LINKAGE OF THE en AND st GENES IN PEAS

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Pea enation mosaic virus (PEMV) is an important virus disease of peas in the United States. It has also been recorded in the Netherlands, Switzerland, West Germany, England, and Czechoslovakia (Hagedorn, Amer. Phytopath. Soc. Monograph No. 9, 1974). The virus produces characteristic blister-like ridges or "enations" on the underside of leaflets, stipules, and pods and causes vein clearing and mottling **OF** the leaves.

Resistance to PEMV was found in PI 140295 and was introduced into commercial cultivars through backcrossing. Resistance is conditioned by a single dominant gene, En (Schroeder and Barton, Phytopathology 48:628-632, 1958).

A number of lines carrying resistance to PEMV were crossed with a number of marker stocks. We scored greenhouse-grown F2 plants for resistance and susceptibility following inoculation with the virus. These same plants were scored for a number of marker traits. Among the many traits scored, only st showed a relationship to reaction with PEMV.

Classification of the plants of the three crosses which segregated for st and en are given in Table 1. All crosses were made in coupling. Recombination values were similar and were statistically homogeneous. Data combined over all crosses resulted in a crossover percentage of 31.3 as calculated by the method of maximum likelihood.

Table 1. F2 segregation of normal size stipule (St) vs reduced stipule (st) in relation to susceptibility to pea enation mosaic virus (en) and resistance (En)

Cross	Number of plants EnSt	Enst	enSt	enst	Total	P*	Recombination %
Pure Line Freezer Lot 503-3-1 x Wellensiek Tester	94	25	18	20	157	< .005	30.7 ± 4.53
Rogers PR 6650 x L 01493	106	27	21	18	172	< .05	34.05 ± 4.63
Gallatin Valley Lot 72949 x B 267	100	19	16	18	153	<.005	25.01 ± 4.15
Heterogeneity (2df)						0.80-0.50	
Combined ratio							
Observed	300	71	55	56	482	<.01	31.28 ± 2.62
Expected 9:3:3:1	271	90	90	30	482		

Probability values were based on a 9:3:3:1 ratio.

The st gene is located on chromosome 3 so en is also a member of this linkage group. We detected no linkage with   which may indicate that en lies on the far side of st [M side-- Ed.]. Our data with f is incomplete but a greater number of parental types than expected was found in the segregation of en and f, thus suggesting that en may lie on the same side of st as f.

> Editor's Note:
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> The results reported in the above paper are in accord with unpublished results secured by I). W. Barton in 1959. Barton obtained negative evidence for linkage with markers on chromosomes 1, 2, 4, 5, 6, and 7 but positive evidence for linkage with M and st on 3. The CrO estimates between En-M and En-St were calculated as 33 and 38, respectively. In the case of the En-M linkage, a combined population of over 2200 plants was involved, but the population size for the En-st linkage was only 171 plants The estimate of linkage with b was 45% but the Chi-square was not significant. He concluded that En probably lies between M and St.

WITHIN-LINE HETEROGENEITY FOR GENE sbm IN THE U.S. PISUM COLLECTION

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During a recent search (1) for sources of immunity to pea seedborne mosaic virus [gene *sbm* (2)] among 668 untested U.S. Plant Introduction accessions of *Pisum*, 16 lines homogeneous for immunity were identified. The 16 lines were released to U.S. plant breeders by special memorandum in October, 1976. Having been selected specifically for PSbMV-immunity, these lines represented the usual gamut of non-horticultural plant characteristics. Numerous other lines, however, consisted of obvious mixtures of seed and plant type, but contained a majority of immune plants, and still others contained a minority of immune plants.

These results prompted the question: is the sbm allele relatively common in the USDA collection of *Pisum*? If so, might a diverse source of sbm provide breeders with a better choice of horticultural characteristics for breeding purposes than is available in the released lines?

I therefore examined data from the above 668 lines to identify those that were previously excluded on the basis of either seed or plant type mixtures, or heterogeneity for gene sbm (not pure for sbm/sbm plants). Resistance was found in 160 lines in addition to the 16 previously released to