are not given here because of problems in achieving high germination frequencies for the bronze endosperm class, which also has a defective (sh) endosperm phenotype.

References:

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Wayne Carlson

KRASNODAR RESEARCH INSTITUTE OF AGRICULTURE
Krasnodar-12, USSR

1. Combining ability of high protein opaque-2 maize lines for protein content in diallele crosses.

Twelve opaque-2 high protein lines were included in this study (Table 1).

Lines 1 to 9 were related by their high protein source, IHP, which in the local environment of Krasnodar Region shows 24-28% protein; lines 10, 11 and 12 were not related either to each other or to lines 1-9. All lines except 1 and 8 have a common opaque-2 source, Synthetic A o_2 (S Ao_2); line 1 had the source B 37 o_2, and line 8 had the genetic stock $o_2 ra_1 gl_1$ as a source of o_2. The lines from 9 to 12 were heterozygous for o_2.

Two-directional diallel crosses were made in 1972 in 3-5 female ears. A pollen mixture from 5-7 plants was used. The kernel protein content of the absolute dry matter was determined in separate ears, sibbed and female as well. The lack of outcrossing for protein made it possible to utilize the results of analyses for evaluation of the lines for protein. The morphological traits of lines were relatively uniform and corresponded to S_2, S_3 generations.

In 1973 all F_1 crosses and parental lines were sown in a randomized block design (plots of 10 sq.m.) using four replications. The grain

Table 1

Utilized lines

Line number	Pedigree	Generation	1972						1973
			Sibs			Crosses			
			No. of analyzed ears	Protein means (%)	Lysine (g)	No. of analyzed ears	Protein means (%)	Protein variation (%) min.-max.	Protein (%)
1.	[(Rustler x $B370_2$) x IHP]	S_3	1	16.8	4.3	39	17.8	16.2-19.9	18.9
2.	[(BC_2wF_9 x SAO_2) x IHP]	S_3	2	17.7	3.5	40	17.0	14.7-19.4	17.6
3.	[(MT305 x SAO_2) x IHP]	S_3	6	16.9	3.3	38	17.4	14.8-18.9	16.8
4.	[(MT324 x SAO_2) x IHP]	S_3	7	17.3	4.1	49	17.3	15.3-20.1	17.6
5.	[(D6 x SAO_2) x IHP]	S_3	4	19.3	4.0	48	17.1	15.8-20.1	17.2
6.	[(Grushevskaya x SAO_2) x IHP]	S_3	5	20.0	3.6	41	19.9	16.2-26.4	17.5
7.	[(A344 x IHP) x (BC_2A344 x O_2ra_1)]	S_3	3	17.9	4.3	41	16.9	15.2-19.1	15.9
8.	[(BC_1Cg25 x SAO_2) x IHP]	S_3	3	16.8	3.3	46	17.6	15.0-19.6	16.5
9.	BC_2(IHP x SAO_2)	S_3	4	22.9	3.0	49	24.1	20.7-27.9	23.4
10.	BC_3(Grushevskaya x SAO_2)	BC_3	5	13.8	4.0	46	13.8	12.3-15.5	12.7
11.	BC_1(Odessa 10 x SAO_2)	BC_1	3	15.1	-	43	15.5	13.2-17.8	16.0
12.	[BC_2(A96 x SAO_2) x IHP]	BC_2	5	15.0	4.0	55	14.7	13.2-16.5	14.3

Table 2

Means of opaque-2 hybrid yields** (q/ha) and protein content (%) of diallel crosses (reciprocal means)

Line	1	2	3	4	5	6	7	8	9	10	11	12
1	18.9	17.9	17.2	16.7	15.8	16.8	16.0	16.6	18.7	14.2	15.6	14.9
2	33.9	17.6	18.6	17.6	17.1	17.2	15.9	17.3	19.2	14.0	15.6	14.4
3	37.3	40.0	16.8	16.7	16.7	17.3	16.6	17.4	18.9	14.2	16.2	14.3
4	37.8	43.8	44.3	17.6	16.7	17.3	16.5	16.5	17.5	14.2	16.2	14.6
5	40.7	42.1	42.8	43.8	17.2	16.7	14.7	16.7	18.3	14.0	15.4	14.5
6	43.8	36.5	37.5	42.6	36.4	17.5	16.3	17.0	17.6	14.3	15.0	14.2
7	39.4	48.2	46.5	40.4	52.0	40.2	15.9	15.8	15.7	13.4	14.2	12.6
8	35.4	38.9	44.6	35.6	35.4	36.1	42.2	16.5	20.0	14.2	16.6	15.0
9	44.3*	35.8*	46.9	44.2	42.6*	37.4	40.2	22.5	23.4	15.2	18.8	16.9
10	44.2	45.5	50.9	53.6	46.0	42.3	45.4	39.2	48.7	12.7	13.0	12.0
11	51.3	54.1	40.7	60.0*	49.2	46.8	49.7	33.7	48.2*	48.2	16.0	13.9
12	57.1	52.6	57.3	56.7	48.4	48.5	58.2	43.5	74.0*	52.0	83.2*	14.3

* kernel yield for hybrids with +/+ and o_2/+ genotypes.

** kernel yield to be read below underlined values.

yield was evaluated in Q/ha at 14% moisture level. The protein content was evaluated separately in replicates 1 and 3 of each cross.

The same test included as standards some opaque-2 hybrids yielding approximately at the same level as the commercial dent hybrids. The protein level of the standards was about 10-11%. The data on yield and protein content are listed in Table 2 as means of the reciprocal crosses.

Hereafter, only results of the combining ability analysis for protein content are discussed.

The dispersion analysis showed a highly significant genotypical difference among crosses (for protein content: $F(165,495) = 24.41$). This allowed us to proceed with the combining ability analysis using Method 1 by Griffing (Model 1).

All variability sources significantly influenced the changes in test results (Table 3). The General Combining Ability (GCA) is the most significant in determining the protein level. The GCA variance was about 40 times more than the Specific Combining Ability (SCA). The variation of reciprocal differences was much less pronounced; the mean square of reciprocal effects was three times less than the SCA variance. Thus, we may conclude that the combining ability for protein content is mainly influenced by additive genes.

Table 3

Dispersion analysis of combining ability for protein content

Source	DF	Sum of squares	Mean squares	F	
				Estimate	Reference p 0.01
G C A	11	406.40	36.95	266.31	2.24
S C A	66	61.60	0.94	6.72	1.44
Reciprocal effects	66	18.95	0.29	2.01	1.44
Errors	495	--	0.14	--	--

The lines when compared individually showed important differences in general combining ability: the GCA effects varied from -2.3% to +2.3% (Table 4). Lines 2, 3 and 9 showed a high combining ability (they were related to IHP). Lines 5 and 7, also related to IHP, showed an intermediate combining ability, and lines 1, 4, 6 and 8 had a somewhat lower GCA than the previous lines. The lowest GCA effects were shown by lines 10, 11 and 12, which were unrelated to IHP.

In analyzing the SCA constants, it should be noted that for most of the hybrids non-additive genes do not affect the protein level; their constants do not significantly differ from 0. However, a relatively high specific interaction may occur in some cases (crosses 2x3, 4x9, 7x9, 8x9, etc.). The variances of SCA constants show a non-additive type of gene action; they may be a property not only of some crosses, but of the lines themselves. Thus, lines 7 and 9 showed SCA variances of 0.81 and 0.36, respectively, which are 2-8 times more than in other lines.

The effect of "negative heterosis" for protein level is confirmed by the SCA constants of parental lines, which are, as a rule, higher than in their crosses. None of the crosses of lines 1, 4, 5, 6, 7, 9, 10, 11 and 12 had SCA constants significantly higher than the parental ones. However, in crosses of lines 2, 3 and 8, some combinations showed constants significantly higher than the parentals; this gives us some hope that the negative heterosis for protein level in some combinations may be not only reduced, but excluded as well.

Though the reciprocal differences were significant in the whole experiment, the individual effects in most cases had moderate values: from 66 reciprocal combinations, only 12 differed significantly from 0 in both directions. The reciprocal effects variances were very low.

To evaluate the influence of the procedure on the results obtained, we analyzed separately the experimental data from nine lines related to IHP, using Methods 1 and 3 after Griffing (Model I). We obtained similar results, though numerical values differed slightly, and the order of lines in GCA and SCA was the same. The difference was due to the exclusion of unrelated lines, which reduced the variation in GCA and SCA.

The comparison of yield of high protein opaque-2 hybrids (Table 2) with that of the standard hybrid Krasnodarsky 82 o_2 [which in nine

Table 4

Analysis of combining ability of lines for protein content (Griffing, 1956, procedure, Model 1)

Line	SCA constants (sij) and reciprocal effects (rij)*												GCA effects (gi)	Variances	
	1	2	3	4	5	6	7	8	9	10	11	12		GCA	SCA
1	1.9	0.6	-0.0	-0.2	-0.8	-0.1	0.2	-0.5	-0.2	-0.1	-0.5	-0.4	0.4	0.16	0.43
2	-0.1	0.0	1.1	0.3	-0.1	0.6	-0.7	-0.1	0.1	-0.6	-0.7	-0.6	0.7	0.48	0.28
3	0.4	-0.5	-0.6	-0.5	-0.1	0.1	0.7	0.1	-0.2	-0.2	0.2	-0.5	0.7	0.48	0.19
4	-0.3	-0.4	-0.1	0.7	0.2	0.1	0.9	-0.5	-1.2	0.0	0.3	-0.1	0.4	0.16	0.16
5	-0.2	0.7	-0.1	0.1	1.1	0.2	-0.6	0.0	-0.1	0.2	-0.2	0.2	0.0	0.00	0.16
6	0.5	-0.6	0.1	0.4	0.0	0.5	0.6	-0.1	-0.5	0.1	-0.9	-0.5	0.4	0.16	0.16
7	0.0	-0.2	1.2	0.5	-0.1	0.2	1.5	0.0	-1.9	0.5	-0.5	-0.8	-0.1	0.00	0.81
8	0.0	0.1	-0.2	-0.3	-0.3	0.1	-0.4	-0.7	1.1	-0.7	0.5	0.2	0.5	0.24	0.22
9	-0.1	-0.2	-0.5	0.2	-0.1	-0.2	-1.3	0.4	2.7	-0.9	0.9	0.3	2.3	5.28	1.36
10	-0.2	-0.2	-0.2	0.1	0.0	0.0	-0.1	0.0	0.0	1.2	-0.2	0.1	-2.3	5.28	0.26
11	0.4	0.2	-0.2	0.0	0.4	0.2	-0.8	-0.5	-0.6	0.4	1.0	0.2	-0.5	0.24	0.31
12	-0.3	0.0	-0.2	-0.2	-0.1	0.4	-0.4	0.1	0.5	0.4	0.3	1.9	-1.8	3.24	0.44
RC variances	0.03	0.09	0.16	0.03	0.03	0.04	0.39	0.01	0.22	0.00	0.14	0.04			

Standard errors:

$\hat{g}_i - \hat{g}_j = 0.10$ $\quad \hat{s}_{ii} - \hat{s}_{ij} = 0.60$ $\quad \hat{s}_{ij} - skl = 0.30$

$\hat{s}_{ii} - \hat{s}_{jj} = 0.50$ $\quad \hat{s}_{ij} - \hat{s}_{ik} = 0.40$ $\quad \hat{r}_{ij} - rkl = 0.40$

*Reciprocal effects are below underlined means.

tests in this experiment yielded 61.0 Q/ha (P 0.05; LSD=5.9 Q/ha) at a protein level of 10.7%], showed that most of the experimental hybrids yielded much less than the standard. However, some crosses of lines 10, 11 and 12 with lines unrelated to the protein source yielded very close to the standard Krasnodarsky 82 o_2, even when a negative correction of 10 - 12% was made in the yield of dent hybrids.

The results of the study of inheritance of protein level in F_1 crosses lead us to expect a relatively high protein level (16 - 17%) in hybrids.

The fact that the lines are related both to the high protein source and to the allele o_2 source as well prevents us from making a conclusion about the possible level of heterosis attainable if totally unrelated high protein lines, pre-selected for combining ability, had been used.

The results of this work emphasize the necessity of creating high protein lines of different origin, totally unrelated to IHP. This would be essential for a breeding program of high protein o_2 hybrids.

M. I. Hadjinov
K. I. Zima
A. A. Normov
V. Z. Pakudyn

2. A simplified procedure of backcrossing for transferring the recessive trait to the recurrent parent.

The routine procedure of developing counterparts differing from the recurrent parents in only one trait, determined by the recessive allele of a gene, may be further simplified with regard to the backcrossing and controlling the allele transfer (AT). The resulting reduction of the work needed will be about two times less.

The AT presence in BCn plants is commonly monitored by selfing or by crossing with a form homozygous for the transferred trait (TT).

We propose a procedure by which the backcrossing and control of AT may be achieved on the same ear of the plant selected for backcrossing. A tester is needed, possessing in homozygous condition, the AT and a dominant trait for kernel color. Such a tester can easily be developed in three generations by crossing the AT source with a genetic marker of the ACR type, for example, the Purple Embryo Marker.