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Abstract

Project Title: Breeding Peanuts for Multiple Disease Resistance

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Summary: This project accelerates the process of development of multiply disease-resistant virginia-type peanut cultivars. Each year a new set of crosses is made, usually a set of agronomically good parents crossed with another set with the most disease resistance available. The program uses a winter seed nursery in Puerto Rico to achieve two generations per calendar year, and it uses early generation testing to identify the families most resistant to the four diseases that commonly have economic impact in North Carolina: early leaf spot caused by *Cercospora arachidicola*, *Cylindrocladium* black rot caused by *C. parasiticum*, Sclerotinia blight caused by *S. minor*, and tomato spotted wilt caused by the *Tomato spotted wilt tospovirus*. We grow separate tests for the four diseases in trials specially managed to promote specific diseases in different trials, but we score other diseases as opportunity allows. In each trial we grow the same set of families. This series of disease trials is called the "Disease Selection Test (DST)" series.

In 2011 we had 135 $F_{2:4}$ (selected as F_2 plants two generations removed from the cross, tested as F_4 grand-progeny of those selected plants), 60 $F_{4:6}$, and 16 $F_{6:8}$ families. Most of these families were either high oleic or carrying the gene for the high oleic trait. We consider the $F_{6:8}$ families to be genetically stable "breeding lines," and we select the best among them but not within them. For the $F_{2:4}$ and $F_{4:6}$ family types, we select good looking plants within the most disease-resistant families, send the progeny to the winter nursery, and return enough seed to have our replicated trials and a selection nursery in North Carolina. In addition to the disease evaluations, the $F_{6:8}$ families are generally tested in replicated trials for yield and grade at two locations in North Carolina, but in 2010 we did not get back enough $F_{6:8}$ seed from Puerto Rico to allow this, so we tested only for disease resistance in 2011.

Once a line has been tested for disease reaction as an $F_{6:8}$ family, we "graduate" resistant families into our ongoing program of evaluating lines for reactions to the four diseases, our "Disease Advanced Line Test (DAT)" series, or we graduate high-yielding lines into our Advanced Yield Test (AYT) with yield trials conducted at three locations in North Carolina and leading to the multi-state Peanut Variety and Quality Evaluation program and ultimately to cultivar release. Most years there is some overlap of the sets of lines graduated to the DAT and AYT. Because we had not collected yield data on $F_{6:8}$ families in 2011, we graduated all of them to the 2012 AYT. Only four graduated to the DAT. We moved other F_6 -derived families from previous years' testing forward in the DAT and AYT programs. Note that we do test disease reactions of lines in the AYT starting in the second year of AYT testing, and that lines in the DAT can move into the AYT program if their performance so warrants.

Bailey was released from this program in 2008, Sugg in 2009. We did not release a new cultivar in 2011. The area's shellers do not want to absorb a new cultivar every year, preferring them to come out every three to five years. We intend to replace Bailey with one of the high-oleic versions once we have collected sufficient disease, yield and grade data to warrant release. In the meantime, a number of lines that have passed through the NPB-funded program will have been sufficiently tested by the end of the 2012 season, and a release will be made if the data support it. Our ultimate aim is to replace all the cultivars currently on the seed market with high-oleic, disease-resistant releases.

Report

Project Title: Breeding Peanuts for Multiple Disease Resistance

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Objectives: Develop high-oleic peanut cultivars with resistance to CBR, Sclerotinia blight, TSWV, and early leafspot using early generation selection augmented by a winter nursery.

Procedures: A new set of crosses was made in the greenhouse on the NCSU campus in 2011. In the winter months a factorial mating was made between a set of agronomically “good” parents (N08070oJJC, N08081oJJC, N08082oJJC, N09049oIC, and N09053oICSm) and a set of 10 highly disease resistant parents selected from an earlier cycle of the program. The disease-resistant parents all traced to N06056LT or to SPT 06-06 or SPT 06-07, two wild species-derived lines from Dr. Shyamalrau P. Tallury’s program at NCSU. In the summer of 2011, each F_1 hybrid made in the winter was crossed back to its agronomically good parent. The BC_1F_1 seeds were planted in the 2011-2012 winter seed nursery at Juana Diaz, PR (PRWN) in November.

The F_2 seeds produced at the 2010-2011 PRWN were planted at the NCDA&CS Peanut Belt Research Station (PBR) at Lewiston, NC in the spring of 2011. After digging in the October, individual plant selections were made on the basis of pod appearance, and $F_{2,3}$ progenies of selected plants were planted at the 2011-2012 PRWN in November.

The corresponding $F_{2,3}$ progenies from the 2010-2011 PRWN were harvested in March 2011 by first collecting a single pod from each plant from which a single seed was planted for selection in the $F_{2,4}$ Nursery, Accelerated at PBR (11 L F4A). After performing “single seed descent” (SSD), each PRWN $F_{2,3}$ plot was harvested in bulk to provide sufficient seed to allow for replicated testing for reactions to diseases in the 2011 Disease Selection Test (DST) series. Once we identified the “best” $F_{2,4}$ families on the basis of DST data, individual plant selections were made within those families, and selected $F_{4,5}$ progenies of selected plants were planted at the 2011-2012 PRWN in November.

The $F_{4,5}$ progenies from the 2010-2011 PRWN were harvested in March 2011 with both SSD and bulk harvest as previously described for the $F_{2,3}$ families. The single seed per plant was planted in May in the 2011 $F_{4,6}$ Nursery, Accelerated at PBR (11 L F6A); the bulk-harvested seed was planted in the 2011 DST series. Once we identified the “best” $F_{4,6}$ families on the basis of DST data, individual plant selections were made within those families, and selected $F_{6,7}$ progenies of selected plants were planted at the 2011-2012 PRWN in November.

The $F_{6,7}$ progenies from the 2010-2011 PRWN were harvested in March 2011 with only bulk harvest. We consider F_6 -derived families to be sufficiently genetically stable and uniform that we classify them as “breeding lines” and do no further within-family plant selection. The bulk-harvested seed was planted in the 2011 DST series and in the 2011 Disease Preliminary Line Nursery (11 L DPN) although we did not get enough seed back from the 2010-2011 PRWN to allow for yield testing of the $F_{6,8}$ lines at PBR and UCPRS as is customary. After performing “single seed descent” (SSD), each PRWN $F_{2,3}$ plot was harvested in bulk to provide sufficient seed to allow for replicated testing for reactions to diseases in the 2011 Disease Selection Test (DST) series.

We had separate tests for four diseases with 135 $F_{2,4}$, 60 $F_{4,6}$, 16 $F_{6,8}$ families, and 14 cultivars and checks in each. The plots at PBR for early leaf spot caused by *Cercospora arachidicola* were not provided with any fungicidal spray. In late September we rated defoliation on the plots using a proportional scale of 1 (representing no defoliation) to 9 (complete defoliation usually accompanied by death of the plants). The plots at PBR for tomato spotted wilt caused by the *Tomato spotted wilt tospovirus* (TSWV) received no insecticide treatment to manage the thrips that vector the virus and were planted at 20” seed spacing to maximize thrips feeding and TSWV incidence. The plots at the NCDA&CS Upper Coastal Plain Research Station (UCPRS) near Rocky Mount, NC for *Cylindrocladium* black rot (CBR) caused by *C. parasiticum* were not treated with metam sodium fumigant nor were the seeds treated with prothioconazole to control CBR. Plots at UCPRS for Sclerotinia blight caused by *S. minor* (plots not treated with fluazinam or to control blight. All DST trials were conducted in single rows in rectangular lattice designs with two replicates. For CBR, SB, and TSWV, emerging plants were counted approximately one month after planting, then symptomatic plants were counted at appropriate times during the season, and disease incidence was expressed as a proportion of emerged plants for purposes of statistical analysis.

After analyzing the data for all four diseases, mean disease reaction values for the families were expressed on a zero-to-one scale with a score of zero for the mean indicating the greatest level of susceptibility and a score of one indicating the most resistant family. We calculated the arithmetic mean for each family across the four diseases and identified the best 20% of the $F_{2,4}$ families, $F_{4,6}$ families, and $F_{6,8}$ families. We also identified the best 20% of all families. We selected the best looking plants in the F4A, and F6A nurseries at PBRs from within the families identified as “best.”

We have the option of “graduating” resistant families into our ongoing program of evaluating lines for reactions to the four diseases, our “Disease Advanced Line Test (DAT)” series, or of graduating high-yielding lines into our Advanced Yield Test (AYT) with yield trials conducted at three locations in North Carolina and leading to the multi-state Peanut Variety and Quality Evaluation program and ultimately to cultivar release. Most years there is some overlap of the sets of lines graduated to the DAT and AYT.

Results and Discussion: Because we had not collected yield data on $F_{6,8}$ families in 2011, we graduated all of them to the 2012 AYT. Only four graduated to the DAT. We moved other F_6 -derived families from previous years’ testing forward in the DAT and AYT programs. We perform an annual summary of disease reactions and yield using databases maintained for this purpose (Fig 1.). Note that we do test disease reactions of lines in the AYT starting in the second year of AYT testing, and that lines in the DAT can move into the AYT program if their performance so warrants.

The DAT series had 64 common entries tested for the four diseases that were measurable in 2011: seven $BC_1F_{9,12}$ families selected from the 2007 DPT for further testing of yield, grade, and disease resistance; five $F_{8,11}$ families selected from the 2008 DPT, five $F_{9,10}$ families selected from the 2009 DPT, five lines entered upon the request of Dr. Roy Pittman, the USDA-ARS peanut germplasm curator, nine lines derived from interspecific hybrids developed by Dr. S.P. Tallury, and 15 checks including released cultivars (Florigiant, NC-V 11, NC 12C, Gregory, Perry, Phillips, Brantley, Bailey, Sugg, CHAMPS, Florida Fancy and runner-type cultivar Floida-07) and disease-resistant lines (Georgia Green, GP NC 343, NC 3033, N96076L, and PI 576636). There were also seven lines that made their way into the DAT by expressing superior disease resistance after surviving in the conventional cultivar development stream through a second year in the three-location Advanced Yield Test (AYT) and Early Maturity Advanced Test (EAT) series. Some of these lines originated in the DST program but fell out of the accelerated program because they did not exhibit sufficient resistance to be retained. Such families enter the conventional cultivar development stream that achieves only one generation per year and in which selection and retention in the program are based solely on pod characteristics, yield and grade. Of the 32 experimental lines developed by the breeding program rather than the species program, 16 were also entered in the multiple-location Advanced Yield Test series for broader evaluation of yield and grade, and two were entered in the multiple-location Early Maturity Advanced Test.

Disease data from the 2011 season on preliminary and advanced F_6 -derived lines was combined with data collected from 2000-2010, and means adjusted to a common environmental effect were computed. Adjusted means were converted to a zero (worst) to one (best) scale for each of the four diseases, and an arithmetic mean disease score was computed. All diseases were weighted equally. Similarly, an adjusted mean yield was computed using all data collected from plots with conventional disease management from 2000 through 2011. Of the 20 best lines for disease resistance, 8 came from the accelerated resistance selection program (Fig. 1), all of them high-oleic selections from the 2007 through 2010 DPT. Although it is often the case that the most disease-resistant lines are not the highest yielding or have the best grade, many of these selections yielded extremely well. The top 20 disease resistant lines included Bailey, released in 2008 and now widely available to growers as certified seed. The commercial value of the experimental selections cannot be known with certainty until they have passed through the multiple-year multiple-location testing program, but several of them appear to combine high yield with good disease resistance. One of Dr. Tallury’s lines, SPT 07-01, combined outstanding disease resistance with high yield based on the data available to date. It must be noted that means based on more replication are more reliable, means based on less replication less so.

Bailey was released from this program in 2008, Sugg in 2009. We did not release a new cultivar in 2011. The area’s shellers do not want to absorb a new cultivar every year, preferring them to come out every three to five years. We intend to replace Bailey with one of the high-oleic versions once we have collected sufficient disease, yield and grade data to warrant release. In the meantime, a number of lines that have passed through the NPB-funded program will have been sufficiently tested by the end of the 2012 season, and a release will be made if the data support it. Our ultimate aim is to replace all the cultivars currently on the seed market with high-oleic, disease-resistant releases.

2011 Summary of Yield and Disease Resistance

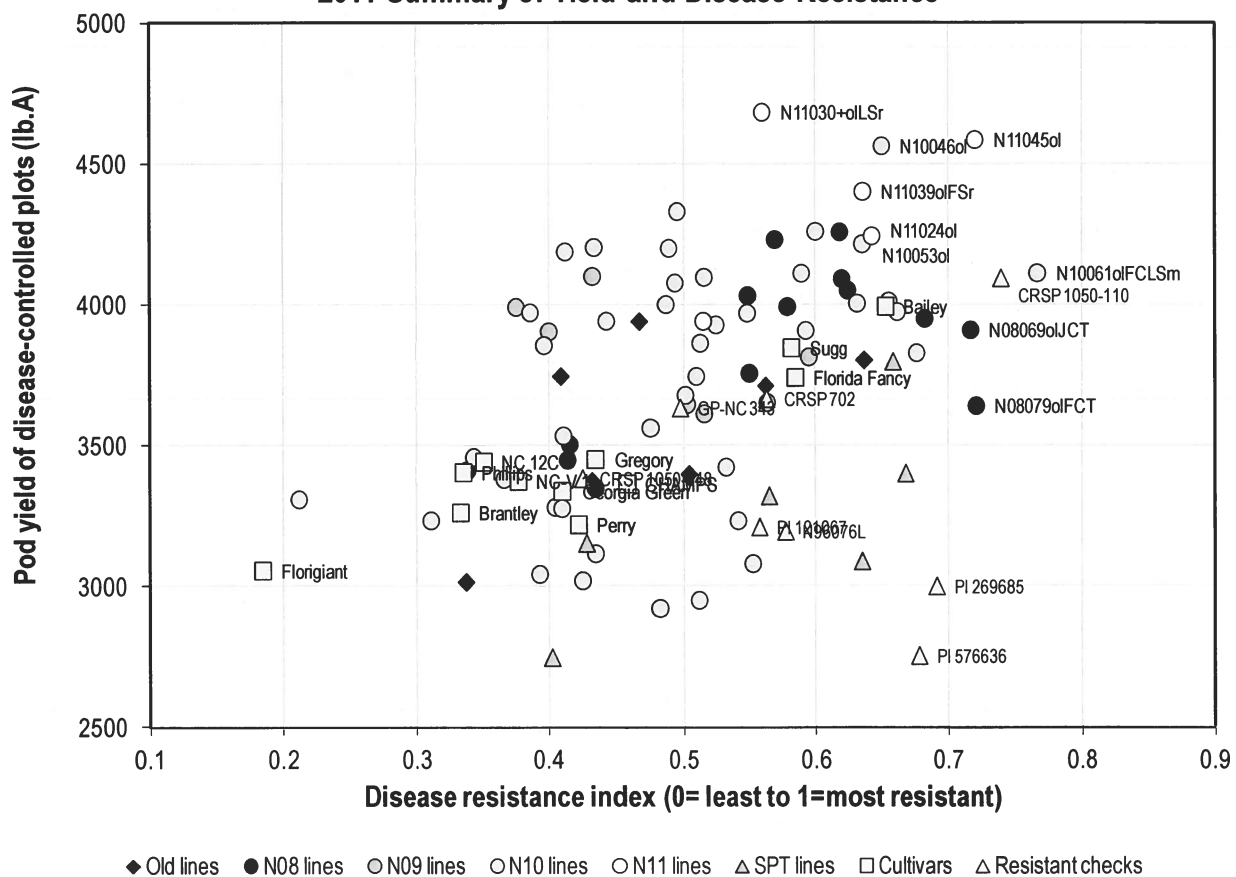


Figure 1. Pod yield with disease control versus arithmetic disease resistance index (mean of three disease scores adjusted to a scale of 0=worst to 1=best).