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Relationships of CBR and Insect Resistance and Yield Among Progenies of a CBR-Resistant x Insect-Resistant Cross[1]

C. C. Green, J. C. Wynne*, M. K. Beute and W. V. Campbell[2]

ABSTRACT

The potential for the development of large-seeded, high-yielding virginia-type peanuts (*Arachis hypogaea* L.) with resistance to Cylindrocladium black rot (CBR) and three insects was examined. Forty randomly selected F_2 families in F_5 generation from a cross of the CBR-resistant germplasm NC 3033 and the cultivar NC 6 were evaluated for yield, fruit traits, and resistance to CBR, thrips (*Frankliniella fusca* Hinds), corn earworm (*Heliothis zea* Bodie) and potato leafhopper (*Empoasca fabae* Harris). Significant differences were found among families for all traits measured except corn earworm damage and number of seed. Transgressive segregation was observed for six of the nine traits measured. Heritabilities were high for pod length, pod weight, and seed weight; moderate for pod yield, CBR resistance, thrips and potato leafhopper damage and low for corn earworm damage. Large negative genotypic correlations were found between CBR resistance (percent dead and diseased plants) and traits indicative of insect resistance. Genotypic correlations between percent dead and diseased plants and yield and fruit traits were large and positive. Based on the predicted response in the other unselected traits when selection is for one trait, selection for increased CBR resistance should result in lines with decreased insect resistance, pod size and weight, seed weight, and yield. These data suggest that unfavorable linkages or pleiotropy among these traits may exist that would prevent selection of desirable genotypes from this cross.

Key Words: *Arachis hypogaea*, heritability, genotypic correlations, thrips, potato leafhopper, corn earworm, *Cylindrocladium crotalariae*.

Development of a new peanut (*Arachis hypogaea* L.) cultivar with disease resistance also requires selection for a number of other economically important traits. Not only must selection be practiced for increased levels of resistance to the disease of interest but selection for acceptable pod and seed characteristics, as well as high yield, must be made. Resistances to other diseases and insect problems may also be considered during selection.

A disease of peanuts that has become a major problem in North Carolina over the past decade is Cylindrocladium black rot (CBR). The causal organism of CBR is the soil-borne fungus *Cylindrocladium crotalariae* (Loos) Bell and Sobers which causes a severe peg, pod and root rot of peanut (5, 7, 10).

At present there is no effective management scheme, either through the use of chemicals or cultural practices, for the control of CBR (9, 10, 11). The germplasm NC 3033 and some related lines were found to be resistant to CBR in field tests conducted in North Carolina in 1973-74 (12). NC 3033 has small fruit and seeds, is low yielding and is susceptible to the major insect pests of North Carolina-grown peanuts. These common insect pests include tobacco thrips (*Frankliniella fusca* Hinds), the potato leafhopper (*Empoasca fabae* Harris), and the corn

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[1] Paper No. 8821 of the Journal Series of the North Carolina Agricultural Research Service, Raleigh, NC 27650.

[2] Graduate Assistant and Associate Professor, Department of Crop Science; Professor, Department of Plant Pathology; Professor, Department of Entomology; N.C. State University, Raleigh, NC 27650, respectively.

earworm (*Heliothis zea* Bodie). Development of a high-yielding, large-seeded virginia-type peanut with both disease and insect resistance would be highly desirable.

The objective of this study was to determine the potential for the selection of large-fruited, high-yielding CBR and insect-resistant cultivars from a cross of the CBR-resistant line NC 3033 and the insect-resistant cultivar NC 6 (2). Estimates of genetic variances, ratios of genetic variance to phenotypic variance (heritability), genotypic and phenotypic correlations among traits, and expected advances from selection were determined for a number of yield, fruit, and CBR and insect-resistant traits. This information indicates the usefulness of the populations and aids in planning an efficient breeding strategy for the development of high-yielding, multiple pest-resistant lines.

Materials and Methods

NC 3033 was crossed to the cv. NC 6 in an effort to develop a new cultivar with large fruit, high yield and CBR resistance as well as insect resistance. NC 6 is high yielding, has large fruit and is resistant to tobacco thrips and potato leafhopper (2). NC 3033 is a small-seeded virginia line with CBR resistance (1). Forty randomly selected F_5 generation lines advanced in bulk from individual F_2 plants from the cross were planted at four locations in 1980. Yield and fruit traits were measured at two locations: Lewiston, NC (three replications) and Rocky Mount, NC (four replications). Insect resistance alone was measured in a naturally infested field at Lewiston (two replications) where no insecticides were applied. A field in Bladen County, NC (four replications) naturally infested with *Cylindrocladium crotalariae* was used only to measure resistance to CBR. The unequal number of replicates was due to an insufficient seed supply and the loss of one replicate during harvest of the yield test at Lewiston. Each test was planted in a randomized complete block design. Each plot consisted of two 2.44 m rows planted 90 cm apart with 10 seeds per row. Stand counts were made approximately 6 weeks after planting at each location. Dead and diseased plants per plot were counted (September 23, 1980) at Bladen County, divided by the stand count for that plot, and reported as percent dead and diseased plants/plot. The following traits were also measured at their respective locations:

a) Pod yield (kg/ha)
b) Length of 20 random mature pods (cm)
c) Weight of 50 random mature pods (g)
d) Number of seed from 50 random mature pods
e) Weight of seed from 50 random pods (g)
f) Total number of thrip damaged leaves/(no. of plants/plot)
g) Percent corn earworm damage/plot (rated visually)
h) Number of leafhopper-damaged leaves/plot

Transformations were used on the data where needed to reduce the coefficients of variation. The data for percent dead and diseased plants and percent corn earworm damage were transformed using an arcsin transformation. A log transformation was used on the potato leafhopper data. The individual characters were analyzed by analysis of variance and all possible pairs of traits with the same number of replications (*i.e.*, all possible pairs between yield traits and all possible pairs between insect resistance traits) were analyzed by analyses of covariance (Table 1). Due to differences in numbers of replications and locations, genetic covariances between yield, insect and CBR traits were estimated as

$$\sigma_{s_{ij}} = r_{ph_{ij}}\sqrt{\sigma^2_{ph_i}\sigma^2_{ph_j}}$$

where:

$r_{ph_{ij}}$ = the phenotypic correlation coefficient among means between the i^{th} and j^{th} trait for the 40 segregates;

$\sqrt{\sigma^2_{ph_i}}, \sqrt{\sigma^2_{ph_j}}$ = the phenotypic standard deviations of the 40 segregates for the i^{th} and j^{th} traits, respectively.

Estimates of genetic variance or covariance components ($\sigma_{s_i}^2$, $\sigma_{s_{ij}}$) were used to obtain estimates of genotypic correlations among traits, heritabilities, and expected genetic advance from selection as follows:

$$\text{Genotypic correlations } r_{g_{ij}} = \frac{\sigma_{s_{ij}}}{\sqrt{\sigma^2_{s_i}\sigma^2_{s_j}}}$$

$$\text{Heritability (H)} = \frac{\sigma^2_{s_i}}{\sigma^2_{ph_i}}$$

where

$\sigma_{ph_i}^2 = \sigma_{s_i}^2 + \sigma_{e_i}^2/b$ for the disease and insect traits with b equaling the number of blocks, or

$\sigma_{ph_i}^2 = \sigma_{s_i}^2 + \sigma_{sl_i}^2/l + \sigma_{e_i}^2/bl$ for the yield traits with l and b equaling the number of locations and blocks, respecitvely and

$$\text{Genetic advance (GS)} = \frac{\sigma^2_{s_i}}{\sigma^2_{ph_i}} \times K\sigma_{ph_i}$$

where:

$K\sigma_{ph_i}$ is the selection differential expressed in phenotypic standard deviations. The K value for 5% selection was used (K = 2.06).

The expected change in one character as a result of selecting for another character was estimated in the following manner:

$$\text{Expected change in unselected charater (i)} = \frac{K\sigma_{s_{ij}}}{\sqrt{\sigma^2_{ph_j}}}$$

where:

K = 2.06 for 5% selection.

Table 1. Form of the analysis of variance and covariance with the relevant mean square and mean cross products expectations.

Source	df	Mean square expectation[a]	Mean cross product expectations[a]
A. Analysis of CBR resistance (1 location, 1 year)			
Blocks	3		
Entries	41		
Parents vs segregates	1		
NC 3033 vs NC 6	1		
Among segregates	39	$\sigma^2_{e_i} + 4\sigma^2_{s_i}$	
Error	123	$\sigma^2_{e_i}$	
B. Analysis of each insect resistance trait (1 location, 1 year)			
Blocks	1		
Entries	41		
Parents vs segregates	1		
NC 3033 vs NC 6	1		
Among segregates	39	$\sigma^2_{e_i} + 2\sigma^2_{s_i}$	$\sigma_{e_{ij}} + 2\sigma_{s_{ij}}$
Error	41	$\sigma^2_{e_i}$	
C. Analysis of yield traits (2 locations, 1 year)			
Location	1		
Blocks (Loc)	5		
Entries	41		
Parents vs segregates	1		
NC 3033 vs NC 6	1		
Among segregates	39	$\sigma^2_{e_i} + 3.6\sigma^2_{sl_i} + 7\sigma^2_{s_i}$	$\sigma_{e_{ij}} + 3.6\sigma_{sl_{ij}} + 7\sigma_{s_{ij}}$
Location x Entry	41		
Loc x Parents vs segregates	1		
Loc x NC 3033 vs NC 6	1		
Lox x Among segregates	39	$\sigma^2_{e_i} + 3.4\sigma^2_{sl_i}$	$\sigma_{e_{ij}} + 3.4\sigma_{sl_{ij}}$
Error	205	$\sigma^2_{e_i}$	$\sigma_{e_{ij}}$

[a] $\sigma^2_{s_i}$, the among segregate variance of the i^{th} trait which is predominantly additive genetic variance;

$\sigma^2_{sl_i}$, the segregate x location variance for the i^{th} trait;

$\sigma_{s_{ij}}$, the among segregates covariance component between the i^{th} and j^{th} traits;

$\sigma_{e_{ij}}$, the error covariance for the i^{th} and j^{th} trait;

$\sigma^2_{e_i}$, the error variance for the i^{th} trait.

Results and Discussion

Significant differences were found among families (segregates) for all traits measured except percent corn earworm damage and number of seed. There was a significant location x families (segregates) interaction for three of the five yield traits measured over two locations – pod length, pod weight, and seed weight.

The 40 families plus the parents were ranked according to means for each trait. NC 3033 was the most CBR-resistant entry and NC 6 had the highest level of resistance to potato leafhopper. There were families that exceeded NC 6 for resistance to the remaining two insects and for all five of the yield and fruit traits measured (Table 2).

Table 2. Means and ranges of agronomic, CBR and insect resistance traits.

Trait	Mean			Range of 40 families
	NC 3033	NC 6	40 families	
% Dead & diseased plants (CBR)[a]	15.4	51.4	60.9	21.5-95.4
Thrip damage	25.0	11.7	14.9	7.8-26.0
% Corn earworm damage[a]	60.6	41.1	45.9	33.3-65.9
Potato leafhopper damage[b]	2.8	0.4	2.0	0.6-4.4
Pod yield (kg/ha)	1522.9	2413.2	2574.0	1695.1-3234.3
Length/20 pods (cm)	55.4	74.9	71.9	59.9-78.7
Weight/50 pods (g)	63.8	110.3	102.2	78.6-119.1
Number seed/50 pods	96.9	94.9	89.0	65.9-96.7
Seed weight/50 pods (g)	50.8	81.9	75.7	57.3-86.4

[a] Percent dead and diseased plants and percent corn earworm transformed to the arcsin of $\sqrt{\%}$.

[b] Potato leafhopper data transformed to $\log_e$ of (no. of leafhopper-damaged leaves/plot).

Although there were no significant differences among families for percent corn earworm damage, NC 6 was significantly different from the susceptible parent NC 3033.

Variance components among segregates were computed from expected mean squares. All traits except number of seed had positive and relatively large genetic variance components in respect to the scale of measure for the trait (Table 3). There was a negative estimate of genetic variance ($\sigma_{s_i}^2$) for number of seed with the most reasonable estimate being zero. The segregates x location variances (σ_{sli}^2) or interaction variances were small in comparison to the genetic variance components for all fruit and yield traits except pod yield. The interaction variance component for pod yield was approximately one-half as large as the genetic variance component. This was also true of the error variance for this trait. Estimates of the error variances exceeded the genetic variances for the disease and insect resistance traits. Large error components are typical of disease and insect data collected in the field due to the natural variability in infestations of these organisms.

Table 3. Estimates of variance components for agronomic, CBR and insect resistance traits[a].

Trait	$\sigma_{s_i}^2$	$\sigma_{sl_i}^2$	$\sigma_{e_i}^2$
% Dead & diseased plants (CBR)	227.88		921.35
Thrip damage	8.11		10.64
% Corn earworm damage	22.13		87.26
Potato leafhopper damage	0.79		0.80
Pod yield (kg/ha)	71663.87	33427.28	39333.63
Length/20 pods (cm)	33.92	0.81	5.95
Weight/50 pods (g)	12407.90	136.25	471.40
Number seed	-20.07	35.58	479.29
Seed weight/50 pods (g)	785.72	94.70	591.13

[a] $\sigma_{s_i}^2$ = among segregates variance for the i^th trait which is predominantly additive genetic variance;

$\sigma_{sl_i}^2$ = among segregates x location variance for the i^th trait;

$\sigma_{e_i}^2$ = error variance for the i^th trait.

The variance component estimates are probably biased upwards because they are not clean estimates of the genetic variance alone. The variance among segregates ($\sigma_{s_i}^2$) for traits measured at only one location in one year (disease and insect traits) includes not only predominately additive genetic variance but also variances due to genotype x environment interactions – segregates x location variance ($\sigma_{sl_i}^2$), segregates x year variance ($\sigma_{sy_i}^2$) and segregates x location x year variance ($\sigma_{sly_i}^2$). For the yield traits measured at two locations in one year the genetic variance estimated is actually ($\sigma_{s_i}^2 + \sigma_{sy_i}^2$). The other quantity, that can be estimated for the yield traits only, is the genotype x location interaction variance ($\sigma_{sl_i}^2$) which actually estimates ($\sigma_{sl_i}^2 + \sigma_{sly_i}^2$).

Heritability estimates based on per plot variances were high for length of pods, weight of pods and weight of seed (Table 4). A moderate heritability estimate of 0.50 was obtained for pod yield. These heritability estimates are in agreement with those reported for yield and fruit traits by Mohammed *et al.* (8) although they reported heritabilities for pod yield ranging from 0.42-0.82 for eight estimates. The variance component estimates reported by Mohammed *et al.* (8) were based on the F_2 and F_3 generations of two crosses between a virginia and two spanish lines evaluated at two locations in separate years. Heritabilities were high for thrips and potato leafhopper damage (0.60 and 0.66, respectively) and low for corn earworm (0.34). There are no previous reports of estimates of heritabilities for resistance to peanut insect pests. The heritability estimate for CBR resistance was

Table 4. Estimates of heritability, genetic advance and means for agronomic, CBR and insect resistance traits.

Trait	Heritability[c]	GS[d] in % of mean	Mean
% Dead & diseased plants (CBR)	0.50	35.99	60.90
Thrip damage	0.60	30.68	14.87
% Corn earworm damage[a]	0.34	12.36	45.94
Potato leafhopper damage[b]	0.66	73.10	2.03
Pod yield (kg/ha)	0.50	15.09	2573.96
Length/20 pods (cm)	0.96	16.37	71.94
Weight/50 pods (g)	0.98	221.16	102.24
Number seed	0	0	89.00
Seed weight/50 pods (g)	0.86	22.32	75.68

[a] Percent dead and diseased plants and percent corn earworm data transformed to the arcsin of $\sqrt{\%}$.

[b] Potato leafhopper data transformed to $\log_e$ of (no. of leafhopper-damaged leaves).

[c] Variance component estimates of heritability on a per-plot basis for one year, two locations for the fruit and yield traits and one year, one location for the disease and insect resistance traits.

[d] Genetic advance expected from selection expressed in percent of the mean for the respective trait.

0.50. Hadley (6) reported heritability estimates of 0.48-0.65 for CBR resistance based on a greenhouse evaluation of the F_1 and F_2 generations of a four-parent diallel between two spanish and two virginia lines. The heritability estimates obtained in this study for disease and insect traits may be biased upward because the estimates of genotypic variances also included the genotype x environment variances as mentioned previously in the discussion of the variance components. Heritability estimates provide an indication of the effectiveness with which selection of genotypes can be based on phenotype (4). The most useful application of heritability estimates in conjunction with the selection differential is to predict the progress from selection. Genetic advance is predicated as the product of the heritability ratio and the selection differential. The expected genetic advance from selection for single traits in this populaiton was low for percent corn earworm damage, pod yield and length of pods, and moderate for percent dead and diseased plants, thrips damage and seed weight (Table 4). The advance from selection was high for potato leafhopper damage and pod weight.

Phenotypic correlations among means (r_p) and genotypic correlations (r_g) calculated from genetic variances and covariances were determined for all pairs of traits measured except for number of seed (Table 5). Genotypic correlations with number of seed were not computed due to a negative estimate of genetic variance for this trait. All genotypic correlations were significant. These correlations among traits were used to predict the expected change in one character as a result of selecting for another. Progress expected in the unselected character (i) from selection for character (j) is expressed in percentage of the change expected when selection was for that character (i) itself (Table 6).

Table 6. Progress expected in trait (i) resulting from selection for other traits (j), expressed in the percentage of the change expected when selection was for trait (i) itself.

	Trait (i)			
Trait (j)	Pod yield (kg/ha)	% Dead & diseased plants (CBR)	Thrip damage	Potato leafhopper damage
% Dead & diseased plants (CBR)	-109.01[a]		-79.82	-86.49
Thrip damage	62.83	-97.24		88.12
% Corn earworm damage	39.37	-60.05	7.52	26.78
Potato leafhopper damage	96.20	-114.53	96.04	
Pod yield (kg/ha)		-108.77	51.54	72.48
Length/20 pods (cm)	136.23	-150.03	87.06	86.84
Weight/50 pods (g)	167.91	-172.34	111.08	114.47
Seed weight/50 pods (g)	125.07	-146.89	92.54	88.87

[a]- Denotes direction of progress or a decrease in the unselected trait.

Table 5. Phenotypic (r_p) and genotypic correlation coefficients (r_g) for CBR resistance, insect resistance and yield.

		Thrip damage	% Corn earworm damage	Potato leafhopper damage	Pod yield (kg/ha)	Length/20 pods (cm)	Wt/50 pods (g)	Number seed	Seed wt/50 pods (g)
% Dead & diseased plants (CBR)	(r_g)	-0.88**	-0.73**	-0.99**	1.09**	1.08**	1.22**	--[a]	1.12**
	(r_p)	-0.48**	-0.30	-0.57**	0.54	0.75**	0.69**	-0.001	0.73**
Thrip damage	(r_g)		0.63**	0.92**	-0.57**	-0.69**	-0.89**	--	-0.78**
	(r_p)		0.28	0.58**	-0.31**	-0.53**	-0.56**	0.11	-0.56**
% Corn earworm damage	(r_g)			0.37*	-0.48**	-0.54**	-0.66**	--	-0.45**
	(r_p)			0.32*	-0.20	-0.31*	-0.31**	0.12	-0.24
Potato leafhopper damage	(r_g)				-0.83**	-0.71**	-0.90**	--	-0.78**
	(r_p)				-0.48**	-0.57**	-0.59**	0.03	-0.58**
Pod yield (kg/ha)	(r_g)					0.96**	1.18**	--	0.95**
	(r_p)					0.68**	0.63**	0.06	0.64**
Length/20 pods	(r_g)						1.23**	--	1.04**
	(r_p)						0.98**	0.17	0.96**
Weight/50 pods (g)	(r_g)							--	-1.00**
	(r_p)							-0.14	-0.92**
Number seed	(r_g)								--
	(r_p)								0.18

*,**Denote significance at the 0.05 and 0.01 probability levels, respectively.

[a]Genotypic correlations with number of seed not reported due to a negative estimate of genetic variance for number of seed.

There was a highly significant ($p = 0.01$) negative genotypic correlation between percent dead and diseased plants due to CBR and insect damage to all three insects (Table 5). Thus, there is an association between high levels of CBR resistance and low levels of insect resistance. A decrease in insect resistance would be expected in families selected for CBR resistance, as indicated by the large negative percentages in Table 6. The genotypic correlations between percent dead and diseased plants and all fruit and yield traits were positive and approximately one. This indicates an association between low percentages of dead and diseased plants (high level of CBR resistance) and low values for fruit and yield traits. Families selected for CBR resistance in a *C. crotalariae* -infested field would not be expected to perform well in a yield trial on disease-free land. Thus, there are large negative values exceeding 100% for expected gain in fruit and yield traits when selection is for CBR resistance measured as low percentages of dead and diseased plants. A moderate but highly significant genotypic correlations coefficient was found between thrips damage and percent corn earworm damage ($p = 0.01$) and a low but significant ($p = 0.05$) correlation between potato leafhopper damage and percent corn earworm damage. Thrips and potato leafhopper resistances were highly correlated. All three insect traits had a significant ($p = 0.01$) and negative correlation (r_g) with all yield and fruit traits. Thus, it is possible to obtain high yielding lines from this population by selecting for insect resistance. For example, selection for pod yield alone would result in 96% of the gain in potato leafhopper resistance expected when selection is for potato leafhopper resistance alone. There are no previous reports on correlations among CBR and insect resistance or between these traits and yield and fruit traits for comparison.

Genotypic correlation coefficients between pod yield, length of pods, weight of pods and weight of seeds were all positive and approximately one (Table 5). Mohammed *et al.* (8) and Coffelt and Hammons (3) reported significant and positive genotypic correlations between yield and fruit traits, although correlations reported by Mohammed *et al.* (8) were not as high as those found in this study. Progress would be expected in pod yield by selection by any of the remaining traits except percent dead and diseased plants (Table 6). Greater increases in pod yield would be expected from selection for length of pods, weight of pods,or weight of seeds than from selection for pod yield itself as indicated by positive values exceeding 100% for expected gain in an unselected character.

In summary, the families separated into two groups, those resembling NC 3033 in CBR resistance with small seeds and low yields, and those resembling NC 6 in insect resistance, large seeds and high yields. Segregates were found that exceeded the parents for most traits but none had high levels of both disease and insect resistance with large seed and high pod yields. The genotypic correlation coefficients of approximately one between percent dead and diseased plants and all other traits suggests unfavorable linkages (*i.e.*, CBR resistance linked with insect susceptibility) or possibly pleiotropy. The possibility of unfavorable linkages needs to be further investigated. A breeding scheme incorporating additional recombination to break up unfavorable linkages may enable the recovery of high-yielding, large-fruited lines with CBR and insect resistance. A population could be developed by intermating F_2 plants after crossing NC 3033 and NC 6 or by intermating the desirable transgressive segregates identified in this study. A recurrent selection scheme could then be practiced. Progress could not be made if pleiotropy existed among CBR and insect resistance and yield traits.

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