LINKAGE RELATIONS OF mo

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Pea mosaic, caused by hean yellow mosaic virus (BYMV=BV₂), is a disease of economic importance in many pea growing areas of the world (Schroeder and Provvidenti, New York State Agr. Exp. Sta. Bui. 806. 1964). Resistance to the virus is conferred by a single recessive gene pair, mo/mo CYen and Fry, Australian J. Agr. Res. 7:272-280. 1956).

Although BYMV resistance is routinely incorporated into our breeding and genetic stocks, till now we have never undertaken a formal linkage study involving mo. Preliminary tests pointed to a linkage of mo with wb and k on chromosome 2 (Table 1).

Entry	Wb Mo	Wb mo	wb Mo	wb mo	Total
C276-373	42	18	22	1	
C276-374	12	11	4	0	
	54	29	26	1	110
	К Мо	K mo	k Mo	k mo	
C276-373	45	19	14	0	
C276-374	13	11	2	0	1
	58	30	16	$\overline{0}$	104-

 $\frac{1}{2}$ Six plants not scored for k-k and therefore excluded

Following this, populations were grown and tested for crossover segregants carrying wb, k and mo in coupling. Triply recessive plants were then crossed with triply dominant plants and the F_2 progenies were grown and tested for resistance in the greenhouse along with the respective resistant and susceptible parents and with a traditional set of control varieties, viz. 'Bonneville' (R) and 'Ranger' (S).

Each plant in the test was artificially inoculated twice in a manner outlined by Schroeder and Provvidenti (loc cit). A total of 404 F_2 plants were tested for reaction to the virus but this was done in two separate groups of approximately 200 plants each, planted about two weeks apart in September 1978. The greenhouse night temperature was maintained at approximately 15°C +/- 5° and daytime temperatures were approximately 22°C (rarely over 27°C). Natural daylight was supplemented by fluorescent and incandescent light to a total of 16 hrs illumination daily. The raw data of the three-point test were sent to Dr. Blixt for computer analysis where the two groups were analyzed separately and together (Table 2).

cou	pling phas sses were	e crosses grown and	<u>Wb-Mo</u> , of <u>k</u> . Populat l analyzed two weeks	ions from in two se	the sam
trezs bně bř	Wb Mo	Wb mo	wb Mo	wb mo	Total
C278-103-109	130	20	20	37.	207
C278-155-160	135	20	6	36	197
	265	40	26	73	404
	К Мо	K mo	k Mo	k mo	
C278-103-109	149	9	1	48	207
C278-155-160	138	8	3	48	197
	287	17	4	96	404
	Wb K	Wb k	wb K	wb k	
C278-103-109	138	12	20	37	207
C278-155-160	141	14	5	37	197
	279	26	25	74	404
Materoders	Per	cent cros	sing over		
		Wb-K	K-Mo	Wb-Mo	
C27	8-103-109	15.5	4.8	20.3	
C27	8-155-160	9.6	5.6	15.2	
Com	bined	12.6	5.2	17.8	

The results confirmed the preliminary findings and establish mo on chromosome 2 rather closely linked with k. All three single gene segregations, in both groups, were statistically not significant; moreover, the relative order of the three genes was the same. However, the calculated linkage intensity was different in both instances so the data are presented separately and combined. Using the combined data, the map distances in that segment of chromosome 2 are as follows: