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Executive Summary for NPB Project ID 53 Breeding Peanuts for Resistance to Sclerotinia Blight, Leaf Spot, CBR and TSWV.

This long-term project was initiated to implement simultaneous selection for resistance to four diseases of consistent economic importance in the North Carolina and Virginia: Sclerotinia blight caused by soilborne fungus *Sclerotinia minor*, early leaf spot caused by foliar fungus *Cercospora arachidicola*, *Cylindrocladium* black rot (CBR) caused by soilborne fungus *Cylindrocladium parasiticum*, and tomato spotted wilt (TSW) caused by the thrips-vectored *Tomato spotted wilt tospovirus*. Each year, agronomically superior parents are crossed with sources of high-level resistance that are often not agronomically desirable in the VC area. We often make an initial cross in the winter then next summer cross the F₁ plants back to the agronomically desirable parent before the hybrid progeny are subjected to an accelerated program of inbreeding and selection as outlined below:

Crosses are made in the greenhouse at the N.C. State University campus in Raleigh, NC. The F₁ or first backcross F₁ (BC₁F₁) hybrid plants from the annual summer crossing program are grown at our Puerto Rico Winter Nursery (PRWN) in Juana Diaz, PR. The F₂ populations are subjected to selection for pod and seed characteristics at the Peanut Belt Research Station (PBRS) at Lewiston, NC, in plots provided a full disease control program. There is no chemical control for TSW, and the plants must be spaced 10 inches or more apart to allow for selection of individual plants, so TSW does contribute to the appearance of plants in the selection nursery. F₃ progeny of F₂ plant selections (F_{2:3} families) are grown at the PRWN that winter. At harvest a single pod is harvested from each plant in an F_{2:3} family to provide a single seed representing that plant in an F_{2:4} selection nursery at PBRS, then the rest of the pods are harvested in bulk to provide seed for replicated testing for resistance to the four diseases at sites specially chosen and managed to promote development of diseases: Sclerotinia blight, leaf spot and CBR on infested fields left untreated with the protectant fungicides used to control them, TSW in a trial in which plants are spaced 20 inches apart and left untreated with insecticides that would reduce the population of the thrips that vector the virus. The F_{2:4} or BC₁F_{2:4} families with the best overall resistance to the four diseases are identified, then we make plant selections in those families in the nursery planted for the purpose at PBRS from the F_{2:4} single-seed descent harvest. Progeny of those selections are sent back to the PRWN for another cycle of inbreeding and selection among and within F_{4:6} and BC₁F_{4:6} families the following summer. F_{6:7} progeny of selected F₆ plants are grown at the PRWN, but harvested only in bulk as we do not make single-plant selections beyond the F₆ generation. The F_{6:8} families, now considered genetically stable breeding lines, are tested for disease reactions and also in replicated preliminary trials for yield and grade at PBRS and another research station on the upper coastal plain near Rocky Mount, NC. The most disease-resistant families are retained for continued evaluation in disease trials; those with the best yields and grades advance into the "conventional" testing program (conducted with disease controls) that leads to cultivar release. There is usually some overlap between the two groups, but highly resistant lines that do not make the grade agronomically are used as parents for another cycle of the program. Any line that survives in the conventional advance yield test series for a second or greater year is also evaluated in disease trials.

Two cultivars have been released from this project: 'Bailey' in 2008 and 'Sugg' in 2009. Certified seed of Bailey was available to growers for the 2011 growing season, as were limited amounts of Sugg. Both have partial resistance to all four diseases and also have excellent yield potential. At federal support prices for peanuts, saving one or two applications of leaf spot fungicide or a single application of Sclerotinia preventives could mean the difference between profit and loss. Reduction of chemical inputs requires improvement of the disease resistance available in virginia-type cultivars. Resistant cultivars will help to maintain peanut production and the peanut seed market in North Carolina. In recent years, we have incorporated greater levels of disease resistance and have advanced only families carrying the University of Florida's high-oleic seed oil gene in our accelerated selection program.

Lay Interpretation of Results for NPB Project ID 53 Breeding Peanuts for Resistance to Sclerotinia Blight, Leaf Spot, CBR and TSWV.

A series of peanut variety releases by N.C. State University gave evidence of a problem in our program. We had separate subprograms of selection for resistance to the four diseases of consistent economic importance in the North Carolina and Virginia: Sclerotinia blight caused by soilborne fungus *Sclerotinia minor*, early leaf spot caused by foliar fungus *Cercospora arachidicola*, Cylindrocladium black rot (CBR) caused by soilborne fungus *Cylindrocladium parasiticum*, and tomato spotted wilt (TSW) caused by the thrips-vectored *Tomato spotted wilt tospovirus*. When we released a variety resistant to one or even two, it often was badly susceptible to another. We needed to select for resistance to all four simultaneously.

Each year, we cross agronomically superior parents with sources of high-level resistance that are often not agronomically desirable in the Virginia-Carolina area, including runner-type sources. After the cross, we use a form of "shuttle" breeding to get to genetically stable inbred lines in three years. Starting the second generation after the cross, we make plant selections for pod and seed characteristics in North Carolina. We use a winter seed nursery in Puerto Rico to grow a second generation each year, then test the selected families for resistance to the four diseases in separate trials, identifying the best families overall and making plant selections within those families. By the sixth generation after the cross, the families are genetically stable breeding lines that have improved disease resistance and then proceed through the multi-year multi-location testing program that eventually leads to variety release. Highly resistant lines that do not measure up agronomically are recycled as parents in the crossing program.

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IMPACT STATEMENT

Two cultivars have been released from this project: Bailey and Sugg. Certified seed of Bailey should be available to growers for the 2011 growing season, and limited amounts of Sugg the same. Both cultivars have partial resistance to the four most common economically important diseases of peanut in North Carolina: early leafspot, *Cylindrocladium* black rot, *Sclerotinia* blight, and tomato spotted wilt virus. With current peanut prices, saving one or two applications of leafspot fungicide or a single application of *Sclerotinia* preventives could mean the difference between profit and loss. Reduction of chemical inputs requires improvement of the disease resistance available in virginia-type cultivars. Resistant cultivars will help to maintain peanut production and the peanut seed market in North Carolina.

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NCARS / NCCES CODE: **NC-20**
ON CAMPUS RESEARCH
REPORT PERIOD **01/01/2010-12/31/2010**
 INTERIM FINAL

Small

**PROGRESS REPORT
TO
NORTH CAROLINA PEANUT GROWERS ASSOCIATION, INC.**

TITLE: Breeding peanuts for multiple disease resistance
LEADER: T.G. Isleib
DEPARTMENT: Crop Science

REPORT:

Grades of the 67 F₈ progenies of F₆ plants selected from resistant F_{4:6} families from the 2005 crossing program were measured in pod samples obtained from the Disease Preliminary Test (DPT) conducted at two locations, the Peanut Belt Research Station (PBRS) and Upper Coastal Plains Research Station (UCPRS) in 2009. Ten F_{6:9} families were selected for further testing of yield, grade, and disease resistance as part of the 2010 Disease Advanced Test; three of those ten plus 20 additional lines (23 total) were selected for entry into the 2010 NCSU Advanced Yield Test (AYT). All of the lines carry the high oleic acid trait patented by the University of Florida.

Disease data were recorded for the 2010 Disease Selection Test (DST) and Disease Advanced Test (DAT) series: Sclerotinia tests with no application of fluazinam were grown at an infested site in Bertie 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 application of leafspot fungicide, 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 182 genetic entries including F₄ progeny of 82 F_{2:4} plants (all carrying the high-oleic gene, 42 of them high-oleic), F₆ progeny of 27 BC₃F₄ plant selections (all carrying the high-oleic gene, 15 of them high oleic) from superior BC₃F_{2:4} families from 15 crosses made in 2007, and F₈ progeny of 52 F₄ selections (all carrying the high-oleic gene, 50 of them high oleic) from superior F_{4:6} families derived from 5 crosses made in 2006. 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 their yield and grade. For each F_{2:4} and BC₃F_{4:6} family, there was a selection plot at PBRS from which plant selections were be made if that family proved 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 and Sclerotinia blight but not leaf spot disease. Leaf spot trials were irrigated to provide sufficient humidity to promote disease development. Due to the hot dry weather of the 2010 growing season, there was very little development of three of the four diseases monitored in the program: there was good development only of TSWV. However, Southern stem rot caused by *Sclerotium rolfsii* also was observed in the tests.

Because the Disease Selection Tests had 182 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 three different crosses made in 2008, all of which share breeding line N08059oIFCT as a common parent while the resistance comes from three different sources, each derived from exotic parentage (*Arachis hypogaea* var. *hirsuta*, and diploid wild species *Arachis cardenasii*). The best ten BC₃F_{4:6} families came from three different crosses made in 2007 to move the high-oleic trait into Bailey and

Bailey sister line N03090T. The best $F_{6:8}$ families came from three crosses made in 2006 to combine high-oleic disease-resistant but small-seeded selections with larger seeded parents including Sugg and N03084T. There were differences in the average level of different diseases observed in the different family types. We expected the $F_{6:8}$ families, *i.e.*, those subjected to the most selection for resistance, to have the greatest average level of disease resistance. However, contrary to expectation, the $F_{2:4}$ families showed a greater average level of resistance than did the $F_{6:8}$ families, probably reflecting the high levels of disease resistance in the exotic parents used to produce the $F_{2:4}$ families. In making within-family selections, special attention was paid to the top 5, 10 and 20% of the $F_{2:4}$ and $BC_3F_{4:6}$ 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. It is of interest to note that N08075olCT, an advanced line entered as a check, ranked among the best ten out of 182 families and lines with respect to average disease resistance.

The Disease Advanced Test (DAT) series had 49 common entries tested for the diseases that were measurable in 2010: three $F_{6:16}$ families selected from the 2002 Disease Preliminary Test (DPT) for further testing of yield, grade, and disease resistance; one $F_{6:14}$ family selected from the 2004 DPT, six $F_{6:11}$ families selected from the 2007 DPT, two $F_{6:10}$ families selected from the 2008 DPT; ten $F_{6:9}$ lines selected from the 2009 DPT, six lines entered upon the request of Dr. Roy Pittman, the USDA-ARS peanut germplasm curator, four lines derived from interspecific hybrids developed by Drs. H.T. Stalker and S.P. Tallury, and 15 checks including released cultivars (NC-V 11, NC 12C, Gregory, Perry, Phillips, Brantley, Bailey, Sugg, VA 98R, CHAMPS, and Florida Fancy) and disease-resistant lines (Georgia Green, N96076L, and PI 576636). There were also two lines that made their way into the DAT by expressing superior disease resistance after surviving in the conventional cultivar development stream through a second or greater year in the three-location 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 24 experimental lines developed by the breeding program rather than the species program, six were also entered in the multiple-location Advanced Yield Test series for broader evaluation of yield and grade.

Table 1. Adjusted means from the 2009 Disease Selection Tests: best ten BC₃F_{2,4}, F_{4,6} and BC₁F_{6,8} families compared with 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, and Sclerotinia plots at Roxobel in Bertie Co. on infested soil without application of fluazinam or boscalid.

Entry	Defoliation score	Rank among 182	Disease at Upper Coastal Plain Res. Station		Disease at Joey Baker farm, Roxobel		Tomato spotted wilt virus incidence	Rank among 182	Arithmetic disease index [§]	Rank	
			incidence	Rank among 182	incidence	Rank among 182				Over-all	Among families I
	1=none to 9=complete								0=worst to 1=best		
F_{2,4} families	2.81±0.04^α	1	.312±.019^α	4	.152±.010^α	1	.602±.011^α	1	.642		1
X08051 (F1-01-01-S: F04)	1.94±0.30 ^{†a}	17	-.047±.157 ^{†a}	116	.000±.097 ^{†a}	14	.693±.099	130	.840	4	4
X08051 (F1-01-03-S: F04)	2.38±0.30 ^{†a}	28	.079±.157 ^{†a}	151	.121±.097 ^{†a}	71	.436±.099 ^a	6	.815	8	8
X08054 (F1-01-02-S: F04)	2.63±0.30 ^{**a}	6	-.026±.157 ^{†a}	116	.154±.097 ^{†a}	91	.481±.099 ^a	15	.827	7	7
X08054 (F1-02-02-S: F04)	2.13±0.30 ^{†a}	35	.103±.157 ^{†a}	116	.088±.097 ^{†a}	58	.385±.099 ^{**a}	2	.839	5	5
X08054 (F1-03-01-S: F04)	2.51±0.30 ^a	70	.103±.157 ^{†a}	116	.000±.097 ^{†a}	14	.539±.099	31	.791	11	10
X08055 (F1-02-01-S: F04)	2.11±0.30 ^{†a}	10	.000±.157 ^{†a}	116	.000±.097 ^{†a}	14	.416±.099 ^a	6	.909	1	1
X08055 (F1-03-02-S: F04)	2.05±0.30 ^{†a}	3	.288±.157 ^{†a}	129	.077±.097 ^{†a}	48	.461±.099 ^a	20	.814	9	9
X08055 (F1-03-04-S: F04)	2.00±0.30 ^{†a}	11	.042±.157 ^{†a}	142	.136±.097 ^{†a}	82	.529±.099	27	.828	6	6
X08055 (F1-03-05-S: F04)	1.87±0.30 ^{†a}	1	.080±.157 ^{†a}	116	.000±.097 ^{†a}	14	.594±.099	61	.882	2	2
X08055 (F1-04-04-S: F04)	2.50±0.30 ^{†a}	2	-.096±.157 ^{†a}	123	.125±.097 ^{†a}	75	.473±.099 ^a	14	.870	3	3
BC₃F_{4,6} families	2.93±0.07^{αβ}	3	.458±.037^β	1	.210±.019^β	3	.680±.019^{βγ}	3	.534		3
X07076 (BC3F1-03-01-S-03-S: F06)	3.17±0.30 ^z	90	.455±.157	116	.160±.097 ^{†a}	96	.594±.099	61	.581	98	7
X07076 (BC3F1-03-02-S-01-S: F06)	3.05±0.30 ^z	135	.307±.157 ^a	142	.045±.097 ^{†a}	28	.617±.099	74	.641	69	3
X07078 (BC3F1-03-01-S-02-S: F06)	2.55±0.30 ^a	65	.193±.157 ^{†a}	116	.050±.097 ^{†a}	32	.707±.099 ^z	139	.690	42	1
X07084 (BC3F1-02-01-S-02-S: F06)	3.05±0.30 ^z	42	.288±.157 ^{†a}	116	.183±.097 ^{†a}	110	.566±.099	39	.656	63	2
X07091 (BC3F1-06-02-S-03-S: F06)	2.75±0.30 ^{**}	40	.391±.157 ^{**}	129	.181±.097 ^a	108	.609±.099	64	.636	71	4
X07096 (BC3F1-03-01-S-01-S: F06)	3.05±0.30 ^z	137	.232±.157 ^{†a}	116	.243±.097 ^{**a}	139	.681±.099	126	.559	114	10
X07102 (BC3F1-05-01-S-01-S: F06)	2.82±0.30	104	.258±.157 ^{†a}	146	.063±.097 ^{†a}	34	.783±.099 ^z	169	.603	87	5
X07102 (BC3F1-05-01-S-02-S: F06)	2.45±0.30 ^{†a}	106	.384±.157 ^{**}	116	.245±.097 ^{**a}	141	.616±.099	69	.595	91	6
X07102 (BC3F1-05-03-S-01-S: F06)	2.91±0.30	150	.327±.157 ^{**a}	116	.136±.097 ^{†a}	82	.681±.099	122	.577	101	8
X07102 (BC3F1-05-03-S-02-S: F06)	2.95±0.30 ^z	73	.283±.157 ^a	163	.208±.097 ^{**a}	123	.753±.099 ^z	159	.560	110	9
F_{6,8} families	2.95±0.05^β	2	.355±.026^α	2	.154±.013^α	2	.639±.014^β	2	.594		2
X06127 (F2-01-S-01-S-01-S: F08)	2.95±0.30 ^z	38	.215±.157 ^{†a}	116	.080±.097 ^{†a}	49	.538±.099	29	.730	26	4
X06127 (F2-01-S-01-S-03-S: F08)	2.41±0.30 ^{†a}	33	.237±.157 ^{†a}	116	.042±.097 ^{†a}	24	.705±.099	139	.710	31	6
X06130 (F2-09-S-01-S-02-S: F08)	1.95±0.30 ^{†a}	13	.085±.157 ^{†a}	116	.129±.097 ^{†a}	78	.707±.099 ^z	140	.754	19	3
X06130 (F2-09-S-01-S-04-S: F08)	3.04±0.30 ^z	43	.076±.157 ^{†a}	116	.077±.097 ^{†a}	48	.454±.099 ^a	7	.779	13	1
X06130 (F2-09-S-01-S-06-S: F08)	2.33±0.30 ^{†a}	55	.224±.157 ^{†a}	142	.091±.097 ^{†a}	60	.490±.099 ^a	16	.759	17	2
X06130 (F2-14-S-03-S-02-S: F08)	2.96±0.30 ^z	88	.183±.157 ^{†a}	153	.042±.097 ^{†a}	24	.490±.099 ^a	26	.728	27	5
X06130 (F2-14-S-04-S-01-S: F08)	2.46±0.30 ^{†a}	83	.238±.157 ^{†a}	116	.151±.097 ^{†a}	88	.524±.099	25	.705	34	8
X06130 (F2-14-S-04-S-07-S: F08)	2.66±0.30 ^{**a}	50	.242±.157 ^{†a}	168	.208±.097 ^{**a}	123	.499±.099 ^a	20	.694	38	9
X06132 (F2-03-S-01-S-01-S: F08)	3.42±0.30 ^z	110	.258±.157 ^{†a}	129	.083±.097 ^{†a}	56	.302±.099 ^{†a}	4	.689	43	10
X06132 (F2-03-S-01-S-02-S: F08)	3.00±0.30 ^z	102	.111±.157 ^{†a}	116	.050±.097 ^{†a}	32	.605±.099	62	.709	33	7
Cultivars and advanced lines	3.02±0.10^{αβ}	4	.555±.054^β	3	.296±.029^γ	4	.702±.030^{βγ}	4	.453		4
NC-V 11	3.30±0.30 ^z	142	.282±.157 ^a	116	.400±.097	172	.792±.099 ^z	171	.425	168	6
Bailey	2.75±0.30 ^{**}	136	.594±.157 ^z	164	.232±.097 ^{**a}	134	.735±.099 ^z	150	.473	152	4
Sugg	3.69±0.30 ^z	173	.453±.157	116	.394±.097	171	.668±.099	109	.385	176	9
Phillips	3.59±0.30 ^z	180	.512±.157 ^z	116	.267±.097 ^a	148	.847±.099 ^z	176	.336	179	10
Gregory	2.97±0.30 ^z	153	.566±.157 ^z	116	.292±.097	154	.700±.099	142	.442	164	5
Perry	3.34±0.30 ^z	95	.647±.157 ^z	177	.348±.097	167	.772±.099 ^z	164	.386	175	8
Brantley	3.47±0.30 ^z	182	.657±.157 ^z	163	.663±.097 ^z	181	.763±.099 ^z	164	.180	181	11
N08070oJc	2.93±0.30 ^z	76	.682±.157 ^z	116	.000±.097 ^{†a}	14	.704±.099	144	.562	109	3
N08075oJcT	1.93±0.30 ^{†a}	37	.286±.157 ^a	116	.091±.097 ^{†a}	60	.420±.099 ^a	3	.797	10	1
N08081oJc	2.47±0.30 ^{†a}	23	.636±.157 ^z	116	.250±.097 ^{**a}	145	.560±.099	37	.595	92	2
N08086oJcT	2.81±0.30	72	.786±.157 ^z	116	.325±.097	163	.762±.099 ^z	158	.404	173	7
Disease checks	3.14±0.15^β	5	.461±.078^{αβ}	5	.320±.043^γ	5	.774±.044^γ	5	.425		5
NC 3033	3.67±0.30 ^z	181	.741±.157 ^z	136	.470±.097 ^z	174	.982±.099 ^z	182	.129	182	5
N96076L	2.97±0.30 ^z	154	.442±.157	142	.310±.097	160	.695±.099	151	.455	159	3
Georgia Green	2.92±0.30	151	.266±.157 ^a	116	.675±.097 ^z	182	.801±.099 ^z	172	.339	178	4
PI 576636	3.06±0.30 ^z	47	.642±.157 ^z	153	.000±.097 ^{†a}	14	.705±.099	141	.579	100	2
Mean of all entries	2.43		.365		.175		.426		.595		
Standard value	2.00		.000		.000		.000		--		

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

α,β Group means followed by the same Greek letter are not significantly different by t-test (P<0.05).

,,† 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.