Linkage relationship between genes *Fw* and *Fnw*

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Fusarium oxysporum Schlecht. emend. Snyd. and Hans. f. sp. *pisi* (van Hall) Snyd. and Hans. is a causal agent of wilting in peas. Four races, 1, 2, 5 and 6, are economically important. Races 1 and 2 of the pathogen have a worldwide distribution while races 5 and 6 are mostly confined to the western part of Washington State in the U.S.A. and to British Columbia in Canada (1). Resistance to race 1 of the pathogen is conferred by a single dominant gene *Fw* that has been reported to be located 30 map units from *Le* (4). Resistance to race 2 of the pathogen is also conferred by a single dominant gene *Fnw* (2, 5). Wells et al. (5) reported loose linkage between *Fnw* and *Fw* with 40% recombination; however, no linkage was found between *Fnw* and *Le*. The putative location of *Fnw* has been on chromosome 4 but not linked to *Le*. Since the data of Wells et al (5) for F_3 families did not support linkage between *Fnw* and *Fw*, it was our goal to determine where the two genes are located and whether or not they are linked.

Crosses between lines resistant or susceptible to races 1 and 2 of the fungus were made, and the F_3 families were evaluated for their response to the two races. Resistance or susceptibility to race 1 was evaluated in the field in a disease nursery, while resistance to race 2 of the pathogen was evaluated under greenhouse conditions following standard inoculation procedures (3). Crosses used in this study were: Mini 93 (*Fw, Fnw*) x M410 (*fw, fnw*), 74SN5 (*Fw, Fnw*) x WA788 (*fw, fnw*), and 74SN5 (*Fw, Fnw*) x M410 (*fw, fnw*).

We analysed the data for each cross separately and later combined the data (123 F_3 families). *Fw* and *Fnw* segregated as expected for single dominant genes (Table 1).

The joint segregation data for the two loci (Table 2) indicated a recombination fraction of around 46%, and the likelihood that the two genes assorted independently. The linkage relationship of 40% between the two loci reported by Wells et al. (5) was never confirmed in subsequent studies. Based on our data, it appears that the genes are transmitted independently; however, the possibility that the two genes are in the same linkage group has not been ruled out. We are conducting further studies on linkage of various genes with *Fw* and *Fnw* which may help to determine the linkage groups that contain these genes.

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Table 1. Single locus goodness of fit to a 1:2:1 ratio for F_3 families from crosses segregating for *Fw* and *Fnw*.

Gene	Cross	F_3 families			χ^2	df	P
		+/+	+/-	-/-			
Fw	Mini 93 x M410	8	22	12	0.85	2	0.65
	74SN5 x WA788	6	15	8	0.31	2	0.86
	74SN5 x M410	14	26	11	0.37	2	0.83
	Combined	28	63	31	0.28	2	0.87
Fnw	Mini 93 x M410	12	18	6	2.00	2	0.37
	74SN5 x WA788	7	14	8	0.10	2	0.95
	74SN5 x M410	7	28	16	3.67	2	0.15
	Combined	27	59	30	0.19	2	0.91

Table 2. Joint segregation data for *Fw* (resistance to race 1) and *Fnw* (resistance to race 2) for 116 F_3 families from three crosses.

Race 2	Race 1			Joint seg. χ^2 (df = 4)	Prob.	Recomb. fraction	SE
	+/+	+/-	-/-				
+/+	9	12	6	2.58	0.63	46.2	4.0
+/-	11	32	16				
-/-	6	17	7				