ON THE GENES FOR RESISTANCE TO FUSARIUM WILT

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Several races of the pea wilt fungus (*Fusarium oxysporum* f. sp. *pisi*) cause economic losses in the pea growing regions of the U. S. and other countries. Resistance to four races of the fungus (races 1, 2, 5, and 6) is reportedly controlled in each case by single dominant genes (1,2,3,4,6). Wade (6) was able to show that resistance to race 1 was controlled by a single dominant gene (Fw) linked by about 30 map units to Le on chromosome 4. Resistance to race 2 or "near wilt" is controlled by a single dominant gene designated as *Fnw* (7). The gene for resistance to race 2 (*Fnw*) was reported by Wells *et* al. (7) to be about 40 map units from *Fw*; however, his F3 data indicated independence of the two genes, and no linkage of *Fnw* with Le was found. The chromosomal locations of the genes for resistance to races 5 and 6 of wilt are unknown and no linkage studies have been reported.

For our study, we tentatively designated the gene for resistance to race 5 as '*Fwf*'. To determine the chromosomal locations and linkage relationships of the genes for resistance to races 2, 5, and 6, we crossed known wilt-resistant material with genetic stocks that were chosen for marker genes on the seven chromosomes. Because the gene for resistance to race 1 (Fw) is reportedly on chromosome 4, we initially concentrated our studies on that chromosome and attempted to determine whether *Fnw* and *Fwf* were located there as well. Our approach was to develop F2 populations that were well characterized for the morphological markers and various isozyme loci followed by scoring F3 families from individual F2 plants for resistance or susceptibility to the races of wilt.

In F3 families from populations of F2 plants segregating for morphological genes in chromosome 4 (v, *le*, *Np*, *Td*, *fa*, *was*, and n), it appeared that *Fwf* is linked to Le (Table 1) with a recombination fraction estimated at 29%. *Fwf* did not show linkage with n; however, *Fwf* appeared to be loosely linked to v as expected based on the apparent close linkage of v with Le. *Fwf* and Le appeared to be linked in two other segregating families (Tables 2 and 3) with recombination fractions of 34% and 39%. respectively. The probabilities associated with the chi-squares were 0.07, 0.09, and 0.08, respectively; however, the consistency of results among populations indicate a likely linkage of Fwf with *Le*. *Fwf* showed some linkage with *lum*, a gene tentatively placed on chromosome 4. However, *Fwf* did not appear to be linked to *fa*, n, or *Np*.

Table 1. Joint segregation (A285-283 to A285 286)

Pairs of genes	F3 families n	+/+	+/-	-/+	-/-	X^2	Probability	Recomb. Fraction
n, 'Fwf'	51	21	18	7	5	0.07	0.78	0.47 ± .10
v, 'Fwf'	51	25	14	3	9	5.66	0.02	0.33 ± .12
le, 'Fwf'	51	20	21	8	2	3.16	0.07	0.29 ± .12
le, v	51	29	12	10	0	3.82	0.05	0.004 ± .14
le, n	51	32	9	7	3	0.29	0.59	0.44 ±.11

Table 2. Joint segregation (A285 280 to A285-282)

Pairs of genes	F3 families n	+/+	+/-	-/+	-/-	X^2	Probability	Recomb. Fraction
le, 'Fwf'	77	37	16	21	3	2.78	0.09	0.34 ± .10
lum, 'Fwf'	77	41	12	14	10	2.93	0.09	0.37 1 .10
1e, 1um	77	42	13	16	6	0.11	0.74	0.47 ± .09

In populations segregating for Fwf, Td, and fa, it was apparent that Fwf was not linked to Td as would be expected if Fwf were located on chromosome 4 in proximity to Le (Table 4). Also, Fwf, was very loosely linked to fa as would be expected based on where fa is placed in that linkage group.

The genes for resistance to races 1 and 5 (Fw and Fwf, respectively) both appear to be linked with Le and with similar recombination fractions. The results indicate a probable close linkage of Fw with Fwf. We are currently developing the lines needed to test this apparent linkage. Fwf was also linked to v and to lum indicating that chromosome.4 is the probable location of Fwf. The lack of linkage with Td and other markers on chromosome.4 may indicate that the gene is in a distal position to Le; however, further information (5) indicates that Td may be located elsewhere in the genome.

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Families A283-250 to A283-259, shown in Table 3, were provided by G. A. Marx.

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Table 3. Joint segregation of pairs of loc1 (A283-250 to A283-259)

Pairs of genes	F3 families n	+/+	+/-	-/+	-/-	X^2	Probability	Recomb. Fraction
fa:le	117	79	24	13	1	1.92	0.17	0.39 ± 0.08
n:le	117	6/	21	25	4	1.32	0.25	0.41 ± 0.08
Np:le	117	76	8	16	17	24.80	0.00	0.23 ± 0.08
Fwf:le	114	66	14	23	11	3.07	0.08	0.39 ± 0.08
Fwf:fa	114	71	9	29	5	0.26	0.61	0.49 ± 0.07
Fwf:n	114	61	19	24	10	0.40	0.53	0.46 ± 0.07
Fwf:Np	114	59	21	23	11	0.44	0.51	0.45 ± 0.07

Table 4. Joint segregation of pairs of lod (W286-104, W286-89 and W286-92 families

Pairs of genes	F3 families n	+/+	+/-	-/+	-/-	X^2	Probability	Recomb. Fraction
Fwf:fa	66	36	10	17	3	0.40	0.53	0.43 ± 0.10
Fwf:Td	26	13	6	5	2	0.02	0.88	0.48 ± 0.15
Fwf:Td	50	10	15	13	12	0.72	0.39	0.44 ± 0.07

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