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QUARTERLY PROGRESS REPORT to
National Peanut Board
North Carolina Peanut Growers Association

TITLE: Breeding peanuts for resistance to Sclerotinia blight, early leafspot, *Cylindrocladium* black rot, and tomato spotted wilt virus

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REPORT: Since the last quarterly report, the disease data were recorded for the 2007 Disease Selection Test (DST) and Disease Advanced Test (DAT) series: Sclerotinia tests with no application of fluazinam were planted at an infested site in Northampton County, NC, CBR tests with no application of metam sodium in an infested field at the Upper Coastal Plain Research Station (UCPRS) in Edgecombe County; early leafspot tests at the Peanut Belt Research Station (PBRS) at Lewiston, NC in plots that received no fungicide application, and tomato spotted wilt virus tests at PBRS in plots that received no insecticide treatment to manage thrips and that were planted at 20" seed spacing to maximize TSWV incidence. Each test had two replications and 169 genetic entries including F₄ progeny of 52 BC₁F₂ plant selections (all carrying the high-oleic gene, 13 of them high oleic) from 11 crosses made in 2005, F₆ progeny of 22 F₄ selections (all carrying the high-oleic gene, 21 of them high oleic) from superior F_{2.4} families derived from 8 crosses made in 2003, and F₈ progeny of 79 F₆ selections (all carrying the high-oleic gene, 67 of them high oleic) from superior F_{4.6} families derived from 4 crosses made in 2003. The F_{6.8} families, which will not be subjected to further within-family selection, also were tested in replicated trials (Disease Preliminary Tests) grown at PBRS and UCPRS with full disease control programs to assess yield and grade of those families. For each F_{2.4} and F_{4.6} family, there was a selection plot at PBRS from which plant selections will be made if that family proves to have superior disease resistance based on performance in the Disease Selection Tests. These tests were planted in May. Stand counts were made in June to permit calculation of disease incidence for CBR, Sclerotinia blight, and TSWV. Few early-season symptoms of TSWV were observed in any of the tests but symptoms developed later. Weather conditions in the early season were conducive to development of CBR but not Sclerotinia blight or leaf spot diseases. Due to high heat and drought in the mid- and late season, Sclerotinia blight failed to develop in the Northampton County trials, but TSWV was present there. The dry conditions also reduced the severity of leafspot at PBRS in spite of regular irrigation. CBR symptoms did develop at UCPRS although they were less pronounced in the DST than in the DAT due to better moisture conditions in the part of the field where the DAT was planted.

Because the Disease Selection Tests had 169 entries, only the means for the best ten families of each type and the checks are presented (Table 1). The best ten F_{2.4} families came from eight different backcrosses crosses made in 2005 to move the high-oleic trait into N03073FT, N03076FT, N03081T, N03088T, and N03090T. The best ten F_{4.6} families came from four crosses made in 2004 between disease-resistant lines (N03075FT, N04046JCSmT, N04052FCSmT, and N04070CSmT) and high-oleic parents N00098ol and N02060ol. The best ten F_{6.8} families came from three crosses made in 2003 to move the high oleic trait into disease-resistant lines N03079FT and N03081T. There were differences in the average level of different diseases observed in the different family types with the F_{6.8} families having the greatest average level of disease resistance as might be expected for the families subjected to the most selection for resistance. However, contrary to expectation, the F_{2.4} families showed a greater average level of resistance than did the F_{4.6} families, probably reflecting the conservation of disease resistance genes in the F_{2.4} families derived by backcrossing to a resistant parent versus the F_{4.6} families with equal ancestry from the resistant and high-oleic parents. In making within-family selections, special attention will be paid to the top 5, 10 and 20% of the F_{2.4} and F_{4.6} families. Again, there will be no more selection within the F_{6.8} families; we will simply be identifying the best with respect to diseases, yield, and grade.

The Disease Advanced Test series had 72 common entries tested for the three diseases that were measurable in 2007: two advanced lines selected separately for resistance to one or more diseases; 14 F_{6.13} families selected from the 2002 Disease Preliminary Test (DPT) for further testing of yield, grade, and disease resistance; one F_{6.12} families selected from the 2003 DPT; one F_{6.11} families selected from the 2004 DPT, six F_{6.10} families selected from the 2005 DPT, 12 F_{6.9} families selected from the 2006 DPT, ten lines derived from interspecific hybrids developed by Drs. H.T. Stalker and S.P. Tallury, and 16 checks including released cultivars (NC 7, NC-V 11, NC 12C, Gregory, Perry, Phillips, Brantley, VA 98R, Wilson, and CHAMPS) and disease-resistant lines (Georgia Green, GP-NC 343, N96076L, PI 121067, PI 269685, PI 270806, and PI 276636). There were also 11 lines that made their way into the DAT by expressing superior disease resistance after surviving in the conventional cultivar

develop stream through a second year in the Advanced Yield Test series. Some of these lines originated in the DST program but fell out of the accelerated program because they did not exhibit sufficient resistance to be retained. Such families enter the conventional cultivar development stream that achieves only one generation per year and in which selection and retention in the program are based solely on pod characteristics, yield and grade. Of the 46 experimental lines developed by the breeding program rather than the species program, 21 were also entered in the multiple-location Advanced Yield Test series for broader evaluation of yield and grade.

Of the 20 best lines for disease resistance, 16 came from the accelerated resistance selection program (Figure 1), 15 of them selections from the 2006 DPT (lines symbolized by open circles in Figure 1) and the remaining one from the 2005 DPT (lines symbolized by open circles in Figure 1). Although it is often the case that the most disease-resistant lines are not the highest yielding or have the best grade, many of the 2006 DPT selections, all of them high-oleic, yielded extremely well. As one would expect for a set of lines yield-tested for the first time, among the 79 selections from the 2006 DPT are several with poor yields. There is not yet any grade data for those selections; it will be obtained in the winter of 2007-2008. The commercial value of these selections cannot be known with certainty until they have passed through a multiple-year multiple-location testing program.

Table 1. Adjusted means from the 2007 Disease Selection Tests: best ten F_{2.4}, F_{4.6} and F_{6.8} families compared with cultivars and checks. Early leafspot tested at PBRS in plots without fungicide; TSWV at PBRS in plots with 20" seed spacing and without insecticide, CBR at UCPRS on infested soil without metam sodium. Sclerotinia plots were grown near Galatia in Northampton Co., but disease did not develop well, and only TSWV data were recorded.

Entry	Defoliation score <i>1=none to 9=complete</i>	Rank among 169	CBR		TSWV		Arithmetic disease index§ <i>0=worst to 1=best</i>	Rank	
			incidence	Rank among 169	incidence	Rank among 169		Among families	Overall
F_{2.4} families									
X05249 (BC1F1-12-02: F04)	3.12±0.34 ^{†a}	18	0.063±0.084 ^{†a}	125	0.070±0.096 ^{†a}	11	.871	1	11
X05242 (BC1F1-02-02: F04)	3.19±0.34 ^{**a}	25	0.000±0.084 ^{†a}	91	0.163±0.096 ^{†a}	56	.837	2	21
X05253 (BC1F1-07-02: F04)	3.42±0.34 ^a	46	0.000±0.084 ^{†a}	91	0.130±0.096 ^{†a}	39	.836	3	22
X05254 (BC1F1-01-01: F04)	3.00±0.34 ^{†a}	10	0.000±0.084 ^{†a}	91	0.197±0.096 ^{**a}	79	.834	4	23
X05243 (BC1F1-11-02: F04)	3.12±0.34 ^{†a}	18	0.000±0.084 ^{†a}	91	0.182±0.096 ^{†a}	68	.832	5	26
X05252 (BC1F1-08-01: F04)	2.85±0.34 ^{†a}	5	0.000±0.084 ^{†a}	91	0.224±0.096 ^{**a}	94	.831	6	27
X05239 (BC1F1-06-01: F04)	2.85±0.34 ^{†a}	5	0.071±0.084 ^{†a}	130	0.163±0.096 ^{†a}	56	.827	7	28
X05242 (BC1F1-02-01: F04)	3.46±0.34	52	0.000±0.084 ^{†a}	91	0.141±0.096 ^{†a}	43	.824	8	29
X05242 (BC1F1-04-01: F04)	3.42±0.34 ^a	46	0.045±0.084 ^{†a}	107	0.119±0.096 ^{†a}	29	.814	9	34
X05250 (BC1F1-06-02: F04)	3.54±0.34	62	0.083±0.084 ^{†a}	133	0.096±0.096 ^{†a}	20	.793	10	43
F_{4.6} families									
X04045 (F2-02-S-03: F06)	3.81±0.34	99	0.000±0.084 ^{†a}	91	0.210±0.096 ^{**a}	86	.738	1	75
X04045 (F2-02-S-02: F06)	4.54±0.34	148	0.083±0.084 ^{†a}	133	0.050±0.096 ^{†a}	3	.719	2	85
X04056 (F2-02-S-04: F06)	3.42±0.34 ^a	46	0.056±0.084 ^{†a}	120	0.243±0.096 ^{**az}	111	.718	3	87
X04045 (F2-01-S-01: F06)	4.38±0.34	145	0.000±0.084 ^{†a}	91	0.167±0.096 ^{†a}	58	.707	4	95
X04041 (F2-01-S-02: F06)	4.77±0.34 ^z	157	0.000±0.084 ^{†a}	91	0.209±0.096 ^{**a}	85	.636	5	124
X04056 (F2-02-S-03: F06)	4.42±0.34	146	0.000±0.084 ^{†a}	91	0.287±0.096 ^{az}	131	.617	6	128
X04045 (F2-02-S-01: F06)	4.35±0.34	142	0.000±0.084 ^{†a}	91	0.334±0.096 ^z	145	.591	7	138
X04056 (F2-02-S-06: F06)	4.15±0.34	132	0.000±0.084 ^{†a}	91	0.381±0.096 ^z	161	.578	8	139
X04009 (F2-01-S-02: F06)	4.58±0.34	150	0.000±0.084 ^{†a}	91	0.321±0.096 ^z	143	.575	9	141
X04046 (F2-04-S-02: F06)	3.85±0.34	105	0.000±0.084 ^{†a}	91	0.442±0.096 ^z	168	.567	10	142
F_{6.8} families									
X03155 (BC1F1-04-02-S-04-S-04: F08)	2.92±0.34 ^{†a}	8	0.000±0.084 ^{†a}	91	0.061±0.096 ^{†a}	8	.940	1	1
X03155 (BC1F1-04-01-S-04-S-01: F08)	3.19±0.34 ^{**a}	25	0.000±0.084 ^{†a}	91	0.040±0.096 ^{†a}	1	.926	2	2
X03157 (BC1F1-04-01-S-01-S-01: F08)	3.19±0.34 ^{**a}	25	0.000±0.084 ^{†a}	91	0.048±0.096 ^{†a}	2	.920	3	3
X03157 (BC1F1-04-01-S-04-S-04: F08)	2.88±0.34 ^{†a}	6	0.000±0.084 ^{†a}	91	0.102±0.096 ^{†a}	25	.914	4	4
X03153 (BC1F1-01-02-S-02-S-03: F08)	3.35±0.34 ^{**a}	35	0.000±0.084 ^{†a}	91	0.058±0.096 ^{†a}	6	.897	5	5
X03155 (BC1F1-04-02-S-04-S-01: F08)	3.23±0.34 ^{**a}	27	0.000±0.084 ^{†a}	91	0.080±0.096 ^{†a}	14	.893	6	6
X03157 (BC1F1-04-01-S-05-S-01: F08)	3.08±0.34 ^{†a}	14	0.000±0.084 ^{†a}	91	0.104±0.096 ^{†a}	26	.892	7	7
X03157 (BC1F1-04-01-S-04-S-05: F08)	3.42±0.34 ^a	46	0.000±0.084 ^{†a}	91	0.058±0.096 ^{†a}	7	.888	8	8
X03155 (BC1F1-04-02-S-04-S-03: F08)	3.27±0.34 ^{**a}	28	0.000±0.084 ^{†a}	91	0.082±0.096 ^{†a}	15	.888	9	9
X03157 (BC1F1-04-01-S-04-S-02: F08)	3.35±0.34 ^{**a}	35	0.000±0.084 ^{†a}	91	0.083±0.096 ^{†a}	16	.878	10	10
Cultivars									
Wilson	5.27±0.34 ^z	165	0.000±0.084 ^{†a}	91	0.237±0.096 ^{**az}	105	.562	1	143
NC 12C	4.19±0.34	135	0.071±0.084 ^{†a}	130	0.335±0.096 ^z	146	.559	2	144
NC 7	4.65±0.34	155	0.056±0.084 ^{†a}	120	0.417±0.096 ^z	165	.462	3	156
Phillips	4.38±0.34	145	0.250±0.084	159	0.285±0.096 ^{az}	129	.456	4	157
NC-V 11	4.65±0.34	155	0.400±0.084 ^z	167	0.125±0.096 ^{†a}	33	.442	5	160
Perry	4.73±0.34 ^z	156	0.136±0.084 ^{†a}	146	0.436±0.096 ^z	167	.386	6	162
Gregory	3.69±0.34	86	0.336±0.084 ^z	162	0.413±0.096 ^z	164	.380	7	163
Brantley	3.92±0.34	114	0.400±0.084 ^z	167	0.361±0.096 ^z	156	.350	8	165
VA 98R	5.31±0.34 ^z	166	0.464±0.084 ^z	168	0.279±0.096 ^{az}	124	.218	9	168
NC 9	5.35±0.34 ^z	167	0.381±0.084 ^z	164	0.407±0.096 ^z	163	.177	10	169
Checks									
N03081T	3.77±0.34	93	0.000±0.084 ^{†a}	91	0.063±0.096 ^{†a}	9	.848	1	18
N03090T	2.50±0.34 ^{†a}	1	0.071±0.084 ^{†a}	130	0.255±0.096 ^{az}	115	.798	2	42
N96076L	3.46±0.34	52	0.143±0.084 ^{†a}	148	0.242±0.096 ^{**az}	109	.657	1	119
PI 576636	3.15±0.34 ^{†a}	20	0.391±0.084 ^z	165	0.098±0.096 ^{†a}	21	.628	2	127
GP-NC 343	2.73±0.34 ^{†a}	3	0.331±0.084 ^z	161	0.255±0.096 ^{az}	116	.600	3	134
Mean of all entries	3.80		0.060		0.215		.695		
Mean of F _{2.4} families	3.63±0.06 ^b	2	0.036±0.012 ^a	2	0.242±0.013 ^{bc}	3	.709		3
Mean of F _{4.6} families	4.60±0.09 ^b	4	0.101±0.018 ^b	3	0.279±0.021 ^{cd}	4	.538		4
Mean of F _{6.8} families	3.64±0.04 ^a	3	0.033±0.009 ^a	1	0.166±0.011 ^a	1	.766		1
Mean of cultivars	4.62±0.12 ^c	5	0.249±0.027 ^c	5	0.329±0.030 ^d	5	.399		5
Mean of checks	3.12±0.17 ^{ab}	1	0.187±0.038 ^c	4	0.182±0.043 ^{ab}	2	.726		2
Standard value	2.50		0.000		0.000				

§ Average of three disease scores, each adjusted to a 1 (best) to 0 (worst) scale.

**,*† Indicate means not significantly different from the standard value at the 1%, 5%, and 10% levels of probability, respectively, by t-test from a standard value.

a,z Denote means not significantly different from the best and worst in the test, respectively, at the 5% level by t-test.

