Inheritance of Horizontal Resistance to Crown Rust in Oats

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ABSTRACT

Horizontal resistance to crown rust in Red Rustproof oats was found to be controlled by a small number (2.16) of genes, showing slight partial dominance for susceptibility. A high heritability value (87%) was found; therefore, selection should be effective.

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A superior type of horizontal resistance (HLR) was demonstrated in certain cultivars of Red Rustproof (RRP) oats (*Avena byzantina* C. Koch) (4). We observed that RRP-14 expressed crown rust (*Puccinia coronata* Cda. f. sp. *avenae* Fraser & Led.) symptoms 10-14 days later than susceptible cultivars, and possessed a low percentage of infection at the end of the growing season. This pronounced form of HLR has remained stable for more than 20 years (4). Cultivars with this type of HLR escape significant rust damage, and are not influenced by changes in rust races. Under field conditions, cultivars with HLR do not show signs of rust infection until a given point, at which time they are susceptible to most races. A recent report indicated that the grain yield of a slow-rusting cultivar was as good as those with vertical resistance (VR) (5). Slow-rusting is a form of HLR. Other reports indicated that HLR may be superior to VR (3, 7). We, therefore, initiated studies to determine the inheritance of HLR.

Cultivars used as parents were RRP-14 (C.I. 4876) and Fulghum (C.I. 708). RRP-14 is a selection from RRP. The latter originated in southwest Georgia about a century ago (6). Reciprocal crosses were made. Seeds were space-planted in the field in early December 1973. A rust spreader (Fulghum) that circumscribed the F_1, F_2, and parental seedlings was planted about 3.2 m from the test area. Seeds of the parental cultivars were planted at the ends and middle of each test plot. Crown rust evaluations were expressed as the percentage of affected area of the most severely diseased leaves. In the spring of 1974, F_1, F_2, and parental plants were evaluated for reaction to crown rust.

No significant variation was observed in plants from F_2 populations derived from different crosses. Therefore, the data from F_2 plants from three crosses between the parents were combined and analyzed. When rust evaluations were initiated, no lesions were found on any plants of the RRP-14 parent, but some variation was observed among plants of the Fulghum parent (Table 1). This variation resulted from differences in rust evaluation rather than in heterogeneity within the cultivars. The observed means of the F_1 and F_2 generations were slightly above the calculated arithmetic mean, indicating a partial dominance for rust susceptibility in each generation.

The frequency distributions of all generations are presented in Figure 1. Considerable segregation was

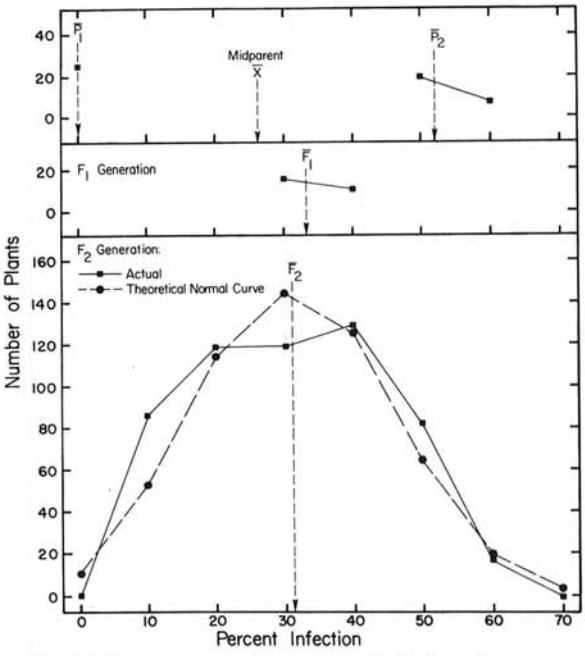

Fig. 1. The percentage of crown rust infection observed on plants of oat cultivars Red Rustproof-14 (P_1) and Fulghum (P_2), and F_1 and F_2 plants derived by crossing these two cultivars.

TABLE 1. Characteristics of parents and F_1 and F_2 generations derived from crosses of Red Rustproof-14 and Fulghum

Generation	Cultivar	Plants classified (no.)	Mean infection		Standard deviation	Variance	Standard error
			Observed (%)	Arithmetic[a] (%)			
P	Red Rustproof-14	25	0	...	0.0	0.0	0.0
P	Fulghum	25	52.4	...	4.4	19.4	0.9
F_1	...	23	34.3	26.2	5.1	26.0	1.1
F_2	...	549	31.0	30.3	13.9	193.2	0.6

[a] $F_1 = (P_1 + P_2)/2$; $F_2 = (P_1 + 2F_1 + P_2)/4$.

found in the F_2 generation. The distribution of the F_2 generation did not fit a theoretical normal curve ($\chi^2 = 49.39^{**}$, df = 7). The deviations occurred primarily at the 10, 30, and 50% infection level, with an excess at the 10 and 50% level and a shortage at the 30% level. Evidence for slight partial dominance was indicated by the frequency distribution of the F_2 generation (skewness = 0.65).

The gene number and broad-sense heritability value associated with this character were estimated. The estimated broad-sense heritability value was 87%, which is relatively high. Using the assumptions described by Burton (2), the gene number was estimated to be 2.16. This value is relatively low. The low number of genes differs with a recent report concerning the horizontal resistance to tomato early blight (1).

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