

Table 1
Yield response (kg/ha) of four varieties at three sites with applied zinc

Variety	Zinc	Site		
		Narrabri	Trangie	Breeza
Bragg	+	3347	2106	2494
	Nil	3013	1161	549
Lee	+	2798	1771	2640
	Nil	2768	1714	1707
Forrest	+	3610	1002	2471
	Nil	3139	677	322
Dodds	+	3329	1192	2161
	Nil	2678	920	583
1.s.d. (0.05)				
Variety x Zinc means		411	309	564

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1) Soybean linkage tests.

F_2 linkage results are presented in Table 1 with $a = XY$, $b = Xy$, $c = xY$ and $d = xy$ for the eight gene pairs listed in the form of Xx and Yy . Percentage recombination was obtained from the ratio products following Immer and Henderson (1943). The data for each of the gene pairs gave a good fit to a 3:1 ratio.

Rps_1/rps_1 was evaluated using race 1 of *Phytophthora megasperma* var. *sojae* in hypocotyl tests of F_3 seedlings. Rmd/rmd was evaluated for adult plant resistance and susceptibility to powdery mildew using greenhouse inoculation of F_3 progenies with *Microsphaera diffusa*.

The previously reported possibility that Rmd/rmd is in Linkage Group 1 (Buzzell, 1978) was supported by the linkage of Fg_3/fg_3 with Rmd/rmd . Fg_3/fg_3 is between T/t and Rmd/rmd but is closer to T/t . A combined estimate using data from 'Blackhawk' x 'Kingwa' (Buzzell, 1977) and Table 1 indicates $13.6 \pm 4.4\%$ recombination between Fg_3/fg_3 and T/t .

Table 1
Soybean F₂ linkage tests
Blackhawk (Rps t w₁l₁fg₁fg₂Fg₃Rmd) x PI 65,388 (rps₁T W₁L₁Fg₁Fg₂fg₃rmd)

Genes		a	b	c	d	%R	SE	Phase
Rps ₁ rps ₁	T t	168	44	48	16	53.2	4.4	R
	W ₁ w ₁	169	48	40	17	> 55	-	R
	L ₁ l ₁	153	64	42	17	44.5	4.5	R
	Fg ₁ fg ₁	160	56	44	14	48.4	4.6	R
	Fg ₂ fg ₂	167	49	41	17	54.8	4.3	R
	Fg ₃ fg ₃	161	56	44	14	51.2	4.6	C
	Rmd rmd	164	51	50	7	> 55	-	C
Rmd rmd	T t	171	45	48	10	46.7	4.7	R
	W ₁ w ₁	163	53	46	12	47.0	4.7	R
	L ₁ l ₁	156	60	39	19	53.2	4.4	R
	Fg ₁ fg ₁	159	55	46	13	47.2	4.7	R
	Fg ₂ fg ₂	163	50	46	14	49.9	4.5	R
	Fg ₃ fg ₃	167	51	34	23	39.1	3.9	C
	T t	W ₁ w ₁	171	49	36	16	45.0	4.3
Fg ₁ fg ₁		157	64	50	7	> 55	-	C
Fg ₂ fg ₂		164	57	48	10	> 55	-	C
Fg ₃ fg ₃		150	70	56	1	13.5	5.9	R
L ₁ l ₁	T t	161	36	61	21	44.0	4.2	C
	W ₁ w ₁	148	47	62	18	50.5	4.5	C
	Fg ₁ fg ₁	146	48	61	22	48.7	4.4	C
	Fg ₂ fg ₂	151	44	59	23	45.9	4.3	C
	Fg ₃ fg ₃	146	50	61	22	50.6	4.5	R
Fg ₁ fg ₁	W ₁ w ₁	155	48	53	17	49.5	4.5	C
	Fg ₂ fg ₂	163	50	53	17	49.3	4.4	C
	Fg ₃ fg ₃	157	56	53	17	48.5	4.5	R
Fg ₂ fg ₂	W ₁ w ₁	161	46	47	18	45.8	4.3	C
	Fg ₃ fg ₃	165	51	44	23	> 55	-	R
Fg ₃ fg ₃	W ₁ w ₁	154	49	53	17	50.1	4.5	R

N = 272-283.

References

- Buzzell, R. I. 1977. Soybean linkage tests. Soybean Genet. News1. 4: 12-13.
 Buzzell, R. I. 1978. Soybean linkage tests. Soybean Genet. News1. 5: 14-15.
 Immer, F. R. and M. T. Henderson. 1943. Linkage studies in barley. Genetics 28: 419-440.

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2) Soybean parental lines.

Seed of five improved breeding lines (Table 1) is available upon request for use in crosses or experimental work. Disease reactions are given in Table 2 and physiological attributes in Table 3.

The lines are somewhat improved over the unadapted parents; however, only OX610I has been yield tested. It yielded 16% less than 'Harcor' over 3 locations in 1978, but its yield and photosynthetic rate could have been reduced by leafhopper damage. Apparently the pubescence on OX610I is less dense than normal.

Table 1
Origin and description of parental lines

Line	Origin	Color		
		Flower	Hilum	Pubescence
OX298	Harwood x Toyosuzu	Purple	Yellow	Gray
OX610I	Harwood x Tokachishiro	Purple	Yellow	Gray
OX615	Harcor ² x Raiden	Purple	Yellow	Gray
OX693	Harosoy 63 x Altona	Purple	Black/Brown	Brown
OX696	Harosoy x Kingwa	Purple	Yellow*	Gray

*Seed are yellow/green.

Table 2
Disease reactions of parental lines

Line	% plant loss*	Phytophthora megasperma var. sojae								PM	SMV
		Hypocotyl reaction** to races									
		1	2	3	4	5	6-7	8-9			
OX298	-	R	R	R	R	R	R	R	R	S	S
OX610I	-	R	R	S	S	S	R	R/S	R/S	RJ	-
OX615	-	R	R	R	S	S	R	R	R	S	R
OX693	-	R	R	R	R	S	S	S	S	RJ	S
OX696	-	R	R	R	R	R	R	R	R	RA	-
Harcor	17	R	R	S	S	S	S	S	S	S	S
Harosoy 63	49	R	R	S	S	S	S	S	S	S	S

*Average of 1977-78 in an infested field (races 3, 7 and 9).

**R = resistant; S = susceptible.

PM = powdery mildew caused by Microsphaera diffusa. RJ = juvenile and adult resistance; RA = adult resistance.

SMV = soybean mosaic virus (race or races unknown). R = resistance to leaf symptoms and seedcoat mottling; appears to be controlled by a single dominant gene.

Table 3
Physiological characteristics of parental lines

Line	Days to mature	Plant ht, cm	Leaflet* area, cm ²	SLW** mg/cm ²	Chlorophyll** mg/dm ²	P _A ** mgCO ₂ /dm ² /h
OX298	121	66	87	5.6	3.8	28
OX610I	124	75	86	5.2	3.7	24
OX615	114	80	72	5.4	4.1	31
OX693	104	57	72	6.8	4.3	31
OX696	128	72	78	4.6	3.6	25
Harcor	125	78	82	5.4	3.9	28
Harosoy 63	122	81	94	5.2	3.7	25
L.S.D. 0.05	-	-	ns	1.19	0.68	5.5
C.V. %	-	-	12.4	9.6	8.1	16.5

*Most recently fully-expanded leaves sampled July 26; 9 per plot in 4 replicates.

**Average of 6-replicate determinations July 28 and August 16, 1978.

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1) Genetic analysis of factors controlling nodulation response in soybeans.

Two of the genes controlling nodulation response in soybeans were tested for linkage associations with genes controlling pubescence color (T) and flower color (W₁), chlorophyll deficiency (y₉) and absence of pubescence (P). The rj₁ gene (Williams and Lynch, 1954) in homozygous recessive condition results in a non-nodulating phenotype with a broad spectrum of Rhizobium japonicum strains. The dominant gene, Rj₄ (Vest and Caldwell, 1972) conditions an ineffective nodulation response when inoculated specifically with R. japonicum strain 61 of the Beltsville Culture Collection.

Genetic stocks (T lines) and Clark rj₁ rj₁ were obtained from the Soybean Genetic Type Collection (Bernard and Weiss, 1973). Crosses were made in the field and F₁ seed were advanced to the F₂ generation in the greenhouse. F₃ seed was produced in the field at Beltsville. F₃ progeny rows derived from individual F₂ plants of rj₁ crosses were evaluated for phenotype in the field at Beltsville. Crosses with Rj₄ were evaluated in plastic growth tray assemblies (Devine and Reisinger, 1978) and inoculated with 7-day-old broth cultures of R. japonicum strain 61. F₂ genotypes were rationalized from F₃ phenotypes. Results of these linkage tests (Table 1) indicate independent assortment of rj₁ and T, rj₁ and W₁, rj₁ and P, and Rj₄ and y₉. A linkage association is apparent between Rj₄ and P in linkage group 2. Reasoning from this