Genetic Variability and Heritability Estimates Based on the F_2 Generation from Crosses of Large-Seeded Virginia-Type Peanuts with Lines Resistant to Cylindrocladium Black Rot[1]

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ABSTRACT

Selection of large-fruited, high-yielding Cylindrocladium black rot - (CBR) resistant lines from two sets of crosses, each set consisting of crosses in F_2 generation between a virginia and two CBR-resistant lines, was evaluated to determine the potential for selecting cultivars with these traits. Heritabilities, phenotypic and genotypic correlations and estimates of additive and nonadditive genetic effects were determined for yield and fruit traits at two locations and CBR resistance at one location. Crosses with NC 2 as a parent had higher levels of CBR resistance than those with Florigiant as the common virginia-type parent. Heritability estimates for the necrosis index (CBR resistance) were high while estimates for yield and fruit traits were variable over crosses and locations. The necrosis index was significantly and negatively correlated with all fruit and yield traits for three of the four crosses indicating it should be possible to select high-yielding, large-fruited lines with low levels of disease from three crosses. Only significant additive genetic effects were found for CBR resistance. Significant additive and nonadditive genetic effects were found for the yield and fruit traits. Estimates of additive and nonadditive genetic effects indicate that early generation selection for CBR resistance should be effective, whereas selection for yield and fruit traits would be more effective in later generations.

Key Words: Arachis hypogaea L., disease resistance, genetic variance, additive and nonadditive genetic effects.

A relatively new disease problem of North Carolina-grown peanuts (Arachis hypogaea L.) is Cylindrocladium black rot (CBR) caused by the soil-borne fungus Cylindrocladium crotalariae (Loos) Bell and Sobers (3). Since the first report of CBR in North Carolina in 1970, no consistently effective chemical or cultural control practices have been established (8,9). Resistance lines of spanish descent were identified in field tests conducted in North Carolina during 1973-74 and NC 3033 was released in 1976 as a resistant germplasm (1,10). Although NC 3033 has a high level of resistance to CBR, it has small seeds and is low yielding. CBR-resistant lines have since been developed with improved yield and seed size although

further improvements in the agronomic qualities of these lines are still needed. Efforts towards development of lines with high levels of CBR resistance, large fruits and seeds, and high yields can be maximized by knowledge of the heritabilities and genetic relationships between these traits.

Hadley (4) reported only significant general combining ability effects in a diallel analysis of CBR resistance for crosses in the F_1 and F_2 generations, thus indicating additive genetic control. Estimates of heritability ranged from 0.48 to 0.65 for CBR resistance depending on the method of calculation.

Reviews of quantitative genetic studies in peanuts by Hammons (5) and Coffelt and Hammons (2) cite numerous reports of heritabilities and correlations among yield and fruit traits from a diverse group of peanut materials. Positive correlations have been reported among yield traits such as number of fruit per plant, weight of fruit per plant, number of seed per plant and fruit length. Heritabilities for yield and fruit weight have been reported as being both low and high. Presently there are no reports on genetic variability, heritability, and correlations among yield traits and CBR resistance in populations derived from crosses of large-seeded virginia-type lines with CBR-resistant lines.

This study was conducted to determine the potential for selection of large-seeded, high-yielding lines with CBR resistance from crosses of large-seeded, high-yielding virginia lines with CBR-resistant lines. Selection potential was determined by estimating genetic variability, heritability and correlation coefficients for yield and fruit traits and CBR resistance. Estimates of additive and nonadditive genetic effects for these traits were also obtained as indicators of the progress expected from selection in early generation.

Materials and Methods

The F_2 populations used in this study were from crosses of NC 17941A x Florigiant, NC Ac 18323 x Florigiant, NC Ac 18016A x NC 2 and NC Ac 18229 x NC 2. These populations plus the six parents were tested in 1981. The 10 entries composed two 5-entry sets. Each set consisted of the two F_2 populations with a common large-fruited parent and the three parental lines. Of the parental lines two were large-

fruited, virginia-type cultivars, Florigiant (set 1) and NC 2 (set 2), and four were CBR-resistant lines - NC Ac 17941A and NC Ac 18323 (set 1) and NC Ac 18016A and NC Ac 18229 (set 2). The CBR-resistant parents are advanced lines derived from crosses of high-yielding cultivars and CBR-resistant sources. The parentages of the four lines are as follows: NC Ac 17941A = (NC Ac 3139 x Florigiant), NC Ac 18323 = (NC 3033 x Va 61R), NC Ac 18016A = (NC Ac 9088 x NC 3033) and NC Ac 18229 = (NC 3033 x NC 2). The parents were coded as follows: A_1 = Florigiant, B_1 = NC Ac 17941A, and C_1 = NC Ac 18323 for set 1 and A_2 = NC 2, B_2 = NC Ac 18016A, and C_2 = NC Ac 18229 for set 2.

The 10 entries were planted in a randomized complete block design with five replications at three locations. The three locations included the Upper Coastal Plain Research Station, Rocky Mount, NC; the Peanut Belt Research Station, Lewiston, NC: and the Byrd Farm in Bladen County, NC, where CBR has been a problem. Two-row plots of 15 seed per row were planted. Stand counts were made early in the season. Prior to harvest the number of dead and diseased (CBR) plants for each plot at the Byrd Farm were counted on September 9 and October 2, 1981. Numbers of dead and diseased plants per plot were divided by their respective stand counts and recorded as percent dead and diseased plants. Ten plants per plot were harvested at each location and the fruit were hand-picked. Roots from the harvested plants were also collected at the Byrd Farm. These roots were split longitudinally down the center and CBR root rot was evaluated based on the distance the root rot extended toward the center of the root. A necrosis index scale of 0 (no disease) to 5 (completely decayed) was used. The following fruit and yield traits were measured on a per-plant basis at all three locations:

a) Pod yield (g)
b) Length of 20 random pods (cm)
c) Weight of 20 random pods (g), and
d) Weight of seed from 20 random pods (g).

An analysis of variance for percent dead and diseased plants for each of the two count dates was performed for the 10 entries combined. An arcsin transformation was used on data recorded as percent (% dead and diseased plants) to stabilize the error variance. A Waller-Duncan Bayesian LSD was computed to compare entry means. Data for the remaining traits were analyzed separately for each location and each of the two sets of entries. A separate analysis of variance was performed for each of the F_2 entries and each of the two sets of parental lines excluding the parents Florigiant and NC 2 from the sets. Estimates of parental within-plot or plant-to-plant variability for each of the two sets of parents were equated to environmental variance. Florigiant and NC 2 were excluded from these estimates of environmental variance because these cultivars are not typical inbred lines and thus probably not good indicators of environmental variance. Florigiant is a multiline cultivar composed of seven full-sib lines, and NC 2 was selected in an early generation which probably resulted in some variability in the line. Estimates of within-plot variance for NC 2 and Florigiant were high in comparison to the other parental lines as well as to the F_2's for the root rot index and for pod yield. Total F_2 genotypic variance for each cross was estimated by subtracting the estimate of environmental variance from F_2 within-plot variance. The assumptions for this method are: (a) environmental variances are the same for the heterozygous F_2 as for the homozygous parent and (b) there is no genotype-environment correlation as would exist with differential competitive abilities. The genetic covariances between pairs of traits for the F_2 were estimated in a similar manner using parental within-plot covariances as estimates of environmental covariances.

The F_2 within-plot variances and covariances were used to estimate heritabilities (H), and genotypic (r_g) and phenotypic (r_p) correlations for each location, set and F_2 cross as follows:

$$H = \frac{\sigma^2_{G_i}}{\sigma^2_{F_{2_i}}}$$

$$r_p = \frac{\hat{cov}_{F_{2_{ij}}}}{\sigma_{F_{2_i}}\sigma_{F_{2_j}}}$$

$$r_g = \frac{\hat{cov}_{G_{ij}}}{\sigma_{G_i}\sigma_{G_j}}$$

where:

$\hat{\sigma}^2_{G_i}, \hat{\sigma}^2_{G_j}$ are the genotypic variances of the ith and j^{th} traits,

$\hat{\sigma}^2_{F_{2_i}}, \hat{\sigma}^2_{F_{2_j}}$ are the total phenotypic or F_2 within-plot variances for the ith and j^{th} traits, and

$\hat{cov}_{F_{2_{ij}}}, \hat{cov}_{G_{ij}}$ are the phenotypic and genotypic covariances for the ith and j^{th} traits.

A combined analysis over locations was performed on plot means for each set. All effects in the model were considered random, thus entries were tested by their interaction with location. The sums of squares for entries were partitioned into pooled sums of squares for additive and nonadditive effects and these pooled estimates were further partitioned into single degree of freedom contrasts. Additive effects (Ba, Ca) were estimated as differences between the A parent and each of the B and C parents and the nonadditive effects (Bd, Cd) were estimated as differences betwen the F_2's and the midparental values. This is a modification of Hayman's generation means analysis (6) applied to two crosses simultaneously. The effects are not orthogonal so adjusted sums of squares are reported; that is, each additive effect is adjusted for the other additive effect and each nonadditive effect is adjusted for the other nonadditive effect as well as both additive effects. The entry x location interaction sum of squares are partitioned similarly.

Results

Significant differences were observed between entries grown at the Byrd Farm for percent dead and diseased plants on both scoring dates (Table 1). The necrosis index, also measured at this location, plus mean pod yields and seed weights from one of the yield locations (Lewiston) are included for comparison. The susceptible virginia-type parents, Florigiant and NC 2, had high numbers of dead and diseased plants. The necrosis index value was not as high for NC 2 as Florigiant, although the two cultivars did not differ significantly in this respect. The four CBR-resistant parents had low percentages of dead and diseased plants and low necrosis index values. The F_2's with Florigiant as a parent tended to have greater percen-

Table 1. Means for six parental lines and four F_2 crosses for percent dead and diseased plants, necrosis index, pod yield and seed yield.

Line or cross	% Dead & diseased (CBR)[a]	% Dead & diseased (CBR)[b]	Necrosis index (CBR)[c]	Pod yield (g)[d]	Seed weight (g/20 pods)
Florigiant (A_1)	24.44	33.00	1.38	103.34	32.78
NC 2 (A_2)	26.94	38.40	0.98	154.18	29.56
NC Ac 17941A (B_1)	13.84	25.38	0.54	111.10	25.54
NC Ac 18016A (B_2)	7.98	16.58	0.22	113.34	24.80
NC Ac 18323 (C_1)	0.00	5.41	0.22	95.50	25.32
NC Ac 18229 (C_2)	0.00	18.50	0.36	127.08	25.64
NC Ac 17941A x Florigiant	19.77	28.15	1.30	111.40	33.78
NC Ac 18323 x Florigiant	23.00	44.42	1.56	112.38	31.04
NC Ac 18016A x NC 2	8.24	17.67	0.46	134.60	29.30
NC Ac 18229 x NC 2	15.35	26.49	0.90	128.30	28.60
LSD[e]	15.69	24.89	0.54	15.80	1.68

[a]Counts made September 9; LSD and means computed from data with arcsin transformation.

[b]Counts made October 2; LSD and means computed from data with arcsin transformation.

[c]Necrosis index on a scale of 0 (no disease) to 5 (completely decayed).

[d]Pod yield and seed weight reported for Lewiston, a nondiseased location.

[e]Waller-Duncan LSD, K-ratio = 100.

tages of dead and diseased plants and higher necrosis index values than the F_2's with NC 2 as the virginia-type parent. There were F_2 crosses that yielded as well or better than Florigiant. Both F_2 crosses with NC 2 as a parent had high yields and large seed weights in comparison with the F_2 crosses with Florigiant as a parent as well as in comparison to the CBR-resistant parents.

Estimates of heritability computed from variance components are reported in Table 2. Heritability estimates of zero are reported for traits where the estimate of genetic variance was zero (negative genetic variance estimates). Heritabilities for the necrosis index (CBR resistance) measured at one location were high (0.69-0.73) for all crosses except A_2 x B_2 (NC 2 x NC Ac 18016A) for which there was a moderate heritability estimate of 0.43. Estimates of heritability for pod yield were low to moderate (0.12-0.60) for all crosses at all three locations. The range in estimates of heritabilities was large for fruit length (0-0.90), pod weight (0-0.80) and seed weight (0-0.70) compared over all crosses and locations. The cross A_1 x B_1 (Florigiant x NC Ac 17941) had consistently low estimates for fruit length, pod weight and seed weight whereas moderate to high heritability estimates were obtained for A_2 x C_2 (NC 2 x NC Ac 18229) over all three locations for the same traits. The crosses A_1 x C_1 (Florigiant x NC Ac 18323) and A_2 x B_2 (NC 2 x NC Ac 18016) were variable in heritability estimates for fruit length, pod weight, and seed weight compared over locations.

Phenotypic and genotypic correlations among all pairs of traits for the four crosses were calculated from within-plot variances and covariances for each location (Table 3). Genotypic correlations were generally higher than phenotypic correlations. In the case of traits with negative estimates of genetic variance which were considered as zero, the genotypic correlations with these traits or among pairs of traits both with negative genetic variances could not be estimated and were thus reported as zero.

The necrosis index was negatively and significantly correlated with all other fruit and yield traits both genotypically and phenotypically for crosses A_1 x B_1, A_1 x C_1 and A_2 x C_2. The only significant correlations between the necrosis index and fruit and yield traits for the cross A_2 x B_2 were positive genotypic correlations of the root rot index with fruit length and seed weight.

Genotypic correlations could not be estimated for most pairs of fruit and yield traits for cross A_1 x B_1 at any of the

locations although there were moderate but significant correlations betwen pod yield and seed weight at the Byrd Farm and between pod yield and pod weight at Lewiston. Correlation coefficients for the cross A_1 x C_1 were generally moderate to high for pod yield with the remaining three fruit and yield traits and consistently high between fruit length, pod weight and seed weight. In set 2, genotypic correlation coefficients between pod yield and the other fruit and yield traits were generally not significant or could not be estimated for the cross A_2 x B_2. Correlation coefficients tended to be moderate and significant between pod yield and the remaining fruit and yield traits for the cross A_2 x C_2. Both crosses in set 2 had moderate to high correlation coefficients between fruit length, pod weight and seed weight except for cross A_2 x B_2 at Rocky Mount for which genotypic correlations were not estimable.

An analysis of variance was performed separately for the two sets of entries for each of the traits combined over locations (Table 4). There were significant differences among entries in sets 1 and 2 for fruit length, pod weight and seed weight and for the necrosis index in set 2 only. Total additive effects were significant for pod yield, fruit length, pod weight and seed weight in set 1 and for the necrosis index, fruit length, pod weight and seed weight in set 2. There were significant additive effects for both parents B and C crossed with the common parents A for all traits with significant total additive effects except in the case of pod yield in set 1 for which only parent C crossed with parent A exhibited significant additive effects.

Total nonadditive effects were significant between the A parents and the B and C parents for fruit length, pod weight and seed weight in sets 1 and 2. Partitioning of the total nonadditive effects revealed that there were significant nonadditive effects for only the B_1 parent with the A_1 parent for fruit length but for both the B_1 and C_1 parents with the A_1 parent for pod weight and seed weight in set 1. In set 2 there were significant nonadditive effects between only the B_2 parent with the A_2 parent for fruit length and pod weight.

The total entry x location interaction was significant for fruit length in set 1 only. However, partitioning of the total interaction revealed significant interactions for some entries which in all but one case were due to the interaction of additive effects with location. The one exception was the significant interaction of nonadditive effects with

Table 2. Heritability estimates based on variances for traits measuring yield, fruit size and CBR resistance for four crosses at three locations.*

| Characters | Byrd Farm | | | | Rocky Mount | | | | Lewiston | | | |
| | Set 1 | | Set 2 | | Set 1 | | Set 2 | | Set 1 | | Set 2 | |
	A_1xB_1	A_1xC_1	A_2xB_2	A_2xC_2	A_1xB_1	A_1xC_1	A_2xB_2	A_2xC_2	A_1xB_1	A_1xC_1	A_2xB_2	A_2xC_2
Necrosis index	0.69	0.73	0.43	0.71								
Pod yield (g)	0.46	0.38	0.43	0.12	0.39	0.13	0.18	0.40	0	0.25	0.60	0.44
Fruit length (cm)	0	0.83	0.48	0.90	0	0.38	0	0.78	0	0.44	0.44	0.57
Pod weight (g/20)	0	0.49	0.38	0.82	0	0.36	0	0.66	0	0.66	0.57	0.50
Seed weight/20 pods (g)	0.16	0.68	0.20	0.74	0.03	0.41	0	0.60	0	0.65	0.49	0.49

*A_1 = Florigiant, B_1 = NC Ac 17941A, B_2 = NC Ac 18323, A_2 = NC 2, B_2 = NC Ac 18016A, C_2 = NC Ac 18229.

Table 3. Genotypic (rg) and phenotypic (rp) correlations among traits for four crosses grown at three locations.

Location/trait	Pod yield r_p	r_g	Fruit length r_p	r_g	Pod weight r_p	r_g	Seed weight r_p	r_g	Pod yield r_p	r_g	Fruit length r_p	r_g	Pod weight r_p	r_g	Seed weight r_p	r_g
							Set 1									
					$A_1 \times B_1$							$A_1 \times C_1$				
Byrd Farm																
Necrosis index	-.47**	-.61**	-.28	-.43**	-.52**	-.45**	-.48**	-1.03**	-.64**	-1.01**	-.37**	-.44**	-.36**	-.45**	-.45**	-.53**
Pod yield			.07	+	.30*	+	.29*	.41**			.36**	.54**	.46**	.78**	.54**	.84**
Fruit length					.86**	+	.72**	+					.59**	.52**	.87**	.90**
Pod weight							1.02*	+							.84**	.80**
Lewiston																
Pod yield			.12	+	.22	.38**	.30*				.41**	.81**	.44**	.68**	.44**	.58**
Fruit length					.70**	+	.68**	+					.87**	.89**	.73**	.78**
Pod weight							.92*	+							.79**	.75**
Rocky Mount																
Pod yield			.11	+	.46**	+	.50**	+			.22	-.22	.29*	.08	.45**	.70**
Fruit length					.65**	+	.50**	+					.81**	.73**	.66**	.56**
Pod weight							.93**	+							.89**	.86**
							Set 2									
					$A_2 \times B_2$							$A_2 \times C_2$				
Byrd Farm																
Necrosis index	-.16	-.28	.09	.39**	-.006	.22	.07	.67**	-.53**	1.11**	-.47**	-.56**	-.37**	-.44**	-.40**	-.49**
Pod yield			.19	.14	.18	.12	.21	.34*			.25	.56**	.25	.52**	.27	.66**
Fruit length					.57**	.51**	.47**	.27					.55**	.55**	.68**	.71**
Pod weight							.85**	.66**							.84**	.81**
Lewiston																
Pod yield			.08	.16	.14	.13	.22	.09			.40**	.47**	.24	.17	.33*	.30*
Fruit length					.58**	.50**	.58**	.58**					.76**	.82**	.75**	.91**
Pod weight							.69**	.66**							.83**	.50**
Rocky Mount																
Pod yield			.39**	+	.55**	+	.53**	+			.44**	.45**	.54**	.57**	.57**	.55**
Fruit length					.79**	+	.73**	+					.91**	.96**	.87**	.92**
Pod weight							.93**	+							.95**	.95**

*,**Denote significance at the .05 and .01 probability levels, respectively.

†Estimates of zero obtained due to negative genetic variance estimates.

Table 4. Generation means analysis for yield, fruit size and CBR resistance traits for two sets of entries.

Source	df	Necrosis index	Mean squares Pod yield (g)	Fruit length (cm)	Pod weight (g/20)	Seed weight/20 pods (g)
			Set 1‡			
Entries	4	1.71	1349.50	414.88**	411.05**	148.48**
Additive	2	1.80	2239.11*	558.52**	273.89**	169.02**
(Ba/Ca)	1	1.76	186.45	982.74**	447.16**	181.68**
(Ca/Ba)	1	3.36	2491.88*	663.23**	371.99**	309.43**
Nonadditive	2	1.62	45.99	271.25**	548.21**	127.93**
(Bd/Ca,Cd,Ba)	1	0.38	44.14	21.58	86.67**	57.23*
(Cd/Ba,Bd,Ca)	1	1.92	336.90	212.29**	694.47**	105.41**
Entries x Location	8		423.31	13.54*	15.25	7.76
Loc x (Ba/Ca)	2		47.61	7.89	32.21*	9.86
Loc x (Ca/Ba)	2		866.44*	11.20	23.11	6.00
Loc x (Bd,Ca,Cd,Ba)	2		835.19*	2.18	17.90	11.66
Loc x (Cd,Ba,Bd,Ca)	2		270.14	0.07	1.56	4.00
Error	16	0.80				
	48		262.93	5.48	10.03	4.86
			Set 2†			
Entries	4	0.57*	485.97	92.77**	91.37**	38.04**
Additive	2	0.82*	292.20	110.57**	115.42**	49.81**
(Ba/Ca)	1	1.44**	555.37	208.63**	172.54**	55.59**
(Ca/Ba)	1	0.96*	53.65	107.74**	175.49**	90.29**
Nonadditive	2	0.32	679.73	74.97**	67.32**	26.27*
(Bd/Ca,Cd,Ba)	1	0.06	1031.92	67.35**	45.81**	14.48
(Cd/Ba,Bd,Ca)	1	0.18	232.51	24.52	24.08	10.81
Entries x Location	8		606.93	7.83	6.91	3.39
Loc x (Ba/Ca)	2		1890.07**	10.80	16.95**	11.43**
Loc x (Ca/Ba)	2		1089.74**	1.51	0.73	0.68
Loc x (Bd,Ca,Cd,Ba)	2		371.25	5.33	6.66	3.57
Loc x (Cd,Ba,Bd,Ca)	2		197.38	9.46	2.54	1.41
Error	16	0.16				
	48		320.09	5.93	4.97	3.14

*,**Denote significance at the .05 and .01 probability levels, respectively.

†Set 1 = entries A_1, B_1, C_1, $A_1 \times B_1$ and $A_1 \times C_1$; set 2 = entries A_2, B_2, C_2, $A_2 \times B_2$ and $A_2 \times C_2$.

location for pod yield for the B_1 parent with the A_1 parent in set 1.

Discussion

A comparison of entry means for percent dead and diseased plants and the necrosis index indicated that CBR-resistant lines crossed to Florigiant produced progeny that resembled Florigiant in susceptibility, whereas CBR-resistant lines crossed to NC 2 produced progeny with higher levels of disease resistance as well as high yields and large seed weights.

Heritability estimates from variance components for the necrosis index (CBR resistance) were high (0.69-0.73) for all crosses except $A_2 \times B_2$ for which a moderate heritability estimate (0.43) was obtained. The smaller heritability estimate for this cross resulted from little total F_2 variance for the necrosis index, thus a small estimate of genetic variance was obtained upon removal of the environmental variance. Although little variability existed among the progeny of $A_2 \times B_2$ for this trait, the means for the necrosis index indicated that the progeny, though not significantly different from either parent, tended to be more like the resistant B_2 parent. Hadley (4) reported heritability estimates for CBR resistance evaluated in controlled greenhouse experiments ranging from 0.42-0.65 for three methods of calculation. The high heritability estimates obtained in the present study for the necrosis index indicate that it should be possible to select in early generations for CBR resistance. High heritabilities obtained for the necrosis index for the F_2's with Florigiant as a parent indicate selection progress is possible. Despite this fact, the high means (susceptibility) for this trait, as well as for percent dead and diseased plants, indicate that a majority of the progeny from these two crosses are susceptible.

Low to moderate heritability estimates were found for pod yield and generally higher estimates were found for fruit length, pod weight and seed weight. These estimates are in agreement with those reported by Mohammed *et al.* (7) for the F_2 and F_3 generations from crosses of virginia and spanish peanuts. Heritability estimates for each trait tended to be inconsistent when compared over locations for individual crosses and in some cases the range was considerable (*e.g.*, a range in heritability estimates for fruit length of 0.38-0.83 over three locations was obtained for the cross $A_1 \times C_1$). Inconsistent heritability estimates over environments indicate the problem of estimates reported for a single environment. Variable heritability estimates indicate the need to select or evaluate lines over several environments. The heritability estimates obtained indicate that improvement in the individual traits should be possible by selection within some of the F_2 crosses evaluated. Improvement of fruit and yield traits beyond that attained in the F_2's of crosses $A_1 \times B_1$ or $A_2 \times B_2$ would not be expected from selection because the heritability estimates were low to zero. The parental line, NC Ac 17941A, in the cross $A_1 \times B_1$ is a line derived from NC Ac 3139 x Florigiant. In the second cross $A_2 \times B_2$, NC Ac 18016A, is a line derived from Ac 9088 (NC 2 x Ga 119-20) x NC 3033. The lack of genetic variability in these F_2 lines may be a result of the close relationship of the CBR-resistant lines to the virginia lines to which they were crossed. Although there appears to be little, if any, genetic variability in these F_2's, the means of these crosses ($A_1 \times B_1$, $A_2 \times B_2$) for the fruit and yield traits indicate improvement in these traits over that of the advanced CBR lines used as parents.

Another indication of the progress that can be expected from selection is the correlation among traits. Significant negative correlations between the necrosis index and the fruit and yield traits indicate an association between high yields and large fruit with low values for the necrosis index (resistance). Thus, it should be possible to select for high-yielding, large-fruited CBR-resistant lines. The significant positive correlations between the necrosis index and fruit length and seed weight for the cross $A_2 \times B_2$ indicate that progress would not be expected in improving these traits simultaneously. Conversely, a nonsignificant negative correlation between the necrosis index and pod yield for this cross indicated progress in improving both CBR resistance and yield would not be hindered, although further progress in improvement of fruit and seed size would not be expected as mentioned previously.

Correlations between pod yield and remaining fruit and yield traits were moderate to high and correlations between fruit length, pod weight and seed weight were generally high for all crosses where estimable. This indicates that selection for an easily measured and highly heritable trait, such as fruit length, would tend to result in large-seeded, high-yielding progeny.

Partitioning of the additive and nonadditive effects between the virginia and CBR-resistant parents for the necrosis index indicated significant additive effects for both crosses in set 2 but not set 1 for which there were no significant differences among entries. This, in addition to the

fact that set 1 had high means for percent dead and diseased plants and the necrosis index, indicates that progress in improving these traits would not be expected by selection in crosses in CBR-resistant lines to Florigiant. Results suggest that resistant progeny can be identified in crosses of CBR-resistant lines to NC 2 and because only additive effects were significant for the necrosis index selection in early generations should be effective in improving resistance. Hadley (4) also reported only significant general combining ability effects for a four-parent diallel indicating additive genetic effects for CBR resistance.

Although additive effects were large in both sets for fruit and yield traits, significant nonadditive effects observed for these traits for some cross combinations would hinder progress from selection in early generations.

In summary, crosses of virginia-type cultivars to CBR-resistant lines resulted in improvement of yield and fruit traits in comparison to the CBR-resistant parents but only those crosses of NC 2 with CBR-resistant lines gave CBR-resistant progeny with large seeds and high yields. Results indicate that it should be possible to develop high-yielding, large-fruited CBR-resistant lines from the crosses involving NC 2 and the CBR-resistant lines. Early generation screening and selection for CBR resistance in inoculated soil in the greenhouse would be expedient provided these results were shown to correlate well with field performance. Early generation selections with CBR resistance could then be increased and advanced to later generations when selection for yield traits would be more effective.

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