

## The North Carolina State University Peanut Breeding Program: A Summary of Field Research Conducted in 2016

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**INTRODUCTION.** The peanut breeding program in the Department of Crop Science at NCSU was initiated in the 1920s when Mr. P. H. Kime collected peanut plant specimens from growers and used them as the basis for a program of mass selection. Later, Drs. Paul Harvey and G. K. Middleton, the department's corn and small grains breeders, worked part-time in peanuts, assembling and evaluating a germplasm collection until Dr. Walton C. Gregory was hired in 1944 as a full-time peanut breeder. Dr. Gregory was joined in 1958 by Dr. Donald A. Emery who took on the responsibility for cultivar development while Dr. Gregory focused on collection and phylogenetic studies of the diploid wild species of genus *Arachis*. When Dr. Emery moved on to full-time teaching and administrative duties in 1974, Dr. Johnny C. Wynne took over as peanut breeder. Dr. Thomas G. Isleib was hired in 1990 after Dr. Wynne became head of the department. The project has released 24 public cultivars and 7 germplasm lines. The cultivars were all of the virginia market-type and include NC 4, NC 1, NC 2, NC 4X, NC 5, NC 17, NC-Fla 14, NC 6, NC 7, NC 8C, NC 9, NC 10C, NC-V 11, VA-C 92R, NC 12C, Gregory, Perry, Phillips, Brantley, Bailey, Sugg, Sullivan, Wynne, and Emery. The germplasm releases included insect- and disease-resistant line GP-NC 343, *Sclerotium rolfsii*- and CBR-resistant line NC 3033, leafhopper-resistant lines NC 10247, NC 10272, NC 15729, and NC 15745, and multiple-disease-resistant line N96076L. Several other lines have been released exclusively, including three in Australia, one to a private seed company in North Carolina, two to a private seed company in Virginia, and two to private companies in Georgia.

That the project has been successful is evidenced by the support with which it has been provided over the years by clientele organizations including the North Carolina Peanut Growers Association, the N.C. Foundation Seed Producers, Inc., the N.C. Crop Improvement Association, the Virginia-Carolina Peanut [Shellers] Association, the Peanut Foundation, and the National Peanut Board. Funding has also been obtained in the past from the USAID Peanut Collaborative Research Support Program (CRSP) and from USDA competitive grants in biological nitrogen fixation, genetic vulnerability, and organic production. In recent years, substantial support for the program has come from royalties charged on sales of seed of new releases, over six million dollars since 1992. However, the main source of funding for the project remains the state of North Carolina. The N.C. Agricultural Research Service provides salaries, facilities, and basic operating funds on the NCSU campus while the N.C. Department of Agriculture and Consumer Services (NCDA&CS) provides field facilities.

The general objective of the program is to provide peanut growers of North Carolina, South Carolina and Virginia with high-yielding cultivars that meet the needs of the area's shelling and processing industries. Although this objective has not changed over the years, production constraints and industry needs have, necessitating incorporation of new germplasm and methodologies into the program. The specific objectives of the program include: high yield, resistance to prevalent diseases, and improved quality (conformation to market type, pod brightness, seed oil content and composition, and flavor). To achieve these objectives, a system of hybridization, selection, testing, and seed multiplication has been established.

**BREEDING FOR YIELD AND GRADE.** The simplest yield breeding concept is to intermate the best cultivars and breeding lines among themselves, then to try to select something better from the hybrid populations as segregation and assortment recombine the genes of the parents. The trick is picking the winners out of the huge number of genotypes found in the segregating generations following the initial cross. Most peanut cultivars are derived from a single-plant selection made in the F<sub>6</sub>, *i.e.*, the sixth filial generation after the cross, or later generation. In earlier generations, the progeny of individual plants do not "breed true," *i.e.*, they do not resemble the parent exactly. In the case of yield, there is so much variation due to environmental factors or to genotype-by-environment interaction that it is difficult to identify the best genotypes even when they are true-breeding. A great deal of effort has been expended over the years trying to identify easily measurable characteristics that can be evaluated in the early segregating generations and used to identify the individual plants whose progeny will have the greatest yield potential. These characteristics have ranged from morphological traits such as number of branches or pods per plant to physiological traits such as leaf area index, or timing and duration of the reproductive phase, to molecular genetic traits such as DNA markers. In general, these techniques have not worked well, nor have they been sufficiently inexpensive to permit the evaluation of tens of thousands of individual plants in a single season. Our approach has been to select in the early generations for characteristics with high heritability (such as plant type, or pod and seed size and shape), narrow the population down to a subset that conforms to

the virginia market type, and then begin screening for yield and other traits once the lines are sufficiently inbred to breed reasonably true. All field work except some disease evaluation is conducted on research stations run by the NCDA&CS. All plant selection is conducted at the Peanut Belt Research Station (PBRS) at Lewiston, NC.

TESTING PROGRAM. Like most plant breeding programs, we have an elaborate system of performance testing (Table 1). At present, we make our last single-plant selection in elite populations in the  $F_6$  generation. The following year we grow  $F_{6,7}$  progenies that are subjected to among-family selection. Enough seed is recovered from a single selected plot to plant three plots in the following season, one in each of two Preliminary Yield Tests (PYTs) grown at two sites, the PBRS at Lewiston and the Upper Coastal Plain Research Station (UCPRS) at Rocky Mount, and a seed increase plot at PBRS. The set of selections, usually 125 to 250 in number, are grouped into subsets of 20 to 25 that are planted in an unreplicated trial at each site. A small number of checks are included in each subset, so there is extensive replication of the checks, providing an estimate of experimental error within the test at a site, but no within-site replication of the new experimental lines. After harvest, yields are measured, and a pod sample is taken back to the grading laboratory at NCSU where the sample is divided into jumbo and fancy pod fractions, each of which is subjected to colorimetry to determine pod brightness and hue. On the basis of this data, 10 to 20% of the lines are promoted to the Advanced Yield Test (AYT) in the following year. This test is grown at three sites with two reps per site: the PBRS at Lewiston, the UCPRS at Rocky Mount, and the Border Belt Tobacco Research Station (BBTRS) at Whiteville. Full grade, pod color, and oil content of SMK are measured on each AYT plot. If a line is selected for testing in the AYT for a second or greater year, then it is

Table 1. A generalized summary of the NCSU peanut breeding program's cultivar development process.

Year	Season	Action
1	Summer	Select parents and make crosses
1	Winter	$F_1$ generation grown in Puerto Rico Winter Nursery (PRWN)
2	Summer	Single-plant selection (SPS) among $F_2$ plants for plant, pod, and seed traits at Peanut Belt Research Station (PBRS) at Lewiston, NC.
3	Summer	SPS among and within $F_{2,3}$ progenies for plant, pod, and seed traits at PBRS <sup>†</sup> .
4	Summer	SPS among and within $F_{3,4}$ progenies for plant, pod, and seed traits at PBRS <sup>†</sup> .
5	Summer	SPS among and within $F_{4,5}$ progenies for plant, pod, and seed traits at PBRS <sup>†</sup> .
6	Summer	SPS among and within $F_{5,6}$ progenies for plant, pod, and seed traits at PBRS <sup>†</sup> .
7	Summer	Family selection among $F_{6,7}$ progenies for plant, pod, and seed traits at PBRS <sup>†</sup> .
8	Summer	Preliminary Yield Test (PYT) of $F_{6,7}$ progenies at PBRS and Upper Coastal Plain Research Station (UCPRS) at Rocky Mount, NC. Selection divided into sets, each including the same 3-4 checks. Yield, jumbo and fancy pod content and color measured at harvest. Seed increased on 0.003 A in Preliminary Yield Line Nursery (PYN) or harvested by hand from the yield plot at PBRS.
9	Summer	Advanced Yield Test (AYT) at PBRS, UCPRS, and Border Belt Tobacco Research Station (BBTRS) at Whiteville, NC. Two-rep test at each site, full grade, pod color, and oil content measured at harvest. Seed increased in 0.003 A in Small-Plot Increase Nursery (SPI).
10	Summer	AYT at PBRS, UCPRS, and BBTRS. Disease reaction evaluated in Advanced Line Disease Test, Leafspot (ALL) without chemical leafspot control at PBRS, Advanced Line Disease Test, CBR (ALC) at a CBR-infested site, Advanced Line Disease Test, Sclerotinia Blight (ALS) at a Sclerotinia-infested site, and Advanced Line Disease Test, TSWV (ALT) planted at wide (20") seed spacing without insect control at PBRS. Seed increased in SPI and on 0.02 A in Large Plot Increase (LPI).
11	Summer	AYT at PBRS, UCPRS, and BBTRS. Disease reactions evaluated in ALL, ALC, ALS, and ALT. Regional performance testing in small-plot phase of the Virginia-North Carolina Peanut Variety and Quality Evaluation (PVQE) program coordinated by Dr. Maria Balota of VPI&SU's Tidewater Agricultural Research and Extension Center in Suffolk, VA. Two sites in Virginia, three in North Carolina, and one in South Carolina. Two separate trials dug at 10- to 14-day intervals one NC and one VA site. Seed increased in SPI and LPI.
12	Summer	AYT at PBRS, UCPRS, and BBTRS. Disease reactions evaluated in ALL, ALC, ALS, and ALT. PVQE small-plot test at six sites. Seed increased in SPI and LPI; 1 A breeder seed increase at PBRS <sup>§</sup> .
13	Summer	AYT at PBRS, UCPRS, and BBTRS. Disease reactions evaluated in ALL, ALC, ALS, and ALT. PVQE small-plot test at six sites. PVQE large-plot test comparing one or two lines with a check in 0.5 A plots at two sites; extensive processing of pods and seeds from large plots by area shellers and processors to determine suitability <sup>§</sup> . Uniform Peanut Performance Test (UPPT) in seven states, coordinated by W.D. Branch of the University of Georgia. Seed increase in SPI and LPI. Foundation seed increase by North Carolina Foundation Seed Producers, Inc.
14	Spring	Release decision. Released lines are included as checks in the AYT, ALL, ALC, ALS, ALT and PVQE small-plot test.

<sup>†</sup> Selection procedures may include single-seed descent at the PRWN to reduce the number of years required to reach the  $F_6$  generation.

<sup>§</sup> This phase may be delayed until a fourth or fifth year of testing in the PVQE small-plot trials, depending on how many lines reach a third year of PVQE testing.

also evaluated for resistance to four prevalent diseases: early leaf spot, *Cylindrocladium* black rot (CBR), *Sclerotinia* blight, and tomato spotted wilt virus (TSWV) in the Advanced Line Disease (ALD) test series.

Historically, the domestic market for in-shell peanuts has been primarily a fancy pod market while the European export market demanded more jumbo pods. In the late 1990s, area shellers expressed concern about the high jumbo pod content of NCSU releases NC 12C and Gregory, saying that they produced too few fancy pods and that the fancy pods that were produced generally were dark in color, especially after roasting. In response to these concerns, we instituted a program of measuring the brightness and hue of jumbo and fancy pods separated out of farmer stock grade samples using a colorimeter acquired with support from the Virginia-Carolina Peanut Association, the area shellers' organization.

We have also made an effort to select more lines with a jumbo-to-fancy ratio closer to the long-time industry standard Florigiant which has a ratio of about 1:1 averaged over years. We do also retain PYT entries that have a high ratio of jumbo to fancy pods (greater than 2) provided the jumbo pods are sufficiently shapely and bright. After starting our emphasis on high fancy pod content, we retained these "jumbo" lines hoping that they might fit into the boiling peanut market niche where very large pods and seeds are preferred. We conducted a separate Jumbo Advanced Test (JAT) conducted at only two locations, PBRS and UCPRS. However, with abandonment of the quota production system in the federal farm program, there is more of a domestic market for these large-podded lines, and we have discontinued the JAT.

After two years in the AYT, a line is eligible for entry in the Peanut Variety and Quality Evaluation (PVQE) program's small-plot trials. The program is jointly funded by the Virginia Agricultural Experiment Station, the North Carolina Agricultural Research Service, and grower and sheller organizations and is coordinated by Dr. Maria Balota of the Virginia Polytechnic Institute and State University's (VPI&SU's) Tidewater Agricultural Research and Extension Center (TAREC) in Suffolk, VA. In 2016, PVQE trials are grown at one location in Virginia (TAREC in the City of Suffolk), three in North Carolina (Martin, Edgecombe and Bladen Counties), and one in South Carolina (Clemson University's Edisto Agricultural Research and Education Center at Blackville, SC). There are two separate replicated trials at Suffolk and two at Martin Co., planted at the same time but harvested at two-week intervals 135 to 155 days after planting (DAP). At the other three sites there is one trial dug at an intermediate date. After two or more years in the small-plot test, a line is eligible for entry in the large-plot phase of the PVQE program: 0.5 A of the line is grown in alternating strips with a similar check cultivar at two sites, yield and grade are measured, then the harvested pods are subjected to extensive quality evaluation by area shellers and processors. Because the Virginia variety selection program also uses "slots" in the large-plot test, lines from the two states usually are entered in alternating years. In 2016, there is no large-plot test.

Concurrently with a third or greater year of testing in the PVQE program, our most advanced lines may be entered in the Uniform Peanut Performance Test (UPPT), the national cooperative test of runner- and virginia-type breeding lines. The UPPT is grown at nine sites in eight states and is coordinated by Dr. William D. Branch of the University of Georgia's Coastal Plain Experiment Station. NCSU's UPPT test is grown each year at PBRS with three reps dug near October 1 (145 to 155 DAP) and three reps dug approximately 10 to 14 days later to allow late-maturing lines from the Florida and Georgia programs to mature more fully. Each year, breeding programs are permitted to submit up to three "official" or "common" entries in the UPPT. Additional lines called "local options" may be included in a particular state's UPPT, but only official entries are grown at all locations. Beginning with the 2000 season, a composite pod sample from each UPPT entry was sent to Dr. Marshall Lamb at the USDA-ARS National Peanut Research Laboratory at Dawson, GA, for analysis of physical properties including size distribution and bulk density of pods and seeds. Beginning in 2001, ELK, jumbo runner, and/or medium kernels from the samples processed at Dawson were forwarded to Dr. Timothy H. Sanders (now to Dr. Lisa Oehrl Dean) of the USDA-ARS Market Quality and Handling Research Unit at Raleigh, NC, for evaluation of composition and sensory quality. Quality evaluation of Georgia lines was discontinued in the 2014 season due to a dispute between the University of Georgia and USDA-ARS over ownership of data generated in the program. Prior to the 2001 season, the NCSU program did not include local options in the UPPT, but with the advent of extensive quality testing of UPPT samples, we have been including as local options any lines that were entered in the PVQE trials for a second or greater year, sometimes all PVQE entries if there were enough "slots" available.

Each time a line is promoted to the next level in the testing program, it is retained in all previous test levels except the Preliminary Yield Test. High-yielding lines with acceptable grade identified in disease resistance or other subprograms can be entered in the Advanced Yield Test whether or not they possess the special characteristic for which they were initially tested. A release decision usually is made following the third year of PVQE small-plot evaluation. If a line is released, it is included in the AYT and PVQE as a check in subsequent years.

The seed multiplication phase of the program is designed to provide sufficient seed for the maximum possible need in the following season: single 0.003 A plots (two 24-ft rows at 36-in row spacing) for use strictly within the NCSU program, 0.02 A plots (six standard plots laid end to end) when the line might be entered in the PVQE small-plot trials the

following year, a 0.05 to 0.10 A increase when the line may be tested in the PVQE large-plot phase of the PVQE trials or the UPPT, and a seed “purification” (bulk harvest of individual plant progenies conforming to a standard for that line) concurrently with the third year of small-plot PVQE testing. Seed increase plots are rogued to eliminate off-types at least once during the growing season, and seed is examined for uniformity prior to planting the following season.

Tests in the cultivar development stream in 2016 are listed below:

**Advanced Yield Test (AYT):** a replicated ( $r=2$ ) test of 77 advanced breeding lines from the NCSU breeding program, 1 species-derived line from Dr. H. Thomas Stalker, and 5 virginia-type and 7 runner-type checks arranged in 10x9 double rectangular lattice designs in PBRs Field D2, UCPRS Field F1, and BBTRS Field B. Entries include lines selected from the main cultivar development stream, disease-resistant lines, and lines with high contents of jumbo pods and super-extra-large kernels. All of the NCSU experimental lines carry the Univ. of Florida high oleic acid trait. Seed of all 77 breeding lines in this test is increased in the **Small Plot Increase (SPI)** in PBRs Field C6; seed of 39 lines entered for a second or greater year is increased in the **Large-Plot Increase (LPI)** in PBRs Field D2; seed of 9 lines that are candidates for entry in a cooperative large-plot test in 2017 is increased in the **Big-Ass Nursery (BAN)** in PBRs Field D6.

**Disease-Resistant Line Preliminary Test (DPT):** a replicated ( $r=2$ ) test of 41  $F_{6,8}$  families, 4 checks, and 4 advanced breeding lines in 7x7 simple square lattice designs in PBRs Field D2 and UCPRS Field F1. The 41  $F_6$ -derived families represent 10 crosses, 10  $F_1$ -derived families, each from a different cross, 10  $F_2$ -derived families, 13  $F_3$ - and  $F_4$ -derived families, and 41  $F_5$ -derived families from the 6x6 **Disease-Resistant-by-High-Oleic-Line Factorial (DHOL)** mating made in 2012 of 6 high-oleic “agronomic” lines (including the line later released as Emery) crossed with 6 disease-resistant lines (three of which were the  $BC_3F_4$ -derived families that became high-oleic Bailey lines N12007ol, N12008olCLSMT, and N12010ol). The families are simultaneously tested for disease reactions in the **Disease Selection Test, Leaf Spot** in PBRs Field C6, **Disease Selection Test, CBR** in UCPRS Field D1, **Disease Selection Test, Sclerotinia Blight** in UCPRS Field C2, and **Disease Selection Test, TSWV** in PBRs Field C7. Seed of the families is increased in the **Disease-Resistant Preliminary Line Nursery (DPN)** in PBRs Field C6.

**Early Maturity Advanced Test, Early and Late Diggings (EAE and EAL):** a replicated test of 13 breeding lines and 7 checks in PBRs Field D2 (early and late diggings with  $r=3$ ) and UCPRS Field F1 (early and late diggings with  $r=3$ ), each test arranged in a 5x4 triple rectangular lattice design. Seven experimental lines have normal “tan” pods while six are “black-podded,” that is, possessing the gene for the trait that causes the exocarp of an individual pod to darken as it reaches physiological maturity, much as the mesocarps of pods darken in “normal” tan-podded lines. All tan-podded lines carry the Florida high oleic acid trait. The six black-podded lines are normal-oleic. All experimental lines have been tested previously in the EAE and EAL. This test is to evaluate maturity, yield and grade for lines descended from early maturing parents. The early plots will be dug at 125 to 135 days after planting (DAP) and the late plots dug at 145 to 155 DAP. Pod blasting will be used to assess the maturity of the lines. Seed of the high-oleic breeding lines is increased in the **Large-Plot Increase (LPI)** in PBRs Field D2; seed of the normal-oleic lines is increased in the **Breeder Seed Increase** in PBRs Field D2.

**Preliminary Yield Test (PYT):** a partially replicated test ( $r=1$  or  $r=8$ ) of 214 experimental  $F_{6,8}$  or  $BC_1F_{6,8}$  families and five checks arranged in eight 6x5 double rectangular lattice designs with Rep 1 in PBRs Field D2 and Rep 2 in UCPRS Field F1. The 214 families represent 39 crosses, 67  $F_1$ - or  $BC_1F_1$ -derived families, 83  $F_2$ - or  $BC_1F_2$ -derived families, 118  $F_3$ - or  $BC_1F_3$ -derived families, 134  $F_4$ - or  $BC_1F_4$ -derived families, and 187  $F_5$ - or  $BC_1F_5$ -derived families. The 214 families (plus two “fillers” N11020olJ and N11028ol) were divided into eight sets of 27, each set tested with the same set of three checks (Bailey, Sullivan, and Emery). Experimental lines are replicated only across locations while each check has eight replicate plots at each test site. All experimental lines are high oleic. Seed of the 214 lines is increased in the **Preliminary Yield Line Nursery (PYN)** in PBRs Field C4b.

**Uniform Peanut Performance Test (UPT):** a replicated ( $r=6$ , three dug 145-155 DAP, three dug 7 to 14 days later) test of 30 advanced breeding lines and checks arranged in a 6x5 triple rectangular lattice design in PBRs Field D2. Reps 1 (dug early) and 2 (dug late) are in Arrangement 1, Reps 3 and 4 in Arrangement 1, and Reps 5 and 6 in Arrangement 3. This test is grown cooperatively at nine locations in eight states and is coordinated by Dr. William D. Branch of the University of Georgia’s Coastal Plain Experiment Station. The cooperative test includes 16 “official” or “common” entries of which two are the checks Georgia-06G and Bailey. These 16 lines are grown at all locations. All of the 14 experimental breeding lines originated at state and federal breeding programs in other states; three NCSU lines (high-oleic Bailey backcross derivative lines N12008olCLSMT, N12009olCLT, and N12010ol) are included as official UPPT entries that are grown by test participants in other states. The balance of the 30 entries grown at PBRs are 14 “local options” grown at the PBRs location only, including 12 high-oleic NCSU lines, virginia-type line ARSOK-V85-7 from the USDA-ARS program at Stillwater, OK, and runner-type line AU/NPRL-14-29 from the state program at Auburn Univ. in Alabama.

**TESTING FOR DROUGHT TOLERANCE.** Drought is a common constraint to yield and quality in the Virginia-Carolina peanut production area where only about 15% of the acreage is irrigated, leaving the rest of the area rainfed and subject to drought if the rain expected during the growing season fails to fall. Large-seeded peanuts are more subject to drought

stress than are smaller-seeded types because the subterranean pod acts as a water-absorbing organ. Demand for water and calcium from the soil solution are functions of pod volume while the ability of the pod to absorb moisture is a function of pod surface area. Large pods have a smaller surface-to-volume ratio than small pods. Drought tolerance is difficult to measure. In fact, there is not universal agreement among crop physiologists how best to do it. There are two drought physiologists working on peanut in this area: Dr. Thomas R. Sinclair in the Department of Crop and Soil Sciences at NCSU and Dr. Maria Balota at VPI&SU's Tidewater Agricultural Research and Extension Center in Suffolk, VA. These two scientists do not agree as to the best method to use in assessing drought reaction. We provide seed to our collaborator Dr. Balota, and participate more actively with Dr. Sinclair. Drought tolerance experiments in the field in 2016 include:

**Sinclair Drought Resistance Test (SDT):** a replicated ( $r=4$ ) test of 9 entries for their wilting reactions on drought-prone soil, grown in PBRS Field A2 and at the Tidewater AREC in Suffolk, VA, under rain-out shelters. The first six entries are  $F_{4:7}$  families derived from the cross between large-seeded virginia-type NCSU breeding line N08086oJCT, a sister line of the 'Wynne' cultivar, and drought-resistant Spanish-type line ICGV 86015 (PI 505005) from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), an institute of the Consultative Group for International Agricultural Research (CGIAR). The last three lines are advanced NCSU breeding lines N12006oI, N13042oI, and N13045oL. These are lines previously tested by Dr. Avat Shekoofa, a post-doctoral research fellow in Dr. Sinclair's laboratory, for wilting under increasing water stress in a greenhouse assay or for reaction to inhibition of water movement within cells when treated with silver ions. These lines will be subjected to drought stress during the season by withholding irrigation, and ratings of plant wilt, measurements of canopy temperature, and other physiological measures will be made to assess their tolerance. Dr. Balota will use spectral imaging from her UAV platform to try to relate rapidly obtained imagery with more laborious conventional measures of drought tolerance. Seed of all these lines is increased in the **Sinclair Drought-Resistant Line Nursery (SDN)** in PBRS Field D8.

**Sinclair Drought Resistance Resistance Test, Outside Shelters (SDO):** a replicated ( $r=4$ ) test of 8 entries for their wilting reactions on drought-prone soil, grown in PBRS Field A2, on deep sandy soil (Candor series) at the Sandhills Research Station (SRS) at Jackson Springs, in Moore Co., NC, and at the Tidewater AREC in Suffolk, VA, outside of the rain-out shelters. The entries are all advanced NCSU breeding lines including the same three that are included in the **Sinclair Drought Resistance Resistance Test (SDT)** (N12006oI, N13042oI, and N13045oL). The other five entries are: N04074FCT, N05006 (currently proposed for release by VPI&SU as ' '), N13047oIJ, N13048+oI, and N13059oI. These are lines previously tested by Dr. Avat Shekoofa, a post-doctoral research fellow in Dr. Sinclair's laboratory, for wilting under increasing water stress in a greenhouse assay or for reaction to inhibition of water movement within cells when treated with silver ions. These lines will be subjected to drought stress during the season by withholding irrigation, and ratings of plant wilt, measurements of canopy temperature, and other physiological measures will be made to assess their tolerance. Dr. Balota will use spectral imaging from her UAV platform to try to relate rapidly obtained imagery with more laborious conventional measures of drought tolerance. Seed of these lines is increased in the **Sinclair Drought-Resistant Line Nursery (SDN)** in PBRS Field D8 or in the **Breeder Seed Increase (BSI)** in PBRS Field D2.

**SELECTION NURSERIES.** Our primary breeding method in elite-by-elite populations is straight pedigree method in which we make single-plant selections in the  $F_2$  through  $F_6$  generations, growing one generation per year at PBRS and planting the progeny of each selected plant in the next year's selection nursery. However, we do incorporate populations into the cultivar development stream that originated in other subprograms such as multiple disease resistance breeding. Single-seed descent in odd-numbered segregating generations ( $F_3$  and  $F_5$ ) is a common feature of those populations. We do grow the  $F_1$  hybrids of almost all crosses at the winter nursery in order to "save" at least one year in North Carolina. Selection nurseries in the field at PBRS in 2016 include:

**$F_2$  Selection Nursery (F2N):** a selection nursery of 127 plots in PBRS Field C6. The 127  $BC_1F_2$  plots derive from 55 crosses made in the  $9 \times 6$  **Disease-Resistant-by-High-Oleic Backcross** crossing program made in the summer of 2015. In the original factorial mating, we used agronomically superior high oleic lines (N12007oI, N12010oI, N13047oIJ, N13048+oI, N13052oIL, N13057oIL, N14046oIT, and N14049oILSmT) and Sclerotinia blight-resistant plant introduction PI 497429 as females and disease-resistant line (N14039oILSmT, N14040oILSmT, N14043oILSmT, 14 DPT 010 [now N15063oILSm], 14 DPT 013 [now N15066oILSmT], and 14 DPT 015 [now N15068oILSmT]) as males in the winter of 2014-2015. The  $F_1$  hybrids were crossed back to the agronomically superior parent in the summer of 2015. We will make individual plant selections within the populations, then send selected  $BC_1F_{2:3}$  families carrying the high-oleic gene to the winter nursery in Juana Diaz, PR (the "PRWN") as part of our program of accelerated breeding for multiple disease resistance. They will be tested as  $BC_1F_{2:4}$  families as part of the 2017 **Disease Selection Test (DST)** series.  $F_{2:3}$  families from plants whose progenies are not selected for the 2016-2017 PRWN will be planted in the 2017  **$F_{2:3}$  Selection Nursery (F3N)**.

**$F_{2:3}$  Selection Nursery (F3N):** a selection nursery of 164  $F_{2:3}$  plots in PBRS Field C6. The 164  $F_2$ -derived families represent 84 crosses and 135  $F_1$ -derived families. The first 111  $BC_1F_{2:3}$  plots derive from the  $10 \times 5$  **Disease-Resistant-by-High-Oleic Backcross** crossing program made in the summer of 2014 (disease-resistant parents N12006oI, N12007oI,

N12009oLCLT, N12010oL, N12014oL, 13 DPT 023 [now N14035oLSmT], 13 DPT 029 [now N14037oLSmT], 13 DPT 034 [now N14039oLSmT], 13 DPT 066 [now N14049oLSmT], and species-derived line SPT 13-05oL used as females and agronomically superior high-oleic lines N11019oLJ, N13041oLJ, N13045oL, N13055oL, and N13056oLSm used as males in the initial factorial mating in the winter, the  $F_1$  hybrids crossed back to the agronomically superior parent in the summer). These are the progenies of  $F_2$  plant selections that were not sent to the winter nursery. Another 53 31  $F_{2:3}$  families represent 11 crosses from the four-parent (N11020oLJ, N11051oLJ, N09042oLF, and Emery) **High Value Diallel** crossing program made in 2014. We will make individual plant selections within the populations,  $F_{3:4}$  or  $BC_1F_{3:4}$  families carrying the high-oleic gene will be grown at PBRS in 2017 in the  $F_{3:4}$  Selection Nursery (F4N). We will make individual plant selections within the populations, then send selected  $BC_1F_{4:5}$  families carrying the high-oleic gene to the winter nursery as part of our program of accelerated breeding for multiple disease resistance. They will be tested as  $BC_1F_{4:6}$  families as part of the 2017 **Disease Selection Test (DST)** series.

**$F_{2:3}$  Oil Content Selection Nursery (F3O):** a selection nursery of 12  $F_{2:3}$  plots in PBRS Field C6. The 12  $F_2$ -derived families represent 8 crosses and 11  $F_1$ -derived families. These families derive from a factorial mating of five families selected for small seed size and high oil content and three high-oleic parents with relatively high oil content selected from the testing program (N13031oLL, N13032oLL, and SPT 10-14oL).  $F_{2:3}$  progenies from small-seeded  $F_2$  plant selections were assessed using nuclear magnetic resonance for oil content, and only those that combined small seeds with high oil were planted for further selection.

**$F_{2:4}$  Selection Nursery, Accelerated (F4A):** a selection nursery of 98 plots in PBRS Field C6. The  $BC_1F_{2:4}$  families represent 55 crosses, 85  $BC_1F_1$ -derived families, and 98  $BC_1F_{2:3}$ -derived families. These crosses were made as part of the 10x5 **Disease-Resistant-by-High-Oleic Backcross** crossing program made in the summer of 2014 (disease-resistant parents N12006oL, N12007oL, N12009oLCLT, N12010oL, N12014oL, 13 DPT 023 [now N14035oLSmT], 13 DPT 029 [now N14037oLSmT], 13 DPT 034 [now N14039oLSmT], 13 DPT 066 [now N14049oLSmT], and species-derived line SPT 13-05oL used as females and agronomically superior high-oleic lines N11019oLJ, N13041oLJ, N13045oL, N13055oL, and N13056oLSm used as males in the initial factorial mating in the winter, the  $F_1$  hybrids crossed back to the agronomically superior parent in the summer). These are the progenies of  $F_2$  plant selections that were sent to the winter nursery.

**$F_{3:4}$  Selection Nursery (F4N):** a selection nursery of 30 plots in PBRS Field C5b. The 30  $F_3$ -derived Families trace to 10 crosses and 17  $F_2$ -derived families. Sixteen of the families are derived from the **Runner-by-Virginia Factorial** mating made in 2013 (Georgia-06G, Georgia Greener, Tifguard, and Georgia-07W as females; N08069oLJCT, Sullivan, Emery, N10061oLFCLSm, N10066oLSmT, N11021oLSrT, N11038oLSrT, N12003oLCSmT, N12008oLCLSmT, N12009oLCLT, N07018JCSm, and N07019JCSm as males), the objective being to find virginia-type progeny with the flat “runner” growth habit typical of runner-type cultivars. The rest of the  $F_{3:4}$  families were selected from crosses involving species-derived parents. These families will be subjected to single-plant selection in October.  $F_{4:5}$  progenies of selected  $F_{3:4}$  plants will be planted in the 2017  **$F_{4:5}$  Selection Nursery (F5N)**.

**$F_{4:5}$  Selection Nursery (F5N):** a selection nursery of 238 plots in PBRS Field C6. The 238  $F_4$ -derived families represent 86 crosses, 109  $F_1$ -derived, 163  $F_2$ -derived, and 211  $F_3$ -derived families. The first 77 families derive from a 6x6 **Disease-Resistant-by-High-Oleic Backcross** mating made in 2012 using six (high-oleic NCSU breeding lines N09037oL, N09039oLF, N09042oLF, Emery, N10047oL, and N10053oL used as females; disease resistant lines N12007oL, N12008oLCLSmT, N12010oL, CRSP 1050-110, N10061oLFCLSm, and N11035oLSrT used as males in the initial factorial mating in the winter; the  $F_1$  hybrids then crossed back to the agronomically superior parent). Another 161 families trace to the 2013 10x6 **Disease-Resistant-by-High-Oleic Factorial** (disease-resistant parents N08069oLJCT, Sullivan, Emery, N10061oLFCLSm, N10066oLSmT, N11021oLSrT, N11038oLSrT, N12003oLCSmT, N12008oLCLSmT and N12009oLCLT used as females; six high-oleic breeding lines N10043oLJ, Emery, N11020oLJ, N11043oL, N11045oL, and black-podded line N11054B used as males in the winter). Because that year’s summer crossing program failed,  $F_2$  seeds from the  $F_1$  plants produced in the 2013 winter greenhouse and used as males in the summer backcrossing program were sent to Puerto Rico where individual  $F_2$  plants were harvested and their progenies planted in the field in 2014. We will make individual plant selections within the populations, then selected  $F_{5:6}$  families carrying the high-oleic gene will be grown in the 2017  **$F_{5:6}$  Selection Nursery (F6N)**.

**$F_{4:6}$  Selection Nursery, Accelerated Program (F6A):** a selection nursery of 65 plots in PBRS Field C6. The 65  $F_{4:6}$  families represent 19 crosses, 20  $F_1$ -derived, 25  $F_2$ -derived, and 25  $F_4$ -derived families. The populations derive from the 2013 10x6 **Disease-Resistant-by-High-Oleic Factorial** (disease-resistant parents N08069oLJCT, Sullivan, Emery, N10061oLFCLSm, N10066oLSmT, N11021oLSrT, N11038oLSrT, N12003oLCSmT, N12008oLCLSmT and N12009oLCLT used as females; six high-oleic breeding lines N10043oLJ, Emery, N11020oLJ, N11043oL, N11045oL, and black-podded line N11054B used as males in the winter). Because that year’s summer crossing program failed,  $F_2$  seeds from the  $F_1$  plants produced in the 2013 winter greenhouse and used as males in the summer backcrossing program were sent to Puerto Rico where individual  $F_2$  plants were harvested and their progenies planted in the field in 2014. Because of the failure of the summer crossing program, these are actually  $F_{5:7}$  families, but to keep the nomenclature of the program consistent across years, we are calling them “ $F_{4:6}$ .” These are the families being tested in the **Disease Selection Test (DST)** series. Five seeds from each  $F_{3:4}$  selection were individually assayed for fatty acid profile, and only the families that were uniformly high-oleic

or that were segregating for the high-oleic trait were retained. Single-plant selections will be made at harvest with special attention paid to those families that exhibited resistance to two or more diseases based on data from the DST series. Selections will be made from all families, and those from families found to possess multiple disease resistance will be sent to the PRWN for increase and further selection in the multiple disease resistance program. Surviving families will be tested for disease resistance as  $F_{6,8}$  families in the 2017 **Disease Selection Test (DST)** series, for yield and grade as 2017  $F_{6,8}$  families in the **Disease Preliminary Test (DPT)**, and as advanced disease-resistant lines in the 2018 **Disease Advanced Tests (DAT)** and high-yielding lines in the 2018 **Advanced Yield Test (AYT)**. Progeny of selections from  $F_{4,6}$  families not identified as having multiple disease resistance will be grown for further among-family selection in the 2017  **$F_{6,7}$  Selection Nursery (F7N)**.

**$F_{5,6}$  Selection Nursery, Insect Resistance (F6I):** a selection nursery of 86 plots grown in PBRS Field C7 without any application of insecticides. The 86  $F_5$ -derived families represent 30 crosses, 42  $F_1$ -derived, 44  $F_2$ -derived, 58  $F_3$ -derived families, and 75  $F_4$ -derived families. The crosses were made as part of the 2010 **Insect Resistance Topcross** using eight insect-resistant lines (NC Ac 02214, NC Ac 02232, NC Ac 00343, NC Ac 10247, NC Ac 10272, NC Ac 15729, NC Ac 15745, and PI 121067) as females and two high-yielding high-oleic lines N08070oIJC and N08083oIJCT as males. Single-plant selections will be made for pod characteristics including freedom from damage by pod-feeding insects at harvest. Selections will be grown without insect control in the 2017  **$F_{6,7}$  Selection Nursery, Insect Resistance (F7I)**.

**$F_{5,6}$  Selection Nursery (F6N):** a selection nursery of 424 plots in PBRS Field C6. The 424  $F_5$ -derived families represent 103 crosses, 156  $F_1$ -derived, 200  $F_2$ -derived, 256  $F_3$ -derived families, 331  $F_4$ -derived families, and 424  $F_5$ -derived families. The first 223 families derived from 2011's 5x11 **Disease-Resistant-by-High-Oleic Backcross** (agronomically superior lines N08070oIJC, Wynne, N08082oIJCT, N09049oIC, and N09053oICSm used as females; ten progenies of  $F_2$  plant selections thought to be sources of superior disease resistance [X08051 (F1-01-01: F04), N08059oIFCT / N06056LT; X08051 (F1-01-03: F04), N08059oIFCT / N06056LT; X08054 (F1-01-02: F04), N08059oIFCT / SPT 06-06; X08054 (F1-02-02: F04), N08059oIFCT / SPT 06-06; X08054 (F1-03-01: F04), N08059oIFCT / SPT 06-06; X08055 (F1-02-01: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-02: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-04: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-05: F04), N08059oIFCT / SPT 06-07; and X08055 (F1-04-04: F04), N08059oIFCT / SPT 06-07] used as males in the winter; the  $F_1$  hybrid backcrossed to the agronomically superior parent in the summer). They contain either species-derived germplasm or a *hirsuta*-type ancestor. Another 79 families derive from 2012's 6x6 **Disease-Resistant-by-High-Oleic Backcross** mating (high-oleic NCSU breeding lines N09037oI, N09039oIF, N09042oIF, Emery, N10047oI, and N10053oI used as females; disease resistant lines N12007oI, N12008oICLSmT, N12010oI, CRSP 1050-110, N10061oIFCLSm, and N11035oISrT used as males in the initial factorial mating in the winter; the  $F_1$  hybrids then crossed back to the agronomically superior parent). Another 122  $F_{5,6}$  families derive from 2013's 10x6 **Disease-Resistant-by-High-Oleic Factorial** (disease-resistant parents N08069oIJCT, Sullivan, Emery, N10061oIFCLSm, N10066oISmT, N11021oISrT, N11038oISrT, N12003oICSmT, N12008oICLSmT and N12009oICLT used as females; six high-oleic breeding lines N10043oIJ, Emery, N11020oIJ, N11043oI, N11045oI, and black-podded line N11054B used as males in the winter). Because that year's summer crossing program failed,  $F_2$  seeds from the  $F_1$  plants produced in the 2013 winter greenhouse and used as males in the summer backcrossing program were sent to Puerto Rico where individual  $F_2$  plants were harvested and their progenies planted in the field in 2014. These populations will be subjected to single-plant selection.  $F_{6,7}$  families from the will be grown in the 2017  **$F_{6,7}$  Selection Nursery (F7N)** for among-family selection.

**$F_{6,7}$  Selection Nursery (F7N):** an among-family selection nursery of 399 plots in PBRS Field C6. The 399  $F_6$ - and  $BC_1F_6$ -derived families represent 114 crosses, 184  $F_1$ - and  $BC_1F_1$ -derived, 207  $F_2$ - and  $BC_1F_2$ -derived, 211  $F_3$ - and  $BC_1F_3$ -derived families, and 330  $F_4$ - and  $BC_1F_4$ -derived families. The first 188 families derived from 2010's **Elite Line Diallel** mating among nine elite lines (N08070oIJC, Wynne, N09024oIJ, N09037oI, N09053oICSm, N10066oISmT, N10078oIJC, N10080oIJCL, and Sugg). An additional 120 families derive from 2011's 5x11 **Disease-Resistant-by-High-Oleic Backcross** (agronomically superior lines N08070oIJC, Wynne, N08082oIJCT, N09049oIC, and N09053oICSm used as females; ten progenies of  $F_2$  plant selections thought to be sources of superior disease resistance [X08051 (F1-01-01: F04), N08059oIFCT / N06056LT; X08051 (F1-01-03: F04), N08059oIFCT / N06056LT; X08054 (F1-01-02: F04), N08059oIFCT / SPT 06-06; X08054 (F1-02-02: F04), N08059oIFCT / SPT 06-06; X08054 (F1-03-01: F04), N08059oIFCT / SPT 06-06; X08055 (F1-02-01: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-02: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-04: F04), N08059oIFCT / SPT 06-07; X08055 (F1-03-05: F04), N08059oIFCT / SPT 06-07; and X08055 (F1-04-04: F04), N08059oIFCT / SPT 06-07] used as males in the winter; the  $F_1$  hybrid backcrossed to the agronomically superior parent in the summer). They contain either species-derived germplasm or a *hirsuta*-type ancestor. Another 91 families derive from 2012's 6x6 **Disease-Resistant-by-High-Oleic Backcross** mating (high-oleic NCSU breeding lines N09037oI, N09039oIF, N09042oIF, Emery, N10047oI, and N10053oI used as females; disease resistant lines N12007oI, N12008oICLSmT, N12010oI, CRSP 1050-110, N10061oIFCLSm, and N11035oISrT used as males in the initial factorial mating in the winter; the  $F_1$  hybrids then crossed back to the agronomically superior parent). These populations will be dug on or near October 1 and subjected to visual selection among families after having had a chance to dry. Selected families will be tested in the 2017 **Preliminary Yield Test (PYT)** at PBRS and UCPRS.

**RECOMBINANT INBRED LINE (RIL) DEVELOPMENT.** Most economically important traits in peanut exhibit continuous variation and are subject to genotype-by-environment interaction. In order to obtain accurate and precise estimates of phenotypic value to use in identifying quantitative trait loci (QTLs), it is necessary to replicate genotypes within and across macro-environments (year-by-location combinations). Peanut is not readily amenable to cloning, so inbred families must be used to achieve that desired replication. We attempt to develop 200 to 400 RILs per cross, so it is important to initiate only those populations that might be valuable; otherwise the cost of developing and maintaining the populations is prohibitively high. Because we have observed segregation distortion in RILs developed using single-seed descent, we attempt to reduce the potential frequency-shifting effect of natural selection within populations by employing “small bulk population” breeding from the  $F_{2:3}$  generation on. We harvest individual  $F_2$  plants and plant  $F_{2:3}$  progenies the following generation. Although there may be some natural selection within the plot, in general there will be some surviving plants for each  $F_{2:3}$  progeny. We harvest (without intentional selection) a group of plants from the  $F_{2:3}$  plot and shell enough seed to plant an  $F_{2:4}$  plot the next generation. We continue this process up to the  $F_{2:6}$  at which point we harvest a single plant to represent that  $F_2$ -derived family. The separate progeny of the  $F_6$  plants are our RILs. They can be genotyped and increased as genetically stable inbred families to allow planting of replicated plots.

**F<sub>5:6</sub> Drought-Resistance RIL Development Nursery (F5D):** a RIL-development nursery in PBRS Field B5 of 340 one-row, 14-foot plots representing replicate crosses of high-oleic Bailey derivative N08086oJCT with ICGV 86015 (PI 585005), a drought-resistant spanish-type parent from ICRISAT. A single  $F_6$  plant (sufficient to provide seed for a small plot the following year) will be harvested from each plot in the fall of 2016 and  $F_{6:7}$  families will be planted at PBRS in 2017. The objective of this population is to develop recombinant inbred lines for drought studies.

**RECURRENT SELECTION PROGRAMS.** Recurrent selection is designed to increase the frequency of desirable alleles in a closed population, increasing the frequency of desirable homozygous lines obtained when the population is selfed to a high level of inbreeding. There were two long-standing recurrent selection programs within the NCSU peanut breeding program: one based on an interspecific cross and the other on elite germplasm.

**The *Arachis cardenasii* Recurrent Selection (ACRS)** program was initiated in 1975 with 10 large-seeded tetraploid lines derived from a cross between diploid ( $2n=2x=20$ ) *A. cardenasii* GKP 10017 (PI 262141) and tetraploid ( $2n=4x=40$ ) purple-seeded valencia-type *A. hypogaea* subsp. *fastigiata* var. *fastigiata* PI 262942. The initial interspecific cross was made in 1963. Following colchicine-induced chromosome doubling in the sterile triploid ( $3x=30$ ) hybrid, the fertile hexaploid ( $2n=6x=60$ ) produced seed. Several generations later, descendants of the hexaploid had spontaneously lost chromosomes, reverting to the tetraploid level. Dr. Johnny Wynne chose ten lines that had large virginia-type pods and seeds, intermated them in 45 pairwise combinations, grew the  $S_0$  ( $F_1$ ) generation of the crosses at the Puerto Rico winter nursery, then yield-tested the  $S_{0:1}$  ( $F_{1:2}$ ) progenies of the crosses in replicated trials. The highest yielding ten crosses were identified, and remnant  $S_1$  seed of the selected crosses were planted for use as parents for the second cycle of recurrent selection. The ACRS program is currently in its eleventh cycle with  $C_{11}$  crosses having been made in the greenhouse in 2008.

**The Elite Germplasm Recurrent Selection (EGRS)** program was based on 40 cultivars, elite virginia-type breeding lines, and high-yielding plant introductions. The 40 parents were intermated in a partial diallel cross in 1975, each parent being used five times for a total of 100 crosses. The  $S_0$  generation was grown at the PRWN, the  $S_1$  at PBRS the following summer when a single  $S_1$  plant representing the cross was selected for seed increase at the PRWN the following winter. The  $S_{1:3}$  families were yield-tested, the highest yielding 40 identified, and the next cycle initiated by intermating remnant seed of the 40 selected  $S_{1:3}$  families. The EGRS program is currently in its ninth cycle with  $C_9$  crosses having been made in the greenhouse in 2008. NC-V 11, a widely grown cultivar in the Virginia-Carolina production area, was selected from the first cycle of the EGRS program, but no cultivar has been released from later cycles.

We replicated the yield test for each cycle of the ACRS and EGRS programs at two sites if seed supply was adequate, using completely random designs with unequal replication at each site. The families used as parents for the next cycle of each recurrent selection program were subjected to further inbreeding and single-plant selection to develop true-breeding lines that were fed into the cultivar development stream. Neither the ACRS nor the EGRS population included the high-oleic trait, a trait that is required for future releases. Therefore, the recurrent selection populations must be viewed as a genetic resource separate from the cultivar development stream unless an effort is made to backcross the high-oleic trait into each parent before continuing with additional cycles. There are no recurrent selection nurseries in the field at PBRS in 2016.

**BREEDING FOR DISEASE AND ARTHROPOD PEST RESISTANCE.** The array of economically important diseases and pests in the Virginia-Carolina production area is constantly changing. New problems appear from time to time, and old problems vary in importance from year to year depending on the weather or on changes in cultural practices that affect the interaction between host and pathogen or pest. At present, there are four diseases that have sufficiently large and consistent impact on producers to warrant effort in breeding for resistance: leaf spots caused by *Cercospora arachidicola*

and *Cercosporidium personatum*, Cylindrocladium black rot (CBR) caused by *Cylindrocladium parasiticum*, Sclerotinia blight (SB) caused by *Sclerotinia minor*, and tomato spotted wilt (TSW) caused by *Tomato spotted wilt tospovirus*. Other diseases of sporadic importance include web blotch caused by *Phoma arachidola*, southern stem rot caused by *Sclerotium rolfsii*, pod rots caused by *Pythium myriotylum*, *Rhizoctonia solani*, and *Fusarium* spp., and collar rot caused by *Lasiodiplodia theobromae*.

**LEAF SPOTS.** We have had a long-standing program of breeding for resistance to leaf spots, initiated before there were effective chemical controls. Even though excellent control usually is easy to achieve with modern fungicides, the expense of control has become more of an issue with the change in the farm program. When Hurricane Floyd flooded peanut fields in eastern counties in 1999, many growers were reminded that chemical control cannot always be applied, especially when saturated soils make it impossible for growers to enter the fields for the last one or two sprays needed to maintain control. The end of the quota system and the concomitant artificially high federal support price has made the relatively modest cost of leaf spot control more of an economic issue to growers. There has been renewed grower interest in our leaf spot resistance program since those two events. Most of the resistance in our program traces to PI 121067 through its descendant GP-NC 343. Recently, we have incorporated resistance derived from *A. cardenasii* GKP 10017 through tetraploid lines developed by Dr. H. Thomas Stalker, and from PI 203396 through lines provided by Dr. Daniel W. Gorbet of the Univ. of Florida. Preliminary leaf spot lines are tested for defoliation in short (12 ft) one- or two-row plots in replicated tests grown without chemical control of leafspot. Defoliation is rated late in the season on a proportional scale of 1 (no defoliation) to 9 (complete defoliation). Advanced lines are grown in our standard 24-ft two-row plots in replicated trials, two reps grown without chemical leafspot control and two adjacent reps grown with control. Defoliation ratings are made prior to harvest, then yield and full grade data are recorded. Dr. Shyamalrau P. Tallury (now Dr. Stalker since Dr. Tallury's departure) enters his species-derived advanced lines in these tests to obtain yield and grade data. Any line that has been retained for a second or greater year of testing for yield or some other disease resistance is entered in a separate leaf spot test in which defoliation and yield data are recorded. Leaf spot tests grown in 2016 are listed below:

**Advanced Line Disease Test, Leafspot (ALL):** a replicated ( $r=2$ ) test of 52 advanced breeding lines from the breeding program, 8 virginia- and runner-type cultivars, and 4 checks arranged in a 8x8 simple square lattice design without chemical control of leaf spot in PBRs Field D8. The lines are entered for a second or greater year in advanced tests for some purpose other than leaf spot resistance. Defoliation will be scored late in the season, and only yield will be measured at harvest. Grades are measured for these lines in tests grown with chemical control of leaf spots. This test is part of the **Advanced Line Disease Test** series, our program of monitoring disease reactions of all advanced lines that includes the **Advanced Line Disease Test, CBR (ALC)**, the **Advanced Line Disease Test, Sclerotinia minor (ALS)**, and the **Advanced Line Disease Advanced Test, TSWV (ALT)**.

**Disease Selection Test, Leafspot (DSL):** a replicated ( $r=2$ ) test of 210 entries including 98 BC<sub>1</sub>F<sub>2,4</sub>, 65 F<sub>4,6</sub>, 41 F<sub>7,9</sub> families and 6 checks (Bailey, Sullivan, GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) in one-row plots arranged in a 15x14 double rectangular lattice design without chemical control of leaf spot in PBRs Field D8. Defoliation will be scored late in the season. Ordinarily, the F<sub>7,9</sub> families would be BC<sub>1</sub>F<sub>6,8</sub> progenies of BC<sub>1</sub>F<sub>4,6</sub> plants selected the previous year, but the backcross phase of this factorial mating failed in the greenhouse in the summer of 2013 so we sent F<sub>2,3</sub> progenies (self-pollinated seed from the F<sub>1</sub> hybrids made in the winter of 2012-2013 and used as males for the backcross phase in summer of 2013) to the winter nursery at Puerto Rico. The 41 F<sub>7,9</sub> families are tested for yield and grade along with checks in the replicated ( $r=2$ ) **Disease Preliminary Test (DPT)** in PBRs Field D2 and UCPRS Field F1. Seed of the 41 F<sub>7,9</sub> families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. The BC<sub>1</sub>F<sub>2,4</sub> and F<sub>4,6</sub> families will be subjected to single-plant selection at harvest in the **F<sub>2,4</sub> Accelerated Selection Nursery (F4A)** and the **F<sub>4,6</sub> Accelerated Selection Nursery (F6A)** in PBRs Field C6. This test is part of our program for simultaneous selection for multiple disease resistance that includes the **Disease Selection Test, Leaf Spot (DSL)**, the **Disease Selection Test, CBR (DSC)**, the **Disease Selection Test, Sclerotinia minor (DSS)**, and the **Disease Selection Test, TSWV (DST)**.

**Leafspot Advanced Test, Sprayed (LAS) and Unsprayed (LAU):** replicated ( $r=2$ ) tests of 39 advanced breeding lines, 8 species-derived lines from Dr. H.T. Stalker's program, 5 virginia-type cultivars (Bailey, Sugg, Sullivan, Wynne, Emery), and 4 checks (GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) arranged in a 8x7 double rectangular lattice design without chemical control of leaf spot in PBRs Field D8. The entries include breeding lines common to the **Disease Advanced Test (DAT)** series for all four important diseases, 5 released virginia-type cultivars, and 4 disease-resistant checks. The advanced lines exhibit resistance to two or more of the four main diseases that affect peanuts in North Carolina. Defoliation will be scored late in the season, and yield and grade will be measured at harvest. These tests are part of the **Disease Advanced Test** series that includes the **Disease Advanced Test, CBR (DAC)**, the **Disease Advanced Test, Sclerotinia minor (DAS)**, and the **Disease Advanced Test, TSWV (DAT)**. Seed of the advanced lines is increased in the **Disease Advanced Line Nursery (DAN)** in PBRs Field D8.

**CBR AND SCLEROTINIA BLIGHT.** CBR became a problem in North Carolina in the 1970s. A resistance breeding program was initiated by Drs. D.A. Emery and J.C. Wynne and has resulted in the release of several partially CBR-resistant cultivars: NC 8C, NC 10C, NC 12C, Perry, Bailey, Sugg, Sullivan, Wynne, and Emery. Sclerotinia blight, formerly found only in a few of the northernmost counties of North Carolina, used to be more of a problem in Virginia. Sclerotinia resistance was a primary objective of the USDA-ARS breeding program at Suffolk, VA until its closure in 1994. We began screening CBR-resistant lines for their reactions to Sclerotinia the following season. In the unusually cool growing season of 1996, Sclerotinia blight appeared in every peanut-growing county in North Carolina, causing severe damage in some fields. It remains a problem throughout most North Carolina peanut acres. Recognizing that resistance to both of these soil-borne diseases was necessary to the success of a cultivar, we began testing all CBR selections for their Sclerotinia reactions, dropping our practice of selecting single plants on CBR-infested soil in favor of early-generation testing of CBR and Sclerotinia resistance in progenies of plants selected at PBRS. In these tests, short (12 ft) single-row plots are planted at 10-in seed spacing in fields known to be infested with the respective pathogens, stand counts are taken four to five weeks after planting, and the number of symptomatic dead and diseased plants in each plot is monitored throughout the season. Most CBR and Sclerotinia symptoms appear in the second half of the season, especially as warm summer weather moderates in September. Disease incidence values are calculated and used as the basis for retaining lines for further testing. CBR and Sclerotinia tests conducted in the field in 2016 are listed below:

**Advanced Line Disease Test, CBR (ALC):** a replicated ( $r=3$ ) test of 52 advanced breeding lines from the breeding program, 8 virginia- and runner-type cultivars, and 4 checks arranged in a 8x8 triple square lattice design without chemical control of CBR in UCPRS Field D1. Symptomatic plants will be counted as they appear. The lines are entered for a second or greater year in advanced tests for some purpose other than CBR resistance. This test is part of the **Advanced Line Disease Test** series, our program of monitoring disease reactions of all advanced lines that includes the **Advanced Line Disease Test, Leafspot (ALL)**, the **Advanced Line Disease Test, Sclerotinia minor (ALS)**, and the **Advanced Line Disease Advanced Test, TSWV (ALT)**.

**Advanced Line Disease Test, Sclerotinia minor (ALS)** a replicated ( $r=3$ ) test of 52 advanced breeding lines from the breeding program, 8 virginia- and runner-type cultivars, and 4 checks arranged in a 8x8 triple square lattice design without chemical control of Sclerotinia blight in UCPRS Field C2. Symptomatic plants will be counted as they appear. The lines are entered for a second or greater year in advanced tests for some purpose other than Sclerotinia blight resistance. This test is part of the **Advanced Line Disease Test** series, our program of monitoring disease reactions of all advanced lines that includes the **Advanced Line Disease Test, CBR (ALC)**, the **Advanced Line Disease Test, Leaf Spot (ALL)**, and the **Advanced Line Disease Advanced Test, TSWV (ALT)**.

**Disease Advanced Test, CBR (DAC):** a replicated ( $r=3$ ) test of 39 advanced breeding lines, 8 species-derived lines from Dr. H.T. Stalker's program, 5 virginia-type cultivars (Bailey, Sugg, Sullivan, Wynne, Emery), and 4 checks (GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) arranged in a 8x7 triple rectangular lattice design without chemical control of CBR in UCPRS Field D1. Symptomatic plants will be counted as they appear. The entries include breeding lines common to the **Disease Advanced Test (DAT)** series for all four important diseases, 5 released virginia-type cultivars, and 4 disease-resistant checks. The advanced lines exhibit resistance to two or more of the four main diseases that affect peanuts in North Carolina. This test is part of the **Disease Advanced Test** series that includes the **Leafspot Advanced Test, Sprayed (LAS) and Unsprayed (LAU)**, the **Disease Advanced Test, Sclerotinia minor (DAS)**, and the **Disease Advanced Test, TSWV (DAT)**. Seed of the advanced lines is increased in the **Disease Advanced Line Nursery (DAN)** in PBRS Field D8.

**Disease Advanced Test, Sclerotinia minor (DAS):** a replicated ( $r=3$ ) test of 39 advanced breeding lines, 8 species-derived lines from Dr. H.T. Stalker's program, 5 virginia-type cultivars (Bailey, Sugg, Sullivan, Wynne, Emery), and 4 checks (GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) arranged in a 8x7 triple rectangular lattice design without chemical control of Sclerotinia blight in UCPRS Field C2. Symptomatic plants will be counted as they appear. The entries include breeding lines common to the **Disease Advanced Test (DAT)** series for all four important diseases, 5 released virginia-type cultivars, and 4 disease-resistant checks. The advanced lines exhibit resistance to two or more of the four main diseases that affect peanuts in North Carolina. This test is part of the **Disease Advanced Test** series that includes the **Leafspot Advanced Test, Sprayed (LAS) and Unsprayed (LAU)**, the **Disease Advanced Test, Sclerotinia minor (DAS)**, and the **Disease Advanced Test, TSWV (DAT)**. Seed of the advanced lines is increased in the **Disease Advanced Line Nursery (DAN)** in PBRS Field C4b.

**Disease Selection Test, CBR (DSC):** a replicated ( $r=2$ ) test of 210 entries including 98 BC<sub>1</sub>F<sub>2,4</sub>, 65 F<sub>4,6</sub>, 41 F<sub>7,9</sub> families and 6 checks (Bailey, Sullivan, GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) in one-row plots arranged in a 15x14 double rectangular lattice design without chemical control of CBR in UCPRS Field D1. Symptomatic plants will be counted as they appear. Ordinarily, the F<sub>7,9</sub> families would be BC<sub>1</sub>F<sub>6,8</sub> progenies of BC<sub>1</sub>F<sub>4,6</sub> plants selected the previous year, but the backcross phase of this factorial mating failed in the greenhouse in the summer of 2013 so we sent F<sub>2,3</sub> progenies (self-pollinated seed from the F<sub>1</sub> hybrids made in the winter of 2012-2013 and used as males

for the backcross phase in summer of 2013) to the winter nursery at Puerto Rico. The 41  $F_{7,9}$  families are tested for yield and grade along with checks in the replicated ( $r=2$ ) **Disease Preliminary Test (DPT)** in PBRs Field D2 and UCPRS Field F1. Seed of the 41  $F_{7,9}$  families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. The  $BC_1F_{2,4}$  and  $F_{4,6}$  families will be subjected to single-plant selection at harvest in the  **$F_{2,4}$  Accelerated Selection Nursery (F4A)** and the  **$F_{4,6}$  Accelerated Selection Nursery (F6A)** in PBRs Field C6. This test is part of our program for simultaneous selection for multiple disease resistance that includes the **Disease Selection Test, Leaf Spot (DSL)**, the **Disease Selection Test, CBR (DSC)**, the **Disease Selection Test, *Sclerotinia minor* (DSS)**, and the **Disease Selection Test, TSWV (DST)**.

**Disease Selection Test, *Sclerotinia minor* (DSS)**: a replicated ( $r=2$ ) test of 210 entries including 98  $BC_1F_{2,4}$ , 65  $F_{4,6}$ , 41  $F_{7,9}$  families and 6 checks (Bailey, Sullivan, GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) in one-row plots arranged in a 15x14 double rectangular lattice design without chemical control of *Sclerotinia* blight in UCPRS Field C2. Symptomatic plants will be counted as they appear. Ordinarily, the  $F_{7,9}$  families would be  $BC_1F_{6,8}$  progenies of  $BC_1F_{4,6}$  plants selected the previous year, but the backcross phase of this factorial mating failed in the greenhouse in the summer of 2013 so we sent  $F_{2,3}$  progenies (self-pollinated seed from the  $F_1$  hybrids made in the winter of 2012-2013 and used as males for the backcross phase in summer of 2013) to the winter nursery at Puerto Rico. The 41  $F_{7,9}$  families are tested for yield and grade along with checks in the replicated ( $r=2$ ) **Disease Preliminary Test (DPT)** in PBRs Field D2 and UCPRS Field F1. Seed of the 41  $F_{7,9}$  families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. The  $BC_1F_{2,4}$  and  $F_{4,6}$  families will be subjected to single-plant selection at harvest in the  **$F_{2,4}$  Accelerated Selection Nursery (F4A)** and the  **$F_{4,6}$  Accelerated Selection Nursery (F6A)** in PBRs Field C6. This test is part of our program for simultaneous selection for multiple disease resistance that includes the **Disease Selection Test, Leaf Spot (DSL)**, the **Disease Selection Test, CBR (DSC)**, the **Disease Selection Test, *Sclerotinia minor* (DSS)**, and the **Disease Selection Test, TSWV (DST)**.

**TOMATO SPOTTED WILT VIRUS. TSWV** appeared in North Carolina in the early to mid-1990s. Late-season symptoms of TSWV are easily confused with those of CBR. We noticed anomalous results in our CBR trials in the mid-1990s, with some lines known to be CBR-susceptible appearing to be resistant and some known to be CBR-resistant appearing to be susceptible. We have learned how to differentiate symptoms of the two diseases. Incidence of TSWV has grown in severity since the mid-1990s, and in 1997 we began to include field evaluation of TSWV reaction as part of our program of monitoring resistance to prevalent diseases. In our TSWV trials, we space seed 20 inches apart within rows and apply no insecticide to the plots either at planting or subsequently. The wide intra-row plant spacing and absence of insecticide fosters feeding by tobacco thrips (*Frankliniella fusca*), the primary insect vector of TSWV in the Virginia-Carolina production area. Plant stands are recorded shortly after emergence in the spring, and disease incidence is monitored throughout the growing season. Early in our screening of germplasm extant within the NCSU collection, we observed that TSWV incidence was particularly low in some Mexican *hirsuta*-type lines (*A. hypogaea* subsp. *hypogaea* var. *hirsuta* Köhler). We had used the *hirsuta* lines as parents in breeding for reduced oil content, so there are several *hirsuta*-derived lines in our program. We also have used the runner-type cultivar Georgia Green as a source of TSWV resistance in a program of family-based selection. A similar program has been initiated by crossing some *hirsuta*-by-virginia selections back to virginia-type parents. TSWV tests conducted in the field in 2016 are listed below:

**Advanced Line Disease Test, TSWV (ALT)**: a replicated ( $r=3$ ) test of 52 advanced breeding lines from the breeding program, 8 virginia- and runner-type cultivars, and 4 checks arranged in a 8x8 triple square lattice design in wide (20 in) seed spacing and without insecticide in PBRs Field C7. Symptomatic plants will be counted as they appear. The lines are entered for a second or greater year in advanced tests for some purpose other than leaf spot resistance. This test is part of the **Advanced Line Disease Test** series, our program of monitoring disease reactions of all advanced lines that includes the **Advanced Line Disease Test, CBR (ALC)**, the **Advanced Line Disease Test, Leafspot (ALL)**, and the **Advanced Line Disease Advanced Test, *Sclerotinia minor* (ALS)**.

**Disease Advanced Test, TSWV (DAT)**: a replicated ( $r=3$ ) test of 39 advanced breeding lines, 8 species-derived lines from Dr. H.T. Stalker's program, 5 virginia-type cultivars (Bailey, Sugg, Sullivan, Wynne, Emery), and 4 checks (GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) arranged in a 8x7 triple rectangular lattice design in wide (20 in) seed spacing and without insecticide in PBRs Field C7. Symptomatic plants will be counted as they appear. The entries include breeding lines common to the **Disease Advanced Test (DAT)** series for all four important diseases, 5 released virginia-type cultivars, and 4 disease-resistant checks. The advanced lines exhibit resistance to two or more of the four main diseases that affect peanuts in North Carolina. This test is part of the **Disease Advanced Test** series that includes the **Leafspot Advanced Test, Sprayed (LAS) and Unsprayed (LAU)**, the **Disease Advanced Test, *Sclerotinia minor* (DAS)**, and the **Disease Advanced Test, TSWV (DAT)**. Seed of the advanced lines is increased in the **Disease Advanced Line Nursery (DAN)** in PBRs Field D8.

**Disease Selection Test, TSWV (DST)**: a replicated ( $r=2$ ) test of 210 entries including 98  $BC_1F_{2,4}$ , 65  $F_{4,6}$ , 41  $F_{7,9}$  families and 6 checks (Bailey, Sullivan, GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) in one-row

plots arranged in a 15x14 double rectangular lattice design with wide (20 in) seed spacing and no insecticide in PBRs Field C7. Ordinarily, the  $F_{7,9}$  families would be  $BC_1F_{6,8}$  progenies of  $BC_1F_{4,6}$  plants selected the previous year, but the backcross phase of this factorial mating failed in the greenhouse in the summer of 2013 so we sent  $F_{2,3}$  progenies (self-pollinated seed from the  $F_1$  hybrids made in the winter of 2012-2013 and used as males for the backcross phase in summer of 2013) to the winter nursery at Puerto Rico. The 41  $F_{7,9}$  families are tested for yield and grade along with checks in the replicated ( $r=2$ ) **Disease Preliminary Test (DPT)** in PBRs Field D2 and UCPRS Field F1. Seed of the 41  $F_{7,9}$  families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. Seed of the 41  $F_{7,9}$  families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. The  $BC_1F_{2,4}$  and  $F_{4,6}$  families will be subjected to single-plant selection at harvest in the  $F_{2,4}$  **Accelerated Selection Nursery (F4A)** and the  $F_{4,6}$  **Accelerated Selection Nursery (F6A)** in PBRs Field C6. This test is part of our program for simultaneous selection for multiple disease resistance that includes the **Disease Selection Test, Leaf Spot (DSL)**, the **Disease Selection Test, CBR (DSC)**, the **Disease Selection Test, Sclerotinia minor (DSS)**, and the **Disease Selection Test, TSWV (DST)**.

**MULTIPLE DISEASE RESISTANCE.** When NC 12C was released in 1996 as a CBR-resistant cultivar, it quickly became apparent that it was highly susceptible to Sclerotinia blight. Likewise, Perry, released in 2000 as a cultivar with good resistance to CBR and partial resistance to Sclerotinia blight, proved to be highly susceptible to TSWV under heavy disease pressure. Even though we had been monitoring the reactions of every advanced breeding line to all four important diseases for a number of years, these examples underscore the importance of selecting simultaneously for resistance to all four diseases rather than selecting for resistance to one and hoping that there will be resistance to the others as well. Monitoring of reactions to “other” diseases often reveals a line with one to resistance to be susceptible to others. Future releases must carry field resistance to TSWV, CBR, and Sclerotinia blight in order to succeed in the current virginia-type peanut marketplace. Resistance to leaf spots is not absolutely necessary because growers are accustomed to the trouble and expense of leaf spot fungicide programs. However, any reduction in the cost of leaf spot control achieved through even partial resistance would be helpful to the growers. Multiple resistance is the most important goal for the breeding program for the foreseeable future as our growers try to reduce their cost of production in order to remain competitive. We broadened our program of simultaneous selection for resistance to CBR and Sclerotinia blight to include TSWV and leaf spots. The procedure involves early generation selection based on family performance, and it uses a winter nursery to speed the process of inbreeding to the  $F_6$  generation when the last single-plant selections are made (Table 2).

We have applied best linear unbiased prediction (BLUP) of breeding value to databases of disease reactions of NCSU breeding lines and checks in order to identify parents that would have the greatest impact on disease resistance. Unfortunately, there have been no lines with outstanding breeding values for all four diseases. It appears that it will be necessary to combine the resistances two or three at a time and then intermate those lines to find ones with resistance to all four diseases. Tests and nurseries involved in the multiple disease resistance program in 2016 include:

**Disease Advanced Test series (DAT):** a replicated ( $r=2$  or  $r=3$ ) test of 39 advanced breeding lines, 8 species-derived lines from Dr. H.T. Stalker’s program, 5 virginia-type cultivars (Bailey, Sugg, Sullivan, Wynne, Emery), and 4 checks (GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) arranged in 8x7 double or triple rectangular lattice designs without chemical control of the critical disease for a given test. The entries include breeding lines common to the **Disease Advanced Test (DAT)** series for all four important diseases, 5 released virginia-type cultivars, and 4 disease-resistant checks. The advanced lines exhibit resistance to two or more of the four main diseases that affect peanuts in North Carolina. The lines are tested for yield and grade when planted at 10-in seed spacing and with disease and insect control in the replicated ( $r=2$ ) **Leafspot Advanced Test, Sprayed (LAS)** in PBRs Field D8. This is the **Disease Advanced Test** series that includes the **Leafspot Advanced Test, Sprayed (LAS)** and **Unsprayed (LAU)** in PBRs Field C6, the **Disease Advanced Test, CBR (DAC)** grown without metam sodium fumigation on infested soil in UCPRS Field D2, the **Disease Advanced Test, Sclerotinia minor (DAS)** grown without fluazinam or boscalid on infested soil in UCPRS Field C2, and the **Disease Advanced Test, TSWV (DAT)** grown at wide (20 in) seed spacing and without insect control in PBRs Field D9a. Seed of the lines is increased in the **Disease Advanced Line Nursery (DAN)** in PBRs Field C4b.

**Disease Selection Test Series (DST):** replicated ( $r=2$ ) tests of 210 entries including 98  $BC_1F_{2,4}$ , 65  $F_{4,6}$ , 41  $F_{7,9}$  families and 6 checks (Bailey, Sullivan, GP-NC 343, NC 3033, N96076L, and *hirsuta*-type plant introduction PI 576636) in one-row plots arranged in a 15x14 double rectangular lattice designs. Ordinarily, the  $F_{7,9}$  families would be  $BC_1F_{6,8}$  progenies of  $BC_1F_{4,6}$  plants selected the previous year, but the backcross phase of this factorial mating failed in the greenhouse in the summer of 2013 so we sent  $F_{2,3}$  progenies (self-pollinated seed from the  $F_1$  hybrids made in the winter of 2012-2013 and used as males for the backcross phase in summer of 2013) to the winter nursery at Puerto Rico. In this test, symptomatic plants will be counted as they appear. The DST series includes the **Disease Selection Test, Leafspot (DSL)** grown without leaf spot control in PBRs Field D8, the **Disease Selection Test, CBR (DSC)** grown without metam sodium fumigation in UCPRS Field D1, the **Disease Selection Test, Sclerotinia minor (DSS)** grown on Sclerotinia-infested soil without chemical control in UCPRS Field C2, and the **Disease Selection Test, TSWV (DST)** grown at wide (20 in) seed spacing and without insect control in PBRs Field C7. The 41  $F_{7,9}$  families are tested for yield and grade along with checks in the replicated ( $r=2$ )

Table 2. A generalized summary of the NCSU peanut breeding program's "accelerated" multiple disease resistance breeding procedure.

Year	Season	Action
1	Summer	Select parents and make crosses.
1	Winter	F <sub>1</sub> generation grown in Puerto Rico Winter Nursery (PRWN).
2	Summer	Single-plant selection (SPS) among F <sub>2</sub> plant for plant, pod, and seed traits at Peanut Belt Research Station (PBRs) at Lewiston, NC.
2	Winter	F <sub>2,3</sub> families grown at PRWN, single-seed descent (SSD, harvest one seed from each plant in the family) followed by bulk harvest of each family.
3	Summer	F <sub>2,4</sub> bulk-harvested families entered in replicated Disease Selection Tests for leafspot (DSL), CBR (DSC), Sclerotinia blight (DSS), and TSWV (DST); collect disease incidence data and identify the best families. SPS for plant, pod, and seed traits in selected F <sub>2,4</sub> SSD families grown at PBRs.
3	Winter	F <sub>4,5</sub> families grown at PRWN, SSD followed by bulk harvest of each family.
4	Summer	F <sub>4,6</sub> bulk-harvested families entered in replicated Disease Selection Tests for leafspot (DSL), CBR (DSC), Sclerotinia blight (DSS), and TSWV (DST); collect disease incidence data and identify the best families. SPS for plant, pod, and seed traits in selected F <sub>4,6</sub> SSD families grown at PBRs.
4	Winter	F <sub>6,7</sub> families grown at PRWN as a seed increase step, bulk harvest of each family.
5	Summer	F <sub>6,8</sub> bulk-harvested families entered in replicated Disease Selection Tests for leafspot (DSL), CBR (DSC), Sclerotinia blight (DSS), and TSWV (DST); replicated yield trials, the Disease Preliminary Test (DPT), at PBRs and Upper Coastal Plain Research Station at Rocky Mount, NC; identify the best families for diseases, yield, and grade; seed increase on 0.003 A in Disease preliminary Line Nursery (DPN) at PBRs. SPS for plant, pod, and seed traits in selected F <sub>4,6</sub> SSD families grown at PBRs.
6	Summer	Assign accession numbers to selected F <sub>6,9</sub> lines; replicated Disease Advanced Tests (DAT) for leafspot, (Leafspot Advanced Test or LAT), CBR and Sclerotinia blight (Soil-borne Pathogen Advanced Test or SAT), and TSWV (TSWV Advanced Test or TAT); lines selected for yield and grade placed in Advanced Yield Test (AYT) at PBRs, UCPRS, and Border Belt Tobacco Research Station (BBTRS) at Whiteville, NC. Seed increased in 0.003 A in Small-Plot Increase Nursery (SPI) at PBRs. (See Table 1 for testing sequence after initial year in AYT)
7	Summer	Selected F <sub>6,10</sub> lines in replicated DAT for leafspot, CBR, Sclerotinia blight, and TSWV; AYT at PBRs, UCPRS, and BBTRS; seed increase in SPI and on 0.02 A in Large Plot Increase (LPI) at PBRs.
8	Summer	Selected F <sub>6,11</sub> lines in replicated DAT for leafspot, CBR, Sclerotinia blight, and TSWV; AYT at PBRs, UCPRS, and BBTRS; lines selected for yield and grade may be entered in the Peanut Variety and Quality Evaluation (PVQE) program small-plot test conducted at two sites in VA and two in NC with two digging dates per site; seed increase in SPI and LPI at PBRs.
9	Summer	Selected F <sub>6,12</sub> lines in replicated DAT for leafspot, CBR, Sclerotinia blight, and TSWV; AYT at PBRs, UCPRS, and BBTRS; PVQE small-plot test at four sites; seed increase in SPI, LPI, and breeder seed increase at PBRs.
10	Summer	Selected F <sub>6,13</sub> lines in replicated DAT for leafspot, CBR, Sclerotinia blight, and TSWV; AYT at PBRs, UCPRS, and BBTRS; PVQE small-plot test at four sites; PVQE large-plot test at two sites for processor evaluation of quality; foundation seed increase in SPI, LPI, and 1 A breeder seed increase at PBRs.
10	Winter	Release decision. Released lines are included as checks in the AYT and PVQE small-plot test.

**Disease Preliminary Test (DPT)** in PBRs Field D2 and UCPRS Field F1. Seed of the 41 F<sub>7,9</sub> families are increased in the **Disease Preliminary Line Nursery (DPN)** in PBRs Field C6. The F<sub>3,5</sub> and F<sub>4,6</sub> families will be subjected to single-plant selection at harvest in the **F<sub>2,4</sub> Accelerated Selection Nursery (F4A)** and the **F<sub>4,6</sub> Accelerated Selection Nursery (F6A)** in PBRs Field C6. These tests are part of our program for simultaneous selection for multiple disease resistance.

**F<sub>2</sub> Selection Nursery (F2N)**: a selection nursery of 127 plots in PBRs Field C6. The 127 BC<sub>1</sub>F<sub>2</sub> plots derive from 55 crosses made in the 9x6 **Disease-Resistant-by-High-Oleic Backcross** crossing program made in the summer of 2015. In the original factorial mating, we used agronomically superior high oleic lines (N12007oI, N12010oI, N13047oIJ, N13048+oI, N13052oIL, N13057oIL, N14046oIT, and N14049oILSmT) and Sclerotinia blight-resistant plant introduction PI 497429 as females and disease-resistant line (N14039oILSmT, N14040oILSmT, N14043oILSmT, 14 DPT 010 [now N15063oILSm], 14 DPT 013 [now N15066oILSmT], and 14 DPT 015 [now N15068oILSmT]) as males in the winter of 2014-2015. The F<sub>1</sub> hybrids were crossed back to the agronomically superior parent in the summer of 2015. We will make individual plant selections within the populations, then send selected BC<sub>1</sub>F<sub>2,3</sub> families carrying the high-oleic gene to the winter nursery in Juana Diaz, PR (the "PRWN") as part of our program of accelerated breeding for multiple disease resistance. They will be tested as BC<sub>1</sub>F<sub>2,4</sub> families as part of the 2017 **Disease Selection Test (DST)** series. F<sub>2,3</sub> families from plants whose progenies are not selected for the 2016-2017 PRWN will be planted in the 2017 **F<sub>2,3</sub> Selection Nursery (F3N)**.

**F<sub>2,4</sub> Selection Nursery, Accelerated (F4A)**: a selection nursery of 98 plots in PBRs Field C6. The BC<sub>1</sub>F<sub>2,4</sub> families represent 55 crosses, 85 BC<sub>1</sub>F<sub>1</sub>-derived families, and 98 BC<sub>1</sub>F<sub>2,3</sub>-derived families. These crosses were made as part of the 10x5 **Disease-Resistant-by-High-Oleic Backcross** crossing program made in the summer of 2014 (disease-resistant parents

N12006ol, N12007ol, N12009olCLT, N12010ol, N12014ol, 13 DPT 023 [now N14035olSmT], 13 DPT 029 [now N14037olLSmT], 13 DPT 034 [now N14039olLSmT], 13 DPT 066 [now N14049olLSmT], and species-derived line SPT 13-05ol used as females and agronomically superior high-oleic lines N11019olJ, N13041olJ, N13045ol, N13055ol, and N13056olSm used as males in the initial factorial mating in the winter, the F<sub>1</sub> hybrids crossed back to the agronomically superior parent in the summer). These are the progenies of F<sub>2</sub> plant selections that were sent to the winter nursery.

**F<sub>4,6</sub> Selection Nursery, Accelerated Program (F6A):** a selection nursery of 65 plots in PBRS Field C6. The 65 F<sub>4,6</sub> families represent 19 crosses, 20 F<sub>1</sub>-derived, 25 F<sub>2</sub>-derived, and 25 F<sub>4</sub>-derived families. The populations derive from the 2013 10x6 **Disease-Resistant-by-High-Oleic Factorial** (disease-resistant parents N08069olJCT, Sullivan, Emery, N10061olFCLSm, N10066olSmT, N11021olSrT, N11038olSrT, N12003olCSmT, N12008olCLSmT and N12009olCLT used as females; six high-oleic breeding lines N10043olJ, Emery, N11020olJ, N11043ol, N11045ol, and black-podded line N11054B used as males in the winter). Because that year's summer crossing program failed, F<sub>2</sub> seeds from the F<sub>1</sub> plants produced in the 2013 winter greenhouse and used as males in the summer backcrossing program were sent to Puerto Rico where individual F<sub>2</sub> plants were harvested and their progenies planted in the field in 2014. Because of the failure of the summer crossing program, these are actually F<sub>5,7</sub> families, but to keep the nomenclature of the program consistent across years, we are calling them "F<sub>4,6</sub>." These are the families being tested in the **Disease Selection Test (DST)** series. Five seeds from each F<sub>3,4</sub> selection were individually assayed for fatty acid profile, and only the families that were uniformly high-oleic or that were segregating for the high-oleic trait were retained. Single-plant selections will be made at harvest with special attention paid to those families that exhibited resistance to two or more diseases based on data from the DST series. Selections will be made from all families, and those from families found to possess multiple disease resistance will be sent to the PRWN for increase and further selection in the multiple disease resistance program. Surviving families will be tested for disease resistance as F<sub>6,8</sub> families in the 2017 **Disease Selection Test (DST)** series, for yield and grade as 2017 F<sub>6,8</sub> families in the **Disease Preliminary Test (DPT)**, and as advanced disease-resistant lines in the 2018 **Disease Advanced Tests (DAT)** and high-yielding lines in the 2018 **Advanced Yield Test (AYT)**. Progeny of selections from F<sub>4,6</sub> families not identified as having multiple disease resistance will be grown for further among-family selection in the 2017 **F<sub>6,7</sub> Selection Nursery (F7N)**.

**RESISTANCE TO AFLATOXIN PRODUCTION.** In spite of millions of dollars spent over the past 25 to 30 years in search of management and genetic solutions, aflatoxin produced in peanuts colonized by *Aspergillus flavus* or *A. parasiticus* remains a problem for peanut growers, shellers, processors, and consumers. In the main peanut-producing areas of the Southeast and Southwest, aflatoxin contamination that develops before harvest in hot, dry weather is more of a problem than contamination that results from storage of peanuts under high relative humidity. In the Virginia-Carolina production area, droughty conditions during the critical phase of seed development are less common, and post-harvest contamination remains a problem. Dr. Huiqin Xue, a former student from the People's Republic of China, screened peanut germplasm for its ability to support aflatoxin production under very adverse storage conditions. She determined that lines with the high-oleic trait can support nearly twice as much aflatoxin production as lines without the trait. She also screened disease- and pest-resistant germplasm derived from interspecific crosses, lines reported in the literature to carry resistance to IVSCAF ("in vitro seed colonization by *A. flavus*"), and lines reported by Dr. C. Corley Holbrook to carry resistance to preharvest aflatoxin contamination. Since Dr. Xue's graduation and departure from the project, field work in this area has been discontinued. However, Dr. Susana R. Milla examined the species-derived lines assayed by Dr. Xue for their capacity to support aflatoxin production, trying to determine whether any DNA markers are associated with the observed variation in aflatoxin production. This study was the basis for the MS research program of Ms. Christina Rowe. There is no aflatoxin resistance test in the field in 2016.

**ARTHROPOD PEST RESISTANCE.** The arthropod complex of the Virginia-Carolina production area includes leaf feeders tobacco thrips (*Frankliniella fusca*), potato leafhopper (*Empoasca fabae*), corn earworm (*Helicoverpa zea*), fall armyworm (*Spodoptera frugiperda*), and two-spotted spider mite (*Tetranychus* spp.), and pod feeders southern corn rootworm (*Diabrotica undecimpunctata howardi*), lesser cornstalk borer (*Elasmopalpus lignosellus*), and tobacco wireworm (*Conoderus vespertinus*). The most serious pest in terms of direct damage to yield and/or quality is the southern corn rootworm (SCR) which feeds on succulent developing pods, sometimes destroying the entire pod either by itself or by making a wound through which soil-borne fungi enter and consume the pod, or by scarifying the pod, reducing its value. In terms of the importance of their effect, thrips are now the most serious problem because they vector TSWV, which can greatly reduce yield and quality. Most of the insect resistance in our program is derived from PI 121067 through its descendant GP-NC 343, one of the parents of the SCR-resistant cultivar NC 6. The only arthropod resistance nursery in the field in 2016 is:

**F<sub>5,6</sub> Selection Nursery, Insect Resistance (F6I):** a selection nursery of 86 plots grown in PBRS Field C7 without any application of insecticides. The 86 F<sub>5</sub>-derived families represent 30 crosses, 42 F<sub>1</sub>-derived, 44 F<sub>2</sub>-derived, 58 F<sub>3</sub>-derived families, and 75 F<sub>3</sub>-derived families. The crosses were made as part of the 2010 **Insect Resistance Topcross** using eight insect-resistant lines (NC Ac 02214, NC Ac 02232, NC Ac 00343, NC Ac 10247, NC Ac 10272, NC Ac 15729, NC Ac

15745, and PI 121067) as females and two high-yielding high-oleic lines N08070oIJC and N08083oICT as males. Single-plant selections will be made for pod characteristics including freedom from damage by pod-feeding insects at harvest. Selections will be grown without insect control in the 2017 **F<sub>6,7</sub> Selection Nursery, Insect Resistance (F7I)**.

**BREEDING FOR IMPROVED QUALITY.** The word “quality” has different meanings to different people. To the grower, high quality peanuts are those that fetch the best price, so under the old price support program in which price of virginia peanuts was determined largely by meat and ELK content, cultivars with thin hulls and large seeds were considered by the grower to have the highest quality. Shellers desire cultivars that will meet their need for shapely, bright-hulled jumbo and fancy in-shell peanuts and for the various fractions of shelled goods (ELK, medium, No. 1, etc.) that they produce from the peanuts that do not make good in-shell products. We regularly measure jumbo and fancy pod content, brightness and hue as part of our conventional grading process as well as measuring seed grade factors. Peanut processors want peanuts that will make a superior product that will retain its peanut flavor beyond the point of sale. We have incorporated as a breeding objective the development of only high-oleic cultivars that have longer shelf-life. The consumer wants peanut products with intense roasted peanut flavor and lengthy shelf life. We annually measure flavor on advanced breeding lines and released cultivars. Consumers also have at times expressed concern over the high oil content of peanut products.

**HULL BRIGHTNESS.** We have incorporated measurements of hull color into our normal grading process, even in the short grade taken on pod samples from the Preliminary Yield Tests, and hull brightness is now just another trait under consideration as we decide which lines will graduate through the various levels of testing in the cultivar development stream. However, there are three other market-oriented aspects of quality that we are addressing through special breeding subprograms: oil content, oil composition, and flavor.

**OIL CONTENT.** In the mid-1990s when US peanut consumption was in decline and fat content was the main reason given by consumers for their increasing aversion to peanuts, we initiated a subprogram to select peanuts with less than 75% of the normal oil content of over 500 g kg<sup>-1</sup> expressed on a dry matter basis, *i.e.*, at 0% moisture or “% DM.” Elimination of one quarter of the normal amount of oil is a prerequisite to marketing a “reduced fat” product under federal Food and Drug Administration labeling regulations. We measure oil content by nuclear magnetic resonance (NMR) in an SMK sample from every replicated yield plot in our program. Although there is a substantial range of average oil values across elite lines, oil contents under 450 g kg<sup>-1</sup> are rare in that population. A few lines with oil contents near the critical 375 g kg<sup>-1</sup> level were found among *hirsuta*-type lines introduced into the USA in 1993 from the central Mexican highland states of Puebla and Guanajuato. Other low-oil lines were found among mutants selected by Drs. W. C. Gregory and D. A. Emery from the progeny of mutant plants grown from irradiated seeds of the old cultivar NC 4. We crossed low oil lines with relatively low elite lines and selected segregating progeny on the basis of plant type, apparent maturity, and oil content. A replicated trial of selections was completed in 2001, and several lines met the criteria for reduced fat content, but they were mostly purple-seeded and had unusual raw seed texture. One side benefit of this subprogram is that the low-oil selections appear to have substantial resistance to TSWV, probably derived from their *hirsuta*-type parent. These lines have been used as parents in our disease-resistance breeding program. In the meantime, public concern over the high fat content of peanut appears to have subsided. This may have resulted in part because of the emergence of popular reduced-carbohydrate diets that supplanted reduced-fat diets in US society, and through the public relations efforts of and the nutritional studies funded by the Peanut Institute and the Peanut Board.

Surging prices for petroleum products since 2005 have resulted in intensified interest in development of biofuels, *i.e.*, ethanol from fermentation of starchy or sugary plant tissues and “biodiesel” fuel based on vegetable oil. In spite of the high production cost of peanut relative to soybean or canola, the high oil content of peanut makes it a candidate to be a feedstock for biodiesel. It appears that high oil content should be an objective of the project at least for the near future. The high end of oil content in elite lines is about 55% DM. Higher oil contents have been measured in exotic lines, particularly lines of Bolivian origin.

Only one field nursery is dedicated to oil content populations in 2016, the **F<sub>2,3</sub> Oil Content Selection Nursery (F3O)**:

**F<sub>2,3</sub> Oil Content Selection Nursery (F3O):** a selection nursery of 12 F<sub>2,3</sub> plots in PBRS Field C6. The 12 F<sub>2</sub>-derived families represent 8 crosses and 11 F<sub>1</sub>-derived families. These families derive from a factorial mating of five families selected for small seed size and high oil content and three high-oleic parents with relatively high oil content selected from the testing program (N13031oIL, N13032oIL, and SPT 10-14oI). F<sub>2,3</sub> progenies from small-seeded F<sub>2</sub> plant selections were assessed using nuclear magnetic resonance for oil content, and only those that combined small seeds with high oil were planted for further selection.

**OIL COMPOSITION.** In the 1980s, researchers at the Univ. of Florida identified a natural variant of peanut with unusually high oleic acid level (and correspondingly low linoleic acid level) in its seed oil. Florida patented the trait, making it available for breeding purposes under license. We began transferring the trait into virginia-type cultivars by backcrossing in 1990. Several backcross-derived high-oleic lines have passed through the NCSU Advanced Yield Test

and the PVQE small-plot tests. High-oleic cultivar Brantley, a backcross derivative of the NC 7 cultivar, was released in 2005. Two high-oleic cultivars, Sullivan and Wynne, were released by the program in 2013, a third, Emery, in 2016. Almost all of our advanced breeding lines are now high oleic. We acknowledge that normal-oleic lines may still be released if they meet the requirements of a niche production need, but it is envisioned that all mainstream releases need to be high oleic.

Our fatty acid work was initially performed collaboratively with Dr. Richard F. Wilson, formerly of the USDA-ARS Soybean and Nitrogen Fixation Group in Raleigh, NC, then USDA-ARS National Program leader for Oilseeds, and later science advisor to the Peanut Foundation. The initial program of backcrossing was supported by grants from the North Carolina Peanut Growers Association which withdrew its support for the program following the issue of the US Utility Patent to the University of Florida in 2000. It became evident that the growers were the only group that would be paying a royalty for use of the high-oleic cultivars. Within that time frame, rather than concentrating our efforts on development of new populations incorporating the high-oleic trait, we concentrated on selection of TSWV-resistant lines in the face of very high incidence of TSWV in the 2000-2002 growing seasons. We have since been merging the high-oleic and disease-resistance populations through crossing. As a further impediment to progress in developing high-oleic lines, in 2004 the USDA-ARS South Atlantic area director denied our request to formalize our collaborative relationship with the soybean group in Raleigh with a Non-Funded Cooperative Agreement. He furthermore instructed Dr. Joseph W. Burton, then research leader of the group, to discontinue any work on peanut fatty acids. With funds from royalties on seed sales and a grant from the National Peanut Board, we acquired a dedicated gas chromatograph for measuring fatty acid profiles in peanut seeds. This acquisition restored our ability to select and monitor high-oleic lines. We have been assaying 1,200 to 9,500 individual seeds per year in-house since 2005. We recently acquired a Luminar 3076 "SeedMeister" AOTF-NIR instrument from Brimrose Corp. This near-infrared reflectance device can rapidly and non-destructively determine whether or not an individual seed has the high-oleate trait. There are numerous field plots related to the high-oleate breeding program. Starting in 2008, only high-oleic lines or late-generation families segregating for the high-oleate trait have been advanced in the testing program unless the population under selection met some special requirement.

**FLAVOR.** Consumers buy peanut products because of their unique flavor, yet collection of sensory data is rare in peanut breeding programs, at least prior to the final stages of replicated testing. Our flavor work has been done collaboratively with Dr. Timothy H. Sanders (recently retired and replaced by Dr. Lisa Dean) of the USDA-ARS Peanut Quality and Market Hanopdling Research Unit (MQRHU) in Raleigh and Dr. Harold E. Pattee, formerly of the USDA-ARS MQRHU then a Research Professor in the Dept. of Crop and Soil Sciences at NCSU. In the 1990s, we collected sensory descriptor data on peanut samples from across the three major peanut-producing areas over several years in order to separate the effects of genotype, environment, and genotype-by-environment interaction on sensory attributes roasted peanut, sweet, and bitter. Because the exact chemical basis for roasted peanut flavor remains unknown to this day, all evaluation of flavor has been done using a trained descriptive sensory panel working in the Department of Food, Bioprocessing, and Nutrition Sciences at NCSU. Our database of flavor profiles uses the flavor lexicon developed by Dr. Clyde Young. We found that there were large environmental effects, particularly year-to-year variation and variation among specific sites within years and production areas. It is important to correct roasted peanut, sweet, and bitter for the linear and quadratic effects of roast color and for the fruity attribute, a negative sensory quality that results from immaturity of the seeds or from drying the peanuts too rapidly or at too high a temperature. The genotypic portion of total variation was relatively small, ranging from less than 10% for roasted peanut to about 25% for sweet. Runner-type peanuts on average had better flavor profiles (more intense roasted peanut and sweet, less intense bitter) than virginia- or spanish-type peanuts, but the distributions of market-types overlapped. Best linear unbiased prediction (BLUP) was used to estimate the breeding values of the genotypes evaluated, and useful parents were identified in all market-types. In 2001, a diallel mating was made among 11 parents including 9 selected for their positive effects on flavor, Georgia Green (which subsequently proved to have high positive BLUPS for roasted peanut and sweet), and Perry. In 2004,  $F_{1,4}$  bulk populations from these crosses were grown in replicated test, and SMK samples were processed and sensory analysis performed to determine whether our BLUP values corresponded to combining abilities measured from actual hybrid populations. The correlations between BLUPs and empirical estimates of general combining abilities were not much better than the correlations of means of the parents and GCA, indicating that the additional effort required for development of BLUPs of breeding value may not significantly improve discrimination in choosing parents to improve peanut flavor.

In a separate set of experiments, we assessed the utility of near infrared reflectance (NIR) as a tool for predicting sensory quality of roasted peanuts. We developed a predictive equation for roasted peanut, sweet, and bitter attributes

based on NIR values measured on 35g ground raw SMK samples from our Advanced Yield Test and Disease Preliminary Test in 2003-2012. The correlations between predicted and observed values were weak.

**EARLY MATURITY.** As peanut production has shifted from traditional areas to the high plains of west Texas, it has become evident that peanuts grown where night temperatures are cool taste different from those grown under warm-night temperature regimes. On the high plains as in the Virginia-Carolina area, night temperatures decline markedly in September prior to the usual time of harvest, resulting in potential risk to the flavor quality of the crop. There have been cases of freezing temperatures at or near harvest time, resulting in severe damage to crop quality. M&M/Mars and Kraft Foods (the parent company of Planters Nuts) donated funds to the Peanut Foundation directed toward research on early maturity. Earlier cultivars would mature under warmer night temperatures, and might therefore be expected to have better flavor quality. Similarly, mature seeds are less prone to develop off-flavors when dried too rapidly or at too high temperatures. The NCSU breeding program was involved in early maturity work in the early 1990s but discontinued those efforts after several years when area shellers were unwilling to support the release of early cultivars. Because it served the northernmost extreme of peanut production in the area, the USDA-ARS (now VPI&SU) program at Suffolk, VA, continued to select for early maturity by digging plots on or near September 15 (approximately 135 DAP), and selecting for yield and grade. The program released five early maturing virginia-type cultivars: VA 81B, VA 93B, and very large-seeded Titan with bunch growth habits and VA 98R, Wilson, and CHAMPS with runner, *i.e.*, spreading, growth habits. Of these, VA 98R found the broadest acceptance to date although planted acreage of CHAMPS was appreciable. Wilson was released in 2002 and, in spite of excellent performance in variety trials, did not find wide acceptance in the marketplace. Titan has been grown as a niche cultivar that produces a high content of super-extra large kernels. With the retirement of R. Walton Mazingo in 2001 and the departure of his immediate replacement, Dr. Dennis L. Coker, after less than two years, the future of the VPI&SU program appeared to be unsure, so the NCSU program revived its early maturity subprogram. Field plots related to early maturity in 2016 include:

**Early Maturity Advanced Test, Early and Late Diggings (EAE and EAL):** a replicated test of 13 breeding lines and 7 checks in PBRS Field D2 (early and late diggings with  $r=3$ ) and UCPRS Field F1 (early and late diggings with  $r=3$ ), each test arranged in a 5x4 triple rectangular lattice design. Seven experimental lines have normal “tan” pods while six are “black-podded,” that is, possessing the gene for the trait that causes the exocarp of an individual pod to darken as it reaches physiological maturity, much as the mesocarps of pods darken in “normal” tan-podded lines. All tan-podded lines carry the Florida high oleic acid trait. The six black-podded lines are normal-oleic. All experimental lines have been tested previously in the EAE and EAL. This test is to evaluate maturity, yield and grade for lines descended from early maturing parents. The early plots will be dug at 125 to 135 days after planting (DAP) and the late plots dug at 145 to 155 DAP. Pod blasting will be used to assess the maturity of the lines. Seed of the high-oleic breeding lines is increased in the **Large-Plot Increase (LPI)** in PBRS Field D2; seed of the normal-oleic lines is increased in the **Breeder Seed Increase** in PBRS Field D2.

**SEED PURIFICATION.** Upon its release in 2005, it was quickly observed that the putatively high-oleic cultivar Brantley was contaminated with a line that was not high oleic. Up to 30% contamination was found when Foundation Seed lots were analyzed seed by seed using gas chromatography. Although we strive to maintain purity of  $F_6$ -derived breeding lines, the high oleic character is something that cannot be seen with the naked eye, so it is not amenable to maintenance of purity via visual based roguing. A chemical evaluation is necessary, a one- or two-stage purification step. This purification should be performed at regular intervals to maintain purity.

In the first stage, we grow out plots of a putatively high oleic line. The seeds planted for this stage may have been tested for fatty acid composition, in which case only high-oleic seeds would be planted. However, the fatty acid gas chromatographic assay wounds the seed, affording a point of ingress for seed-rotting fungi that can be problematic even if the seed is treated with fungicide. Most seeds planted in the first stage have not been tested individually. Individual plants are harvested. In the second stage, a progeny plot is planted from each individually harvested plant. We shell enough seeds to perform a five-seed progeny test of each plant for the high oleic trait. If this progeny test is completed before planting, we plant only high-oleic progenies. Otherwise, we mark segregating progenies after digging and do not harvest them with the other plots of that line. Plots are planted in long narrow blocks so we can harvest all acceptable plots of a line in bulk. We also mark any plots that do not resemble the other plots in that block. Only those unmarked plots that do not border other peanut plots are harvested together in bulk.

**Purification Nursery (PUR):** a second-stage purification nursery of 660 plots incorporating nine lines in PBRS Field B5 including progeny rows of cultivars Emery N12006ol, N121007ol, N12008olCLSmT, N12009olCLT, N12010ol, N12014ol, and N12015ol. The progeny rows for a given line are planted in a group and bordered by bulk-harvested seed of the same line so that if a natural outcross occurs, it will most likely be between the line and itself. After bulk harvest of high-oleic plots, the pods will be shelled and, if the line is released, Breeder Seed conveyed to the Foundation Seed organization or company licensed to produce and sell seed of the line.