Brief Description of Major Genetic Maps in MaizeGDB

(see also Tutorial and the Maps Data Center at MaizeGDB for more details)

MaizeGDB currently stores over 1789 genetic maps created by community members. A list of all maps is here- (http://www.maizegdb.org/cgi-bin/mapadvquery.cgi?query=true&locus1box=&locus2box=&locus3box=&chrom=1&source=15901&panel=981040). In the most general sense, genetic maps are made by crossing two lines with different alleles at a number of loci, and measuring the amount of recombination between those alleles in the resulting progeny. The progeny of a mapping cross is generally called a mapping population, but for a defined set of mapping lines, such as the recombinant inbreds used for IBM, the more precise name is "panel of stocks" or "mapping panel". Most genetic maps stored at MaizeGDB have been calculated from single mapping panels. However, commonly used maps are the "composite" genetic maps, meaning that they have data from many different mapping experiments and panels integrated by various means into one map.

It is useful to think separately about the two stages of genetic mapping: the generation of the mapping panel and the assigning of markers to discreet genetic positions. Understanding how the various mapping panels have been generated will lead to an understanding of the resolution and limitations of any genetic map. In a single meiosis, there is one crossover recombination per chromosome arm (Copenhaver et al., Proc. Natl. Acad. Sci. USA 95:247-252, 1998). To increase map resolution, panels of stocks have been developed that can accumulate detectable recombination per chromosome over several or many generations. Below is a description of the most commonly used genetic maps at MaizeGDB.

Genetic 2008: This is the current version of the composite genetic map developed and maintained by Ed Coe for the several decades. The first version, with some 60 loci, was published in 1935 by Emerson et al. (Cornell Univ Agric Exp Stn Memoir 180:1-83). In the 2008 version, with some 3775 loci, " Genes for which a function or phenotype is known are placed in relation to markers on the high-resolution IBM2 map; with sequenced BACs on the physical map; and by best estimates from other maps and other data where sufficient. The coordinates are approximately those of conventional centiMorgans. For each gene, the basis for map placement is given in a comment. Corrections or additions are invited. *Acknowledgment*: Many placements in this map derive from the fingerprinted contig [FPC] map aligned to the genetic map of the Maize Mapping Project (Wei et al., PLoS Genet. 3:e123, 2007); and from BAC sequence data that have been made available prior to publication, deposited in GenBank by the Maize Genome Sequencing Consortium." (E. Coe, personal communication to MaizeGDB). Thus, this map represents data from both defined mapping panels and crosses between many different inbreds, hybrids, and "mongrels". It also contains information from crosses where recombination occurred in the female parent or in the male parent or both. All recombination information used to place markers on this map can be found by clicking on the locus listed within the MaizeGDB map display. This map is continuously updated.

IBM2 (Intermated B73 x Mo17) Genetic Maps: This map is called "high resolution" because the method used to generate the mapping panel of nearly 300 recombinant inbred lines created more detectable recombinations per chromosome than previous methods [Lee et al. Plant Mol. Biol. 48:453-461, 2002; Sharopova et al. Plant Mol. Biol. 48:463-481, 2002]. To generate the mapping panel (Fig. 1), inbreds B73 and Mo17 were crossed to create the F1 hybrid. This was self-pollinated. F2 progeny were then intermated for four generations, followed by repeated selfing to generate Recombinant Inbred Lines (RILs). This type of panel is often referred to as Intermated Recombinant Inbred Lines (IRILs). The successive intermating crosses following F1 provided increased opportunity for recombination between linked loci. These recombinations remain detectable at any genomic position where B73 and Mo17 are polymorphic for the markers used in the subsequent mapping steps. The fact that these inbreds are so polymorphic relative to each other allows higher detection of crossover events. However, markers cannot be mapped any place in the genome where there is no polymorphism between Mo17 and B73.

After genotyping these IRILs with 2,046 markers, the Maize Mapping Project (MMP) constructed a genetic map (IBM2) that contains 2,026 markers (Coe et al., Plant Physiol. 128:9-12, 2002; Cone et al., Plant Physiol. 130:1598-1605, 2002). Markers that are ordered with strong statistical support are called "FRAME" markers. It is useful to keep in mind that the units on the IBM maps are not really centiMorgans.

IBM Neighbors: This description is taken directly from Cone et al. 2002 (see above). "We are implementing a “neighbors” map approach in which we extrapolate locations of loci from non- IBM maps to their nearest neighbors on the IBM map, such that the framework loci on the IBM serve as a fixed backbone onto which additional loci are added. To extrapolate, we look for shared loci on the two maps that define an interval containing a locus of interest, calculate the distance between the shared and target loci on the non-IBM map as a ratio of the distance for the interval, and use the ratio to estimate a map coordinate for the target locus in that interval on the IBM. In choosing which neighbors to extrapolate, we consider the depth of the genetic data and the confidence levels for locus assignment to the non-IBM map. The new map is called “IBM Neighbors.” "The key distinction between the IBM and IBM Neighbors maps lies in the confidence level of locus order; the IBM has fewer well-ordered loci and IBM Neighbors has more loci, but confidence in the order is lower." IBM Neighbors Frame maps are similar to IBM Neighbors, except that they only include the loci (markers) that were “frame” (or “skeleton” in ISU_IBM Map4 maps, see below) on the original, individual maps.

ISU_IBM Map4 was prepared by Fu et al. (Genetics 174:1671-1683, 2006), using a panel of 91 IBM lines, a subset of the 302 member panel used for IBM2. They mapped 1,329 new gene-based insertion-deletion polymorphism markers (called IDPs or indels) and 2,029 previously developed markers on the IBM map. This groups calls markers "skeleton" if there is excellent statistical support to order them accurately on the map, and "muscle" if support is adequate for approximate placements. Coordinates on these maps were corrected to represent meiotic centiMorgans.

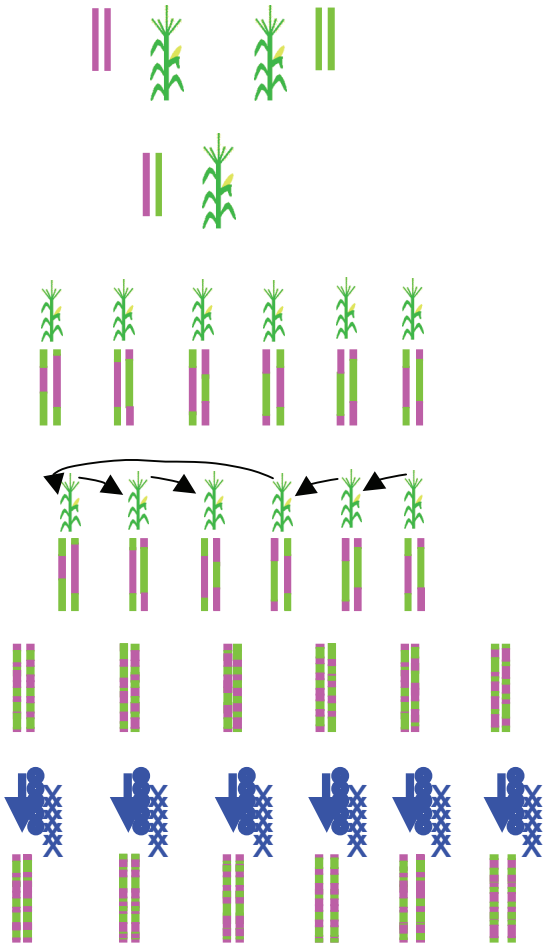
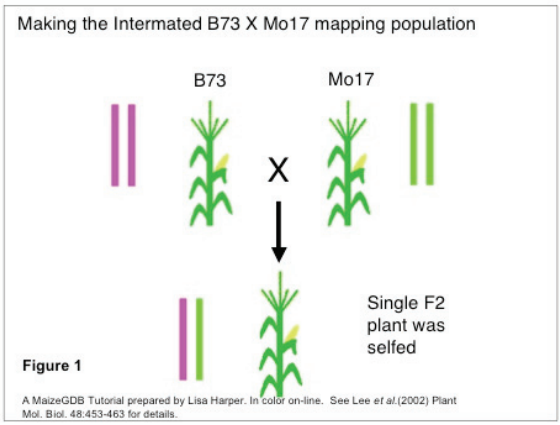


Figure1. Generation of IRILs, a special mapping panel.

LHRF Gnp2004 and IBM GNP2004: Falque et al. (Genetics 170:1957-1966, 2005), generated an IRIL panel from the cross F2 x F252, representing a set of inbreds useful for European maize breeders and permitting mapping a number of markers monomorphic on the IBM panel. In their paper, they state: "We built framework maps of 237 loci from the IBM panel and 271 loci from the LHRF panel. Both maps were used to place 1454 loci (1056 on map IBM_Gnp2004 and 398 on map LHRF_Gnp2004) that corresponded to 954 cDNA probes previously unmapped." Coordinates on these maps were corrected to represent meiotic centiMorgans.

Nested Association Mapping (NAM): The NAM panels are like RILs on steroids. Regarding the IBM map, recall that markers can NOT be genetically mapped in any region that is not polymorphic between B73 and Mo17. To overcome this, Yu et al. (Genetics 178:539-551, 2008) crossed B73 to 26 diverse maize lines (called "founders"). From the 25 F1s that were generated, a total of 5000 RILs where made, with 200 from each F1. The large number of diverse "founders" greatly increases the likelihood that most regions in the genome will be polymorphic in at least one mapping set, allowing markers to be mapped in those genomic regions. Excellent figures describing the process of generating the NAM panels are in the Yu *et al*. paper above. The Diversity Group (panzea.org) is mapping millions of SNP [single nucleotide polymorphism] markers using these lines. This will lead to a very high resolution genetic map and leverages the high throughput genotyping technology available for SNP.

Submitted by:
Lisa Harper
Mary Schaeffer
Taner Sen
Carson Andorf
Darwin Campbell
Carolyn Lawrence


Making the Intermated B73 X Mo17 mapping population
B73
Mo17
X
Single F2 plant was selfed
Figure 1
A MaizeGDB Tutorial prepared by Lisa Harper. In color on-line. See Lee et al.(2002) Plant Mol. Biol. 48:453-463 for details.

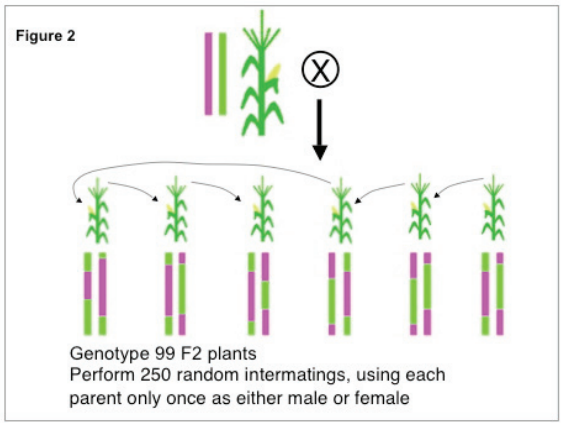


Figure 2
Genotype 99 F2 plants
Perform 250 random intermatings, using each parent only once as either male or female

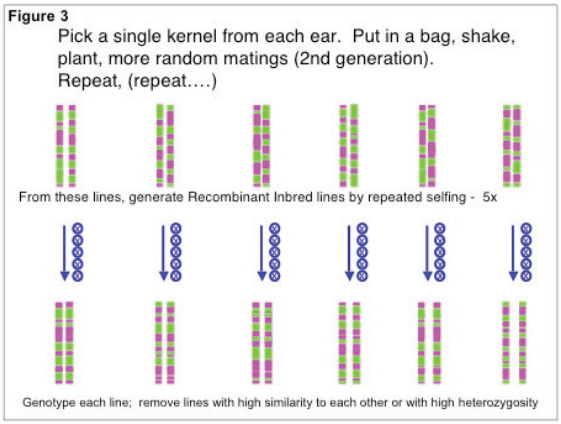


Figure 3
Pick a single kernel from each ear. Put in a bag, shake, plant, more random matings (2nd generation). Repeat, (repeat….)
From these lines, generate Recombinant Inbred lines by repeated selfing - 5x
Genotype each line; remove lines with high similarity to each other or with high heterozygosity

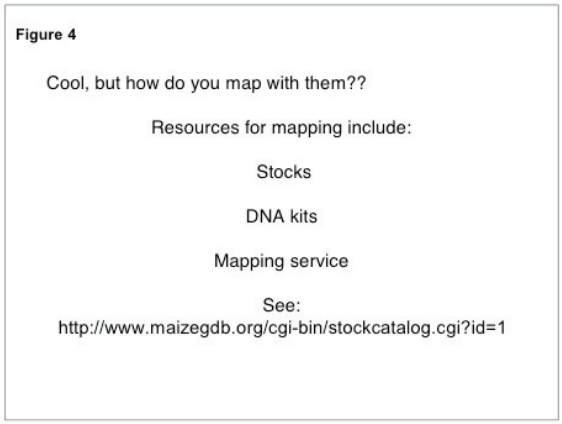


Figure 4
Cool, but how do you map with them??
Resources for mapping include:
Stocks
DNA kits
Mapping service
See:
http://www.maizegdb.org/cgi-bin/stockcatalog.cgi?id=1

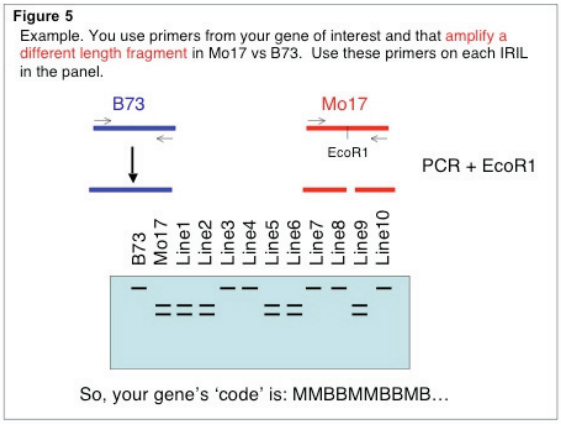
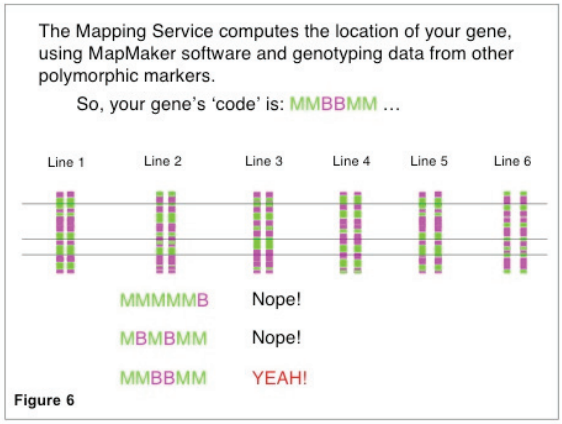


Figure 5
Example. You use primers from your gene of interest and that amplify a different length fragment in Mo17 vs B73. Use these primers on each IRIL in the panel.
B73
Mo17
EcoR1
PCR + EcoR1
B73
Mo17
Line1
Line2
Line3
Line4
Line5
Line6
Line7
Line8
Line9
Line10
So, your gene's 'code' is: MMBBMMBBMB…


The Mapping Service computes the location of your gene, using MapMaker software and genotyping data from other polymorphic markers.
So, your gene's 'code' is: MMBBMM …
Line 1
Line 2
Line 3
Line 4
Line 5
Line 6
MMMMMB
Nope!
MBMBMM
Nope!
MMBBMM
YEAH!
Figure 6