50	yes	IBM2
umc1251	C	7.04	412.10	yes	IBM2
umc1684		7.03	414.15	no	SSR popI
asg32	C	7.04	416.50	yes	IBM2
csu847b(lhcb)		7.04	416.50	no	UMC 98
bnl5.21a		7.04	423.77	no	UMC 98
bnl5.61a		7.04	423.77	no	UMC 98
csu21d(ago)		7.04	423.77	no	UMC 98
umc2062		7.04	426.40	no	SSR popII
ufg17	C	7.04	427.50	yes	IBM2
AY110023	C	7.04	429.20	no	IBM2
bnlg1666	C	7.04	430.50	yes	IBM2
uaz117c		7.04	430.55	no	BNL 2002
uaz200		7.03	430.56	no	BNL 2002
uaz225(lox)		7.04	430.57	no	BNL 2002
npi413b		7.04	430.66	no	BNL 2002
bnlg1161		7.04	430.67	no	BNL 2002
uaz199		7.04	430.82	no	UMC 98
uaz207		7.04	430.82	no	UMC 98
csu213a		7.04	430.82	no	UMC 98
npi240a		7.04	432.30	yes	IBM2
npi263		7.04	433.20	yes	IBM2
tda66c		7.04	438.65	no	UMC 98
npi352		7.04	439.90	yes	IBM2
csu1055		7.04	440.22	no	UMC 98
csu818b(lhca)		7.04	440.22	no	UMC 98
chr111	C	7.04	441.90	no	ChromDB
bnl8.29c		7.04	442.30	yes	IBM2
umc1029	C	7.04	444.70	yes	IBM2
umc1342	C	7.04	444.70	no	SSR popII
tua6		7.04	447.27	no	UMC 98
bnl8.32		7.04	447.27	no	UMC 98
csu749a		7.04	447.27	no	UMC 98
umc125b		7.04	447.27	no	UMC 98
npi217		7.04	447.27	no	BNL 2002
uaz92		7.03	447.28	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz922		7.03	447.28	no	BNL 2002
uaz233c(act)		7.03	447.28	no	BNL 2002
uaz82		7.03	447.43	no	BNL 2002
php20563a		7.04	449.33	no	BNL 2002
umc1593a		7.03	450.17	no	SSR popI
uaz123a		7.02	451.00	no	BNL 2002
bnlg1892a	C	7.04	452.76	no	BNL 2002
bcd249b		7.04	453.19	no	BNL 2002
ukd(hotr)		7.04	453.19	no	BNL 2002
rip2		7.04	453.91	no	SSR popII
e1		7.04	455.10	no	UMC 98
csu996		7.04	455.10	no	UMC 98
bnl7.61		7.04	455.10	no	UMC 98
bnl8.21a		7.04	455.10	no	UMC 98
bnl8.37a		7.04	455.10	no	UMC 98
bnl14.07	C	7.04	455.10	no	UMC 98
umc1543		7.04	457.44	no	SSR popI
mus1		7.04	459.33	no	BNL 2002
pge3		7.04	459.33	no	BNL 2002
ncr(b32c3b)		7.04	459.33	no	BNL 2002
isc(b32b)		7.04	459.33	no	BNL 96
uaz292(gdh)		7.04	464.18	no	BNL 2002
bcd349		7.04	464.50	yes	IBM2
npi398b		7.04	465.04	no	BNL 2002
umc1944		7.04	466.00	no	SSR popI
csu5	C	7.04	468.72	no	UMC 98
umc1708	C	7.04	471.40	yes	IBM2
rgpc12a		7.04	472.17	no	UMC 98
umc137d		7.04	472.17	no	UMC 98
csu175d(eif5A)		7.04	472.17	no	UMC 98
umc2332	C	7.04	472.60	yes	IBM2
phi328175	C	7.04	472.90	no	IBM2
AY110439	C	7.04	473.00	yes	IBM2
ufg79		7.04	473.40	no	IBM2
rgpr440b(gap)		7.04	475.40	no	UMC 98
bnl8.39		7.04	475.51	no	BNL 96
dupssr13		7.04	475.77	no	BNL 2002
csu8		7.04	476.00	yes	IBM2
rz395		7.04	476.00	no	UMC 98
umc1768	C	7.04	481.10	yes	IBM2
asg14a		7.04	487.51	no	UMC 98
asg36a		7.04	487.51	no	UMC 98
bnlg2259	C	7.04	489.20	yes	IBM2
umc1103	C	7.04	493.39	no	SSR popII
umc1295	C	7.04	494.80	yes	IBM2
csu906		7.04	497.10	no	UMC 98
ufg57	C	7.04	497.60	yes	IBM2
uaz119b(rpS6)		7.04	505.23	no	BNL 96
csu904		7.04	511.67	no	UMC 98
rgpr663b		7.04	511.67	no	UMC 98
csu597c(dah)	C	7.04	511.67	no	UMC 98
bnlg2328b		7.05	517.41	no	BNL 2002
AW267377	C	7.04	517.50	no	IBM2
umc1412	C	7.04	518.90	yes	IBM2
uaz241a		7.04	520.70	no	BNL 2002
uaz245(gbp)		7.04	520.70	no	BNL 2002
umc1125	C	7.04	522.79	no	SSR popII
umc80a		7.04	524.71	no	UMC 98
PCO136133	C	7.04-7.05	525.04	no	INDEL
PCO061754	C	7.04-7.05	529.89	no	INDEL
umc245		7.05	532.00	yes	IBM2
umc151		7.04-7.05	532.00	no	UMC 98
umc251		7.04-7.05	532.00	no	UMC 98
npi380		7.05	533.70	yes	IBM2
rgpr44c		7.05	535.19	no	UMC 98
php20523a		7.05	535.71	no	BNL 96
npi433		7.05	536.70	yes	IBM2
ias4b		7.04	536.70	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi385		7.04	536.96	no	BNL 2002
csu894b		7.05	537.27	no	UMC 98
npi113a		7.05	537.27	no	BNL 96
php20593		7.05	537.77	no	UMC 98
php20909b		7.05	538.70	yes	IBM2
npi300b		7.04	539.25	no	BNL 2002
asg28b		7.05	540.74	no	UMC 98
csu920b		7.05	540.74	no	UMC 98
bnl16.06		7.05	540.74	no	UMC 98
mmp67		7.05	540.80	no	IBM2
php20690a		7.05	542.71	no	UMC 98
csu1106		7.05	542.93	no	UMC 98
csu1097a		7.05	542.93	no	UMC 98
mmp25		7.05	543.40	no	IBM2
ncr(sod2)		7.05	543.51	no	BNL 2002
umc2368		7.05	544.55	no	SSR popII
phi069		7.05	545.20	yes	IBM2
umc1671	AC	7.05	547.28	no	SSR popII
umc45		7.05	547.30	no	UMC 98
umc91a		7.05	547.30	no	UMC 98
csu27	AC	7.05	547.30	no	UMC 98
csu578b		7.05	547.30	no	UMC 98
mmp17		7.05	547.70	no	IBM2
umc2379	C	7.05-7.06	555.46	no	SSR popII
bnl8.44a		7.05	558.45	no	UMC 98
csu163a	AC	7.05	558.45	no	UMC 98
std16c(blr)		7.05	558.45	no	UMC 98
umc1154	AC	7.05	558.55	no	SSR popII
csu632b		7.05	564.79	no	UMC 98
cdo38b(ntp)	AC	7.05	564.79	no	UMC 98
csu814a		7.05	568.07	no	UMC 98
bnlg469c	C	7.05	572.56	no	BNL 2002
pbs7		7.06	584.14	no	BNL 2002
cdo938d		7.05	586.60	yes	IBM2
umc2197	C	7.05	587.92	no	SSR popI
umc2333	AC	7.05	593.40	yes	IBM2
umc2222		7.05	598.35	no	SSR popI
umc1406	AC	7.05	598.90	yes	IBM2
umc35a	C	7.05	600.20	no	IBM1
umc1407	AC	7.05	600.20	yes	IBM2
umc2334	AC	7.05-7.06	600.40	no	IBM2
umc1799		7.04-7.06	600.79	no	SSR popI
ufg39	C	7.05	602.90	yes	IBM2
umc1760	AC	7.05	607.60	no	IBM2
umc168	AC	7.06	608.20	yes	IBM2
npi45b		7.06	608.20	no	BNL 2002
kin1		7.06	609.01	no	BNL 2002
phi116	AC	7.06	611.50	yes	IBM2
php20020		7.06	611.90	yes	IBM2
csu705		7.05-7.06	611.90	no	UMC 98
npi611a		7.06	614.80	yes	IBM2
php20728		7.06	615.42	no	BNL 96
abg373		7.06	616.31	no	BNL 2002
AY109703	AC	7.06	618.40	yes	IBM2
bnl(tas1j)		7.06	640.08	no	BNL 96
pbs13d		8.00-8.02	-43.20	no	BNL 96
cuny19		8.00	-35.19	no	BNL 2002
pbs6c		8.00	-34.86	no	BNL 2002
npi220a	C	8.01	0.00	yes	IBM2
csu891(rpL30)		8.00-8.01	0.00	no	UMC 98
csu597b(dah)	C	8.00-8.01	1.36	no	UMC 98
csu319		8.01	5.90	yes	IBM2
rz382b		8.01	6.70	yes	IBM2
npi114a		8.01	10.10	yes	IBM2
umc1786	C	8.01	10.58	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
rz995a(fbp)		8.00-8.01	10.68	no	UMC 98
csu312		8.00-8.01	11.56	no	UMC 98
npi222b		8.01	14.22	no	BNL 2002
csu1076		8.00-8.01	17.96	no	UMC 98
csu368(phr)		8.00-8.01	17.96	no	UMC 98
umc1139	AC	8.01	26.80	yes	IBM2
umc2042		8.01	30.30	yes	IBM2
mmp148		8.01	31.80	yes	IBM2
umc1592		8.01	33.80	yes	IBM2
bnl13.05c		8.01	36.48	no	SSR popI
rnp2		8.01	40.68	no	UMC 98
csu29c	C	8.01	40.68	no	UMC 98
bnlg1252		8.00-8.01	42.39	no	BNL 2002
bnl8.08k		8.01	42.69	no	BNL 2002
bnl13.05a		8.01	44.40	yes	IBM2
umc1414		8.01	48.00	yes	IBM2
CL16874_1	C	8.01	49.05	no	INDEL
AY109699	AC	8.01	49.40	yes	IBM2
umc1327	AC	8.01	55.00	yes	IBM2
umc1075		8.01	59.88	no	SSR popII
ufg38		8.01	64.52	no	IBM1
ncr(sod3b)		8.01	70.23	no	BNL 96
ufg61		8.01	74.41	no	IBM1
csu332		8.01	74.41	no	UMC 98
mpik41b(mem1)		8.01	74.41	no	UMC 98
umc1483	AC	8.01	83.10	yes	IBM2
isu1410a		8.02	84.14	no	BNL 96
csu675b(prh)	C	8.01	98.40	no	UMC 98
mmp85		8.01	99.60	yes	IBM2
bnlg1194	AC	8.02	105.40	yes	IBM2
bnl9.11a(lts)	AC	8.02	106.40	no	SSR popII
umc2352	AC	8.02	107.30	yes	IBM2
hon107b	C	8.02	110.33	no	ChromDB
npi110a		8.02	112.00	yes	IBM2
npi218a		8.02	112.00	no	BNL 2002
bnlg2037		8.01	114.45	no	BNL 2002
cdo460		8.02	115.10	yes	IBM2
umc1817	AC	8.02	115.30	no	IBM2
rz543b	C	8.02	115.32	no	UMC 98
mmp57		8.02	116.40	yes	IBM2
bnlg1073		8.01	116.62	no	BNL 2002
mpik17d		8.02	126.57	no	BNL 2002
pic8b		8.02	127.80	no	BNL 2002
umc1304	AC	8.02	128.60	yes	IBM2
umc2004		8.02	131.95	no	SSR popII
bnlg2235	AC	8.02	132.40	yes	IBM2
bnlg1352		8.02	132.40	no	BNL 2002
rgpc131b	AC	8.02	133.53	no	UMC 98
chr117a		8.02	135.00	no	ChromDB
bcd1823b		8.02	135.60	no	IBM1
bcd1823a		8.02	135.60	yes	IBM2
AY106269	AC	8.02	136.80	yes	IBM2
mmp166		8.02	139.70	yes	IBM2
umc1790		8.02	142.80	no	SSR popII
umc103a		8.02	145.42	no	UMC 98
npi585a		8.02	149.00	yes	IBM2
npi276b		8.02	149.00	no	BNL 2002
csu949b		8.02	152.49	no	UMC 98
umc1974	AC	8.02	153.30	yes	IBM2
umc1872		8.02	153.30	no	SSR popII
hsp18c		8.02	155.66	no	BNL 2002
tpi3		8.02	156.27	no	BNL 2002
wusl1042		8.02	156.27	no	BNL 2002
psr598		8.02	156.60	yes	IBM2
cdo328	AC	8.02	159.20	yes	IBM2
umc1913	AC	8.02	160.80	yes	IBM2
bnl21		8.02	163.70	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz252b(ptk)		8.03	164.29	no	BNL 2002
uaz243c(atpb)		8.03	164.29	no	BNL 2002
uaz251a(rpS11)		8.03	164.29	no	BNL 2002
bcd98b		8.02	169.48	no	BNL 2002
bnlg669		8.03	174.17	no	BNL 2002
bnlg1067		8.03	174.17	no	BNL 2002
umc1868		8.02	175.50	no	SSR popII
csu329		8.02	175.90	yes	IBM2
klp1b		8.02-8.03	176.60	no	UMC 98
umc124a(chk)		8.03	176.60	yes	IBM2
umc1530	C	8.03	179.50	yes	IBM2
umc1778	C	8.03	180.53	no	SSR popII
mmp120		8.03	191.00	yes	IBM2
tda52		8.03	193.25	no	UMC 98
umc1034	AC	8.02-8.03	193.83	no	SSR popI
CL51477_1	C	8.03	193.96	no	INDEL
mmp72		8.03	194.10	yes	IBM2
csu849(atpb)		8.03	195.50	no	UMC 98
umc2147	AC	8.03	197.10	no	IBM2
mmp158b		8.03	197.90	yes	IBM2
umc2146	AC	8.03	198.40	no	IBM2
umc32b	C	8.03	199.10	yes	IBM2
bnlg2082	C	8.03	200.30	yes	IBM2
AW244963		8.03	202.00	yes	IBM2
umc2353	C	8.03	203.00	no	IBM2
AY110450	AC	8.03	203.00	no	IBM2
umc120a		8.03	203.60	no	IBM2
ksu1c		8.03	203.90	no	UMC 98
csu279		8.03	203.90	no	UMC 98
csu910		8.03	203.90	no	UMC 98
csu1175		8.03	203.90	no	UMC 98
umc236	C	8.03	203.90	no	UMC 98
umc238b		8.03	203.90	no	UMC 98
rz244a(dia)		8.03	203.90	yes	IBM2
umc206(hsp70)		8.03	203.90	no	UMC 98
bnlg1834	AC	8.03	204.80	yes	IBM2
chr110b		8.03	204.80	no	ChromDB
umc1807		8.03	205.80	yes	IBM2
umc1157	AC	8.03	206.00	yes	IBM2
umc1904	AC	8.03	206.60	yes	IBM2
npi260b		8.03	211.00	yes	IBM2
rpa5c		8.03	215.06	no	UMC 98
gpa1		8.03	215.11	no	UMC 98
lhcb3		8.03	215.11	no	UMC 98
tda164		8.03	215.11	no	UMC 98
rgpc161		8.03	215.11	no	UMC 98
cdo1160a(kri)	C	8.03	215.60	yes	IBM2
umc2354	C	8.03	216.20	no	IBM2
umc1910		8.03	216.90	yes	IBM2
asg24b(gts)	C	8.03	217.14	no	SSR popI
stp1		8.03	217.46	no	UMC 98
mmp195f		8.03	220.60	yes	IBM2
mpik35f		8.02	221.77	no	BNL 2002
cdo202e(mcf)	C	8.03	224.80	yes	IBM2
php3818		8.03	226.10	yes	IBM2
zmm2		8.02	226.26	no	BNL 2002
mpik12b		8.02	226.26	no	BNL 2002
mpik15d		8.02	226.26	no	BNL 2002
mpik15e		8.02	226.26	no	BNL 2002
mpik17c		8.02	226.26	no	BNL 2002
ucsd64b		8.02	226.26	no	BNL 2002
umc1415	C	8.03	228.60	yes	IBM2
umc1470	AC	8.03	231.20	yes	IBM2
umc2355	AC	8.03	232.90	no	IBM2
umc1984		8.03	234.80	yes	IBM2
umc1236	AC	8.03	239.99	no	SSR popII
AY103821	C	8.03	240.70	yes	IBM2
isu2191h		8.03	242.08	no	BNL 2002
bnl17.20		8.03	242.08	no	BNL 96
bnlg1229		8.03	242.12	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
pge2		8.03	242.85	no	BNL 2002
mdh1		8.03	243.50	no	BNL 2002
npi618		8.03	243.90	no	BNL 2002
pbs4		8.03	244.02	no	BNL 2002
ici277		8.03	244.02	no	BNL 2002
umc2075	C	8.03	244.90	no	IBM2
isu1719c		8.03	245.23	no	BNL 2002
isu2191b		8.03	245.23	no	BNL 2002
bnlg1863	AC	8.03	245.70	no	IBM2
tug1		8.03	245.73	no	BNL 2002
AY105457	AC	8.03	245.90	no	IBM2
bnlg1460		8.03-8.04	247.08	no	BNL 2002
uaz249c(ubf9)		8.03	248.61	no	BNL 2002
bnl9.44		8.03	251.01	no	UMC 98
ici286a		8.03	251.01	no	BNL 2002
ucsd61f		8.03	251.01	no	BNL 2002
niu1::Bs1		8.03	251.01	no	BNL 2002
uaz269a(kri)		8.03	251.01	no	BNL 2002
uaz290(SDAg)		8.03	251.01	no	BNL 2002
AY110032	AC	8.03	254.80	yes	IBM2
umc2366	C	8.03	257.31	no	SSR popII
rps28		8.03	257.67	no	SSR popI
umc1802		8.03	257.67	no	SSR popI
uaz244b(prh)		8.03	259.05	no	BNL 2002
uky3a(P450)		8.03	262.16	no	UMC 98
umc1617	C	8.03	262.74	no	SSR popI
csu760b		8.03	263.40	no	UMC 98
csu244(imp)		8.03	263.40	no	UMC 98
umc1377		8.03	263.76	no	SSR popI
umc1289	C	8.03	264.40	no	SSR popII
umc1385		8.03	265.51	no	SSR popI
umc1615		8.03	265.51	no	SSR popI
csu275a(mtl)		8.03	268.36	no	UMC 98
AY109740	AC	8.03	268.60	yes	IBM2
bnl1.45a		8.03	274.56	no	UMC 98
phi100175	AC	8.03	274.90	yes	IBM2
umc1735	AC	8.03	279.90	yes	IBM2
AY109626	AC	8.03	282.70	no	IBM2
umc1457	AC	8.03	284.60	yes	IBM2
umc1471		8.03	285.04	no	SSR popI
oec23		8.03	286.23	no	SSR popII
umc1302		8.03	287.42	no	SSR popII
uor1b(rpS12)		8.03	289.43	no	UMC 98
phi121	C	8.03	289.80	yes	IBM2
php20714		8.03	291.30	yes	IBM2
tub2	C	8.03	291.91	no	UMC 98
tda217e		8.03	293.15	no	UMC 98
mbd101a	C	8.03	294.20	no	ChromDB
bnl8.06a		8.03	294.24	no	BNL 96
umc2154	AC	8.03	295.30	yes	IBM2
dupssr3		8.03	296.42	no	BNL 2002
bnlg2289		8.02	297.68	no	BNL 2002
ncr(sod3c)		8.03	298.21	no	BNL 2002
uaz121b		8.03	299.32	no	BNL 2002
csu620		8.03	300.59	no	UMC 98
bnlg119		8.04	302.36	no	BNL 2002
uaz25a		8.03	302.65	no	BNL 2002
bnl9.08		8.03-8.04	303.04	no	BNL 2002
umc1460	AC	8.04	304.20	yes	IBM2
PCO147505	C	8.03-8.04	304.73	no	INDEL
umc1427	C	8.03	307.33	no	SSR popI
umc1487		8.03	307.33	no	SSR popII
bnl7.08a		8.04	309.27	no	SSR popII
umc1765		8.03	310.37	no	SSR popI
AY110056	AC	8.04	310.40	yes	IBM2
act1	C	8.03	311.97	no	BNL 2002
agrc1		8.04	312.38	no	UMC 98
umc1858	AC	8.04	312.40	yes	IBM2
ucsd106h		8.04	312.45	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
uaz202		8.04	312.90	no	BNL 2002
umc209(prk)		8.04	313.60	no	UMC 98
umc1343		8.04	314.51	no	SSR popII
bnlg2046	C	8.04	315.20	yes	IBM2
pdc1	C	8.04	315.20	no	SSR popII
ufg58	C	8.04	315.70	no	IBM2
bnl17.16(bt2)	C	8.03	315.87	no	BNL 2002
bnl10.39		8.03	316.22	no	BNL 2002
csu1101b		8.04	316.72	no	UMC 98
npi224c		8.04	316.94	no	BNL 2002
bnlg1446		8.05	316.94	no	BNL 2002
npi(pdk2)		8.04	316.94	no	BNL 2002
csu226a(elf1A)		8.04	319.39	no	UMC 98
AY104017	C	8.04	320.60	no	IBM2
wusl(pdc1)		8.04	320.63	no	BNL 2002
csu720a		8.04	322.95	no	UMC 98
gta101d		8.04	323.80	yes	IBM2
csu807a		8.04	323.95	no	UMC 98
uwm1a(uce)		8.04	324.06	no	UMC 98
csu179d(hsp70)		8.04	324.06	no	UMC 98
csu204(uce)		8.04	324.17	no	UMC 98
caat1		8.04	324.73	no	UMC 98
cdo1395e		8.04	324.73	no	UMC 98
csu254d		8.04	326.29	no	UMC 98
pge21		8.03	327.31	no	BNL 2002
sdg105a		8.04-8.05	327.47	no	ChromDB
sb32		8.04	328.29	no	UMC 98
csh9(cyc1)		8.04	328.40	no	UMC 98
bnl2.369	AC	8.05	329.40	yes	IBM2
rgpg81		8.04-8.05	329.40	no	UMC 98
umc1130		8.05	330.10	yes	IBM2
bnlg1176	C	8.05	330.40	no	IBM2
bnl24a		8.04	331.06	no	BNL 2002
ucsd113a		8.03-8.04	331.06	no	BNL 96
bnlg2313a		8.03	331.37	no	BNL 2002
hox1	AC	8.05	337.20	yes	IBM2
koln2c		8.04-8.05	340.35	no	BNL 96
AY104566	AC	8.05	342.00	yes	IBM2
rop7		8.05	342.86	no	SSR popII
pdk2	C	8.04	343.02	no	UMC 98
npi294f		8.04	343.02	no	UMC 98
rip1	C	8.04	343.02	no	BNL 96
uaz147a		8.04	343.58	no	BNL 2002
npi224h		8.04	344.26	no	BNL 2002
umc2367		8.05	344.50	no	SSR popII
csu66b(lhcb)		8.04	346.14	no	BNL 2002
bnlg1246c		8.05	346.35	no	BNL 2002
uaz165		8.04	346.73	no	BNL 2002
mmp15		8.05	348.20	yes	IBM2
umc1959	AC	8.05	352.20	yes	IBM2
csu841b		8.05	352.80	no	UMC 98
umc1562	AC	8.05	353.30	yes	IBM2
umc1263	AC	8.05	353.90	yes	IBM2
chr117b		8.05	353.90	no	ChromDB
jpsb107a		8.05	356.60	yes	IBM2
umc1846	C	8.05	357.90	no	IBM2
csu292		8.05	358.40	no	IBM2
ufg80	C	8.05	359.50	yes	IBM2
ici222		8.05	360.75	no	BNL 2002
mmp195b		8.05	361.20	no	IBM2
bnlg1812		8.05	362.52	no	BNL 2002
bnlg1599	C	8.05	362.71	no	BNL 2002
ucb(anp1)		8.05	362.71	no	BNL 2002
ufg74	C	8.05	363.40	yes	IBM2
bnl8.26		8.05	364.43	no	BNL 2002
umc160b		8.04	366.75	no	BNL 2002
bnlg2181	AC	8.05	366.80	no	IBM2
bnlg162	AC	8.05	367.00	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg666	AC	8.05	367.00	yes	IBM2
umc89a	C	8.05	369.60	yes	IBM2
umc12a	C	8.05	372.60	yes	IBM2
dgg9h		8.05	372.60	no	BNL 2002
knox5		8.05	372.60	no	BNL 2002
npi595		8.05	372.60	no	BNL 2002
mwg645k		8.04	372.60	no	BNL 2002
npi101b		8.05	372.60	no	BNL 2002
csu829		8.05	372.66	no	UMC 98
knox11		8.05	372.66	no	UMC 98
umc2c	C	8.05	372.66	no	UMC 98
csu1023		8.05	372.66	no	UMC 98
scri1(msf)		8.05	372.66	no	UMC 98
rgpc597(prs)		8.05	372.66	no	UMC 98
uaz233a(act)		8.05	372.66	no	BNL 2002
rz390b(cyb5)		8.05	372.67	no	UMC 98
dgg9a		8.05	372.70	no	BNL 2002
mwg645a		8.05	372.70	no	BNL 2002
cdo580a(ivd)		8.05	372.70	no	BNL 2002
uiu1c(pog)		8.05	372.75	no	BNL 2002
cdo708		8.05	372.84	no	BNL 2002
rz390a(cyb5)		8.05	373.50	no	IBM2
bnlg1651	AC	8.05	374.50	yes	IBM2
umc1889	AC	8.05	374.90	yes	IBM2
umc1712	C	8.05	374.90	no	SSR popI
umc2401	C	8.05	374.90	no	SSR popII
hdt102	C	8.05	374.90	no	ChromDB
umc1864		8.05	375.05	no	SSR popI
bcd134a		8.05	376.90	no	UMC 98
umc1340	AC	8.05	377.70	yes	IBM2
bnl12.36b		8.05	377.79	no	SSR popI
umc2378	C	8.05	377.94	no	SSR popII
umc1882		8.05	378.34	no	SSR popII
hda103		8.05	379.20	yes	IBM2
csu1041b(ptk)		8.05	381.20	no	UMC 98
umc1316	AC	8.05	381.70	yes	IBM2
isu114		8.05	382.70	yes	IBM2
chr112b	C	8.05	382.80	no	ChromDB
umc1777	AC	8.05	382.90	no	IBM2
uaz164b		8.05-8.06	383.08	no	BNL 2002
bnl12.30a		8.05	385.50	yes	IBM2
cdo455a	C	8.05	385.50	no	UMC 98
csu742a(rpS7)		8.05	385.50	no	UMC 98
umc2199	C	8.05	387.37	no	SSR popI
hon107a	C	8.05	389.60	no	ChromDB
umc1665		8.05	390.26	no	SSR popI
umc2210		8.05	390.26	no	SSR popI
uaz138b		8.06	391.16	no	BNL 2002
pic6b		8.05	394.24	no	BNL 2002
bnl17.01		8.06	394.69	no	BNL 96
umc1121	AC	8.05	395.86	no	SSR popII
umc1824b	C	8.05	397.86	no	SSR popI
umc1287	C	8.05	399.47	no	SSR popI
umc184c(glb)		8.05	400.68	no	UMC 98
umc93a		8.05	400.99	no	UMC 98
umc189(a1)		8.05	400.99	no	UMC 98
dba2		8.05	401.47	no	UMC 98
umn430		8.05	401.47	no	UMC 98
csu125b(cah)		8.05	401.47	no	UMC 98
csu31a	C	8.06	404.15	no	SSR popII
idh1		8.06	406.30	no	UMC 98
ici95		8.06	406.94	no	BNL 2002
pbs6b		8.06	406.94	no	BNL 2002
umc53b		8.06	406.94	no	BNL 2002
uaz176a		8.06	406.94	no	BNL 2002
isu1774b		8.06	406.94	no	BNL 2002
csu384		8.06	407.97	no	UMC 98
umc1670		8.06	408.29	no	SSR popII
umc1141	AC	8.05	408.69	no	SSR popI
umc2212		8.05	412.34	no	SSR popI
umc2356	C	8.05	412.90	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1960	C	8.05	413.20	no	IBM2
umc1828		8.06	413.75	no	SSR popII
umc1149	C	8.06	413.90	yes	IBM2
sdg118	C	8.05	413.90	no	ChromDB
bnlg1152	C	8.06	414.10	no	IBM2
bnlg240	C	8.06	414.10	no	SSR popI
umc48a		8.06	415.59	no	UMC 98
csu110a		8.06	415.59	no	UMC 98
csu772b		8.06	415.59	no	UMC 98
PCO079694	C	8.06	415.69	no	INDEL
AY109883		8.06	415.70	no	IBM2
mmp32		8.06	416.00	no	IBM2
csu2c		8.06	420.83	no	UMC 98
ksu1d		8.06	420.83	no	UMC 98
umc30a		8.06	420.83	no	UMC 98
npi299		8.06	420.83	no	BNL 2002
uaz119a(rpS6)		8.06	421.48	no	BNL 2002
npi201b		8.06	421.73	no	BNL 2002
bnlg1782		8.05-8.06	422.30	no	BNL 2002
tum1		8.06	422.38	no	BNL 2002
bnl5.33d		8.06	423.69	no	UMC 98
aba2		8.06	425.84	no	UMC 98
rgpc112		8.06	426.32	no	UMC 98
uaz94		8.06	428.18	no	BNL 2002
pbs9a		8.06	429.37	no	BNL 2002
bcd134c		8.06	429.65	no	UMC 98
bnl17.17		8.06	430.33	no	BNL 96
umc117		8.06	431.08	no	UMC 98
umc71a		8.06	431.08	no	UMC 98
umc1728	AC	8.06	432.40	yes	IBM2
umc2031	C	8.06	432.63	no	SSR popII
hdt105		8.06	434.41	no	ChromDB
umc1161		8.06	434.55	no	SSR popII
ald1		8.06	436.56	no	UMC 98
asg17		8.06	436.56	no	UMC 98
umc84c	C	8.06	436.56	no	UMC 98
csu597e(dah)	C	8.06	436.56	no	UMC 98
asg1a		8.06	438.71	no	UMC 98
asg53		8.06	438.94	no	UMC 98
asg52a		8.06	438.94	no	UMC 98
umc1905	AC	8.06	439.60	yes	IBM2
sbe3		8.06	440.07	no	SSR popII
ksu1b		8.06	441.09	no	UMC 98
csu382b(cld)	C	8.06	441.09	no	UMC 98
rgpc198b(sik)		8.06	441.09	no	UMC 98
uaz95		8.06	443.40	no	BNL 2002
sps1	C	8.06	443.40	no	BNL 96
umc2037	AC	8.06	444.96	no	SSR popII
bnlg1607		8.06	445.76	no	BNL 2002
csu685		8.06	448.00	no	UMC 98
umc271		8.06	448.00	no	UMC 98
rgpc949		8.06	448.00	no	UMC 98
chr116b		8.06	448.94	no	ChromDB
umc2361	C	8.06	451.29	no	SSR popII
npi108b		8.06	451.50	no	BNL 96
mmc0181	AC	8.06	453.25	no	SSR popII
umc2395		8.06	453.45	no	SSR popII
uaz174		8.07	453.92	no	BNL 2002
bnlg1031	C	8.06	455.10	yes	IBM2
bnl10.24b		8.06	455.50	no	IBM2
cuny20(psy)		8.06-8.07	456.56	no	BNL 2002
umc1724	C	8.06	457.29	no	SSR popII
CL9311_1	C	8.06-8.07	457.57	no	INDEL
asg61b		8.06	458.21	no	UMC 98
bnl10.11		8.07	459.01	no	BNL 96
npi268a	C	8.07	459.20	yes	IBM2
bnl10.38c		8.06-8.07	459.20	no	UMC 98
bnlg1065	C	8.07	460.80	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc164a		8.07	460.87	no	BNL 2002
umc2014		8.07	463.03	no	SSR popII
rz538a		8.07	464.00	yes	IBM2
umc165b		8.07	464.03	no	UMC 98
rgpc86(ptk)	C	8.07	464.03	no	UMC 98
npi224b		8.08	464.38	no	BNL 96
csu254c		8.07	466.01	no	UMC 98
umc1607	C	8.07	466.50	yes	IBM2
bnlg1350b		8.07	466.93	no	BNL 2002
ucla(obf3B)		8.08	472.87	no	BNL 2002
csu96b(psei)		8.08	472.87	no	BNL 96
bnlg1056		8.08	473.10	no	BNL 2002
umc7		8.08	473.49	no	UMC 98
npi438b		8.08	473.49	no	UMC 98
csu223a(psei)		8.08	473.79	no	UMC 98
uwo1		8.08	476.38	no	BNL 96
umc39b		8.09	477.61	no	BNL 2002
umc3a		8.09	482.43	no	BNL 96
cdo241b		8.08	482.84	no	UMC 98
bnlg1823	C	8.07	483.40	yes	IBM2
AY110569	C	8.07	486.90	no	IBM2
csu1155b		8.09	489.22	no	UMC 98
psy2	C	8.07	489.70	yes	IBM2
csu163b		8.07-8.08	490.27	no	BNL 2002
csu110c		8.07	490.63	no	UMC 98
umc266d(ptk)		8.07	490.63	no	UMC 98
AY110539		8.07	494.20	no	IBM2
umc1268	C	8.07	494.70	yes	IBM2
csu776a		8.07	494.71	no	UMC 98
csu38b(taf)		8.07	494.71	no	UMC 98
uwm1c(uce)		8.07	495.97	no	UMC 98
umc1055		8.07	496.12	no	SSR popI
csu179c(hsp70)		8.07	498.49	no	UMC 98
dupssr14		8.09	500.12	no	UMC 98
lim301		8.07	504.30	yes	IBM2
bnlg1828		8.07	506.80	yes	IBM2
umc1384		8.07	507.36	no	SSR popI
npi414a	AC	8.08	509.80	yes	IBM2
tpi5		8.07-8.08	509.80	no	BNL 2002
csu1155a		8.08	511.87	no	UMC 98
umc2357		8.08	514.20	no	IBM2
mmp64		8.08	515.00	yes	IBM2
umc82d		8.08	522.00	no	UMC 98
php20793		8.08	522.40	yes	IBM2
AY109593	C	8.08	524.60	yes	IBM2
umc1005		8.08	526.60	yes	IBM2
csu786(uce)		8.08	526.60	no	UMC 98
sb21		8.08	529.82	no	UMC 98
csu591(uce)		8.08	529.82	no	UMC 98
umc2218		8.08	533.24	no	SSR popI
csu165a		8.08	534.65	no	UMC 98
csu922(arf)		8.08	534.65	no	UMC 98
csh8a(cyc4)		8.08	536.96	no	UMC 98
umc1032		8.08	538.76	no	SSR popII
umc1933	AC	8.08	540.30	yes	IBM2
mmp146		8.08	544.70	yes	IBM2
umc2052		8.08	545.52	no	SSR popI
umc1673		8.08	546.90	yes	IBM2
AY110053	C	8.08	550.40	yes	IBM2
npi107		8.08	562.50	yes	IBM2
asg50b		8.08-8.09	562.50	no	UMC 98
npi112b		8.08	564.30	yes	IBM2
AY103806	C	8.08	569.00	yes	IBM2
gst1	AC	8.08	571.50	yes	IBM2
bcd98e		8.09	572.17	no	BNL 2002
uaz128		8.08	573.45	no	BNL 2002
umc4b	C	8.09	574.98	no	BNL 2002
csu146b(cdc48)		8.08	575.40	yes	IBM2
agrr21	AC	8.09	580.10	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY110127	AC	8.09	596.40	yes	IBM2
umc1663	AC	8.09	608.10	no	IBM2
phi233376	AC	8.09	609.10	yes	IBM2
umc1638	AC	8.09	621.60	yes	IBM2
umc1916		8.09	626.70	yes	IBM2
bnlg1131		8.09	628.20	yes	IBM2
AY109853	AC	8.09	632.00	yes	IBM2
agrr118b		9.00	-41.50	no	UMC 98
bnl9.07a		9.00	-11.20	no	UMC 98
umc1279	C	9.00	-7.60	no	SSR popII
umc1957	AC	9.00	0.00	yes	IBM2
umc109	AC	9.01	5.00	yes	IBM2
umc148		9.01	7.30	no	UMC 98
rz144a	AC	9.01	9.86	no	UMC 98
bnlg1724	AC	9.01	11.80	yes	IBM2
npi253a		9.01	14.00	yes	IBM2
umc2393		9.00-9.01	16.20	no	SSR popII
umc1370	C	9.01	17.70	yes	IBM2
rz144c	AC	9.01	20.10	no	UMC 98
umc1040	AC	9.01	21.20	no	IBM2
bnlg2122	AC	9.01	21.30	yes	IBM2
umc1867	AC	9.01	24.30	yes	IBM2
php10005		9.01	28.80	yes	IBM2
ucsd72f		9.01	32.83	no	BNL 2002
csu95a	C	9.01	41.68	no	UMC 98
umc248a		9.01	41.68	no	UMC 98
bnlg1288		9.01	43.23	no	BNL 2002
lim343		9.01	46.20	yes	IBM2
ufg41		9.01	50.40	yes	IBM2
gta106b		9.01	55.51	no	ChromDB
koln10b(hox2)		9.01	56.00	no	BNL 2002
bnlg1583	AC	9.01	62.30	yes	IBM2
bnlg1810	AC	9.01	62.30	yes	IBM2
mir3a(thp)		9.01	63.43	no	UMC 98
c1	C	9.01	64.70	yes	IBM2
koln2b(hox)		9.01	65.19	no	BNL 96
umc1809	C	9.01	65.20	yes	IBM2
isu1146		9.01	73.23	no	BNL 96
bnl17.11		9.01	73.23	no	BNL 96
umc2335	AC	9.01 - 9.02	74.80	yes	IBM2
bnlg1272		9.00	74.94	no	BNL 2002
umc113a		9.01	75.86	no	UMC 98
sh1	AC	9.01	80.30	yes	IBM2
umc1588	AC	9.01	82.30	yes	IBM2
umc1967	AC	9.01	84.30	yes	IBM2
umc2362		9.01 - 9.02	86.67	no	SSR popII
csu250b(aba)		9.01	86.72	no	UMC 98
umc1596	AC	9.01	86.80	yes	IBM2
bz1	AC	9.02	90.10	yes	IBM2
umc1958		9.01 - 9.02	90.10	no	SSR popII
umc1764	AC	9.02	94.28	no	SSR popII
umc1131	C	9.02	94.70	no	SSR popII
AY104252	AC	9.02	95.80	yes	IBM2
umc82a		9.02	96.33	no	BNL 2002
csu665b(adt)		9.02	99.07	no	UMC 98
dupssr6		9.02	101.00	no	SSR popI
umc1170	AC	9.02	101.10	yes	IBM2
chr113		9.02	103.86	no	ChromDB
csu471		9.02	105.80	yes	IBM2
csu466(lhcb)		9.02	105.80	no	UMC 98
asg82		9.02	106.01	no	UMC 98
asg19a		9.02	106.01	no	UMC 98
umc256a		9.02	106.01	no	UMC 98
bnl5.67b		9.02	106.01	no	UMC 98
csu733(rpL39)		9.02	106.01	no	UMC 98
csu651(rpL39)	C	9.02	106.01	no	UMC 98
umc1647		9.00	109.37	no	SSR popI
umc1430		9.02	115.36	no	SSR popI

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu486a		9.02	115.39	no	UMC 98
isu111b		9.02	116.60	yes	IBM2
agrc255b		9.02	124.37	no	UMC 98
csu1083b		9.02	124.37	no	UMC 98
umc2336	AC	9.02-9.03	125.70	yes	IBM2
umc2219	C	9.02	127.70	no	SSR popI
csu1077		9.02	130.49	no	UMC 98
umc1636	AC	9.02	131.10	yes	IBM2
npi266		9.02	134.12	no	BNL 96
prc1		9.02	134.57	no	UMC 98
rz2a		9.02	134.57	no	UMC 98
klp1c		9.02	134.57	no	UMC 98
mpik11c		9.02	136.88	no	BNL 2002
mmp162		9.02	139.00	yes	IBM2
dup1379		9.02	139.47	no	BNL 2002
mpik19a		9.01	139.64	no	BNL 2002
ucsd62k(zag4)		9.02	142.12	no	BNL 2002
bnlg244	AC	9.02	142.60	yes	IBM2
bnlg1401	AC	9.02	147.50	yes	IBM2
mpik25(zmm3)		9.02	148.44	no	UMC 98
umc105a		9.02	152.93	no	UMC 98
mmp77		9.02	153.00	yes	IBM2
bnlg1372		9.02	155.16	no	BNL 2002
umc1037	AC	9.02	160.03	no	SSR popI
umc1893		9.02	161.33	no	SSR popII
mmp30		9.02	162.50	yes	IBM2
isu2191d		9.03	163.63	no	BNL 96
bnlg2107		9.02	167.99	no	BNL 2002
uaz237a(prc)		9.02	168.67	no	BNL 2002
umc1698		9.02	170.40	yes	IBM2
dup1384		9.02	172.42	no	BNL 2002
csu94b		9.02	173.33	no	UMC 98
cdo475a		9.02	173.33	no	UMC 98
csu228(pfk)		9.02	173.33	no	UMC 98
umc2213		9.02-9.03	176.14	no	SSR popI
dupssr19		9.02	176.32	no	BNL 2002
dpg1b		9.02-9.03	177.50	no	BNL 2002
npi300a		9.02	178.05	no	BNL 2002
bnlg1082		9.02	178.39	no	BNL 2002
bnlg1913		9.02	178.39	no	BNL 2002
d3	C	9.03	178.69	no	BNL 2002
bnl3.06		9.02-9.03	183.67	no	BNL 2002
mgs3	AC	9.02-9.03	184.17	no	BNL 2002
AY109531	C	9.02	185.20	yes	IBM2
csu616		9.02-9.03	189.65	no	UMC 98
tda66d		9.02-9.03	189.65	no	UMC 98
umc247		9.02-9.03	189.65	no	UMC 98
npi215a		9.02-9.03	189.65	no	UMC 98
umc253b		9.02-9.03	189.65	no	UMC 98
cdo590(ppr)		9.02-9.03	189.65	no	UMC 98
rgpr1908a(acb)		9.02-9.03	189.65	no	UMC 98
lim286		9.02	190.10	yes	IBM2
dhn2		9.03	190.16	no	BNL 2002
wx1	C	9.03	191.70	yes	IBM2
umc1634	AC	9.03	193.20	yes	IBM2
bnl5.21d		9.03	195.27	no	BNL 2002
umc273a		9.03	195.36	no	UMC 98
umc1258	AC	9.03	195.70	yes	IBM2
AY109570	AC	9.03	196.40	no	IBM2
hon104a	C	9.03	196.88	no	ChromDB
umc1586	AC	9.03	199.70	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY109816	C	9.03	200.40	no	IBM2
bnlg469a	C	9.03	200.41	no	BNL 2002
lim101		9.03	202.30	yes	IBM2
ufg71	C	9.03	204.40	yes	IBM2
mmp170b		9.03	208.50	yes	IBM2
PCO061815	C	9.03	209.97	no	INDEL
rf2		9.03	212.52	no	UMC 98
cdo17		9.03	212.52	no	UMC 98
csu680d	C	9.03	212.52	no	UMC 98
uwm1b(uce)		9.03	212.52	no	UMC 98
ucsd1.8a		9.03	214.22	no	BNL 96
psr160d		9.03	216.20	yes	IBM2
umc2338	AC	9.05	219.40	yes	IBM2
umc2337	AC	9.03	220.10	yes	IBM2
psr160c		9.03	220.70	yes	IBM2
chr120		9.03	221.80	no	ChromDB
bnl5.33c		9.03	222.36	no	UMC 98
bnl7.24a		9.03	222.36	no	UMC 98
umc2370	C	9.03	222.51	no	SSR popII
rz273c(ant)		9.03	223.90	yes	IBM2
rz953		9.03	226.30	yes	IBM2
umc81	C	9.03	226.30	yes	IBM2
csu321		9.03	226.30	no	UMC 98
pbs14b		9.03	226.30	no	BNL 2002
rgpr3235a	C	9.03	226.30	no	UMC 98
php20075b(ext)	C	9.03	226.30	no	BNL 2002
bnlg1626		9.03-9.04	226.88	no	BNL 2002
bcd1421		9.03	227.40	yes	IBM2
php20052		9.03	228.30	yes	IBM2
asg37		9.03	229.10	no	UMC 98
asg65a		9.03	229.10	no	UMC 98
asg66a		9.03	229.10	no	UMC 98
asg67a		9.03	229.10	no	UMC 98
bnl5.10		9.03	229.10	yes	IBM2
csu193		9.03	229.10	no	UMC 98
umc153		9.03	229.10	no	UMC 98
bnl26		9.03	229.10	no	BNL 2002
bnlg1730		9.03	229.10	no	BNL 2002
std6a(dba)		9.03	229.10	no	UMC 98
bnl5.46b		9.03	230.00	no	IBM2
umc1599	AC	9.03	230.10	no	IBM2
csu623	AC	9.03	230.60	yes	IBM2
umc1191	C	9.03	232.80	yes	IBM2
mmp2		9.03	235.50	yes	IBM2
umc1420		9.03	236.88	no	SSR popI
asg63a		9.03	238.00	yes	IBM2
umc2340	AC	9.03	238.40	no	IBM2
umc2339	AC	9.03	238.90	yes	IBM2
gtd101	C	9.03	238.90	no	ChromDB
umc1271	AC	9.03	240.50	yes	IBM2
si605086B11	C	9.03	242.58	no	INDEL
umc1691	AC	9.03	244.10	yes	IBM2
umc2412		9.03-9.04	247.06	no	SSR popII
umc1688	AC	9.03	247.60	yes	IBM2
acp1		9.03	249.20	no	UMC 98
umc20	C	9.03	249.20	yes	IBM2
asg68a		9.03	249.20	no	UMC 98
csu857		9.03	249.20	no	UMC 98
gl15	AC	9.03	249.20	no	UMC 98
pbs14d		9.03	249.20	no	BNL 2002
npi222a		9.03	249.27	no	BNL 2002
umc1921		9.03	249.60	yes	IBM2
uaz223(vpp)		9.03	250.40	no	BNL 2002
mwg645g		9.04	250.89	no	BNL 2002
uaz161b(elf)		9.03	251.65	no	BNL 2002
umc1700	AC	9.03	251.80	yes	IBM2
umc2087	AC	9.03	252.30	no	IBM2
npi454		9.03-9.04	253.02	no	BNL 2002
AW257883	AC	9.03	253.70	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg127		9.03	253.77	no	BNL 2002
umc1743	AC	9.03	254.00	yes	IBM2
umc114	C	9.03	254.30	yes	IBM2
AY103770	AC	9.03	254.60	no	IBM2
mmc0051		9.03-9.04	254.74	no	SSR popII
bnl5.04		9.03	256.10	yes	IBM2
csu181b		9.03-9.04	256.10	no	UMC 98
csu252b(cdc2)		9.03-9.04	256.10	no	UMC 98
csu179b(hsp70)		9.03-9.04	256.10	no	UMC 98
umc1267	AC	9.03	257.60	no	IBM2
rz682	C	9.03	258.20	yes	IBM2
csu147	AC	9.04	258.51	no	SSR popII
knox2		9.03	258.91	no	BNL 2002
bnlg430		9.03	258.91	no	BNL 2002
bnlg1687		9.03	258.91	no	BNL 2002
bnlg1688		9.03-9.04	259.76	no	BNL 2002
lim99b		9.04	259.80	yes	IBM2
fd1		9.03	261.09	no	BNL 2002
pic1a		9.04	263.11	no	BNL 96
umc2394		9.03-9.04	263.79	no	SSR popII
bnl7.13	C	9.04	264.90	yes	IBM2
hm2	C	9.03-9.04	264.90	no	UMC 98
csu254a		9.03-9.04	264.90	no	UMC 98
csu214a(grp)		9.03-9.04	264.90	no	UMC 98
csu778(lhcb)		9.03-9.04	264.90	no	UMC 98
sbp4	C	9.04	266.00	yes	IBM2
bnlg1714		9.04	266.40	no	IBM2
isu2191k		9.03	266.46	no	BNL 2002
ici266		9.04	267.04	no	BNL 2002
lim166		9.04	268.40	yes	IBM2
csu263a		9.04	272.79	no	UMC 98
csu56d(ohp)	C	9.04	272.79	no	UMC 98
csu183b(cdc48)		9.04	272.79	no	SSR popI
bnlg1209	AC	9.04	273.20	yes	IBM2
umc1522		9.04	275.14	no	SSR popII
psr547		9.04	278.90	yes	IBM2
psr129a		9.04	283.10	yes	IBM2
uaz112		9.04	283.36	no	BNL 2002
umc2398		9.04	283.58	no	SSR popII
umc1107	C	9.04	285.80	yes	IBM2
bnlg1159b	C	9.04	287.00	yes	IBM2
pbs14c		9.04	287.79	no	BNL 2002
gta101c		9.04	290.10	yes	IBM2
bnlg1012	AC	9.04	298.00	yes	IBM2
umc1878		9.04	298.43	no	SSR popII
ufg66		9.04	300.00	no	IBM2
ufg73		9.04	300.00	no	IBM2
ufg70	C	9.04	300.20	yes	IBM2
ufg35a		9.04	300.60	no	IBM2
npi580a		9.04	302.30	yes	IBM2
csu43	C	9.04	302.89	no	UMC 98
csu557		9.04	302.89	no	UMC 98
rz251b		9.04	302.89	no	UMC 98
csu212a		9.04	302.89	no	UMC 98
csu404a		9.04	302.89	no	UMC 98
rgpc524		9.04	302.89	no	UMC 98
wsu1(ptk)		9.04	302.89	no	UMC 98
isu41a		9.04	304.90	yes	IBM2
ufg68		9.04	306.20	yes	IBM2
umc1492	AC	9.04	308.00	yes	IBM2
umc1120	AC	9.04	309.90	yes	IBM2
sus1	AC	9.04	311.50	yes	IBM2
npi293a		9.05	311.50	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
rgpr3239b		9.04	311.50	no	UMC 98
AY109764	AC	9.04	311.90	no	IBM2
uaz236a(ser)		9.04	312.12	no	BNL 2002
bnlg1270		9.05-9.06	312.20	no	BNL 2002
mmp96		9.04	312.50	yes	IBM2
mmp37		9.04	314.30	yes	IBM2
csu694a(uce)	C	9.04	315.56	no	UMC 98
umc2121	AC	9.04	315.70	yes	IBM2
umc38c	C	9.04	317.00	yes	IBM2
bnl7.50		9.04-9.05	317.01	no	UMC 98
umc1771	AC	9.04	317.27	no	SSR popII
bnl8.17	C	9.04	320.20	no	IBM2
umc95		9.05	320.60	yes	IBM2
umc1519		9.04	320.60	no	SSR popII
rgpr44b		9.04-9.05	320.60	no	UMC 98
uaz119c(rpS6)		9.04	321.79	no	BNL 2002
umc140b		9.05	321.90	yes	IBM2
umc1078	AC	9.05	322.60	yes	IBM2
lim458		9.05	324.20	yes	IBM2
ufg13a		9.05	326.00	yes	IBM2
ufg64		9.05	329.30	yes	IBM2
ufg63	C	9.05	331.20	yes	IBM2
umc1654		9.05	332.24	no	SSR popII
umc1387	AC	9.04-9.05	334.54	no	SSR popI
ufg48		9.05	335.80	no	IBM2
mmp153		9.05	336.10	no	IBM2
php20554		9.05	338.10	yes	IBM2
umc1357	AC	9.05	340.38	no	SSR popI
umc1231	AC	9.05	342.00	yes	IBM2
chr125a		9.05	343.10	no	ChromDB
mmp41		9.05	343.70	yes	IBM2
hsp18a		9.05	344.57	no	BNL 2002
umc1657	AC	9.05	344.80	no	IBM2
csu395b	C	9.05	348.57	no	UMC 98
mmp151d		9.05	348.80	yes	IBM2
dpg6c		9.05	350.07	no	BNL 2002
pge(phyB2)		9.05	350.07	no	BNL 96
bnlg1091		9.05-9.06	351.23	no	BNL 2002
mmp179		9.05	354.40	no	IBM2
uaz266b		9.04	356.53	no	BNL 2002
ncr(sod4b)		9.05	356.53	no	BNL 2002
rpa8		9.05	358.24	no	UMC 98
csu392a		9.05	358.24	no	UMC 98
csu355(ext)		9.05	358.24	no	UMC 98
ufg67		9.05	361.40	yes	IBM2
ufg47		9.05	362.20	yes	IBM2
uaz125		9.05	362.23	no	BNL 2002
AY109792	AC	9.05	369.30	yes	IBM2
csu710e(apx)		9.05	372.40	no	UMC 98
uaz264a		9.05	372.64	no	BNL 2002
AY110217	AC	9.05	373.20	no	IBM2
umc1494	AC	9.05	373.66	no	SSR popI
csu219(tgd)		9.05	376.55	no	UMC 98
csu58b		9.05	378.34	no	BNL 2002
umc2095	AC	9.05	378.90	yes	IBM2
umc2341	AC	9.05-9.06	381.10	yes	IBM2
ibp1		9.05	382.70	no	UMC 98
csu634	AC	9.05	382.70	yes	IBM2
bnl8.08d		9.05	383.14	no	BNL 2002
rz574b(cwp)		9.05	383.80	yes	IBM2
umc2344	AC	9.05-9.06	384.80	no	IBM2
umc2342	AC	9.05-9.06	384.90	no	IBM2
si687046G05	C	9.05	385.03	no	INDEL
umc2343	AC	9.05-9.06	385.30	no	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
npi427a		9.05	386.80	yes	IBM2
ufg24	C	9.05	392.50	yes	IBM2
umc2134		9.05	404.30	yes	IBM2
umc1732		9.05	405.02	no	SSR popI
npi443		9.05	409.90	yes	IBM2
umc1417	C	9.05	411.95	no	SSR popII
umc2371	C	9.05-9.06	418.60	no	SSR popII
umc1794	C	9.05	420.18	no	SSR popII
mmp142		9.06	421.60	yes	IBM2
csu59a	AC	9.05	425.25	no	UMC 98
csu61a	AC	9.06	425.25	no	SSR popII
csu145a(pck)		9.05	427.70	no	UMC 98
AY109550		9.06	429.70	no	IBM2
uaz96a		9.06	430.51	no	BNL 2002
npi439b		9.06	431.70	yes	IBM2
npi425d		9.05	433.35	no	UMC 98
mmp132		9.06	433.50	yes	IBM2
dba4		9.06	438.50	no	UMC 98
csu28a(rpS22)		9.06	438.50	no	UMC 98
asg44		9.06	441.20	yes	IBM2
mmp131		9.06	458.50	yes	IBM2
umc2346	C	9.06	461.60	yes	IBM2
bnlg292a	C	9.06	462.87	no	BNL 2002
csu93a	C	9.06	463.90	yes	IBM2
cdo1387a(emp70)		9.06	465.16	no	UMC 98
bnlg1191		9.07	467.46	no	BNL 2002
ufg75c		9.06	477.20	yes	IBM2
bnl7.57		9.06	480.19	no	BNL 96
mmp168		9.06	486.50	yes	IBM2
nfd104d		9.06	489.40	no	ChromDB
chs5046		9.05-9.06	489.80	no	BNL 2002
umc1366		9.06	489.90	yes	IBM2
umc2345	C	9.06	492.30	yes	IBM2
hb1	C	9.06	494.50	no	IBM2
bnl5.09a		9.06	500.10	yes	IBM2
uom1(hb)		9.06	500.17	no	UMC 98
uaz148		9.06	501.12	no	BNL 2002
bnlg1588		9.07	501.46	no	BNL 2002
mmp110		9.06	504.60	yes	IBM2
mpik28(zmm8)		9.06	508.79	no	UMC 98
AY110141	C	9.06	517.50	yes	IBM2
umc1310	AC	9.06	517.73	no	SSR popII
cdo1395a		9.06	519.32	no	UMC 98
umc2207		9.06	520.76	no	SSR popI
csu1004		9.06	525.07	no	UMC 98
AY109819	AC	9.06	526.00	yes	IBM2
csu877		9.06	528.90	no	UMC 98
bnl14.28a		9.06	528.90	yes	IBM2
npi403a		9.06	528.90	no	BNL 2002
isu49		9.06	530.80	yes	IBM2
umc2358		9.06-9.07	531.03	no	SSR popII
umc1789	AC	9.06	534.20	yes	IBM2
asg12	AC	9.07	536.10	yes	IBM2
npi209a		9.06-9.07	536.10	no	UMC 98
bnlg1525		9.07	536.65	no	BNL 2002
phi448880	AC	9.06-9.07	536.80	no	IBM2
AY109543	AC	9.07	538.50	yes	IBM2
umc1675		9.07	541.40	yes	IBM2
csu1005		9.07	541.42	no	UMC 98
csu860a		9.07	541.42	no	UMC 98
umc1804		9.07	542.26	no	SSR popII
npi291		9.07	542.48	no	BNL 96
std2a(dba)		9.07	544.97	no	UMC 98
bnlg1506		9.07-9.08	547.75	no	BNL 2002
dupssr29		9.07	550.43	no	BNL 2002
umc2359		9.07	550.46	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
bnlg1375		9.07	551.02	no	BNL 2002
AY110382	AC	9.07	551.30	no	IBM2
bnlg619	AC	9.07	554.40	yes	IBM2
csu870		9.07	554.44	no	UMC 98
csu1118		9.07	554.44	no	UMC 98
ucsd61b		9.07	554.57	no	BNL 2002
mmp136		9.07	556.40	yes	IBM2
umc2089	AC	9.07	562.70	yes	IBM2
umc2131	AC	9.07	566.80	yes	IBM2
umc1714	AC	9.07	567.30	no	IBM2
jpsb596		9.07	567.70	yes	IBM2
npi97b		9.07	571.04	no	BNL 96
mmp171a		9.07	577.20	yes	IBM2
umc2347	AC	9.07-9.08	578.60	no	IBM2
bnlg128	AC	9.07	585.93	no	SSR popI
AY106323	AC	9.08	587.90	yes	IBM2
csu50b		9.08	596.44	no	BNL 2002
dpg12c		9.08	601.89	no	BNL 2002
umc1137	C	9.08	603.50	yes	IBM2
csh2c(cdc2)		9.08	604.50	no	BNL 2002
asg59b		9.07	604.73	no	UMC 98
ucsd107a		9.08	606.53	no	BNL 2002
uaz31a		9.08	607.91	no	BNL 2002
umc94b		9.08	607.91	no	BNL 96
PCO127444	C	9.08	622.15	no	INDEL
rz632b		9.07	626.03	no	UMC 98
csu883(rpL21)		9.07	628.99	no	UMC 98
dmt103a	C	9.08	631.09	no	ChromDB
umc1982	C	9.08	633.20	no	IBM2
bnlg1129	C	9.08	633.60	no	IBM2
bnl1.297b		9.08	635.20	no	IBM1
umc1505	C	9.08	635.20	yes	IBM2
mmp53		9.08	636.20	no	IBM2
rz561c		9.07	636.68	no	UMC 98
umc272(vfa)		9.07	636.68	no	UMC 98
AI901738	C	9.08	637.10	yes	IBM2
AW216329	C	9.08	638.70	yes	IBM2
umc1104	AC	9.07	660.54	no	SSR popII
umc1942		9.07	678.34	no	SSR popII
std20a(uce)		9.07	686.38	no	UMC 98
csu285(his2B)		9.07	691.11	no	UMC 98
klp6		9.07	701.76	no	UMC 98
csu54b	C	9.08	708.86	no	SSR popI
umc1277	C	9.07-9.08	708.86	no	SSR popII
csu804a(dnp)		9.07-9.08	708.86	no	UMC 98
ucsd72b		10.00	-24.00	no	BNL 96
mmp48a		10.00	0.00	yes	IBM2
mmp48b		10.00	11.00	yes	IBM2
bnl10.17a		10.00	13.20	no	UMC 98
csu306(fer)		10.00	13.20	no	UMC 98
mpik13a		10.00	13.98	no	BNL 2002
umc1380	C	10.00	16.60	yes	IBM2
php20626		10.00	19.10	yes	IBM2
AY110060		10.00	22.30	yes	IBM2
psr119c		10.00	28.30	yes	IBM2
bnl3.04		10.00	29.60	yes	IBM2
php20725b		10.00	29.90	no	IBM2
php20753a		10.00	30.00	yes	IBM2
phi041	C	10.00	30.90	yes	IBM2
ksu1e		10.00-10.01	34.80	no	UMC 98
php20075a(gast)	C	10.01	34.80	yes	IBM2
umc1293	C	10.00	44.33	no	SSR popI
ksu1f		10.01	44.70	no	UMC 98
mpik33::cin4		10.01	48.08	no	BNL 2002
AW330564	AC	10.01	53.00	yes	IBM2
csu1061b		10.01	55.80	yes	IBM2
agrc561		10.01	57.15	no	UMC 98
umc1291	AC	10.01	58.76	no	SSR popII

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
csu136(plt)		10.01	61.94	no	UMC 98
umc1318	AC	10.01	62.41	no	SSR popI
AW225120	AC	10.01	64.10	yes	IBM2
csu1042		10.01	64.82	no	UMC 98
ksu2		10.01	71.20	no	UMC 98
ksu3		10.01	71.20	no	UMC 98
bnlg1451		10.02	74.44	no	BNL 2002
umc2053	AC	10.01	76.20	yes	IBM2
umc2018	AC	10.01 - 10.02	81.10	yes	IBM2
phi063		10.02	82.25	no	BNL 2002
umc1319		10.01	82.42	no	SSR popII
csu577		10.01	85.25	no	UMC 98
csu359(alp)		10.01	86.21	no	UMC 98
cdo127b(pyk)	C	10.01	86.21	no	UMC 98
npi285a(cac)	AC	10.02	91.00	no	IBM2
umc1152	AC	10.02	91.40	yes	IBM2
gdcp1	AC	10.02	97.90	yes	IBM2
umc1432	AC	10.02	99.63	no	SSR popII
uaz21c		10.01	100.78	no	BNL 2002
cr4	C	10.02	102.46	no	UMC 98
AY110360	C	10.02	104.00	yes	IBM2
ksu5		10.02	105.12	no	UMC 98
mmc0501	AC	10.02	106.70	no	SSR popII
umc2034	AC	10.02	120.10	yes	IBM2
agrc714		10.02	121.64	no	UMC 98
csu250a(aba)		10.02	121.64	no	UMC 98
csu103a(aba)	C	10.02-10.03	123.02	no	BNL 96
rz400(gbp)		10.02	126.17	no	UMC 98
AI795367	AC	10.02	134.80	yes	IBM2
umc1582		10.02	138.79	no	SSR popI
tda217a		10.02	140.82	no	UMC 98
AY109994	C	10.02	142.00	yes	IBM2
umc1337	AC	10.02	143.30	no	IBM2
phi059	AC	10.02	143.50	yes	IBM2
uaz153		10.03	144.73	no	BNL 2002
isu85b		10.02	144.80	yes	IBM2
dpg3		10.03	144.92	no	BNL 2002
upen1		10.02	145.79	no	BNL 2002
rz900c(ahh)		10.02	146.80	no	IBM2
rz900b		10.02	146.80	no	ChromDB
ucsd72k		10.03	148.07	no	BNL 2002
ucsd72m		10.03	148.07	no	BNL 2002
umc152a		10.02	148.59	no	BNL 96
umc2114	AC	10.02	148.90	no	IBM2
csu561b		10.02	150.41	no	UMC 98
csu1054		10.02	155.74	no	UMC 98
umc2069		10.02	155.90	yes	IBM2
PCO062847	C	10.02-10.03	156.93	no	INDEL
umc130	AC	10.03	160.00	yes	IBM2
npi250a		10.03	160.00	no	BNL 2002
csu625		10.03	160.40	yes	IBM2
ov23		10.03	160.88	no	BNL 2002
bnlg1547		10.03	161.85	no	BNL 2002
uaz24a		10.03	161.97	no	BNL 2002
bnlg1085c		10.03	162.40	no	BNL 2002
uaz178		10.03	162.98	no	BNL 2002
ias13c		10.03	163.12	no	BNL 2002
npi105a		10.03	163.20	yes	IBM2
uaz97		10.03	163.20	no	BNL 2002
uaz98		10.03	163.20	no	BNL 2002
npi417b		10.03	163.20	no	BNL 2002
mpik41c(mem1)		10.03	163.20	no	UMC 98
uaz242(clp)		10.03	163.43	no	BNL 2002
umc18b(psaN)		10.03	164.10	yes	IBM2
umc1863		10.03	165.52	no	SSR popI
gcsh1	C	10.03	168.20	yes	IBM2
csu234b(gbp)		10.03	168.20	no	UMC 98
csu237a(psaN)		10.03	168.20	no	UMC 98
lim2		10.03	173.50	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
dpg5		10.03	176.43	no	BNL 2002
bcd1072b(hsp70)		10.03	177.50	yes	IBM2
glu1	C	10.03	178.60	no	UMC 98
csu1050		10.03	178.60	no	UMC 98
php06005		10.03	178.60	yes	IBM2
csu745c(rpPo)	C	10.03	178.60	no	UMC 98
php1		10.03	179.04	no	BNL 2002
npi98c		10.03	179.04	no	BNL 2002
npi327b		10.03	179.04	no	BNL 2002
npi597b		10.03	179.04	no	BNL 2002
bnlg1762		10.03	179.04	no	BNL 2002
umc(orp2)		10.03	179.04	no	BNL 2002
rz261a(sad)		10.03	179.90	no	UMC 98
rgpc1122d(rpL15)		10.03	179.90	no	UMC 98
rgpr440c(gap)		10.03	180.23	no	UMC 98
umc1785		10.03	180.24	no	SSR popI
umc1312	AC	10.03	180.24	no	SSR popI
umc1962	AC	10.03	180.70	yes	IBM2
umc1866		10.03	180.70	no	SSR popII
asg76a		10.03	182.18	no	UMC 98
zmm1		10.03	182.96	no	BNL 2002
eoh1		10.03	183.15	no	UMC 98
rgpc496c(adh)		10.03	183.15	no	UMC 98
bnlg210	AC	10.03	183.40	yes	IBM2
bnlg1037		10.03	183.41	no	BNL 2002
bnlg1716		10.03	183.41	no	BNL 2002
chs5008		10.03	183.44	no	BNL 2002
bcd98c		10.03	183.62	no	BNL 2002
bnlg2216		10.03	183.62	no	BNL 2002
umc1367	C	10.03	183.80	yes	IBM2
chr109a	C	10.03	183.80	no	ChromDB
csu213b		10.03	184.45	no	UMC 98
uaz116		10.03	184.70	yes	IBM2
sdg108b	C	10.03	184.90	no	ChromDB
php20646		10.03	185.10	yes	IBM2
umc1381	AC	10.03	187.00	yes	IBM2
ufg30a		10.03	188.80	no	IBM2
AY110411	C	10.03	191.20	yes	IBM2
AY105746	C	10.03	193.60	no	IBM2
umc2067	AC	10.03	194.50	no	IBM2
umc2016	AC	10.03	195.40	yes	IBM2
bcd147(gbp)	C	10.03	196.40	yes	IBM2
jpsb527c		10.03	197.90	yes	IBM2
umc1345	C	10.03	199.50	yes	IBM2
AY110248	C	10.03	200.50	yes	IBM2
ufg59	C	10.03	203.00	yes	IBM2
mmp63		10.03	204.80	no	IBM2
rps3		10.03	208.50	yes	IBM2
bnlg1079	AC	10.03	213.10	no	IBM2
umc1239	AC	10.03	213.30	yes	IBM2
psr690		10.03	215.80	yes	IBM2
npi445a		10.03	217.20	yes	IBM2
bnlg1712	AC	10.03	217.80	yes	IBM2
ensl003		10.03	217.80	no	BNL 2002
csh::stAc		10.04	219.25	no	BNL 2002
AY112073	AC	10.03	220.10	yes	IBM2
npi602		10.03	222.50	no	SSR popII
umc1938		10.03	222.50	no	SSR popII
mpik20b		10.03	225.11	no	BNL 2002
umc155	AC	10.03	225.70	yes	IBM2
AY111178	C	10.03	227.40	yes	IBM2
umc2349	AC	10.03-10.04	227.90	no	IBM2
umc1739	AC	10.03	228.00	no	IBM2
bnlg1655	AC	10.03	228.00	no	IBM2
umc1336	AC	10.03	228.30	yes	IBM2
umc2180	AC	10.03-10.04	228.30	no	IBM2
ncsu2		10.04	230.74	no	BNL 96
fgp1	C	10.03	234.30	yes	IBM2
umc64a		10.04	242.30	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
orp2		10.03-10.04	242.30	no	UMC 98
agrr62a		10.03-10.04	242.30	no	UMC 98
csu599b		10.03-10.04	242.30	no	UMC 98
umc243a		10.03-10.04	242.30	no	UMC 98
npi327a		10.04	242.39	no	BNL 2002
bnlg640	AC	10.03-10.04	242.39	no	SSR popII
uaz100(prl)		10.03	242.84	no	BNL 2002
bnlg2336		10.04	242.87	no	BNL 2002
bnlg1526		10.04	243.01	no	BNL 2002
acc1		10.04	243.12	no	BNL 2002
uaz99		10.04	243.18	no	BNL 2002
sad1		10.02	243.24	no	BNL 2002
uaz175a		10.04	243.29	no	BNL 2002
umc1873		10.04	243.57	no	SSR popII
uaz117b		10.04	243.61	no	BNL 96
csu815		10.04	244.19	no	UMC 98
csu913		10.04	244.19	no	UMC 98
csu929(his3)		10.04	244.19	no	UMC 98
uaz76b		10.04	244.26	no	BNL 2002
csu797(uce)		10.04	244.40	no	UMC 98
csu951(eno)		10.04	244.40	no	UMC 98
uaz228b(his2b)		10.05	244.48	no	BNL 2002
dupssr31		10.04	244.55	no	BNL 2002
umc2348	AC	10.03-10.04	244.60	no	IBM2
hcf106c		10.04	245.64	no	BNL 2002
umc1995	AC	10.04	245.90	yes	IBM2
csu898		10.04	246.51	no	UMC 98
nac1	AC	10.04	246.51	no	UMC 98
cdo1395b		10.04	246.51	no	UMC 98
umc1589	C	10.04	247.73	no	SSR popII
umc1824c	C	10.04	247.73	no	SSR popII
isu1719a		10.04	247.96	no	BNL 2002
umc1246	C	10.04	248.20	yes	IBM2
csu276		10.04	249.03	no	UMC 98
csu613(acb)		10.04	251.13	no	UMC 98
rgpr1908b(acb)		10.04	251.13	no	UMC 98
mmp16		10.04	251.60	yes	IBM2
csu46a		10.04	253.24	no	UMC 98
umc1077	AC	10.04	253.30	yes	IBM2
rz69	AC	10.04	253.40	no	IBM2
AY110514	AC	10.04	254.50	no	IBM2
amo1	C	10.04	256.18	no	UMC 98
csu298b		10.04	256.18	no	UMC 98
AY109920	C	10.04	256.80	yes	IBM2
AY109876	C	10.04	259.40	yes	IBM2
csu864		10.04	259.97	no	UMC 98
csu671b		10.04	259.97	no	UMC 98
mgs1	AC	10.04	260.50	yes	IBM2
csu333		10.04	260.60	no	UMC 98
tda205		10.04	260.60	no	UMC 98
psu1b(spe)		10.04	260.60	no	UMC 98
csu893(isp)		10.04	260.60	no	UMC 98
umc1836		10.04	261.80	no	IBM2
AY109584		10.04	261.90	no	IBM2
jpsb527d		10.04	264.20	yes	IBM2
npi305b		10.04	265.15	no	BNL 96
umc1827		10.04	267.28	no	SSR popI
mzetc34	AC	10.04	268.10	no	IBM2
PCO086427	C	10.04	268.32	no	INDEL
mmp121	AC	10.04	269.60	yes	IBM2
AY110365	AC	10.04	271.30	yes	IBM2
incw3	AC	10.04	272.20	yes	IBM2
umc1911	AC	10.04	273.60	yes	IBM2
bnlg2127		10.04	274.03	no	BNL 2002
npi264		10.04	274.10	no	IBM2
npi303		10.04	274.10	no	BNL 2002

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc1453	AC	10.04	274.40	no	IBM2
asg2	C	10.04	277.20	yes	IBM2
csu948		10.04	277.23	no	UMC 98
umc261		10.04	277.34	no	UMC 98
npi294h		10.04	277.63	no	UMC 98
AY109698	AC	10.04	280.70	yes	IBM2
umc2350	AC	10.04	283.50	yes	IBM2
bnlg137		10.05	285.73	no	BNL 2002
umc1330	C	10.04	287.90	yes	IBM2
gpa2		10.04	288.38	no	UMC 98
csu86	C	10.04	288.38	no	UMC 98
umc146		10.04	288.38	no	UMC 98
csu981(eif5A)		10.04	288.38	no	UMC 98
dpg6b		10.05	288.57	no	BNL 96
ufg1433		10.04-10.05	288.57	no	BNL 2002
umc1697	C	10.04	290.90	no	IBM2
php15013		10.04	291.60	yes	IBM2
ufg8(grf)		10.04	291.97	no	UMC 98
umc1280	C	10.04	292.26	no	SSR popI
grf2		10.04	292.87	no	UMC 98
PCO126344	C	10.04-10.05	294.80	no	INDEL
umc1115	C	10.04	295.90	yes	IBM2
umc159b		10.04	296.90	no	UMC 98
hag103b	C	10.04	298.04	no	ChromDB
umc1272	C	10.04	299.40	yes	IBM2
umc1648	C	10.04	299.80	no	IBM2
umc2003	AC	10.04	301.60	no	IBM2
std4(dba)		10.04	304.07	no	UMC 98
rz740(sam)		10.04	304.07	no	UMC 98
umc1930		10.04	306.90	yes	IBM2
php20719a		10.04	308.40	yes	IBM2
npi563		10.04	308.70	no	IBM2
umc1678		10.04	308.70	no	IBM2
umc259a	C	10.05	309.00	yes	IBM2
sam1		10.04-10.05	309.00	no	UMC 98
umc162a		10.04-10.05	309.00	no	UMC 98
umc163a		10.04-10.05	309.00	no	UMC 98
umc1507	AC	10.04-10.05	309.00	no	SSR popII
ufg7B		10.05	309.04	no	BNL 2002
npi582		10.04-10.05	309.07	no	BNL 2002
npi578		10.05	309.20	yes	IBM2
umc1898		10.05	309.91	no	SSR popI
umc1677	C	10.05	311.40	yes	IBM2
isu58b		10.05	315.20	yes	IBM2
npi269b		10.05-10.06	318.69	no	BNL 2002
AY110634	AC	10.05	319.50	no	IBM2
npi232a		10.05	323.05	no	UMC 98
PCO129934	C	10.05	324.99	no	INDEL
mmp12		10.05	327.30	yes	IBM2
PCO087182	C	10.05	328.44	no	INDEL
umc1402		10.05	330.98	no	SSR popI
umc2221		10.05-10.06	331.38	no	SSR popI
bnlg1074	AC	10.05	332.10	yes	IBM2
bnlg1250	AC	10.05	335.50	yes	IBM2
ufg81	C	10.05	341.10	yes	IBM2
AY110167		10.05	342.70	no	IBM2
csu745a(rpPo)	C	10.05	343.40	yes	IBM2
umc1506		10.05	344.80	yes	IBM2
ufg3b(ivr)		10.05	348.73	no	UMC 98
ufg37		10.05	352.40	yes	IBM2
ufg28a		10.05	352.40	yes	IBM2
ufg72		10.05	352.60	no	IBM2
umc1477	AC	10.05-10.06	366.30	yes	IBM2

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
umc44a	C	10.06	367.85	no	SSR popII
bnl17.08		10.06	372.35	no	BNL 2002
r1	C	10.06	373.11	no	SSR popI
umc1045	C	10.05-10.06	375.80	no	IBM2
umc57a	C	10.06	375.98	no	BNL 96
npi287b		10.06	376.04	no	BNL 2002
bnl10.13a	C	10.06	376.30	yes	IBM2
mmp71		10.06	376.90	no	IBM2
bnlg1028	C	10.06	380.50	yes	IBM2
por2	C	10.06	381.04	no	SSR popII
jpsb365a		10.06	383.40	yes	IBM2
bnlg594		10.06	386.06	no	SSR popII
csu615b	C	10.06	387.50	no	UMC 98
cdo1417b(ptk)		10.06	387.50	no	UMC 98
bnl17.02		10.06	387.90	yes	IBM2
bnl17.07		10.06	389.94	no	BNL 2002
uaz251c(rpS11)		10.06	390.27	no	BNL 2002
bnlg153		10.06-10.07	390.28	no	SSR popII
tip5	C	10.06	392.50	yes	IBM2
cpx2		10.06	393.75	no	BNL 2002
bnlg236		10.06	394.81	no	BNL 2002
ucsd(lfyA)		10.06	394.81	no	BNL 96
umc1993	AC	10.06	410.60	yes	IBM2
bnlg2190	AC	10.06	412.30	yes	IBM2
ufg56	C	10.06	414.10	no	IBM2
dmt102a	C	10.06	414.11	no	ChromDB
ias6b		10.06	416.42	no	BNL 2002
npi306		10.06	416.42	no	BNL 96
ufg62		10.06	416.60	yes	IBM2
klp1f		10.06	418.25	no	UMC 98
npi290a		10.06	418.25	no	UMC 98
ufg15		10.06	422.70	no	IBM2
isu2192b		10.06-10.07	430.75	no	BNL 96
bnl7.49a(hmd)	AC	10.07	437.60	yes	IBM2
cdo244a(crp)		10.06-10.07	437.60	no	UMC 98
npi321a		10.07	439.27	no	BNL 2002
agrr37c	AC	10.07	442.20	yes	IBM2
rgpc285		10.07	442.78	no	UMC 98
umc1196	AC	10.07	444.80	yes	IBM2
umc1084	AC	10.07	445.70	yes	IBM2
npi421b		10.07	445.75	no	BNL 96
csu1039		10.07	447.96	no	UMC 98
bnlg1677	AC	10.07	449.30	yes	IBM2
csu1028(lhcb)		10.07	449.37	no	UMC 98

Locus	Contig	Bin	Coordinate, cM	Backbone	Source Map
AY110016	AC	10.07	450.80	yes	IBM2
rz590b		10.07	453.14	no	UMC 98
npi208b		10.07	454.60	yes	IBM2
mpik17f		10.00	454.69	no	BNL 2002
mpik12a		10.00	454.85	no	BNL 2002
mpik15f		10.00	454.99	no	BNL 2002
ucsd64d		10.00	454.99	no	BNL 2002
umc1249	C	10.06-10.07	456.65	no	SSR popI
mmp181		10.07	464.60	yes	IBM2
ufg75b		10.07	465.50	no	IBM2
asg50d		10.07	466.33	no	UMC 98
mir3c(thp)		10.07	466.33	no	UMC 98
bnlg1839	AC	10.07	466.40	yes	IBM2
bnlg279b		10.06	467.15	no	BNL 2002
umc1176		10.07	468.40	yes	IBM2
umc2351		10.07	469.40	no	IBM2
bnlg1360		10.07	469.70	yes	IBM2
bnlg2025		10.07	470.89	no	BNL 2002
npi254b		10.07	470.90	yes	IBM2
npi577b		10.07	470.90	no	BNL 2002
npi604b		10.07	475.10	no	BNL 2002
gln1	C	10.07	475.27	no	UMC 98
umc232		10.07	475.27	no	UMC 98
mwg645l		10.07	478.97	no	BNL 2002
csu300b		10.07	479.98	no	UMC 98
umc2203		10.07	481.42	no	SSR popI
umc1640	C	10.07	483.61	no	SSR popII
bnlg1450	C	10.07	483.70	yes	IBM2
umc1877		10.07	488.63	no	SSR popII
bnlg1518		10.04	490.55	no	BNL 2002
csu844		10.07	495.05	no	UMC 98
php20568a		10.07	496.60	yes	IBM2
crr2		10.07	505.50	no	SSR popII
umc2021	C	10.07	505.50	yes	IBM2
bnlg1185	C	10.07	505.93	no	BNL 2002
AY109829	AC	10.07	509.90	no	IBM2
umc2126	C	10.07	513.20	yes	IBM2
isu53b		10.07	522.60	yes	IBM2
asg19b		10.07	524.10	yes	IBM2
umc1038	AC	10.07	525.11	no	SSR popII
umc1556	AC	10.07	527.39	no	SSR popII
umc269(ptk)		10.07	527.55	no	UMC 98
csu781a	C	10.07	528.02	no	UMC 98
csu571b(ipp)		10.07	528.02	no	UMC 98
dba3		10.07	533.20	no	UMC 98
csu199d		10.07	533.20	no	IBM1
csu48	C	10.07	533.20	yes	IBM2
umc1645		10.07	578.09	no	SSR popI

VIII. AUTHOR INDEX
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Working Linkage Maps	MNL69:191; 70:118; 72:118 and **MaizeGDB**
Plastid Genetic Map	MNL 69:268 and **MaizeGDB**
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Cooperators (that means you) need the Stock Center.
The Stock Center needs Cooperators (this means you) to:

(1) Send stocks of new factors you report in this Newsletter or in publications, and stocks of new combinations, to the collection.

(2) Inform the Stock Center on your experience with materials received from the collection.

(3) Acknowledge the source, and advice or help you received, when you publish.

MaizeGDB needs Cooperators (this means you) to:

(1) Look up "your favorite gene or expression" in **MaizeGDB** (see section V in this Newsletter) and send refinements and updates to via the public annotation "button" at http://www.maizegdb.org.

(2) Compile and provide mapping data in full, including the ordered array of map scores for molecular markers or counts by phenotypic classes; recombination percentage and standard error.

(3) Provide probe or primer information per http://www.maizegdb.org/probe.php; fingerprint data and fragment sizes are significantly useful to colleagues.

May you find a Unique corn in MM!