SUPPLEMENTAL MAPPING DATA FOR CHROMOSOME 6

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The gene for resistance to Pea Seedborne Mosaic Virus (PSbMV) in pea has been found in two accessions, PI 193586 and PI 193835 (2). Using these lines as sources of resistance, Hagedorn and Gritton developed horticulturally improved lines designated Wisconsin 7105 and Wisconsin 7106, both resistant to SbMV.

Gritton and Hagedorn (1) then reported the linkage of the gene sbm with wlo in chromosome 6 with recombination fraction of ca. 12%. The linkage was confirmed by Hampton and Marx (3) with the suggestion of using wlo as the marker gene in selection for resistance.

We tested this suggestion in our own breeding work. Two sbm lines, Wis 7105 and Wis 7106, were crossed with wlo lines Wt 11340 and 10341 (from the Wiatrowo pea genebank), a repulsion phase cross. The dihybrid segregation in F2 gave little evidence of linkage:

Wlo Sbm	Wlo sbm	wlo Sbm	wlo sbm	Total
233	146	90	41	510

Although those data do not show linkage between sbm and wlo there was an excess of segregants scored as resistant, so there was a possibility that susceptible plants had been misclassified as resistant. Further studies on the localization of sbm therefore were pursued; these studies included other known Loci oi chromosome 6.

In the first step Wt 11778 = PI 193586 (sbm) was crossed with Wt 16140 (wlo art-1). All F1 plants proved susceptible to PSbMV. Monohybrid segregation with no disturbances was observed in F2 (Table 1A). In a population of 906 plants, the dihybrid segregation for sbm-wlo showed deviations from independence and a CrO value = 23.0 (Table IB); for sbm-art-l the calculated CrO value was 41.2.

Wt 12070 == Wis 7106 (sbm) was also crossed with Wt 16141 (art-1 p). Again the F1 plants were susceptible and an undisturbed monohybrid segregation was observed (Table 2A). The dihybrid segregation (about 800 plants) showed a linkage between Sbm and Art-1 with a CrO value of 34.2 +/- 3.1% and between Sbm and P with CrO value of 24.5 +/- 13.3% (Table 2B).

Thus none of the above genes (wlo, art-1, or p) seems to be a closely Linked marker for sbm. On the basis of the gene order presented by Marx (4) and on our own results described above the following situation is proposed:

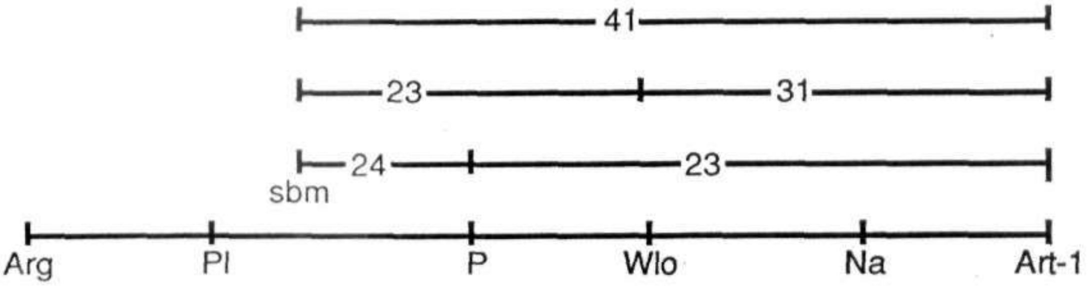

Table 1. Phenotypic distribution in an F_2 population segregating for genes on chromosome 6 from Wt 11778 (sbm) x Wt 16140 (wlo, art-1).

A. Monohybrid F_2 segregation.

Wlo	wlo	Total	Chi-square (3:1)
672	238	910	0.65
Sbm	sbm		
690	216	906	0.65
Art-1	art-1		
701	208	909	2.17

B. Joint segregation of sbm with wlo and art-1.

Wlo Sbm	Wlo sbm	wlo Sbm	wlo sbm	Total	Joint Chi-square	Phase	R.F.	S.E.
464	204	226	12	906	63.42	R	23.0	3.1
Wlo Art-1	Wlo art-1	wlo Art-1	wlo art-1					
568	102	132	106	908	83.53	C	30.5	1.9
Sbm Art-1	Sbm art-1	sbm Art-1	sbm art-1					
516	174	183	33	906	8.86	R	41.2	2.7

Table 2. Phenotypic distribution in an F_2 population segregating for genes of chromosome 6 from Wt 12070 (sbm) x Wt 16141 (art-1, p).

A. Monohybrid $F_?$ segregation.

Sbm	sbm	Total	Chi-square (3:1)
614	186	800	1.31
Art-1	art-1		
620	181	801	2.47
P	P		
611	187	798	1.04

B. Joint segregation of sbm with art-1 and p.

Sbm Art-1	Sbm art-1	sbm Art-1	sbm art-1	Total	Joint Chi-square	Phase	R.F.	S.E.
452	162	167	19	800	21.19	R	34.2	3.1
Sbm P	Sbm p	sbm P	sbm p					
435	177	176	10	798	44.96	R	24.5	3.3
Art-1 P	Art-1 p	art-1 P	art-1 p					
536	82	75	105	798	159.02	C	23.1	1.7

It appears from these data that sbm is located in the Pl end of chromosome 6.

1. Gritton, E. T. and D. J. Hagedorn. 1975. Crop Sci. 15:447-448.
2. Hagedorn, D. J. and E. T. Gritton. 1971. PNL 3:16.
3. Hampton, R. 0. and G. A. Marx. 1981. PNL 13:16.
4. Marx, G. A. 1982. PNL 14:50-52.

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