References

Broich, S. L. 1978. The systematic relationships within the genus *Glycine* Willd. Subgenus *Soja* (Moench) F. J. Hermann. M.S. Thesis, Iowa State University, Ames, IA.

Delannay, X. and R. G. Palmer. 1982. Four genes controlling root fluorescence in soybean. Crop Sci. 22:278-281.

Fehr, W. R. and J. H. Giese. 1971. Genetic control of root fluorescence in soybeans. Crop Sci. 11:771.

Hymowitz, T. and C. A. Newell. 1981. Taxonomy of the genus *Glycine*, domestication, and uses of soybeans. Econ. Bot. 35:272-288.

Christophe Parot[1]

---

[1]Mr. Parot is an undergraduate student in the Ecole National Superieure Agronomique de Toulouse, France. He spent the summer of 1981 working as an assistant in the laboratory of Professor T. Hymowitz.

IOWA STATE UNIVERSITY
Department of Agronomy
UNITED STATES DEPARTMENT OF AGRICULTURE

1) Genetic analysis of a chlorophyll deficient, tan-saddle mutant

In the 1961 Uniform Soybean Test II, seeds with a tan-saddle pattern were found among normally yellow-seeded 'Harosoy' plants. The tan-saddle pattern was found to breed true, and is now designated k_2. The Harosoy line from which k_2 was derived is designated T239 in the Genetic Type Collection.

Among later generations of T239 some plants were found that were chlorophyll deficient. The chlorophyll deficient trait also bred true. One of the progeny of these chlorophyll deficient, tan-saddle plants was harvested and was designated T253 (cd-k_2).

In 1965, an independent mutation to k_2 and to 'chlorophyll deficient' occurred in L67-4323 (suspect cd-k_2). Because of differing times of greening of cd-k_2 and L67-4323, it has been suggested that the chlorophyll deficiency found in L67-4323 might be different from the chlorophyll deficiency found in T253 (R. L. Bernard, personal communication).

Our objective was to determine if the mutation causing the tan-saddle seeds and the chlorophyll deficiency in the suspect cd-k_2 was the same as the mutations in k_2 (T239) and in cd-k_2 (T253).

We made reciprocal crosses with k_2 and suspect cd-k_2 and reciprocal crosses with cd-k_2 and suspect cd-k_2. In addition, reciprocal crosses were made between the suspect cd-k_2 and cyt-Y_2, a new cytoplasmic mutation affecting chlorophyll development (Palmer and Mascia, 1980). It is known that the cd-k_2 mutant (T253) interacts with cyt-Y_2 (Palmer and Cianzio, unpublished). The crosses with cyt-Y_2 were made to determine if the suspect

cd-k$_2$ interacts in the same manner as the known *cd-k*$_2$ in the presence of *cyt-Y*$_2$.

When the suspect *cd-k*$_2$ was crossed as a male parent with k_2 only tan-saddle seeds were found among the progeny in the F_1 and in the F_2 (Table 1). In addition, F_2 progeny segregated 3 green : 1 chlorophyll deficient, thus confirming the hybrid origin of the F_2 (Table 1). In this cross, and others, obvious 'outliers' and plots not exhibiting evidence of hybrid origin, were not included in the analysis. These results show that the mutation causing tan-saddle seeds in the suspect *cd-k*$_2$ is the same as the mutation causing tan-saddle seeds in T239.

When the suspect *cd-k*$_2$ was crossed as a female parent with k_2, again, only tan-saddle seeds were found in the F_1 and in the F_2 (Table 2). F_2 progeny segregated 3 green : 1 chlorophyll deficient, which again confirmed the hybrid origin of the F_2 (Table 2). In this cross, the ratio of green : chlorophyll deficient more represents a 4:1 or a 5:1 segregation than a 3:1 segregation, but this is due mainly to the effects of an early July hailstorm that struck the F_2 plants of this cross before the chlorophyll deficient plants could be identified and tagged. The chlorophyll deficient plants, being weaker, were unable to survive partial defoliation and as a result many died before being identified as chlorophyll deficient.

When the suspect *cd-k*$_2$ was crossed as a male parent with the known *cd-k*$_2$, all F_1 and all F_2 progeny were both chlorophyll deficient, and possessed tan-saddle seeds (Table 1). These results allow us to conclude that the mutations for chlorophyll deficiency and for tan-saddle seeds are the same in both L67-4323 and T253. Similar results were obtained from reciprocal crosses (Table 2). In both types of crosses, W_1 (purple flower) and w_1 (white flower) were used as genetic markers. Among the F_2 of the reciprocal crosses, flower color segregated 3 purple : 1 white, confirming that the progeny were the result of a hybridization (Tables 1 and 2).

When the suspect *cd-k*$_2$ was used as a male parent in crosses involving *cyt-Y*$_2$ all F_1 progeny were yellow (Table 1). All F_2 progeny were also yellow, but none of the F_2 possessed tan-saddle seeds (Table 1). The absence of tan-saddle seeds in the F_2 in the presence of *cyt-Y*$_2$ is the same phenomenon noted in the nuclear-cytoplasmic interaction between the known *cd-k*$_2$ and *cyt-Y*$_2$ (Palmer and Cianzio, unpublished). In this cross, pubescence color was used as the genetic marker and the 3 dominant : 1 recessive segregation (Table 1) in the F_2 population confirmed the hybrid origin of the F_2.

When the suspect *cd-k*$_2$ was crossed as a female parent with *cyt-Y*$_2$ no chlorophyll deficient plants, and no tan-saddle seeds were observed in the F_1 (Table 2). Among the F_2, progeny segregated 3 green, non-saddle : 1 chlorophyll deficient, tan-saddle (Table 2). Tawny pubescence and gray pubescence were used as genetic markers and segregation for these traits was also 3 dominant : 1 recessive (Table 2). If considered as a dihybrid, the segregation pattern in this cross was 9 green, non-saddle, tawny : 3 green, non-saddle, gray : 3 chlorophyll deficient, tan-saddle, tawny : 1 chlorophyll deficient, tan-saddle, gray (Table 2).

The results of our crosses have shown that the mutations responsible for the chlorophyll deficiency and the tan-saddle seeds of plants derived from L67-4323, and of plants derived from T239 and T253, are the same. It would, therefore, be inappropriate to assign a new Genetic Type Collection Number to L67-4323.

Table 1. Crosses involving the suspect *cd-k*$_2$ as a male parent with soybean mutants *k*$_2$, *cd-k*$_2$, and *cyt-Y*$_2$

Cross	F_1	F_2
k$_2$ x suspect *cd-k*$_2$	all green plants	plants segregated 344 green : 95 chlorophyll deficient (3:1) $X^2 = 2.64$, $P<0.25>0.10$
	all tan-saddle seed	all tan-saddle seed
cd-k$_2$ x suspect *cd-k*$_2$	all chlorophyll deficient	all chlorophyll deficient
	all tan-saddle seed	all tan-saddle seed
		plants segregated for flower color (3:1)
cyt-Y$_2$ x suspect *cd-k*$_2$	all yellow plants	all yellow plants
	all non-saddle seed	all non-saddle seed
		plants segregated 805 tawny : 237 gray (3:1) $X^2 = 2.83$, $P<0.10>0.05$

Table 2. Crosses involving the suspect *cd-k*$_2$ as a female parent with soybean mutants *k*$_2$, *cd-k*$_2$, and *cyt-Y*$_2$

Cross	F_1	F_2
suspect *cd-k*$_2$ x *k*$_2$	all green plants	plants segregated 186 green : 40 chlorophyll deficient (3:1) $X^2 = 6.42$, $P<0.025>0.01$
	all tan-saddle seed	all tan-saddle seed
suspect *cd-k*$_2$ x *cd-k*$_2$	all chlorophyll deficient	all chlorophyll deficient
	all tan-saddle seed	all tan-saddle seed
		plants segregated for flower color (3:1)
suspect *cd-k*$_2$ x *cyt-Y*$_2$	all green plants	plants segregated 503 green, non-saddle : 142 chlorophyll deficient
	all non-saddle seed	tan-saddle (3:1) $X^2 = 3.06$, $P<0.10>0.05$
		plants segregated 502 tawny : 143 gray (3:1) $X^2 = 2.75$, $P<0.10>0.05$
		plants segregated 391 green, non-saddle, tawny : 112 green, non-saddle, gray : 111 chlorophyll deficient, tan-saddle, tawny : 31 chlorophyll deficient, tan-saddle, gray (9:3:3:1) $X^2 = 5.82$, $P<0.25>0.10$

References

Palmer, Reid G. and Peter N. Mascia. 1980. Genetics and ultrastructure of a cytoplasmically inherited yellow mutant in soybean. Genetics 95: 985-1000.

Randy C. Shoemaker
Reid G. Palmer - USDA

2) A duplicate-deficient line in soybeans

Satellite chromosomes involved in interchanges, because of their distinct morphology, are useful for special problems. Burnham (1950) determined the frequency of alternate : adjacent 1: adjacent 2 segregation in spore quartets in maize. Kunzel and Nicoloff (1979) modified the karyotype of barley (*Hordeum vulgare* L.) by inducing interchanges in order to distinguish the seven chromosomes from each other, and Langer and Kaul (1979) described an aberrant nucleolar-organizing region in *Allium cepa* L. in which the NOR consists of a fine heterochromatin stalk terminating into a deep-staining satellite.

The satellite chromosome in soybeans can be identified in root tip cells (Palmer and Heer, 1973). It has a prominent secondary constriction separating a small satellite. Although the centromeric constriction is not evident in most of the satellite chromosomes observed, a few chromosomes in which the constriction is distinct indicate that the satellite is on the short arm of the chromosome. No other mitotic chromosomes of the standard complement in soybeans have been identified.

From radiated soybeans (Sadanaga and Grindeland, 1979), three lines with altered satellite chromosomes have been developed. Line 172-11-3 in 'Hodgson' has a reciprocal translocation in which the interchanged chromosomes are identifiable. The interchanged satellite chromosome is short and the other interchanged chromosome is long.

A second line, 175-7-3, derived from 175-7 in cultivar 'Steele', has two chromosomes with a satellite that is 3 to 5 times longer than the standard satellite and two short chromosomes. These two pairs of identifiable chromosomes suggest a reciprocal exchange of asymetrical chromosome segments. An alternative hypothesis is that a chromosome morphologically similar to that postulated from a chromosome interchange arose through an inversion in the short arm with one break in the satellite. Under this hypothesis, the short chromosomes are assumed to be either centric fragments or a pair of interchanged chromosomes that had exchanged segments with a nonsatellite chromosome.

The third line, 175-7-8, derived from 175-7 in Steele, is shorter and matures later than 175-7-3, and its flowers tend to be cleistogamous. Root tip squashes of 175-7-8 revealed two satellite chromosomes with a long satellite as in 175-7-3 but without short chromosomes.

We report the pollen and ovule sterility and chromosome associations in selected parents and hybrids to determine whether 175-7-3 is homozygous for a reciprocal translocation and 175-7-8 is a duplicate-deficient line.

Cross: 175-7-3 x Steele and reciprocal. The average pollen and ovule sterility observed in reciprocal hybrids was 26% and 45.1%, respectively (Table 1). Quadrivalents observed in metaphase I (MI) were either a ring or a chain. A small univalent chromosome observed in the PMC's with a trivalent was the short chromosome. In some PMC's at anaphase I (AI), the short chromosome lagged at the equatorial plate. No anaphase bridges or fragments were observed. The quadrivalent observed in the PMC's and pollen sterility indicated that 175-7-3 is homozygous for a reciprocal translocation.

Cross: 175-7-3 x 175-7-8. The frequency of the different kinds of chromosome associations is shown in Table 1. There was a higher frequency of bivalents and a lower percentage of sterile pollen than in the previous cross. The univalent observed in the PMC was a short chromosome.

Cross: 175-7-8 x Steele. The average pollen sterility in three hybrids of this cross were not significantly different from the pollen sterility in progeny of selfed 175-7-8 (Table 1). Fertile pollen are expected from these hybrids regardless of bivalent or quadrivalent association. Parental chromosomes are expected from alternate and adjacent-1 disjunctions in the quadrivalent.

Origin of 175-7-8. In the translocation heterozygote of 175-7-3, three of the four chromosomes involved in an association of four can be identified in root tip mitotic cells. These are the chromosome with the large satellite, the chromosome with the standard satellite, and the short chromosome. In line 175-7-8, we observed two nucleolar chromosomes with a large satellite but no short chromosomes. Plants of this chromosome constitution can arise from the union of two duplicate-deficient gametes carrying the chromosome with the large satellite (interchanged chromosome) and the standard nonsatellite chromosome involved in the interchange. Cytological analysis of root tip cells of F_2 progeny of a cross between 175-7-3 and T93A indicate that duplicate-deficient gametes are transmitted either through the egg or pollen (unpublished). We conclude that 175-7-8 is a duplicate-deficient line. It is tetrasomic for the interchanged segment on the nucleolar chromosome and deficient for part or all of the small satellite in the standard nucleolar chromosome.

In a cross, 175-7-8 (Y_7Y_8) x T138 (y_7y_8), the F_2 ratio of 90 green: 6 yellow fit the expected 15:1 and indicated that neither the y_7 nor y_8 locus is on the interchanged segment.

Table 1. Chromosome association, pollen and ovule sterility in hybrids involving 175-7-3 and 175-7-8

Identity	Chromosome association			Sterility %	
	20^{II}	$18^{II}+1^{III}+1^{I}$	$18^{II}+1^{IV}$	pollen	ovule
175-7-3 x Steele	11	3	28	26.0	45.1
175-7-3 x 175-7-8	24	1	23	21.8	
175-7-8 x Steele	--[a]	--	--	5.7	2.0
175-7-8 x T138	--	--	--	3.3	8.5
175-7-8 selfs	--	--	--	7.7	

[a] Not analyzed.

References

Burnham, C. 1950. Chromosome segregation in translocations involving chromosome 6 in maize. Genetics 35:446-481.

Kunzel, G and H. Nicoloff. 1979. Further results on karyotype reconstruction in barley. Biol. Zentralbl. 98:587-592.

Langer, A. and A. K. Kaul. 1979. Studies on nucleolus and nucleolar chromosomes in angiosperms. II. An aberrant NOR in *Allium cepa* L. Chromosome Information Service 26:13-14.

Palmer, R. G. and H. Heer. 1973. A root tip squash technique for soybean chromosomes. Crop Sci. 13:389-391.

Sadanaga, K. and R. Grindeland. 1979. Aneuploid and chromosome aberrations from irradiated soybeans. Soybean Genet. Newsl. 6:43-45.

K. Sadanaga - USDA
X. Delannay

3) A dwarf mutation in 'Hodgson' soybean

A dwarf mutation was found in a line derived from radiated 'Hodgson' grown at the Bruner Farm near Ames, IA. The mutant plants were 6 to 10 cm tall, had necrotic leaves, and produced no seeds.

Twenty-four plants randomly picked from segregating plots were progeny-tested in a greenhouse and in the field. The field test data are shown in Table 1. The ratio of normal: dwarf plants in all segregating progeny rows except one fit a 3 normal: 1 dwarf expected for a simple recessive trait. Progeny rows that segregated dwarfs also segregated fertile and semisterile plants. Subsequent testing showed that fertile plants produced only fertile progeny and semisterile plants segregated dwarf, fertile, and semisterile progeny. Dwarfness was linked to semisterility.

Dwarf plants grown in a greenhouse grew 15 to 20 cm tall. We noticed among progeny of semisterile plants, six seedlings with light yellow unifoliolate leaves. These chlorophyll-deficient seedlings subsequently developed into dwarf plants. Evidence of necrosis first appeared along the margins of the unfolding trifoliolate leaves. The trifoliolate leaves of branches were lanceolate and much reduced in size. Almost all floral buds on the dwarf plants were abnormal. However, a few buds bloomed, and about a dozen seeds were harvested from the six dwarf plants. Seeds from the dwarf plants produced dwarf progeny.

The gene for dwarfness was located to the interchange chromosome. F_2 populations of hybrids between 'Hark' and semisterile plants were of two kinds, those that produced all fertile progeny and those that segregated dwarf, semisterile, and fertile plants (Table 2). Dwarf plants, therefore, are homozygous recessive for the dwarf gene and homozygous for the translocation. Hybrids between fertile plants and Hark were all fertile.

The dwarf and chlorophyll-deficiency traits may be controlled by two genes very tightly linked or may be due to pleiotropy of one or the other. No crossover types have been observed in segregating populations, and it has not been determined whether tightly linked genes or pleiotropy control dwarfness and chlorophyll deficiency.

Forty- and 41-chromosome plants were found in progeny of a semisterile plant. In the 40-chromosome group, 18 plants were normal, 9 were dwarfs, and in the 41-chromosome group, 6 plants were normal and 0 plants were dwarf. Interchange chromosomes were not identified in root tip cells. A quadrivalent observed in pollen mother cells of a semisterile plant supported the genetic evidence of the presence of a reciprocal translocation.

Table 1. Segregation of normal and dwarf plants in 13 of 24 randomly picked plants

Identity[+]	Normal	Dwarf	Total	X^2	Probability
35-1	99	32	131	0.02	.50 - .70
35-3	128	25	153	6.12	.01 - .02
35-5	66	26	92	0.52	.30 - .50
35-8	147	46	193	0.14	.70 - .80
36-1	123	31	154	1.95	.10 - .20
36-2	112	32	144	0.59	.30 - .50
36-4	126	43	169	0.02	.80 - .90
36-7	120	31	151	1.61	.20 - .30
39-3	99	26	125	1.18	.20 - .30
39-4	62	20	82	0.02	.50 - .70
39-6	30	11	41	0.07	.70 - .80
39-7	47	16	63	0.01	.90 - .95
39-8	91	27	118	0.28	.50 - .70
	1250	366	1616	12.53	
Chi-square					
Total				12.53	
Deviation				4.76	.02 - .05
Heterogeneity, df = 12				7.77	.80 - .90

[+] 11 plants were homozygous normal.

Table 2. F_2 segregation in crosses of semisterile and fertile plants x Hark

Identity	Fertility	Normal	Dwarf	X^2	P
R47-2-1	semisterile	27	10	0.08	.30 - .50
R47-2-1 x Hark -1		175	0		
" x " -2		180	0		
R47-3	semisterile	36	7	1.74	.10 - .20
R47-3 x Hark		147	44	0.39	.50 - .70
R47-3-1	fertile	40	0		
R47-3-1 x Hark -1		112	0		
" x " -2		173	0		
" x " -3		183	0		
R47-11	semisterile	25	8	0.01	.90 - .95
R47-11 x Hark		212	52	3.96	< .05
R47-15	semisterile	32	8	0.53	.30 - .50
R47-15 x Hark -1		90	0		
" x " -2		51	0		

K. Sadanaga - USDA

R. Grindeland - USDA

4) Chlorophyll-deficient plants in a soybean cross

In 1977, 18 yellow plants were found in an F_2 population of a cross between two strains of soybeans, T235 x PI 86024, both with normal green foliage. Segregation fit a ratio of 15 green: 1 yellow (Table 1). All F_3 seedlings grown from seeds harvested from yellow F_2 plants turned yellow as the plants grew. Yellowing, beginning about 4 to 5 weeks after germination, proceeded from the older to the younger leaves.

The phenotype of the F_2 yellow plants and their F_3 progeny was similar to that of strains homozygous for *g* and y_3, a genotype characterized by yellowing as the plant grew (Bernard and Weiss, 1973). Appropriate crosses were made to test whether the yellow segregates carried y_3. This note presents the results of the tests to determine the alleles in the yellow F_2 progenies and in the parents from which they originated and linkage tests of y_3 with four translocation lines.

The parents homozygous for *G* and y_3 are PI 86024 and 'Kura', for *g* and y_3 are T139, selection 7628 in the original cross, and L63-2346, and for *g* and Y_3 are T235, 'Kent', L61-4222, L61-4558, 171-31-2, 172-11-3, Clark T/T, and L75-0283-4. Lines 171-31-2 and 172-11-3 are homozygous translocations found in radiated 'Hodgson' (Sadanaga and Grindeland, 1979); 'Clark T/T', developed by R. G. Palmer, is near-isogenic Clark incorporating a translocation from PI 101404B (*G. soja*); and L75-0283-4 is a spontaneous translocation found by R. G. Palmer in an F_4 progeny row of a 'Beeson' x 'Amsoy 71' cross from Illinois in 1975.

All F_2 plants of crosses with the translocations were grown in the greenhouse except for crosses with 172-11-3. Semisterile (translocation heterozygote) F_2 plants grown in the greenhouse were identified by staining pollen grains with I_2KI. Field-grown plants were classified semisterile or fertile on the basis of number of pods and seeds per pod.

Chi-squares to test linkage between y_3 and the breakpoints in the translocations were calculated according to the method of Kramer (1954).

Results and Discussion. The hypothesized segregation ratios in the F_2 generation and the associated chi-square probabilities of the different crosses are shown in Table 1. The cross between T235 x PI 86024 again yielded a ratio of 15 green : 1 yellow seedlings. All yellow plants, without exception, were yellow seeded. The absence of yellow plants with green seed coat suggested that the F_2 ratio was not due to duplicate factors. The cross L61-4222 x PI 86024 gave an F_2 ratio of 15 green : 1 yellow; the cross T235 x Kent gave all green F_2 plants. These results indicated that T235 carried the same alleles as L61-4222 and Kent, whereas PI 86024 carried contrasting alleles.

PI 86024 resembles Kura, a cultivar in which the inheritance of seed coat color and chlorophyll deficiency is known. Terao and Nakatomi (1929) first reported the effects of the genes *H h* and *C c*, now symbolized as *G g* and Y_3y_3. *G* is epistatic to y_3 so that hybrids between Kura and yellow-seeded green plants yield 15 green : 1 yellow seedling. Bernard and Weiss (1973) noted, "Several green-seeded Japanese varieties have the *G* y_3 genotype, e.g., 'Kurakake' (Kura or PI 243526 in the USDA soybean collection). Therefore, 1/16 chlorophyll-deficient F_2 plants (*g* y_3) are often observed in breeding populations involving one parent with green seed coat." That PI 86024 may carry *G* and y_3 was surmised from its resemblance to Kura and that both had been introduced from the same region in Japan. If PI 86024

carries the same alleles as Kura, one expects no F_2 segregation for chlorophyll deficiency. The absence of segregating F_2 progeny in the cross Kura x PI 86024 (Table 1) supported the hypothesis that *G* and y_3 are in PI 86024 and that the genotype of the yellow F_2 seedlings from the cross T235 x PI 86024 is $g\ g\ y_3y_3$

In the crosses 7628 x L61-5448 (Table 1) and 7628 x 172-11-3, 7628 x L75-0283-4 and reciprocal (Table 2), segregation was observed for foliage color but not for seed coat color. Selection 7628, therefore, carries the y_3 allele. In cross 7628 x Kura (Table 1), on the other hand, segregation was observed for seed coat and foliage color. All green F_2 plants had green seed coat and all yellow plants had yellow seed coat. In the F_3 generation, 2/3 of the green plants segregated for seed coat and foliage color and 1/3 were homozygous green for seed coat and foliage color. Yellow F_2 seedlings bred true, always producing seeds with yellow seed coat. In crosses between 7628 x T139 and L63-2346, yellow F_1 hybrids with traits characteristic of the $g\ g\ y_3y_3$ genotype confirmed that 7628 has *g* and y_3.

The y_3 locus is not listed on any of the eight linkage groups (LG) reported by Stelly and Palmer (1977); *G* is on LG3. Nonsignificant chi-square values indicated y_3 was not linked to either of the interchanged chromosomes in translocation lines 171-31-2, 172-11-3, Clark T/T, and L75-0283-4 (Table 2). Cytological observations in translocation x translocation crosses (unpublished) indicated that translocation lines 171-31-2 and L75-0283-4 have one common chromosome involved in the interchange; translocation lines 172-11-3 and Clark T/T, also, have one common chromosome involved in the interchange. The y_3 locus, therefore, was tested for linkage to six different chromosomes involved in the interchanges in the four translocation lines. The only known linkage is ms_1 on LG 8 to the breakpoint in Clark T/T (Palmer, 1976). White flower color (w_1), also on LG 8, was independent of the breakpoint. Recently, Hildebrand et al. (1980) reported that LG 9 has genes controlling two chemical components, *Ap* for acid phosphatase and *Ti* for Kunitz trypsin inhibitor, linked with a crossover frequency of 16.2%. PI 86024, which carries the Ti^b allele (Orf and Hymowitz, 1977, 1978) and other mutant genes, may be useful in linkage studies.

Table 1. Segregation of green and yellow plants in F_2 populations of crosses between green x green, yellow x green, and yellow x yellow parents

Cross	Green	Yellow	Chi-square probability 15:1	3:1
Green x Green				
T235 x PI 86024	384	18	.20 - .10	
L61-4222 x PI 86024	118	6	.70 - .50	
T235 x Kent	604	0	.000	
Kura x PI 86024	88	0	.02 - .02	

Table 1. *Continued*

Cross	Green	Yellow	Chi-square probability 15:1 3:1
Yellow x Green			
7628 x L61-5448	188	50	.20 - .10
7628 x Kura	165	52	.80 - .70
Yellow x Yellow			
T139 x 7628	0	346	
7628 x L63-2346	0	323	

Table 2. Observed F_2 segregation of y_3 and the breakpoint in four translocations and their linkage chi-square probability

Cross	Semisterile		Fertile		Chi-square
	Green	Yellow	Green	Yellow	P
7628 x 172-11-3	82	33	84	23	.30 - .20
172-11-3 x T139	99	24	91	26	.70 - .50
Total	181	57	175	49	.70 - .50
7628 x L75-0283-4	47	11	44	13	.70 - .50
L75-0283-4 x 7628	31	10	37	11	.90 - .80
Total	78	21	81	24	.90 - .80
T139 x Clark T/T	62	19	72	17	.50 - .30
L63-2346 x 171-31-2	112	35	95	39	.50 - .30

References

Bernard, R. L. and M. G. Weiss. 1973. Qualitative genetics. Pp. 117-154. *In*: B. E. Caldwell (ed.) Soybeans: Improvement, production, and uses. Am. Soc. Agron., Madison, WI.

Hildebrand, D. F., J. H. Orf and T. Hymowitz. 1980. Inheritance of an acid phosphatase and its linkage with the Kunitz trypsin inhibitor in seed proteins of soybeans. Crop Sci. 20:83-85.

Kramer, H. H. 1954. Recombination in selfed chromosome interchange heterozygotes. Pp. 511-522. *In*: O. Kempthorne, T. A. Bancroft, J. W. Gowen and J. L. Lush (eds.) Statistics and mathematics in biology. The Iowa State College Press, Ames, IA.

Orf, J. H. and T. Hymowitz. 1977. Inheritance of a second trypsin inhibitor variant in seed protein of soybeans. Crop Sci. 17:811-813.

Orf, J. H. and T. Hymowitz. 1979. Inheritance of the absence of the Kunitz trypsin inhibitor in seed protein of soybeans. Crop Sci. 19:107-109.

Palmer, R. G. 1976. Cytogenetics in soybean improvement. Proc. 6th Soybean Seed Res. Conf. Pp. 56-66.

Sadanaga, K. and R. Grindeland. 1979. Aneuploids and chromosome aberrations from irradiated soybeans. Soybean Genet. Newsl. 6:43-45.

Stelly, D. M. and R. G. Palmer. 1977. Genetic linkage groups in soybeans. Soybean Genet. Newsl. 4:83.

Terao, H. and S. Nakatomi. 1929. On the inheritance of chlorophyll colorations of cotyledons and seed-coats in the soybean. Jpn. J. Genet. 4: 64-80. (In Japanese. Resumé in English).

K. Sadanaga - USDA

5) Identifying translocations in soybeans

Six translocations, currently used in linkage studies of marker genes on known linkage groups, have been intercrossed and are being examined cytologically to identify them. The origin of these six translocations are shown in Table 1.

The identification of the translocations is based on the chromosome association of the interchange chromosomes. Two quadrivalents, a quadrivalent and a trivalent + univalent, or two trivalents + two univalents would be expected in the PMCs of F_1 hybrids if the two translocations are different. A ring or chain of six chromosomes would be expected in the PMCs of F_1 hybrids if the two translocations have one common chromosome involved in an interchange.

The percent of sterile pollen and chromosome associations in T x T crosses are shown in Table 2.

The translocation in Clark T/T is different from that in L75-0283-4, PI 189866, and 171-31-2. One common chromosome is involved in an interchange in Clark T/T, 172-11-3, and 175-7-3.

The translocation in L75-0283-4 is different from that in PI 189866, 172-11-3, and 175-7-3. One common chromosome is involved in an interchange in L75-0283-4 and 171-31-2.

PI 189866 and 172-11-3, 172-11-3 and 171-31-2, and 171-31-2 and 175-7-3 have different translocations. One common chromosome (satellite chromosome) is involved in an interchange in 172-11-3 and 175-7-3.

K. Sadanaga - USDA
K. Newhouse

Table 1. Origin of six translocations in soybeans

Translocation	Origin
Clark T/T	Near-isogenic Clark with translocation from PI 101404B incorporated. PI 101404B is introduction from NE China.
L75-0283-4	Spontaneous translocation in an F_4 progeny row of a Beeson x Amsoy 71 cross. Found by R. G. Palmer in Illinois in 1975.
PI 189866	*Glycine gracilis* introduction from NE China.
171-31-2	Translocation from a radiated population of Hodgson. Selected by K. Sadanaga.
172-11-3	Translocation from a radiated population of Hodgson. Selected by K. Sadanaga.
175-7-3	Translocation from a radiated population of Steele. Selected by K. Sadanaga.

Table 2. Percentage of aborted pollen and chromosome associations in T x T crosses

Cross	Aborted pollen (%)			Chromosome association
	KN 1979[a]	KS 1980	KS 1981	
Clark T/T X				
L75-0283-4	74.0 ± 5.5	66.6 ± 2.0		2 IV
PI 189866	78.3 ± 4.6	67.4 ± 2.4		2 IV
171-31-2		73.2 ± 2.2	75.4 ± 4.8	2 IV
175-7-3		61.2 ± 3.2	62.7 ± 4.4	1 VI
172-11-3	68.7 ± 7.0	64.9 ± 1.8	62.9 ± 1.1	1 VI
L75-0283-4 X				
PI 189866	77.9 ± 3.3	72.3 ± 2.4	72.1 ± 4.5	2 IV
175-7-3		63.9 ± 2.8	66.7 ± 3.8	2 IV
172-11-3	77.6 ± 4.7	70.1 ± 2.6	72.6 ± 5.2	2 IV
171-31-2		65.2 ± 1.3	61.7	1 VI
PI 189866 X				
172-11-3	73.5 ± 3.2	68.3 ± 3.1	70.0 ± 3.6	2 IV
175-7-3			58.8 ± 5.1	?[b]
171-31-2			66.1 ± 4.8	?[b]
172-11-3 X				
175-7-3		50.2 ± 8.5	50.9 ± 3.4	1 VI
171-31-2		74.2 ± 7.3		2 IV
171-31-2 X				
175-7-3		72.3 ± 6.0	70.6 ± 3.7	2 IV

[a] Pollen sterility of plants grown in greenhouse. Data of K. Newhouse.
[b] Analysis not complete.