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Inheritance of Resistance to Rhizoctonia Fruit Rot in Cucumber

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Abstract. A wide-base pickling cucumber (*Cucumis sativus* L.) population was formed by intercrossing all available cucumber lines (1063) and selecting for short fruit length. After intercrossing twice, 112 S_0 plants and their half-sib progeny were evaluated for Rhizoctonia fruit rot resistance using a detached-fruit test. Parent-offspring regression indicated a narrow-sense heritability of 0.24, considered low to moderate. Gain from selection was calculated for 2 recurrent selection systems. Based on the heritability estimate, selection using replicated progeny rows was recommended for improving resistance to this trait.

In the southern United States cucumber yield losses to fruit rot caused by *Rhizoctonia solani* Kuehn have averaged 7% to 9%, reaching as high as 40% under optimum disease conditions (7). There is usually an additional loss due to the cost of hand-culling the diseased fruit, and fruit quality is lowered as well, since a certain number of diseased fruit accidently are processed. These problems make Rhizoctonia fruit rot an important disease of commercially-grown cucumbers.

Host resistance would be an economical method of control if a source of resistance were found. Single-gene resistance to Rhizoctonia fruit rot in cucumbers has been identified (1) but may be due to the gene, *H,* for heavy netting on the fruit surface, making the fruit unsuitable horticulturally. Moderate levels of resistance exist in some lines, but heritability of that resistance has not been estimated. Single-gene resistance would offer a source for rapid genetic improvement, but quantitative resistance can be used if high-level single-gene sources for resistance are not available. Recurrent selection can be used to increase the number of minor genes for resistance in a population. To determine the extent of genetic control of resistance, and to estimate the amount of progress that can be made in each cycle of selection, an estimate of heritability is needed. The estimate also permits the determination of the best selection method to use (2, 4). This predictive role is important, since selection only can be applied to the phenotype, and success in changing the characteristics of a population can be predicted only from a knowledge of the degree of correspondence between phenotypic values and breeding values (3).

Table 1. Mean, heritability, variances, and gains from selection for resistance to Rhizoctonia fruit rot resistance in the NCWBP population as determined by parent-offspring regression.

Statistic	Definition	Value[z]
$\bar{x}$	Population mean	2.1 %
x_H	Most susceptible family	12.0 %
x_L	Most resistant family	0.0 %
b_{OP}	Parent-offspring regression coefficient	0.12
h^2_N	Narrow-sense heritability	0.24
σ^2_A	Additive genetic variance	$6.40\%^2$
$\sigma_{P(I)}$	Phenotypic standard deviation (single-plant selection)	5.17%
$\sigma_{P(HS)}$	Phenotypic standard deviation (half-sib family selection)	0.78%
$G_{S(I)}$	Gain from selection (single-plant)	1.6 %
$G_{S(HS)}$	Gain from selection (half-sib family)	3.6 %

[z]Data were half-sib family means of 3 detached fruit per family placed on soil inoculated with *Rhizoctonia solani* at the rate of 3100 grains/m^2 and rated for the percentage (%) of total fruit surface covered with lesions.

The objective of this study was to determine the heritability of Rhizoctonia fruit rot resistance in cucumber using parent-offspring regression analysis in a wide base pickling cucumber population, and to estimate gain from recurrent selection using single-plant and half-sib family testing methods.

A method of screening for resistance developed for use in the North Carolina State University breeding program was used to test the families in the heritability study (5). A similar method was used by Clark and Block (1) to screen the USDA plant introduction collection of cucumbers held at Ames, Iowa, for Rhizoctonia fruit rot resistance.

In 1981, 1063 cucumber cultivars, plant introduction lines, and breeding lines were intercrossed in isolation to construct a wide base population. After eliminating all but the pickling cucumber types, the population was intercrossed a 2nd time in isolation at Clinton, N.C. in 1982 to form the North Carolina Wide Base Pickle (NCWBP) population.

The 4 isolates of *Rhizoctonia solani* used in these studies were obtained from M.J. Goode, Dept. Plant Pathology, Univ. of Arkansas, Fayetteville, AK 72701. All were in anastomosis group 4. The isolates were tested for pathogenicity and then were grown on acidified potato dextrose agar (PDA). Inoculum was produced by introducing 1 cm^2 pieces of the acidified PDA containing *R. solani* growth into autoclavable bags containing 300 ml of oat grains, and 250 ml of tap water, all of which previously had been autoclaved twice. All tests were conducted on fruit having a diameter of about 50 mm.

Plastic flats (450 × 520 mm) were filled to a depth of about 50 mm with steam sterilized field soil classified as a Norfolk-Ruston sandy loam. Soil in the flats then was inoculated with about 3100 oat grains colonized with *R. solani*/m^2.

One fruit was harvested from each of 112 S$_0$ plants chosen at random and tested for Rhizoctonia fruit rot reaction as follows. Fruit free of disease lesions were harvested on 2 dates (16 Aug. and 7 Sept. 1982) to account for differences in maturity. The fruit then were placed on inoculated soil in flats in a greenhouse so that neither end of the fruit was touching the soil. The flats of soil and fruit then were watered and covered with newspaper. The soil was kept damp by watering lightly every 3 days. Temperature

in the greenhouse ranged from 24°C at night to 33° during the day. After 10 days, the fruit were scored individually for the number of lesions per fruit and the percentage of the total fruit surface that was infected.

A 2nd fruit was harvested from each of the 112 S$_0$ plots on 20 Sept. 1982 to produce seed for measuring Rhizoctonia fruit rot resistance of the progeny in 1983. Progeny plots, each a half-sib family, were planted on 13 May 1983 at Clayton, N.C. Plots were 1.3 m long with 1.5 m alleys and 1.5 m between rows. Three fruit from each half-sib family were harvested and rated as described above for the parents in 1982.

Narrow-sense heritability is defined as the ratio of additive genetic variance to phenotypic variance ($h^2_N = \sigma^2_A/\sigma^2_P$). This value can be estimated as twice the regression of breeding value on phenotypic value, or twice the regression of parents on offspring ($h^2_N = 2 b_{OP}$) (3, 8).

Gain from selection can be determined from the following formula. For individual plant selection, the gain from selection (G_s) per year would be: $G_{S(I)} = k (1/2) h^2_N \sigma_{P(I)}$. For half-sib family selection, gain would be: $G_{S(HS)} = k (1/4) \sigma^2_A/\sigma_{P(HS)}$, where k is the selection intensity in SD, h^2_N is narrow-sense heritability, $\sigma_{P(I)}$ is the square root of the phenotypic variance of individual plants, σ^2_A is the additive genetic variance, and $\sigma_{P(HS)}$ is the square root of the phenotypic variance of half-sib families.

The variance of the parental population (σ^2_X) was 26.7 and the additive variance (σ^2_A) was estimated to be 6.4 The half-sib family means were regressed on the maternal parent value using the percentage of fruit surface infected as the measure of Rhizoctonia fruit rot resistance. The covariance of offspring and parent was used to estimate additive genetic variance as shown above, and the variance of the parents was used to esimate phenotypic variance for calculation of gain from selection.

The mean percentage of the fruit surface covered with lesions for the entire population was 2.1% (Table 1). Damage to individual fruit ranged from 0% to 12%, indicating that the population had a moderate level of resistance. The slope (b) of the parent-offspring regression was 0.12. Therefore, the narrow-sense heritability for Rhizoctonia fruit rot resistance was estimated to be 0.24, con-

sidered to be low to moderate. Other estimates for heritability of horticultural traits in cucumber have ranged from 0.17 for yield to 0.68 for number of days to harvest (6).

Gain from selection was estimated for phenotypic recurrent selection (single-plant selection without control of the pollen parent) and modified half-sib family selection (best families intercrossed in isolation for selection control of both parents). Given the resources available in the North Carolina State Univ. breeding program, we estimated that with about the same amount of effort, 8000 plants could be evaluated using phenotypic recurrent selection, and 800 plots (400 families, 2 replications) if modified half-sib family selection were used. We assumed that 80 of 8000 single plants were selected, and that 40 of 400 half-sib families were selected. Therefore, the values of k would be 2.66 and 1.76 for phenotypic recurrent selection and modified half-sib family selection, respectively. Gain from selection was estimated as follows:

$G_{S(I)} = 2.66 \times 0.5 \times 0.24 \times 5.17 = 1.6\%$ fruit surface damaged / cycle; $G_{S(HS)} = 1.76 \times 0.25 \times 6.4 \times 0.78 = 3.6\%$ fruit surface damaged/cycle.

Gain would be made at the rate of one cycle per year for both methods if the season were long enough to test and then intercross the best half-sib families in isolation for modified half-sib family recurrent selection. Thus, the population could be made completely resistant in 1 or 2 cycles (years) of selection, depending on which method were used. Since the unselected population was rated as mostly resistant, it may be desirable to develop a severe test to permit selection for higher levels of resistance. However, the heritability of 0.24 indicates that resistance can be incorporated into adapted cultivars using recurrent selection. As with all traits having low heritability, environmental variation should be controlled during selection by using replicated progeny rows.

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