Late Leaf Spot Progression on Peanut as Affected by Components of Partial Resistance

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ABSTRACT

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Components of partial resistance to late leaf spot (*Cercosporidium personatum*) and disease progression on 14 peanut genotypes were quantified in field experiments at Marianna, Florida, during 1988 and 1989. The resistance components measured were 1) incubation period, 2) latent period, 3) maximum percentage of lesions that sporulated, 4) lesion size, 5) lesion number, 7) degree of sporulation, and 7) percent necrotic area. Lower area under the disease progress curve (AUDPC) values, reduced apparent infection rates, and lower end-of-season disease levels were observed on genotypes UF81206-1, PI 261893, US29-b3-B, and US202-b2 compared to other genotypes in the study. Both apparent infection rate and AUDPC values were highly correlated with latent period ($r = -0.68$ to -0.79, $P \leq 0.01$) and maximum percentage of lesions that sporulated ($r = 0.72$–0.81, $P \leq 0.01$). Latent period and maximum percentage of lesions that sporulated were the components most highly correlated with late leaf spot disease development, and these two components were highly correlated with one another ($r = -0.84$). Using either of these two components to evaluate peanut genotypes for resistance to late leaf spot may facilitate more rapid selection of lines with improved levels of rate-reducing resistance.

Additional keywords: *Arachis hypogaea,* groundnut, *Phaesariopsis personatum*

Late leaf spot of peanut (*Arachis hypogaea* L.), caused by *Cercosporidium personatum* (Berk. & M.A. Curtis) Deighton, is one of the most important diseases of peanut in the southeastern United States (8,20). Losses in pod yield attributed to this disease range from 10 to >50% depending on the cultivar planted and control measures used (9,13,20). Rate-reducing resistance to late leaf spot is a viable breeding strategy, and several studies have identified this type of resistance in peanut (1–4,6,7,9, 15). Southern Runner, a peanut cultivar with improved resistance to late leaf spot, has been released by the University of Florida (7), and other advanced breeding lines with partial resistance are currently being developed (6,15).

Components of resistance in peanut to the early leaf spot pathogen, *Cercospora arachidicola* S. Hori, have been identified, and several components have been shown to impact negatively on the rate of disease development in the field (5,17). Latent period (5) and the maximum percentage of sporulating lesions (MPLS) (17) have proven to be useful components for selection for rate-reducing resistance to early leaf spot. Components of resistance to late leaf spot have been investigated by several other authors (12,15,19,22,23), but there is little quantitative information on the relative importance of these components in reducing the rate of disease development in the field. Watson (23) identified several components of resistance to late leaf spot in two peanut genotypes, one of which was the cultivar Southern Runner. He found that the two genotypes had rate-reducing resistance mediated by reduced sporulation, smaller lesion sizes, and longer latent periods compared to susceptible cultivar Florunner. Chiteka et al (3,4) quantified components of partial resistance to late leaf spot in 116 peanut genotypes under both greenhouse and field environments. The 116 genotypes consisted of commercial cultivars, plant introductions, and advanced breeding lines. They found that the ranking for rate-reducing resistance of genotypes grown in the field was significantly correlated with the ranking of these same genotypes tested in the greenhouse for sporulation, latent period, and lesion size. Sporulation, latent period, and lesion size were also found to be the most important components contributing to disease severity as measured by a plant-appearance scale. Lesion number was not affected by host genotype for any of the genotypes examined by either Chiteka et al (3,4) or Watson (23). Chiteka et al, however, did not determine the relative contributions of individual resistance components towards reducing disease levels in the field, and 10 of the genotypes from their work were selected for the present study.

Evaluating multiple components for late leaf spot resistance is a tedious and lengthy process. Time, space, and facilities often limit the detailed analyses of resistance components on the hundreds of lines that are part of a peanut breeding program. Plants are often selected based on an appearance score. Plant appearance may be a viable way to select peanut genotypes for higher levels of rate-reducing resistance to late leaf spot (3,4, 21), but selection decisions made by plant breeders might be improved if quantitative information on one or more components could also be obtained. It follows that many more advanced lines could be tested if only the best lines were preselected for more intensive screening of disease components in the field. The overall goal of the present study was to determine the effect of different resistance components on late leaf spot progress using germ plasm with known disease resistance characteristics. Incubation period, latent period, sporulation, lesion size, lesion number, and percent necrotic leaf area were quantitatively evaluated and related to the rate of disease progress in the field.

MATERIALS AND METHODS

Experimental germ plasm consisted of 12 peanut breeding lines and two commercial cultivars, Florunner and Southern Runner. Ten of the 12 breeding lines were selected based on previous observations for components of resistance, as denoted in Table 1 (3,4). Except for the cultivars Florunner and Southern Runner, and the breeding line, UF81206-1, the genotypes evaluated in this study will be referred to as genotype lines GT2 through GT12. The criteria for selection of genotypes were 1) evidence for moderate to high level of partial resistance, and 2) observed differences in one or more components of resistance (Table 1). Two additional genotypes, 79×4-6-2-1-1-b3-B

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(GT11) and 79×4-6-2-1-3-b3-B (GT12), were included based on their performance in field tests at the North Florida Research and Education Center near Marianna.

The experiments were conducted in 1988 and 1989 in a field of Tifton loamy sand, pH 5.8, at the Dozier Boy's School, near Marianna. Different test sites at that location were used each year. Genotypes were planted in a randomized complete block design with four replications. In 1988, each plot consisted of two 6.1-m-long rows spaced 0.91 m apart. Four-row plots of the same length and row spacing were planted in 1989. Two rows of UF81206-1, a genotype with high levels of partial resistance to late leaf spot (4,23), were planted as a buffer between plots in both years. Peanuts were seeded at 2.5- to 3.8-cm depth on 28 May 1988 and 19 May 1989 at a rate of 30 seeds per 6.1 m. Because peanut had not been planted at the experimental sites for the past 20 yr, granular inoculum of *Bradyrhizobium* was applied in the furrows at planting. Fields were not irrigated, as rainfall was sufficient in both years for good crop growth and disease development. Standard cultural practices (8) were followed with the exception that no fungicide was applied for leaf spot control. Plots of Florunner were harvested for determination of pod yield 130 days after planting in 1988 and 129 days after planting in 1989. All other genotypes were later in maturity and were harvested 142 days after planting in 1988 and 143 days after planting in 1989. Relative maturities were based on previous knowledge of the experimental lines.

Three plants in 1988 and six plants in 1989 were arbitrarily selected in each plot for inoculation. Selected plants were marked with flags, and three fully expanded tetrafoliate leaves were tagged for inoculation. Inoculum was obtained from 1- to 2-mo-old diseased plants of cultivars Early Bunch and NC 3033. Conidia were collected from sporulating lesions using a cyclone spore collector, suspended in distilled water, and diluted to 10,000 spores per milliliter. The target leaf was inoculated by holding it flat on a wooden board while spraying the adaxial surface with the spore suspension for one second with a Spra-Tool (Fisher Scientific Products, Pittsburgh, PA). All inoculations were performed 1 mo after planting before any leaf spot was detected in the field. Inoculated leaves were used to monitor the components of resistance for 35 days after inoculation. Each target leaf was examined at 2- to 3-day intervals beginning 5 days after inoculation. Incubation period (IP) was measured as the number of days from inoculation to the appearance of the first lesion; latent period was defined as the time (days) from inoculation to the first sporulating lesion (LP_1). The MPLS was obtained by dividing the number of lesions that had sporulated by day 35 by the total number of lesions counted on day 25 (LN). These times were used because primary lesions continued to appear up to 25 days after inoculation without any confounding effects of secondary lesion development (10). Ten mature lesions were selected and measured from each tetrafoliate leaf to calculate mean lesion diameter in mm (LS). Degree of sporulation (SP) was evaluated 35 days after inoculation using a 1–5 scale where 1 = little or no sporulation and 5 = extensive sporulation (20). The percent necrotic area (%NA) per leaf was estimated visually 25 days after inoculation with the aid of standard leaf spot diagrams (23).

Late leaf spot disease was assessed every 7–11 days on five randomly selected plants in each of two rows in each plot following the method used by Plaut and Berger (16). Total disease severity was obtained by integrating visible disease (%NA) with defoliation using the equation: $Y_t = [(1 - d)Y_v] + d$ where Y_t represents total disease severity, Y_v is the proportion of visible disease (%NA), and d is the proportion of defoliation. Defoliation was measured by counting the number of nodes with missing leaflets and the total number of nodes on the main stem of the selected plants. The disease severity was a weighted average of three canopy layers in which the proportions of upper, middle, and lower canopy layers were 1/9, 3/9, and 5/9, respectively (14).

Data analysis. Analysis of variance for resistance components data as affected by peanut genotype was performed and correlation coefficients were computed for the individual components of resistance, in relation to the apparent infection rate and area under the disease progress curve (AUDPC). The number of lesions per leaf was transformed using the square root transformation to normalize data before analysis (21).

Disease severity data were transformed to logits, and apparent infection rates were determined by regressing logits against time. The logistic model was chosen because it had the best fit to the data based on coefficients of determination, standard errors for Y, and visual inspection of residual plots (10,21). AUDPC values were calculated for each genotype (18) and differences among genotypes were examined using analysis of variance. A stepwise regression procedure was used to identify the resistance component(s) that best predicted partial resistance in the field. Regressions were performed using AUDPC and apparent infection rate as the dependent variables to determine the relative contribution of individual components toward reduction of disease.

RESULTS

The components of resistance estimated from inoculated leaves in the field during 1988 and 1989 are shown in Tables 2 and 3, respectively. Genotypes are listed based on descending values for MPLS.

Table 1. Genotypes selected for study of disease progress based on various components of resistance[a]

Genotype no.	Pedigree	IP (days)	LP_1 (days)	Sp (1-5 score)	LS (mm)	PAS (1-10 score)	%NA
1	UF81206-1	8.6–9	>22	1–2	<3.2	<4	<4.0
GT2	72 × 32B-3-2-2-2-2-1-b3-B	>9	>22	1–2	<3.2	4–7	<4.0
GT3	72 × 83B-7-1-1-B	>9	≤22	2	<3.2	4–7	<4.0
GT4	US29-b3-B	>9	>22	1–2	<3.2	<4	<4.0
GT5	76 × 5-3-2-3-1-1-1-b3-B	>9	≤22	1–2	<3.2	<4	<4.0
GT6	76 × 9-10-1-1-1-2-b2-B	<8.6	>22	1–2	<3.2	4–7	>5.5
GT7	76 × 5-3-2-1-1-1-1-b3-B	<8.6	>22	1–2	<3.2	<4	<4.0
GT8	PI 261893	8.6–9	>22	1–2	<3.2	4–7	<4.0
GT9	79 × 6B-10-2-1-2-b3-B	>9	≤22	2	<3.2	4–7	<4.0
GT10	US 202-b2	>9	>22	1–2	<3.2	<4	<4.0
GT11[b]	79 × 4-6-2-1-1-b3-B	...	...	...	...	...	...
GT12[b]	79 × 4-6-2-1-3-b3-B	...	...	...	...	...	...
Southern Runner		<8.6	≤22	2–4	<3.2	<4	4–5.5
Florunner		>9	≤22	4–5	≥3.2	>7	>5.5

[a]IP = incubation period, LP_1 = latent period, Sp = sporulation score, LS = lesion size, PAS = plant appearance score, %NA = percent necrotic leaf area.

[b]Genotypes 11 and 12 were included based on observations and agronomic performance in other trials. Data concerning components of resistance to *Cercosporidium personatum* were not available.

Table 2. Mean values of components of resistance to late leaf spot estimated under field conditions during 1988[a]

Genotype	IP (days)	LP_I (days)	MPLS (%)	LS (mm)	SP	%NA
Florunner	9.6	20.5	81.9	3.7	3.8	5.8
GT9	10.8	22.5	72.6	3.2	3.1	6.1
GT6	9.7	24.2	58.5	3.4	2.9	5.2
GT7	10.2	28.6	39.3	3.4	3.1	5.2
Southern Runner	9.2	24.2	36.9	3.1	3.3	4.9
GT12	9.4	29.5	22.6	2.8	2.3	5.2
GT5	9.5	27.5	21.6	2.8	2.1	4.4
GT3	9.6	32.1	20.1	3.2	2.5	5.1
GT4	10.5	29.7	18.9	2.6	2.2	5.2
GT11	9.5	31.6	17.2	2.7	2.5	4.7
GT2	10.1	32.4	17.1	3.1	2.3	4.6
UF 81206-1	10.3	33.9	14.8	2.9	2.1	4.8
GT10	10.5	29.8	13.8	2.9	2.4	4.7
GT8	10.1	27.4	13.1	2.9	2.1	4.9
$LSD_{0.05}$	NS	3.2	10.1	0.8	0.6	0.2

[a]Components of resistance were obtained from inoculated leaves in the field (IP = incubation period, LP_I = latent period, MPLS = maximum percentage of lesions that sporulated within 35 days after inoculation, LS = lesion size, SP = degree of sporulation (1-5 scale), %NA = percent necrotic area per leaf). Each value represents a mean of data from 36 (1988) or 72 (1989) leaves for each genotype.

Table 3. Mean values for components of resistance to late leaf spot estimated under field conditions during 1989[a]

Genotype	LP_I (days)	MPLS (%)	LS (mm)	SP	%NA
Florunner	22.6	93.6	4.2	4.3	5.1
GT9	22.9	89.1	3.5	3.8	4.8
GT7	23.6	80.7	3.4	3.1	5.2
Southern Runner	24.8	76.5	3.1	3.4	4.9
GT6	21.8	74.3	4.3	2.6	5.1
GT5	24.3	34.5	2.9	2.1	4.6
GT4	26.7	33.9	2.8	2.4	3.9
GT10	27.3	24.5	2.9	2.5	3.1
GT3	28.5	22.6	2.9	2.6	3.4
GT12	27.9	22.5	2.7	2.3	3.3
GT11	30.8	19.8	3.1	3.1	3.5
GT2	31.4	18.7	2.8	2.4	3.1
UF 81206-1	29.9	12.7	2.7	2.0	3.2
GT8	29.1	12.5	2.8	2.1	3.1
$LSD_{0.05}$	2.6	11.4	1.1	0.7	0.4

[a]Components of resistance were obtained from inoculated leaves in the field (LP_I = latent period, MPLS = maximum percentage of lesions that sporulated within 35 days after inoculation, LS = lesion size, SP = degree of sporulation (1-5 scale), %NA = percent necrotic area per leaf. Each value represents the mean of 36 (1988) or 72 (1989) leaves for each genotype.

Table 4. Areas under the disease progress curves (AUDPC), apparent infection rates, and pod yields from field tests in 1988 and 1989

	AUDPC[a]		Apparent infection rate[b]		Pod yield (kg/ha)	
Genotype	1988	1989	1988	1989	1988	1989
Florunner	2,153	2,484	0.118	0.132	432	2,906
GT9	1,126	1,463	0.089	0.112	2,866	3,704
Southern Runner	998	1,120	0.075	0.091	2,896	3,344
GT12	899	789	0.068	0.081	3,694	3,740
GT6	779	834	0.049	0.089	2,266	3,288
GT11	675	761	0.047	0.069	3,679	3,684
GT7	581	792	0.049	0.079	2,403	2,653
GT3	458	799	0.051	0.075	2,535	2,587
GT2	434	804	0.049	0.077	1,976	2,485
GT5	428	809	0.047	0.077	2,307	2,541
UF 81206-1	396	481	0.044	0.057	3,480	3,995
GT8	381	548	0.041	0.061	1,982	2,154
GT4	379	573	0.039	0.064	2,108	1,992
GT10	345	487	0.039	0.059	1,585	1,377
$LSD_{0.05}$	158	251	0.014	0.013	316	349

[a]Measured from day 62 to 121 in 1988 and from day 65 to 125 in 1989. Each value represents the mean of four replicates.
[b]Rates (units/day) were obtained by regressing logit-transformed disease proportions against time.

IP. The time between inoculation and initial appearance of lesions was not significantly different ($P > 0.05$) among the 14 genotypes evaluated for both years (Table 2). The mean incubation period ranged from 9.2 to 10.8 in 1988 and 9.1 to 10.9 in 1989, and no significant differences existed among genotypes.

Latent period (LP). Significant differences ($P \leq 0.05$) in LP_I were observed among genotypes in both 1988 (Table 2) and 1989 (Table 3). Genotypes UF81206-1, GT2, and GT11 had the longest LP_Is both years. Florunner and GT9 had the shortest LPs both years.

MPLS. Fewer than 15% of the total lesions sporulated within the 35-day period following inoculation on genotypes UF81206-1 and GT8 in both years. Florunner and GT9 had the highest MPLS observed. Nine genotypes had a significantly ($P \leq 0.05$) lower MPLS than the moderately resistant cultivar Southern Runner.

LS. LS differed among genotypes, and lesions were significantly smaller ($P \leq 0.05$) on GT4, 5, 8, 10, 11, 12, and UF81206-1 compared to the susceptible standard, Florunner, in both years (Tables 2 and 3). Lesions on Southern Runner were smaller than those on Florunner for both years, but these differences were not significant ($P > 0.05$).

LN. The number of lesions per leaf counted at 25 days after inoculation was not significantly different ($P > 0.05$) among genotypes either year. The average number of lesions per leaf was greater in 1988 (95.2) than in 1989 (75.3).

SP. Sporulation ratings of GT2, 3, 4, 5, 8, 10, 11, 12, and UF81206-1 were significantly lower than those of Florunner and Southern Runner for both years (Tables 2 and 3).

%NA. All genotypes except GT9 had significantly lower percent leaf necrosis than Florunner in 1988 (Table 2). In 1989, all were significantly lower except genotypes 6, 7, 9, and Southern Runner (Table 3).

Disease progression and pod yield. The genotypes are listed in Table 4 based on a descending order of AUDPC values in 1988. Disease increased more rapidly in 1989 than in 1988. The apparent infection rate for Florunner was 0.118 units/day in 1988 and 0.132 units/day in 1989. There were significant differences ($P \leq 0.05$) in apparent infection rates among genotypes. The slowest rates of disease progress were observed for UF81206-1, GT8, GT4, and GT10, whereas Florunner and GT9 had the fastest rates.

Significant differences in AUDPC values were observed among the 14 peanut genotypes. In both years, Florunner and GT9 had the highest AUDPC values, whereas AUDPC values for UF81206-1, GT8, GT4, and GT10 were significantly lower ($P \leq 0.05$). Consistently high pod yield was obtained both years

from UF81206-1, GT11, and GT12. Genotypes 4, 8, and 10 had low AUDPC values but also very low pod yields, in contrast to the high-yielding, partially resistant line UF81206-1.

Correlation analysis. Apparent infection rates and AUDPC values had the highest correlations with MPLS, SP, and LP_I compared to other disease components (Table 5). Disease components of MPLS and SP were highly correlated in 1988 ($r = 0.87$) and in 1989 ($r = 0.80$), $P \leq 0.001$. LP_I was also highly correlated with MPLS ($r = -0.86$ and $r = -0.89$, $P \leq 0.001$, for 1988 and 1989, respectively).

Stepwise regression models. In 1988, MPLS and IP were the two components that explained the greatest amount of the variation in AUDPC values (79.7%) and apparent infection rates (67.9%). In 1989, SP and LN explained 75.4 and 77.7% of the variation in AUDPC values and infection rates in 1988 and 1989, respectively. The best single predictor was SP, which accounted for 70.6–74.0% of the variation in AUDPC values and 65.6–70.6% of the variation in apparent infection rates for the 2 yr.

DISCUSSION

In our study, late leaf spot disease progress was monitored in selected genotypes to examine the effect of the components of partial resistance on the rate of disease progress and AUDPC. Since we generally knew which components of rate-reducing resistance were present in all of the peanut genotypes that we selected except GT11 and GT12, it was our objective to more critically quantify the components of partial resistance in these genotypes and to determine which components might best be used in the breeding selection process.

IP did not differ significantly among genotypes, which is in agreement with previous studies by Watson (23) and Chiteka et al (3). As in our study, incubation period appears to be affected more by environmental factors such as temperature and humidity rather than by genotypic differences (19). The LN is also affected by temperature and humidity such that differences attributable to genotypes, if any, were overshadowed by environmental effects. Thus, genotypic effects on these components might best be quantified using controlled environmental chambers and more precise inoculation techniques (10). Although LP, LS, MPLS, and SP may also be affected by the environment, these resistance components still exhibited significant differences among genotypes.

LP, MPLS, and SP were highly correlated with both the apparent infection rate and AUDPC. All but one of the correlations of these components were higher with AUDPC than with the infection rate. This indicates that, of the two methods, AUDPC provided a more precise measure of genotypic effects on disease progress than did the calculation of apparent infection rates.

The components that had the greatest effect on slowing the rate of disease development were MPLS, SP, and LP, all of which may be useful in breeding for partial resistance to late leaf spot. SP and MPLS were particularly useful for identifying genotypes with a high level of rate-reducing resistance, and these components have the benefit of being relatively easy to evaluate. They are also closely correlated, as both provide a measure of the sporulation capacity of late leaf spot on a given genotype.

The stepwise regression procedure resulted in the selection of different sets of independent variables in each of the 2 yr of the study. Components MPLS and IP explained the highest amount of the variation in AUDPC or apparent infection rate in 1988, while SP and LN explained most of the variation in apparent infection rate and AUDPC in 1989. This indicates that multiple (stepwise) regression procedures may not be helpful in the selection of combinations of resistance components that will have the best impact on reducing AUDPC and apparent infection rates for all locations and years. The selection of two or more independent variables by the stepwise procedure may not have any predictive value because of the high degree of autocorrelation among resistance components (21). It is important to note, however, that a single resistance component (SP) used as the independent variable did account for two-thirds or more of the variation in AUDPC and apparent infection rate, and therefore, this component should have sufficient predictive value to be used as a criterion to identify genotypes with high potential to reduce the rate of disease development. Sporulation may be assessed on genotypes from epidemics occurring in the field by sampling, incubating, and evaluating leaves in the laboratory. Relative comparisons for SP or MPLS could be made among genotypes if known susceptible and resistant standards were used to account for differences in lesion age. Genotypes such as Florunner and Southern Runner were used as standards in our research because these cultivars were well-characterized in previous research studies (3,4,6,11,14,16, 23). Compared to SP, LP is more difficult to determine in the field because it requires inoculation of leaves on a known date and the absence of natural inoculum that might interfere with evaluations. Other researchers (10,18) have defined LP as the time from inoculation to the time that 50% of the lesion (or pustule) population is producing spores (LP_{50}). Because the LP_{50} may not occur on many resistant genotypes (4,23), it is necessary to use some other operational definition of the LP. An LP_{10}, such as reported by Ricker and Beute (17), may be appropriate for some pathosystems. We used the time to the first sporulating lesion (LP_I) because previous research showed that an LP_{10} or LP_{50} could not be calculated for seven of the 14 lines we selected for this study.

Selection for longer LPs should effectively delay late leaf spot disease development in the field. For example, duration of a peanut crop may be 145 days, and the first monocycle of late leaf spot could occur by 35 days after planting. An LP_I of 20 days for Florunner allows 5.8 potential monocycles during the growing season. With the same worst case assumptions, Southern Runner would allow 4.5 monocycles, UF81206-1 would allow 3.7, and GT2 would only allow 3.5. If reduced sporulation is coupled with longer LPs, epidemics should proceed even more slowly.

A reduction in the apparent infection rate should result in higher scores for plant appearance. Chiteka et al (4), showed that SP, LS, and LP were the resistance components most highly correlated with the visual score for overall plant appearance. SP alone accounted for 55% of the total variation in plant appearance. LP also correlated well with sporulation of late leaf spot lesions in

Table 5. Pearson correlation coefficients[a] relating components of resistance, areas under the disease progress curves (AUDPC), and apparent rates of disease progress

	AUDPC[c]		Rate[d]	
Components[b]	1988	1989	1988	1989
IP	0.28	0.08	0.21	0.19
LP_I	−0.77**	−0.55*	−0.75**	−0.67**
MPLS	0.85***	0.72**	0.83***	0.83***
LS	0.66*	0.68**	0.63*	0.75**
LN	0.63*	0.55*	0.55*	0.64*
SP	0.84***	0.86***	0.81***	0.84***
%NA	0.17	0.59*	0.21	0.70**

[a] Coefficients are statistically significant at $P \leq 0.05$ (*), $P \leq 0.01$ (**), and $P \leq 0.001$ (***).
[b] IP = incubation period, LP_I = latent period, MPLS = maximum percentage of lesions that sporulated within 35 days after inoculation, LS = lesion size, LN = lesion number, SP = degree of sporulation, %NA = percent necrotic area per leaf.
[c] Measured from day 62 to 121 in 1988 and from day 65 to 125 in 1989.
[d] Rates were obtained by regressing logit-transformed disease severities against time (units/day).

their study ($r = -0.81$ to -0.86) (3).

Although LS does not appear to be as important as LP and MPLS in slowing an epidemic, it could be a contributing factor. For example, lesions of UF81206-1 were 22% smaller than those of Florunner in this study, and less than 15% of those lesions had produced spores by 35 days after inoculation, compared to 82% for Florunner.

Genotypes with high levels of quantitative resistance often do not have a high yield potential. In this study, the resistant genotypes 4, 8, and 10 had low pod yields. However, UF81206-1 exhibited a high level of resistance and a high yield potential, which agrees with previous reports (3,4,14,23). Southern Runner, GT9, and GT6 had lower levels of rate-reducing resistance than UF81206-1 but maintained similar yields.

Resistances resulting in a longer LP, lower MPLS, reduced SP, or smaller LS should each contribute to slower rates of disease progress when such genotypes are deployed in large plots or grower fields. Several genotypes expressed multiple components of resistance to late leaf spot, and these genotypes significantly slowed epidemic development in the field. Labrinos and Nutter (10) have quantified the effects of a protectant and a systemic fungicide on late leaf spot disease components. This information, coupled with quantitative information concerning the effects of peanut genotype on disease components as described in this paper, could lead to improved integrated control programs, since the effects of fungicides and resistance on disease components could be combined to maximize their effects on disease development and yield (13).

In this study, genotypes with the best rankings by resistance components had lower rates of epidemic development and lower disease levels, as measured by AUDPC. In future breeding efforts, peanut genotypes with long LPs and low numbers of sporulating lesions or lesions with a low degree of sporulation should be selected in order to develop cultivars with improved partial resistance. The close relationship between MPLS and LP indicates that lines selected for low MPLS may also have long LPs. Since sporulation (MPLS and SP) is highly correlated with rate-reducing resistance, it may be the component of choice in screening host populations for late leaf spot resistance (5,11). These components make selection for rate-reducing resistance relatively easy, since rate-reducing resistance can be selected for from a large population of breeding lines in a relatively short time.

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