PROCEEDINGS OF
PEANUT BREEDING SYMPOSIUM
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J. C. WYNNE
T. A. COFFELT

DEPARTMENT OF CROP SCIENCE
NORTH CAROLINA STATE UNIVERSITY
RALEIGH

AND

SEA/USDA
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FOREWORD

A peanut breeding symposium was held in Richmond, Virginia on July 16, 1980 in association with the annual meeting of the American Peanut Research and Education Society. This bulletin is a collection of papers presented at that symposium. The symposium was held in two parts, the first dealing with peanut breeding methods, the second with breeding for resistance. These papers should provide valuable references for peanut breeders concerned with breeding methods and host plant resistance.
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I. PEANUT BREEDING METHODS
USE OF THE PEDIGREE BREEDING METHOD TO DEVELOP MULTILINE PEANUT VARIETIES

A. J. Norden

University of Florida, Gainesville 32611

There are three principal methods of breeding self-pollinated crop species. These are a) introduction, b) selection from within introduced stocks, and c) hybridization followed by selection.

Introductions are generally useful early in a breeding program or in areas that do not have established breeding programs. High yielding materials are released without improvement as new varieties. The second method, selection from within introduced stocks, is limited by the amount of genetic variability present. Either mass selection or pure line selection can be practiced on introduced stocks. The third method, hybridization followed by selection, is used most frequently by peanut (Arachis hypogaea L.) breeders in the U.S.A.

Although the bulk or pedigree method of selection (Poehlman, 1959) is most frequently used as the method of selection following hybridization, all peanut varieties from the University of Florida have been developed through a modification of the regular pedigree system. In the standard pedigree system of selection the F1 generation is grown in a bulk plot (Figure 1) since there is no genetic variability among the plants. Plants of the F2 generation are spaced so that each plant can be observed by the breeder. Selections are made until the F7-F8 generation before testing for yield. The modified pedigree system used in Florida to develop multiline peanut varieties differs from the standard pedigree after the F2 generation. We begin bulking and testing in the F3-F5 generation. In the F3 generation we use 42 plants to represent each F2 family. This is more plants than is generally used by most breeders of self-pollinated crop species. Uniform families in the F3 to F5 can be yield tested or some of the plants in the F3 may be selected, some rogued and the remainder yield tested. After several sublines have been selected, they may be bulked to produce a new variety. This system of multiline breeding is somewhat different from that proposed by other breeders of self-pollinated crops (Borlaug, 1959; Jensen, 1952; Frey et al., 1977). The major difference is that we are interested in selecting for several quantitative traits.

There are several advantages to the multiline varieties. They are as follows:

a) The multiline is productive over wide geographical areas.
b) It produces more stable yields over seasons.
c) The multiline also offers broader protection against disease.

Although the advantages outweigh the disadvantages, there are some disadvantages. The multiline variety may be less uniform and less
attractive than a pure line. It is also more difficult to maintain seed stocks and identify in seed certification programs. We are maintaining Florigiant (10 sublines when released—currently seven lines), Florispan (four lines), Early Runner (four lines), and Dixie Runner (four lines). Florunner also had four lines when released but currently has three lines. Lines are bulked based on phenotypic similarities although disease and chemical differences may be great. The third disadvantage is that the multiline generally yields less than the best line within it in a given year or location. However, since we can't predict the best yielding line, the multiline is superior over all environments.

There are two crucial phases in deciding which sublines should be bulked. Both the vegetative and reproductive characters must be considered. By the F3-F4 generation our field and laboratory observations identify which lines can be bulked. From field observations in a given year we know which lines we may or may not bulk before observing the reproductive characters. Even then all lines are dug and notes are taken on the fruit and seeds. We visually select disease-free plants with uniform pods and seeds. If the entire plot is uniform, it is bulked. If the line is not uniform, but has superior traits, we save the germplasm for possible future use.
Additional data are recorded on the uniform bulked lines in the laboratory during the winter. The fruit and seed of single plant selections are also re-evaluated during the winter. All lines and selections are placed on a table by families. We try to discard by families where possible. Generally about 95% of the F2 material is left in the field and about 75% of the harvested material is discarded in the laboratory evaluation during the winter. Because of the detailed notes required, a breeder and technician can only handle about 7 acres of breeding material.

I would like to elaborate some on the use of multilines in peanut varietal development. Yield data from 1962-1964 for eight component lines of F10rigiant, released in 1961, are shown in Table 1. Line F, the second highest yielding line in 1962, was the lowest yielding line in 1963 and 1964. This type of performance by individual components makes the multiline superior over years and environments.

Table 1. Yields of component lines of Florigiant

<table>
<thead>
<tr>
<th>Line</th>
<th>Year</th>
<th>Mean (kg/ha)</th>
<th>1962</th>
<th>1963</th>
<th>1964</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>1962</td>
<td>1963</td>
<td>1964</td>
<td>Mean</td>
</tr>
<tr>
<td>B</td>
<td></td>
<td>3503</td>
<td>3224</td>
<td>2547</td>
<td>3091</td>
</tr>
<tr>
<td>C</td>
<td></td>
<td>3501</td>
<td>3049</td>
<td>2382</td>
<td>2977</td>
</tr>
<tr>
<td>D</td>
<td></td>
<td>3276</td>
<td>3209</td>
<td>1733</td>
<td>2740</td>
</tr>
<tr>
<td>E</td>
<td></td>
<td>3212</td>
<td>3231</td>
<td>2520</td>
<td>2988</td>
</tr>
<tr>
<td>F</td>
<td></td>
<td>3674</td>
<td>2994</td>
<td>1585</td>
<td>2751</td>
</tr>
<tr>
<td>G</td>
<td></td>
<td>3456</td>
<td>3132</td>
<td>2503</td>
<td>3031</td>
</tr>
<tr>
<td>H</td>
<td></td>
<td>3875</td>
<td>3324</td>
<td>2547</td>
<td>3249</td>
</tr>
<tr>
<td>I</td>
<td></td>
<td>3604</td>
<td>3390</td>
<td>2806</td>
<td>3267</td>
</tr>
</tbody>
</table>

*aLines and years significant at .01 level.
Lines x years significant at .05 level.

Similar results were obtained with Florunner (Table 2). The yield of the component lines of Florunner were not statistically different in 1976 but were in 1977. The two-year mean yield of Florunner line 439-16-1-1 was significantly lower than two of the remaining three lines. However, I would not remove any of the lines from Florunner without many years of performance data because among other things, we know it would greatly alter the chemical composition of the cultivar. In addition, the disease resistance of the variety would be changed if the composition were altered (Table 3). If resistance to *Aspergillus flavus* was of over-riding importance, only line 439-16-10-3 would be selected. Line 439-16-10-3-2 is more susceptible to *A. flavus*. Results found by Porter and Hammons (1975) were similar (Table 4). The variety Florispan had 60% of its plants infected by *Diplodia gossypina*, whereas one of its component lines (334A-B-14) had only 35% (Table 4). Florispan is superior to Florigiant for resistance to *D. gossypina*, however, Porter and Hammons (1975) indicated that the difference in resistance is probably due to the single superior line in Florispan.
Table 2. Yields of component lines of Florunner\textsuperscript{a}

<table>
<thead>
<tr>
<th>Variety or line</th>
<th>Year</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1976</td>
<td>1977</td>
</tr>
<tr>
<td>439-16-10-3</td>
<td>5113 a</td>
<td>4725 ab</td>
</tr>
<tr>
<td>439-16-3-2</td>
<td>4988 a</td>
<td>5096 a</td>
</tr>
<tr>
<td>439-16-3-1</td>
<td>5414 a</td>
<td>4975 ab</td>
</tr>
<tr>
<td>439-16-1-1</td>
<td>4663 a</td>
<td>4637 b</td>
</tr>
<tr>
<td>3-line comp.</td>
<td>5964 a</td>
<td>4875 ab</td>
</tr>
<tr>
<td>4-line comp.</td>
<td>5420 a</td>
<td>4993 ab</td>
</tr>
</tbody>
</table>

| Mean            | 5260 | 4884  | 4978   |
| CV (%)          | 9.5  | 6.4   | 7.0    |

\textsuperscript{a}Data from R. O. Hammons, Tifton, GA (personal communication).

Table 3. Colonization of Florunner genotypes following inoculation with \textit{Aspergillus flavus} in different years\textsuperscript{a}

<table>
<thead>
<tr>
<th>Genotype</th>
<th>% Pod colonization\textsuperscript{b}</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1974</td>
</tr>
<tr>
<td>439-16-10-3</td>
<td>0 e</td>
</tr>
<tr>
<td>439-16-10-3-1</td>
<td>11 de</td>
</tr>
<tr>
<td>439-16-10-3-2</td>
<td>23 cd</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Data from A. C. Kushalappa, Ph.D. dissertation, Univ. of Florida, 1976.

\textsuperscript{b}Values followed by different letters are significant at .05 level.

Table 4. Infection of Florispan by \textit{Diplodia gossypina} compared with one of its component lines and Florigiant\textsuperscript{a}

<table>
<thead>
<tr>
<th>Variety or line</th>
<th>Plants infected by \textit{D. gossypina}, %</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Days after inoculation</td>
</tr>
<tr>
<td></td>
<td>30</td>
</tr>
<tr>
<td>Florispan</td>
<td>0</td>
</tr>
<tr>
<td>Florispan line F 334A-B-14</td>
<td>0</td>
</tr>
<tr>
<td>Florigiant</td>
<td>100</td>
</tr>
</tbody>
</table>

\textsuperscript{a}Data from Porter and Hammons, Peanut Sci. 2:23-25, 1975.
As previously mentioned, I would also like to emphasize one of the disadvantages of multiline varieties— that concerning a possible lack of uniformity (Table 5). The percent flat seeds for the component lines of Florunner range from 28.4 to 40.9 (Table 5). Line 439-16-10-3-1 is significantly poorer in that it contains a higher percentage of flattened seeds than the other component lines. However, this line has other traits which are superior and should not be removed.

Table 5. Percent flat seeds of component lines and Florunner a

<table>
<thead>
<tr>
<th>Variety or line</th>
<th>Mean percent flatness of seed b (1974 season, Tifton, GA)</th>
</tr>
</thead>
<tbody>
<tr>
<td>439-16-10-3</td>
<td>36.1 a</td>
</tr>
<tr>
<td>439-16-10-3-2</td>
<td>28.4 b</td>
</tr>
<tr>
<td>439-16-10-3-1</td>
<td>40.9 c</td>
</tr>
<tr>
<td>439-16-10-1-1</td>
<td>31.9 ab</td>
</tr>
<tr>
<td>Florunner as released</td>
<td>29.7 b</td>
</tr>
</tbody>
</table>


bMeans followed by different letters are significant at .05 level.

In summary we use a multiline concept to maintain as much genetic diversity as possible and yet obtain a fairly uniform peanut variety. The genetic diversity gives improved performance across a range of environments. Since other papers in this symposium deal with multiple crossing, I want to emphasize that the use of parental material that is well adapted and fairly good agronomically is essential if lines are to be composited into multiline varieties in early generations.

Literature Cited


USE OF SINGLE-SEED DESCENT AND POPULATION IMPROVEMENT METHODS IN PEANUTS

T. G. Isleib and J. C. Wynne
North Carolina State University, Raleigh

Historically, peanut (Arachis hypogaea L.) improvement has been achieved primarily through selection within biparental populations. The pedigree method has been the mainstay of most breeding programs, and desirable traits have been fixed either by selfing or backcrossing. However, these conservative traditional methods do not maximize the opportunity for recombination at linked loci nor the expression of "new" blocks of genes.

Hanson et al. (1967) proposed the use of recurrent selection to open the "bottlenecks" in recombination that are common in the improvement of self-pollinated species. A recurrent selection procedure has been developed for use in peanuts (Wynne, 1976) (Fig. 1). This scheme is a modification of Compton's (1968) proposal. To initiate a cycle of selection, 40 lines are crossed in 100 randomly paired matings in the fall, using each line five times as a parent. Only one seed per cross is required, so the number of pollinations per cross can be minimized. A single F1 plant per cross is grown in the greenhouse the following spring,

<table>
<thead>
<tr>
<th>Time</th>
<th>Population: Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>November</td>
<td>40 parents: Greenhouse</td>
</tr>
<tr>
<td>March</td>
<td>100 F1 plants: Greenhouse</td>
</tr>
<tr>
<td>July</td>
<td>100 F2 plants: Greenhouse</td>
</tr>
<tr>
<td>November</td>
<td>100 F2 families in F3: Winter nursery</td>
</tr>
<tr>
<td>May</td>
<td>100 F2 families in F4: Replicated field test</td>
</tr>
<tr>
<td>November</td>
<td>40 selections</td>
</tr>
</tbody>
</table>

Figure 1. One cycle of recurrent selection using 40 parents in a modification of Compton's procedure.

1 This research was partially supported by SEA/CR Research Agreement 701-15-52.
and a single F2 plant for each F1 is grown in the greenhouse during the summer. The F3 progenies are grown as a seed increase generation at a winter nursery, providing enough seed for testing in replicated trials at two locations the following summer. Forty of the 100 F4 progenies are selected as parents for the next cycle.

One such program, initiated with 40 high yielding lines from diverse sources, is currently in its third cycle. While a direct comparison of the first two cycles has not yet been made, it is possible to gauge the effect of selection by the performance of the two cycles relative to the cultivar 'Florigiant' which was included as a check in both cycles. In the first cycle, only five of the 79 lines tested yielded more than the check, while 87 out of 92 second-cycle lines were superior to Florigiant. These findings could be influenced by genotype-environment interactions, but it appears that there has been considerable gain in productivity.

As the entries tested in the field in each cycle are F2 families in the F4 generation, there should be considerable genetic variation within families. This variability can be exploited by standard pedigree or pure line selection methods. Each cycle, then, may be "milked" for superior inbred lines. The long-term utility of this procedure depends on the rate at which alleles become fixed in the population. This, in turn, is a function of population size and selection intensity. With 40 lines selected in each cycle, the rate of fixation is slow, and the population should be a source of improved germplasm for several more cycles. Another recurrent selection program was initiated with the lines derived from an interspecific cross between a cultivated accession (Arachis hypogaea L. PI 261942) and A. cardenasii nom. nud. (Fig. 2). In each cycle, 10 out of 60 crosses are selected in the F2 generation. The rate of fixation of alleles in this population is expected to be much greater than in the first population, so that the recurrent selection procedure should not be continued for more than a few cycles.

<table>
<thead>
<tr>
<th>Time</th>
<th>Population</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>November</td>
<td>10 parents</td>
<td>Greenhouse (random paired matings)</td>
</tr>
<tr>
<td>May</td>
<td>60 F1 rows</td>
<td>Field nursery (bulk harvest)</td>
</tr>
<tr>
<td>May</td>
<td>60 F2 populations</td>
<td>Replicated field test (selection among and within families)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>10 selections</td>
</tr>
</tbody>
</table>

Figure 2. One cycle of recurrent selection using 10 parents in a modification of Compton's procedure.

Another procedure similar to Compton's method is the diallel selective mating system (Fig. 3), proposed by Jensen (1970). Here, a number of selected parents are crossed in diallel. The segregating progeny are again crossed in full or partial diallel. These individuals may be tested as full-sib families or selfed to produce seed for more extensive...
Figure 3. Diallel selective mating system used in peanuts.

tests. In either case, mass selection is practiced in an early generation. Selections are then crossed in full or partial diallelel to produce segregating material for the next cycle. Inbreeding may be used at any stage to produce stable lines for conventional yield testing.

Possibly the most extreme form of recurrent selection is phenotypic recurrent selection (Matzinger and Wernsman, 1968). In this method, yield is measured on individual plants which are also propagated by cutting during the season. After harvest, cuttings of selected plants are used as parents for the next cycle. Random mating can be achieved either by creating a fixed set of randomly paired crosses or simply by retaining unemasculated flowers on each plant and pooling these as a pollen source each morning. The latter method is very simple and eliminates complicated recordkeeping.

By crossing during the winter, one cycle can be completed in a single year. The success of phenotypic recurrent selection depends on several factors:

1. Whether superior single plants can be identified in field tests
2. Whether the performance of a single heterozygous plant will be reflected in its inbred progeny
3. What the effect of genotype-environment interaction will be on a population developed at a single location.

Other population improvement methods that do not utilize recurrent selection are also under study at North Carolina State. These include the convergent and composite cross methods. Dr. Branch will discuss the convergent cross in a paper to follow. The composite crosses in our program were initiated with materials at varying levels of diversity. They are now being subjected to several years of natural selection to see whether evolutionary plant breeding is an effective selection method in peanuts.

Single seed descent, also called the modified pedigree or random method, is a breeding procedure used in self-pollinated crop species for
improvement of quantitative traits with low heritabilities such as seed yield.

The initial step in practically any breeding program is the creation of hybrid populations. This step entails the selection of parents and the actual crossing to create single or composite cross hybrids. The second step is to advance the population to a homozygous state by inbreeding, usually by allowing the plants to self-pollinate.

Single seed descent is based on a concept first addressed by C. H. Goulden in 1939. Goulden (1941) proposed separation of the advance to homozygosity from evaluation of the lines produced. In this regard, single seed descent resembles the bulk method. In practice, the breeder attempts to advance as many lines as possible to homozygosity as quickly as possible. Selection is then practiced among genetically stable lines. To prevent ballooning of population size and to assure adequate seed sampling, progeny size of each plant in a given generation is reduced to one or two which is used to propagate the population. A positive aspect of this procedure is that since little or no selection is practiced in the segregating generations, there is no need to grow the population in the environment of intended use. Therefore, whether a particular generation is grown in the field, in the greenhouse or in a semitropical winter nursery makes no difference. Because of this insensitivity to environmental effects, the approach to homozygosity can be accelerated by growing two, three or more generations per year.

The most widely cited description of single seed descent was published by C. A. Brim (1966). He proposed a modified pedigree selection method for soybeans, basing his proposition on the following rationale. First, the breeder cannot predict with certainty which crosses will produce the highest proportion of superior segregates. Because of this inability, the breeder must examine as many crosses as he can with the resources available. Second, selection becomes more effective as homozygosity increases in a population. Although there is a point at which the increase in effectiveness is not worth the resources expended in inbreeding, it is usually advantageous to inbreed to at least the F3 or F4 before evaluating lines.

Brim's method is to advance each F2 plant in a population to the desired level of inbreeding using single seed descent. That is, the single seed from each F2 plant is used to plant the F3 population. A single seed from each F3 is used to plant the F4, etc. Once the desired level of inbreeding is reached, plants derived from a single F2 are maintained in bulk. Selection may be practiced in the segregating generations for highly heritable traits such as height, maturity, seed quality or disease and shatter resistance. However, such selection should be restricted to elimination of obviously undesirable genotypes. In order to maintain variation in the population for quantitative traits, visual selection may continue during the seed increase in progeny rows. Then yield testing of the lines begins.

Any discussion of single seed descent would be incomplete without some mention of the genetical basis for its use. For species in which self-pollination is obligatory, dominance effects are generally ephemeral; that is, additive effects and additive types of epistasis are the only genetic effects the breeder can utilize in an improvement program.
Single seed descent makes use of these effects. During the development of family structure in a population segregating at a single locus (Fig. 4), the frequency of heterozygotes decreases by one-half with each generation of selfing, following from one-half in the F2 to 1/32 in the F6. In late generations the population is essentially a mixture of homozygous lines. Extrapolating from this distribution to a number of segregating loci, theoretical genetic variances may be calculated, both for the total population and within and among families (Table 1). As the population is inbred to a completely homozygous state, dominance variance in the population decreases until it eventually disappears. The additive component of variance in the population as a whole increases until it doubles.

If we consider a population in which F2 families are maintained in bulk, we see that, when inbreeding is complete, one-half of the additive genetic variance is among families with the remaining half within families. In practical terms, this means that the plant breeder, in selecting among F2 families, can capitalize on only one-half of the additive variance. To utilize the remaining one-half, he must practice mass selection within the selected F2 families.

Looking at genetic variance among and within families produced by each generation of selfing, one sees that the variance among families increases with each generation, while within family variation decreases. If the breeder selects among families in a late generation, he can capitalize on essentially all of the additive genetic variance. In other words, by selecting a single seed from each family in each segregating generation, within family variation is essentially converted to among family variation. The increased additive genetic variance among families makes selection among these families more effective.

With the pedigree method, the breeder uses intense selection to eliminate inferior lines. The effectiveness of such selection hinges
Table 1. Distribution of genetic variance among and within families with inbreeding at a single segregating locus.

<table>
<thead>
<tr>
<th>Generation $(F_n)$</th>
<th>Total $\sigma_A^2$ $\sigma_D^2$</th>
<th>$F_2$ families $\sigma_A^2$ $\sigma_D^2$</th>
<th>$F_n-1$ families $\sigma_A^2$ $\sigma_D^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Among $\sigma_A^2$ $\sigma_D^2$</td>
<td>Among $\sigma_A^2$ $\sigma_D^2$</td>
<td>Among $\sigma_A^2$ $\sigma_D^2$</td>
</tr>
<tr>
<td>$F_2$</td>
<td>1</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>$F_3$</td>
<td>3</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>$F_4$</td>
<td>4</td>
<td>4</td>
<td>1</td>
</tr>
<tr>
<td>$F_5$</td>
<td>15</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>$F_6$</td>
<td>31</td>
<td>31</td>
<td>31</td>
</tr>
<tr>
<td>$F_\infty$</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

upon the breeder's ability to identify superior plants. At the cost of no little effort he may increase the mean of the population but the variance of the lines developed decreases. On the other hand, using single seed descent, the breeder identifies and eliminates only obviously undesirable plants in the segregating generations. This may not raise the mean of the homozygous lines that are eventually developed, but neither does it drastically reduce their variance. So one might expect to find about as many superior lines derived by single seed descent as by the pedigree method. This has been the case in empirical studies comparing the two methods in soybeans, tomatoes, and wheat (Boerma and Cooper, 1975; Casali and Tischler, 1975; Knott and Kumar, 1975).

Single seed descent holds several advantages over the pedigree method. It conserves the breeder's resources in segregating generations. Less space is required for each generation. Less time and effort are required for harvest and the bookkeeping and record taking necessary in the pedigree method are eliminated. In Brim's procedure, the pedigree of the cross and the level of inbreeding are the only records kept during the advance to homozygosity. In addition, less time and effort are spent in selecting homozygotes for simply inherited qualitative traits because in late generations the population resolves into subpopulations homozygous for one allele or another without selection. Because less time is required per population, more crosses can be carried in the program. As we mentioned before, variation for quantitative traits with low
heritabilities is maintained using single seed descent. More importantly, single seed descent allows the breeder to grow more than one generation per year, reducing the time required to develop homozygous lines.

Single seed descent also holds advantages over the bulk method because it assures sampling of progeny from each F2 family. This counters the effects of genetic drift and in genotypic competition in bulk plots, helping to maintain variation for quantitative traits. In addition, the breeder using single seed descent avoids the necessity of practicing mass selection among highly heterogenous bulk populations. Because of the smaller population size required using single seed descent, the breeder can again carry more populations and can utilize the greenhouse in rapid cycling of generations.

Of course, no breeding method is without its drawbacks. We have already discussed the retention of inferior lines in relation to the maintenance of variation. From a practical standpoint these lines represent dead weight in a testing program, serving only to increase the total number that must be evaluated in yield trials. Still, most will be eliminated in preliminary trials. Another disadvantage of the method is that some traits, for example, lodging, are expressed only when a line is planted at field density. Selection for such traits cannot be practiced in segregating generations because each family is represented by only a single plant. Selection must wait until late generations. Lastly, the identity of superior F2 plants is lost. This prevents the breeder from examining superior F2 families and is a result of the simple recordkeeping system used in the procedure.

In summary, single seed descent is a breeding method proposed for use in self-pollinated crop species. It greatly reduces selection in segregating generations, saving the plant breeder substantial time and effort. It permits a rapid approach to homozygosity, two to three times the usual rate for most crops. Selection for quantitative characters is then practiced among advanced generation lines. Lastly, because the breeder spends less time and space evaluating each single population, single seed descent permits the breeder to handle more crosses than he could using the pedigree or bulk methods.

Literature Cited


Convergent Crossing for Peanuts

W. D. Branch

Univ. of Georgia, Coastal Plain Expt. Stn., Tifton, GA 31793

The success of present peanut (Arachis hypogaea L.) breeding programs depends upon the objectives set forth prior to actual initiation, the proper choice of parents, the mating system employed, the quantity and quality of heritable variability, the environmental circumstances, and finally, the breeder's keen judgment in selecting superior genotypes from the more abundant menagerie of less desirable plants within segregating populations.

Within each segment previously mentioned different methods and viewpoints exist, and it ultimately is the responsibility of individual breeders to decide which option is more apt to accomplish his goals. Thus, as in other crops, peanut breeding can be accurately described as both an art and science with just the right amount of God's good will.

In the past, introductions and selections from introduced varieties were the foundation for peanut varietal improvement in the United States. But, as Norden recently pointed out, these practices have now been practically exhausted (5). Consequently present emphasis in peanut breeding has shifted toward planned crossing blocks for combining the desirable attributes of carefully chosen parental lines.

Several crossing procedures are available for the cultivated peanut. These include: single, back, three-way, double, diallel, and multiple or convergent crosses. However, some are used more routinely than others depending upon the breeder's discretion. Additionally reciprocal, top, or test crosses are also used in certain studies.

The convergent hybridization scheme as outlined in Figure 1 was first introduced in barley by Harlan et al. (4). Its concept involves a systematic series of crossing cycles. After the first parental single cross combination, each F1 producing the proceeding generation is continuously crossed in a pyramid fashion. The initial number of single crosses needs to be 2^n, and the number of hybrid seed needs to be increased within each progressing cycle of crossing, since segregation will have begun by the second cycle (4). There are some disadvantages for this crossing method. First, the time and labor involved are directly proportional to the number of parents and crossing cycles. Second, undesirable recombinations are brought together. Third, the loss of genetic control over the cross population. Finally, the probability of obtaining all the desirable genes of the chosen parents decreases with increasing number of parental lines (1).

1Contribution of the Dept. of Agron., Univ. of Georgia, Coastal Plain Expt. Stn., Tifton, GA.
However, practicing selection between crossing cycles and increasing the number of plants per cross should enhance genetic control and desirable recombinations. But, the procedures lengthen the time required to reach the final cross. Other alternatives might be to insert a common good parent in each of the parental single crosses, especially where diverse germplasm is being combined (1), and/or backcross the F1's to a common recurrent parent. Still another modification might be to incorporate diallel matings of the first F1's from the initial single cross combinations and then converge those hybrids (2). Numerous modifications exist for utilization of the convergent crossing technique.

If linkage is regarded as a hindrance to the occurrence of segregation desired, and if linkage blocks can be successfully broken by crossing over or recombination, then as Hanson hypothesized, the inclusion of four or more parents and at least one or more intermatting cycles would be more effective in reducing the length of linkage blocks than a population derived from two parents (3). Thus, it would seem that convergent crossing may be an appropriate mating system for disrupting linkage and increasing the genetic potential of the source population. It would also seem to be advantageous in bringing together, relatively quickly, new recombinations of genes from several parents.

Another optional advantage of this scheme is the many different hybrids available after each crossing cycle which can be grown out separately for screening and selection. One should, thus, deviate from the standard practice of removing 'non-hybrid' flowers among parental F1 cross-combinations.
In 1978, after reviewing the literature and germplasm, a convergent hybridization program in peanuts was initiated at the Coastal Plain Experiment Station. The program consisted of 10 disease-resistant, 4 insect-resistant, and 2 other desirable agronomic germplasm lines to comprise the initial eight single cross-combinations. Currently, the convergent hybridization scheme is in the final cycles of crossing with the objective of combining known resistance to various diseases and insects from distinct germplasm into a desirable multipest-resistant genotype.

In conclusion, the merit of the convergent hybridization method for breeding peanuts remains to be thoroughly tested. However, most assuredly, its potential value warrants further investigation and evaluation by breeders of this "unpredictable legume."

Literature Cited


METHODOLOGY AND SUCCESS IN BREEDING FOR EARLY MATURITY

J. S. Kirby and D. J. Banks

Oklahoma State University and USDA-SEA-AR, Stillwater, Oklahoma

Abstract

In May 1980, 'Pronto', an early maturity Spanish peanut cultivar, was released jointly by the Oklahoma and Georgia Agricultural Experiment Stations and the U.S. Dept. of Agriculture. This cultivar was developed specifically for earliness utilizing 'Chico' (PI 268661), a very early but small-podded and small-seeded Spanish genotype from Russia as the female parent. The male parent was the Spanish cultivar 'Comet'. Pronto traces to one of several single plant selections made in F3 at the Caddo Research Station, Ft. Cobb, Oklahoma in 1973. Criteria used in its selection, besides earliness, were apparent high pod yield, and favorable plant, pod, and seed characteristics.

Based on observations made in the development of Pronto and other early, high-yielding genotypes, we present the following ideas. A successful program aimed at breeding for earliness depends on (1) parents that combine well to give early maturing, agronomically desirable segregates; (2) rigorous selection for earliness by limiting the growing season; (3) selection of desirable plants in the F$_2$-F$_4$ generations; (4) rapid generation advance; and (5) extensive field testing. The early maturing genotypes developed under our conditions appear to exhibit their greatest advantage over typical Spanish varieties when grown under dryland conditions and a short growing season.
The cultivated peanut, *Arachis hypogaea* L., belongs to a large and widely distributed genus native to South America. Species have adapted to a wide range of ecological niches along waterways throughout much of the continent south of the Amazon River and east of the Andes Mountains. Gregory et al. (1973) divided the genus into seven botanical sections based on crossing relationships and morphological similarities. *Arachis hypogaea* belongs to section *Arachis* along with at least 10 other species. Only *A. monticola* Krap. et Rig. (4x) is completely cross-compatible with *A. hypogaea*. Other members of section *Arachis* are diploid and hybrids between these species and the cultigen are sterile due to differences in ploidy levels. Successful germplasm introgression from diploid *Arachis* species is dependent upon restoring fertility in hybrids and then obtaining 40-chromosome plants compatible with cultivated varieties. Hybrids between *A. hypogaea* and members of other botanical sections are unconfirmed (Gregory and Gregory, 1979; Smartt, 1979).

Investigations of chromosomes have closely paralleled biosystematic studies during the past 40 years. Cytogenetic information concerning chromosome numbers of species, chromosome morphology, cytological abnormalities, polyploidy and chromosome behavior have been reported in the literature. Analyses have been used to partially characterize the species of the genus, to explain possible reasons for hybrid sterility, and to propose the most likely pathways for introgressing germplasm into *A. hypogaea*. Cytological characterization of chromosomes and genomes has progressed so that patterns of evolution can now be proposed for some groups of species.

The objective of this paper is to review cytogenetic information in the genus *Arachis*. *Arachis hypogaea*, or hybrids with this cultivated species, have been used in most cytogenetic studies, but data concerning wild species have also been reported. The information pertaining to *A. hypogaea* and then to the wild species of the genus will be presented in separate sections.

I. Cytogenetics of *A. hypogaea*

The chromosome number of *A. hypogaea* was reported as $2n = 40$ by Kawakami (1930) and confirmed by Husted (1931). Chromosomes of *A. hypogaea* are small and mostly median (Ghimpu, 1930). Husted (1933, 1936) analyzed the somatic chromosomes of the cultivated species and found one distinctly smaller chromosome pair, the "A" chromosomes, and one pair with a secondary constriction, the "B" chromosomes. Babu (1955) studied the chromosomes of several peanut varieties and found several types of secondary constrictions plus one variety, Tennessee Red, without a satellited chromosome. D'Cruz and Tankasale (1961) cytologically differentiated four cultivated varieties. Although several chromosome
studies have been reported, a complete karyotype of *A. hypogaea* chromosomes has not been described. The chromosomes of *Arachis* species are small and obtaining high quality preparations for karyotyping is especially difficult for 40-chromosome plants.

Aneuploidy in *A. hypogaea*

A plant with 41 chromosomes plus a fragment was reported by Husted (1936). Other naturally occurring aneuploids were found by Spielman et al. (1979) after observing plants grown from selected small seeds. Chemical treatments (Ashri et al., 1977), or ionizing radiation (Patil and Bora, 1961; Patil, 1968; Madhava Menon et al., 1970) have also resulted in aneuploid plants. A series of aneuploids, either natural or artificially induced, would greatly enhance cytogenetic and genetic studies of cultivated peanuts.

Meiotic Behavior of *A. hypogaea*

*Arachis hypogaea* behaves cytologically like a diploid with 20 bivalents being the most common chromosome configuration during meiosis. Husted (1936) crossed Virginia x Spanish varieties and observed mostly bivalents, but also a few univalents, trivalents and quadrivalents in F₁ hybrids. Mostly because of the multivalent formation, Husted (1936) and Raman (1976) hypothesized structural chromosome differences between the two botanical types. In a more extensive hybridization program, Stalker (unpub. data) cytologically analyzed meiotic behavior of one to five plants from each of the following hybrid combinations: Spanish x Spanish, Valencia x Valencia, Spanish x Valencia, Valencia x Spanish, Valencia x Virginia, Virginia x Valencia, Spanish x Virginia, and Virginia x Spanish. In addition to bivalents in the F₁ hybrids, a few univalents and multivalents were also rarely observed. Only the combination Valencia x Virginia produced as many as 0.51 univalents per cell. Because homoeologous chromosome pairing may be common in the genus, the data do not rule out structural differences among varieties. However, evidence supporting extensive cytological differentiation among varieties is presently lacking. An exception may be chromosome variation between Valencia and Virginia varieties where structural differences for at least one chromosome pair are probable. More extensive chromosome characterization, especially karyotype analyses, is needed to confirm divergence among *A. hypogaea* varieties.

Interspecific *A. hypogaea* Hybrids

*Arachis hypogaea* and *A. monticola* are the only known tetraploid species of section *Arachis*. The F₁ hybrids have regular meiosis and usually 20 bivalents. The two species apparently have the same genomes and barriers to gene exchange are lacking.

The tetraploid species *A. hypogaea* and *A. monticola* will also hybridize with the diploid members of section *Arachis*. Triploid first-generation hybrids have mostly 10 univalents plus 10 bivalents in pollen mother cells, but trivalents are also common in some interspecific hybrid combinations. An average of 0.95 trivalents for *A. hypogaea x A. villosa* var. *correntina* Burk., 2.15 trivalents for *A. hypogaea x A. duranensis* var. *glabra* Bois. 1905.
Krap. et Greg. nom. nud. and 3.40 trivalents for *A. hypogaea* × *A. helodes* (Mart.) Krap. et Rig. F1 hybrids were observed by Smartt (1965). The most plausible assumption is that *A. hypogaea*-wild species chromosomes form bivalents and thus allow genetic crossing-over between taxa. However, since wild species or cultivated meiotic chromosomes have not been karyotyped, interspecific chromosome pairing has not been positively confirmed. Cultivated-wild species chromosome associations were at least present in cells with trivalents.

Fertility is often restored after colchicine treatment of sterile interspecific hybrids between *A. hypogaea* and wild species. Meiosis is irregular in many 6x (*A. hypogaea* × *A. cardenasi* Krap. et Greg. nom. nud.) hybrids and up to 32 univalents per pollen mother cell have been reported (Spielman et al., 1979). Progeny from the meiotically unstable plants all have 60 chromosomes (Moss, pers. comm.). Stalker (unpub. data) also found univalents and a few multivalents in 6x (*A. hypogaea* × *A. cardenasi*) hybrids, but the frequency of univalents was greatly reduced from the data reported by Spielman et al. (1979). In 6x (*A. hypogaea* × *A. chacoense* Krap. et Greg. nom nud.) hybrids up to 18 univalents were recorded by Company and Stalker (unpub. data). Since many hexaploid plants do not produce seeds, most of the cytologically abnormal plants are automatically eliminated by the second generation after colchicine treatment because regular meiosis and associated fertility would be selected in seed nurseries. In a 6x (*A. hypogaea* × *A. batizocoi*) population from the second to fourth generation after colchicine treatments, all hybrids had 30 bivalents and regular meiosis (Stalker, unpub. data).

Aneuploid plants are commonly observed after interspecific *A. hypogaea* hybrids are colchicine treated (Smartt and Gregory, 1967; Spielman et al., 1979; Company and Stalker, unpub. data). Davis and Simpson (1976) reported chromosome numbers ranging from 32 to 48 in derivatives of a 6x (*A. hypogaea* × *A. cardenasi*) hybrid. The 60-chromosome hybrid was either meiotically unstable and thus lost chromosomes or perhaps out-crossed with a plant at a different ploidy level. Stalker et al. (1979) selected plants for agronomic fitness from the same population and found that all selections had 40 chromosomes.

II. Cytogenetics of Wild *Arachis* Species
and Their Interspecific Hybrids

Most *Arachis* species are diploid (2n = 20) but tetraploids are also found in sections *Arachis* and *Rhizomatosae* (Gregory, 1946; Mendes, 1947; Krapovickas and Rigoni, 1957; Krapovickas and Gregory, 1960; Conagin, 1963; Smartt and Gregory, 1967; Gregory and Gregory, 1979). While polyploidy is present in only two section *Arachis* species, a large group of robust tetraploid taxa are present in section *Rhizomatosae*. Because polyploid members of sections *Arachis* and *Rhizomatosae* do not hybridize (Gregory and Gregory, 1979), polyploidy probably evolved independently in the two groups.
Chromosome Morphology of Wild Arachis Species

The chromosomes of Arachis species are small, ranging from 1 to 4 µm in length. A distinctly small chromosome pair was observed in A. villosa var. correntina (Raman, 1959) and in most other section Arachis species except A. batizocoi (Smartt, 1965; Smartt et al., 1978a,b). The distinctly smaller chromosome pair was not observed in A. paraguariensis Chod. et Hassl., a member of section Erectoides (Smartt, 1965). Based on chromosome lengths, centromere position, and differential staining of heterochromatic and euchromatic regions on chromosomes, Stalker and Dalmacio (in review) identified the 10 homologues in each of the following eight section Arachis species: A. batizocoi, A. cardenasii, A. chacoense, A. correntina Krap. et Greg. nom. nud., A. duranensis, A. spegazzinii Greg. et Greg. nom. nud., A. stenosperma Greg. et Greg. nom. nud., and A. villosa Burk. Arachis batizocoi and A. cardenasii were cytologically the most distinct with each species having many slightly submedian chromosomes and unique satellited chromosomes. Arachis batizocoi had a satellite on chromosome 2 while A. cardenasii was the only species observed with two satellites (chromosomes 5 and 10). Arachis chacoense, A. duranensis and A. stenosperma each had a satellited chromosome on one of their medium-sized chromosomes, and A. correntina, A. spegazzinii and A. villosa did not have satellited chromosomes and formed another group. Smartt et al. (1978) hypothesized that two distinct genomes are present in section Arachis with most species having the "A" genome and A. batizocoi having the "B" genome. Based on chromosome morphology, Stalker and Dalmacio (in review) followed their genome designations and further proposed subdividing the "A" genome into the following karyological groups: "A1" = A. cardenasii; "A2" = A. chacoense, A. duranensis and A. stenosperma; and "A3" = A. correntina, A. spegazzinii and A. villosa. Based on single cells, species within a karyological group are difficult to distinguish cytologically. However, after averages of several cells are tabulated, each species analyzed has a unique and identifiable karyotype.

Interspecific Hybridization

All diploid species of Arachis have 10 bivalents and regular meiosis (Raman, 1976; Resslar and Gregory, 1979; Smartt et al., 1978a,b; Stalker and Wynne, 1979). Tetraploid species of section Rizomatoseae may have one to four multivalents per pollen mother cell (Raman, 1976).

Most diploid x diploid section Arachis interspecific hybrids have 10 bivalents and regular meiosis (Raman and Kesavan, 1962; Resslar and Gregory, 1979; Stalker and Wynne, 1979). However, when A. batizocoi is used as a hybrid parent with other diploid section Arachis species, meiosis is irregular and F1 hybrids are sterile (Gibbons and Turley, 1967; Smartt et al., 1978a,b; Stalker and Wynne, 1979). The meiotic analyses confirm the presence of two distinct genomes in the section. Chromosomes of species with the "A" genome apparently pair even though extensive structural rearrangement among chromosomes exists (Stalker and Dalmacio, in review). Homoeologous pairing of morphological different chromosomes must be common in the genus.
Amphidiploid plants produced from semi-fertile interspecific section Arachis hybrids have a range of chromosome associations from 20 bivalents to others with up to 9 quadrivalents per pollen mother cell (Stalker, unpub. data). Pollen fertility in amphidiploids is uniformly greater than in corresponding 2x or F1 hybrids, but most 4x plants do not produce seeds. However, at least some amphidiploids make good pollen parents when used in crossing programs with A. hypogaea. The resulting trispecific hybrids have only 40 to 60% pollen fertility and peg production is rare (Stalker, unpub. data).

Intersectional Arachis hybrids are difficult to produce (Gregory and Gregory, 1979), and cytological analyses of wide hybrids are correspondingly rare. Only cytological data of intersectional hybrids between sections Arachis and Erectoides have been reported (Stalker, 1978; in review). In these crosses, an amphidiploid of A. rigonii Krap. et Greg. (2x) x A. sp. 9841 GKP (2x) was hybridized with section Arachis species A. chacoense and A. steinbacheri. Quadrivalents and bivalents were mostly observed, but a few trivalents were also present in pollen mother cells of the 30 to 32 chromosome hybrids. Intersectional chromosome associations were postulated at least for cells with multivalent associations, and the species of sections Arachis and Erectoides may have a genome in common. Intersectional hybrids between sections Erectoides (E) and Rhiizomatosaes (R) have also been produced and cytologically analyzed (Stalker, unpub. data). Some of the hybrid combinations do not flower while the complexity of others make interpretation of analyses difficult. This is especially true when only bivalents were observed in the polyploid hybrids. In one hybrid combination, 4x [[A. rigonii (E) x A. sp. 9841 GKP (E)]] x 4x [A. sp. 9841 GKP (E) x 9570 GKP (R)], an average of 17.60 bivalents per cell were observed and many of these chromosome pairs represent intersectional homologies.

Discussion

Most species of the genus Arachis are diploid, but polyploidy is found in at least the two sections Arachis and Rhiizomatosaes. Polyploidy probably evolved independently in the two groups, and perhaps more than once in section Rhiizomatosaes.

Diploid species of the genus have normal meiosis. First-generation hybrids of diploid section Arachis species likewise have 10 bivalents, except hybrids with A. batizooi which are sterile and meiotically irregular. The diploid section Arachis species are cytologically identifiable and two distinct genomes are present with most species having the "A" genome and A. batizooi having the "B" genome. Species with the "A" genome can be further grouped into three groups as follows: A1 = A. cardenasi; A2 = A. chacoense, A. duranensis and A. steinbacheri and A3 = A. correntina, A. spagazzini and A. villosa. Because hybrids between cytologically distinct section Arachis species usually have 10 bivalents, homeologous chromosome pairing is common. The allopolyploid A. hypogaea probably has both an A and a B genome. Several progenitor species of A. hypogaea have been hypothesized (Smartt and Gregory, 1978a,b; Gregory and Gregory, 1976; Varisai Muhammad, 1973; Seetharam et al., 1973; Krapovickas et al., 1974), but the ancestors are as yet unconfirmed.
Interpretation of cytological data in polyploid interspecific hybrids is difficult. Bivalent formation does not confirm nor rule out interspecific chromosome associations. Multivalents are more indicative of interspecific homologies, but when an average of only one or two quadrivalents per cell are observed, the amount of chromosome homologies is unknown.

Crossing relationships have been reported by Gregory and Gregory (1979) for species of each botanical section in the genus. Based on compatibilities among species, several genomic groups can be postulated, including: AM (Ambinervosae), C (Caulorhizae), E (Erectoides), EX (Extranervosae) and T (Triseminalae). Members of sections Rhizomatosae, Erectoides and Arachis all hybridize and chromosome homologies are probably present among these groups. After cytological analyses of intersectional hybrids are completed, a clearer picture of chromosome homologies will emerge, and subdivisions of the proposed genomes are expected for some groups.

Plant explorations are continuing and many species still need to be cytologically analyzed. The accumulated cytotegenetic information for cultivated and wild Arachis species should soon be useful for manipulation of chromosomes for the improvement of cultivated varieties.

Literature Cited


II. BREEDING FOR DISEASE RESISTANCE
Throughout the world where peanuts (Arachis hypogaea L.) are produced, Aspergillus flavus Link ex Fr. and related fungi are found associated with the peanut fruit (14,39). Isolates and strains of these fungi produce aflatoxins that are highly toxic and sometimes carcinogenic to animals (5,19,42,45). The aflatoxin contamination of peanuts is of great concern to peanut farmers, brokers, processors and end-use manufacturers. Although it is thought that many advanced cultural, harvesting, curing and handling procedures aid in preventing contamination, the development of a peanut cultivar with appreciable resistance to colonization by the aflatoxin-producing fungus would be of great benefit to the peanut industry.

Some Factors Associated with Peanut Fruit Colonyation and Aflatoxin Development

Environmental conditions (2,3,15,22,38,44), microbial activity (17, 18,36), cultural methods (4,9,31,33,37,38), and peanut genotypes (Arachis hypogaea L.) (6,7,29,30,52,54) may interact to affect the degree of infection of peanut fruit by Aspergillus species and the potential for aflatoxin development during pod development and the subsequent harvesting and drying period. Cultural and management procedures may help control fungal infection and aflatoxin contamination. Such procedures include: rotation of peanuts with other crops that reduce A. flavus population in the soil (16,32,34); prevention of drought stress (10,22,35,44); reducing biological and mechanical harvest damage (8,23, 24,26,43,47,50); harvesting at optimum pod maturity (13,24,25,44), and continuous safe and rapid drying of pods after digging (4,9,31,33,37, 38,47). These factors will continue to be important as peanut varieties are released that minimize the fungal invasion by Aspergillus species. Development of new varieties are being carried out by Mixon (28). Research related to the peanut genotypes exhibiting resistance to seed colonization by aflatoxin-producing strains of Aspergillus species have revealed that several factors are associated with resistance (28). The factors associated with the testa are cell structure (11,12,53), cell arrangement (46,49), permeability (20), waxy surface (21), tannin content (40,41,48), and amino acid components (1).
Progress in Breeding for Resistance

The laboratory procedure of Mixon and Rogers (29) has been utilized to select peanut genotypes for resistance to seed colonization. Selections were made in segregating generations following crosses among genotypes previously identified as being resistant to aflatoxin-producing strains of *Aspergillus flavus* and/or *A. paraciticus* (7109, 72120, 72118, 69, 72116, 7309) (Table 1). Single plant selections were made following the *F*6 and *F*8 generations in populations of two genotypes (7109 and 69) selected for agronomic performance in early generations following hybridization. Data showing the percentage colonization of seed samples from selections in advanced generations following hybridization is presented in Table 2. For four of the lines for which parental colonization data were available were more resistant to colonization than the more resistant parental genotype. Mean colonization percentages for inoculated samples from six replications of these selections and three control genotypes, PI 337409, Florunner, and PI 331326 in 1977-1979 (Table 3) showed that the selections were more resistant to fungal infection than the variety Florunner or the susceptible introduction, PI 331326. Colonization percentages for four of the genotypes selected for resistance were not significantly greater than the resistant genotype PI 337409.

All of the selections that were uninoculated, but incubated in a humid atmosphere, had lower colonization than commercial variety, Florunner, or the susceptible check, PI 331326. Since the uninoculated treatment is only an index of the *Aspergillus* infection resulting from field or pre-laboratory contamination, the incidence of colonization may be associated with inherent differences in resistance of certain pods to penetration and infection. For the 3-year summary there was a highly significant (probability 0.001) year by genotype interaction for both the inoculated and uninoculated incubated samples. From similar studies previously reported (28) there was a correlation \( r = 0.69 \)
Table 2. Advanced line selection for *A. parasiticus* resistance.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Parents</th>
<th>Generation of selection</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Female</td>
<td>Male</td>
<td>F4</td>
</tr>
<tr>
<td>7109b</td>
<td>--</td>
<td>--</td>
<td>7</td>
</tr>
<tr>
<td>72120</td>
<td>20</td>
<td>44</td>
<td>2</td>
</tr>
<tr>
<td>72118</td>
<td>35</td>
<td>77</td>
<td>14</td>
</tr>
<tr>
<td>69b</td>
<td>--</td>
<td>--</td>
<td>(8)c</td>
</tr>
<tr>
<td>72116</td>
<td>60</td>
<td>12</td>
<td>35</td>
</tr>
<tr>
<td>7309</td>
<td>77</td>
<td>15</td>
<td>5</td>
</tr>
</tbody>
</table>

*a Seed colonization expressed as mean percentage of seed in duplicate samples of plant selections with visible infection following inoculation and incubation.

*b No selection for resistance in early generation following cross.

*c Data in parentheses for selection in F8 through F12 generations.

Table 3. Percentage seed colonization of advanced line selections and check genotypes, 1977-1979.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Inoculateda</th>
<th>Uninoculatedb</th>
</tr>
</thead>
<tbody>
<tr>
<td>72116</td>
<td>8.0a*</td>
<td>1.2a</td>
</tr>
<tr>
<td>PI 337409 (res. accession)</td>
<td>9.0a</td>
<td>2.8ab</td>
</tr>
<tr>
<td>69</td>
<td>9.8a</td>
<td>6.5c</td>
</tr>
<tr>
<td>72118</td>
<td>10.0a</td>
<td>3.7abc</td>
</tr>
<tr>
<td>7309</td>
<td>7.9a</td>
<td>2.9ab</td>
</tr>
<tr>
<td>72120</td>
<td>12.4ab</td>
<td>5.5bc</td>
</tr>
<tr>
<td>7109</td>
<td>18.7bc</td>
<td>5.7bc</td>
</tr>
<tr>
<td>Florunner (commercial var.)</td>
<td>39.1d</td>
<td>10.7d</td>
</tr>
<tr>
<td>PI 331326 (sus. accession)</td>
<td>80.1e</td>
<td>15.3e</td>
</tr>
</tbody>
</table>

*a Inoculated with *A. parasiticus*.

*b Contaminated in field or subsequent handling and processing.

*Column means not followed by common letter differ at 0.05 probability level (DNMR) test.

Genotype x year interaction means for inoculated and uninoculated are significant at 0.001 level of probability.

*P < 0.05* between colonization percentages of peanut genotypes for the inoculated and uninoculated treatments.

Yield, market value and seed data for the lines and the Florunner cultivar are presented in Table 4. *Aspergillus*-resistant lines 7109 and 72120 were not significantly different in pod yield per acre or total...
Table 4. Yield, value and seed cata for advanced peanut lines, Tifton, 1977-1979.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Pod yield (lb/A)</th>
<th>Valuea ($/A)</th>
<th>Total meats (%)</th>
<th>Total SMK (%)</th>
<th>Other kernels (%)</th>
<th>ELK (%)</th>
<th>Seed no. (100/g)</th>
<th>Seed damage (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>7109</td>
<td>4944a*</td>
<td>1027</td>
<td>72.5b</td>
<td>69.6ab</td>
<td>2.2a</td>
<td>31.1a</td>
<td>153a</td>
<td>0.8a</td>
</tr>
<tr>
<td>Florunner</td>
<td>4831a</td>
<td>1021</td>
<td>75.3a</td>
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</tr>
</tbody>
</table>

aValue based on 1979 market price.
bVisible damage of seed that are rancid, decayed, moldy or with sprouts, insect or worm damage.
*Column means followed by the same letter are not significant at the 0.05 probability level, DNMR test.

sound mature kernels (SMK) from the commercial variety Florunner. The calculated market value of 7109 was equal to Florunner but 72120 and other resistant lines were lower in value per acre. The seed size data, as indicated by seed/100 g and percentage extra large kernels (ELK), showed that 7109 has a larger seed size than Florunner. In bulk lot processing using a commercial type shelling and grading procedure, it has been determined that the seed remaining on the grading screen for extra large kernels exceeds the 512 seed per pound required for a large-seeded Virginia peanut. Therefore, 7109 would be marketed as a runner market type. However, the peanut processor could use the ELK's to an advantage by selling these at a higher market value. The other four genotypes selected for resistance are probably not acceptable in terms of production, market value, or other characteristics; however, these lines may be improved by crossing or backcrossing.

It is evident that progress has been made in developing agronomically suitable genotypes with resistance to aflatoxin-producing strains of Aspergillus spp. Previous assays of sound undamaged seed with little or no fungal contamination have indicated a low level of aflatoxin content (51). Although breeding for resistance to Aspergillus spp. is hampered by mutagenic factors associated with resistance (27), by variability of fungal isolates (30) and by variation in the incidence of infection resulting from environmental factors and mechanical damage, the development of agronomically acceptable Aspergillus-resistant cultivars is possible.
Literature Cited


DISEASE RESISTANCE BREEDING AT ICRISAT

and S. L. Dwivedi

International Crops Research Institute for the Semi-Arid Tropics,
Patancheru, P.O., Patancheru-502324, A.P., India

The ICRISAT breeding program commenced in 1976 but full-scale hybridization programs did not start until 1977. A great deal of emphasis has been placed on breeding for both pest and disease resistance for the semi-arid tropics because the high cost of pesticides and applicators are often beyond the reach of the small-scale peanut farmers of this large region of the world.

As the program is international in scope, only major diseases occurring on a world-wide basis are presently being considered. When the program expands and has wider responsibilities, it will be possible to cover some other diseases which are important, but only occur on a limited regional basis. The present plan is to place two small teams in Africa, one in eastern/central Africa and one in west Africa, consisting of a breeder and a pathologist during the first third of the present decade. In India there are also possibilities of working on locally occurring diseases particularly when they are present at the research center. A good example of this is bud necrosis virus caused by tomato spotted wilt virus (Ghanekar et al., 1979). This virus is also serious in other areas of India and efforts are being made to locate sources of resistance to it (Gibbons, 1978).

Breeding for Resistance to Foliar Diseases

The main diseases being studied are the leafspots, caused by Cercospora arachidicola and Cercosporidium personatum, and rust, caused by Puccinia arachidis.

Leafspots (A. hypogaea)

Both the leafspot fungi occur in Hyderabad but the late leafspot, C. personatum, is more common and more destructive than C. arachidicola. Therefore much emphasis has been put on breeding for resistance to C. personatum at present until we have other sites where C. arachidicola is the dominant leafspot fungus.

Some 40 cultivars or landraces of A. hypogaea from a germplasm collection of over 7000 lines were found to have promise for resistance to C. personatum (Subrahmanyam et al., 1980b). They received ratings of 3-5 when scored on a 9-point field scale (where 1 = no disease and 9 = severe disease, with total or near total defoliation). These 40 entries showed little or no defoliation and spots were generally few in number, small and sporulation was sparse. Three of the entries--NC Ac 17090, EC 76446 (292), and PI 259747--are also being extensively used as sources of resistance to groundnut rust (Puccinia arachidis) (Subrahmanyam et al.,
1980a). PI 259747 has been reported to be resistant to *C. arachidicola* also in the USA (Sowell et al., 1976). However, at ICRISAT (Subrahmanyan et al., unpubl. data) and in Brazil, PI 259747 gives a susceptible reaction to this fungus. Crosses have been made between the promising resistant lines and high yielding adapted cultivars. Advanced lines will be tested on a multilocational basis to assess yielding ability and disease reaction.

**Leafspots (Wild *Arachis* Species)**

Three sources of resistance to leafspots have been used in this program. *A. chacoense* is highly resistant to *C. arachidicola*, *A. cardenasi* is immune to *C. personatum*, and *A. sp. HLK 410* has been reported to be resistant to both fungi (Abdou, 1966; Sharief, 1972; Abdou et al., 1974; Hammons, pers. comm.). Initial crosses were made with a range of *A. hypogaea* parents and the F1 generation was triploid and sterile. Hexaploids were produced by colchicine treatment of the sterile triploids. At ICRISAT the hexaploids have been evaluated for leafspot resistance and other agronomic characters over several generations. Highly promising material has been backcrossed to *A. hypogaea* and a second backcross of the resulting pentaploids has produced near tetraploid lines which are to be evaluated for leafspot resistance and yield potential. Some of the selected hexaploids are themselves promising for yielding ability and are still segregating. Interspecific hybrids from the same wild species sources, but originating from the North Carolina program, and now at, or around, the tetraploid level are being yield tested and assessed for leafspot resistance this season.

Attempts are also being made to incorporate genes from other wild species into the *A. hypogaea* genome. These species are in other sections of the genus and incompatibility barriers must be overcome. The use of *in vitro* ovule culture and the addition of chemical amendments to developing pegs are being studied (Sastri et al., 1980).

**Rust**

New sources of rust resistance have been found in the germplasm collection at ICRISAT and suitable techniques have been formulated to ensure that large-scale screening of breeding material can be carried out in both the rainy and post-rainy seasons (Subrahmanyan et al., 1980a). A joint USDA/ICRISAT rust nursery is also being grown at ICRISAT in collaboration with Dr. R. O. Hammons to test all reported sources of rust resistance in the world in one trial.

Early generation progenies in the rust breeding program and the rust-resistant parents have been sent to cooperators in several countries. Breeders can therefore select within the segregating populations for agronomically superior resistant lines. The rust-resistant parents, and other cultivars and species which show varying symptoms or reactions to rust at ICRISAT, are being grown at many sites to see whether they exhibit different disease ratings or symptoms from those at Hyderabad. This may give some indication of whether races of rust occur. The 14 FESR lines received from the USDA as F3 progenies (Bailey et al., 1973) have been advanced to the F8 generation at ICRISAT. Initially
single plant selections were made as the F4 generation was still segregating for rust resistance. Since then progenies have been advanced both as single plant selections and bulks. Some of these lines have shown yield advantages over standard cultivars.

**Resistance to Both Leafspots and Rust**

A paper on sources of resistance to both rust and late leafspots is being presented by ICRISAT scientists (Subrahmanyam et al., 1980b) at a session of the APRES meeting. Briefly we have found that several rust-resistant cultivars show a useful degree of resistance to *C. personatum* as well. Advanced breeding lines involving these parents are being evaluated for dual resistance and other agronomic characters.

**Multiple Disease Resistance**

The possibilities of combining several resistances into one genetic background are being investigated. Some of the possibilities are listed below:

1. Some FESR material has been selected for possible combined resistance to rust, late leafspot and thrips.
2. Rosette-resistant lines from Senegal have shown promise for late leafspot resistance.
3. Crosses have been made with rosette-resistant lines and rust-resistant parents (this material will be sent to Africa when our cooperative program starts as rosette almost definitely does not occur in India).

**Other Disease Resistance Programs**

**Resistance to Aspergillus flavus**

This program commenced with two Valencia genotypes reported to have dry seed resistance to this fungus. Recently new sources of resistance have been received from Florida and Georgia (Bartz et al., 1978; Mixon and Rogers, 1973).

A laboratory has recently been set up to rapidly screen material for dry seed resistance. In addition to this test, the production of aflatoxin from inoculated seed will be studied, and any lines that do not produce aflatoxin will be selected.

**Resistance to Pod Rot and Pod Breakdown Fungi**

This work has just commenced and at present the main pathogens being investigated are *Fusarium* species, *Rhizoctonia solani*, and *Macrophomina phaseolina*. Sick plots are being developed and test material will be grown in them to assess their reaction to the pathogens. Useful material will be incorporated into the breeding program. At present some 30 lines have consistently shown less than 10% pod rot over the last three seasons (Mehan et al., unpubl. data).
Resistance to Peanut Mottle Virus (PMV)

Large-scale screening of germplasm is underway to determine whether there is resistance to PMV in the cultivated groundnut or in the wild species. Mass screening techniques have been developed whereby plants are inoculated with PMV using a high pressure sprayer containing infected leaf extracts in phosphate buffer containing celite and mercaptoethanol (Reddy et al., unpubl. data). All lines are also being checked to determine whether the virus is not seedborne in any cultivar, as this would help in controlling the perpetuation of the disease from season to season.

Resistance to Bud Necrosis Virus (BNV)

As stated earlier this disease is caused by TSWV and the vector is a species of thrips. Despite extensive screening no cultivated groundnut has been found with resistance to this disease so far. Certain wild species have not so far been infected by either mechanical inoculation or by grafting but this work needs confirming (Ghanekar et al., unpubl. data).

In the meantime, we are using various methods to control BNV including early planting, close spacing, and limited insecticidal use.

Testing Breeding Material for Reactions to Pests and Diseases

We are attempting to monitor disease and pest reactions of any superior breeding material we produce. This approach is necessary because there is always the possibility that a cultivar which is rust resistant, for example, may be ultra-susceptible to another pest or disease.

Literature Cited


BREEDING FOR RESISTANCE TO CYLINDROCLADIUM BLACK ROT AND SCLEROTINIA BLIGHT IN PEANUTS

T. A. Coffelt, D. M. Porter and K. H. Garren

Agricultural Research, SEA/USDA
Tidewater Research and Continuing Education Center, Suffolk, VA 23437

Cylindrocladium Black Rot

Cylindrocladium black rot (CBR) of peanuts (Arachis hypogaea L.) is caused by Calonectria crotalariae (Loos) Bell & Sobers, Cylindrocladium crotalariae (Loos) Bell & Sobers, a soil-inhabiting fungus (2). Symptoms of CBR first appear in the field as wilted mainstems. As the disease progresses, the entire plant wilts and dies. Finally, large areas of dead and dying plants occur in a field. At the same time these above-ground symptoms occur, pod and root rot occurs below ground. The best way to positively identify CBR in the field is the appearance of reddish-orange fruiting structures (microsclerotia) at or near the soil surface on infected stems, pegs or roots.

Three breeding programs in the United States are involved in CBR research. In Georgia, an effective laboratory screening procedure has been developed for identifying CBR resistance in seedlings (11). As a result of this procedure, 13 lines have been identified for release as CBR-resistant germplasm.

The program in North Carolina has resulted in the release of a small-seeded Virginia-type breeding line, NC 3033, as CBR-resistant germplasm (3). As a result of their breeding program, they currently have three breeding lines in the final stages of testing for possible release as CBR-resistant varieties. Other work in North Carolina (9) has demonstrated that different races of the fungus may be present or may develop in the future if resistant varieties are used extensively. If this has or does occur, breeding for resistance to CBR will be more complex. Additional work in North Carolina (10) has indicated that resistance to CBR is inherited quantitatively, indicating that back-crossing or crossing of resistant x resistant parental lines may be necessary to obtain highly resistant cultivars.

In Virginia, over 200 peanut genotypes have been field-screened for CBR resistance (5,6,8). Generally, most Spanish types (Arachis hypogaea ssp. fastigiata var. vulgaris) are resistant, while most Valencia types (Arachis hypogaea ssp. fastigiata var. fastigiata) are very susceptible. Virginia types (Arachis hypogaea ssp. hypogaea var.

1

Cooperative investigations of the Agricultural Research, Science and Education Administration, U. S. Department of Agriculture, and The Virginia Agricultural Experiment Station of Virginia Polytechnic Institute and State University.
range in susceptibility between resistant to very susceptible. Similar results have been observed in other screening tests (1,12,13,16,17). It is also important to note, however, that exceptions to this generalization have been found. As a result of the screening program in Virginia, the small-seeded Virginia-type breeding line VGP-1 was identified and released as CBR-resistant germplasm (4).

The screening tests have also indicated that significant differences may exist between the pod and root resistances to CBR on the same plant (5,6). In one study (5), Tifspan had below average root damage, but above average pod damage, while Au-3 had below average pod damage and above average root damage. These differences indicate that separate genetic mechanisms may control resistance of pods and roots to CBR. If this is true, knowing the reaction of both plant parts to CBR is essential in choosing parental lines for a breeding program (5,6).

In 1974 a breeding program was initiated in Virginia to produce CBR-resistant peanut cultivars with two objectives: (a) to develop CBR-resistant Virginia-type cultivars and (b) to develop CBR-resistant germplasm more resistant than currently available germplasm. In order to meet these objectives, crosses have been made between resistant x adapted cultivars and resistant x resistant cultivars.

The breeding procedure used is a modified pedigree system (Fig. 1). The crosses are made in a greenhouse crossing bench; the F1 generation is grown in the field or greenhouse, depending upon the time of year crosses are harvested. The F2 generation is grown in the field and selection is made for desirable agronomic traits and CBR resistance when feasible. Individual plant selections are seed increased in the Puerto Rico winter nursery and bulk selections are replanted the following year in the field with the increased seed from individual plant selections for further selection and evaluation. This cycle is repeated each year until CBR-resistant lines with desirable agronomic traits or increased CBR resistance are obtained. Lines with increased resistance will be used as parents, while agronomically accepted lines with CBR resistance will be proposed for release to growers as new cultivars.

![Diagram](image)

**Figure 1.** Modified pedigree breeding procedure being used to develop CBR-resistant cultivars and germplasm.

The major problem that has developed in the system is a lack of adequate disease pressure during the field screening. The method
developed in Georgia (11) and other techniques are being evaluated as possible ways to insure adequate disease pressure during screening. However, based on previous results (5,6) it is important that both the roots and pods be tested for reaction to CBR before a plant is designated as resistant.

In the screening of Spanish cultivars (5), two cultivars (Spancross and Tifspan) with the resistant parent Argentine in common were as resistant as Argentine. The same was true of Spanhoma, a selection from Argentine. Similar results were obtained for Tamnut 74 and Comet which were derived from a cross and selection, respectively, involving the resistant parent Starr. Since resistance was present in these cultivars without selection for resistance, breeders may be able to select for acceptable agronomic and market traits in early generations and for resistance in later generations (5).

Sclerotinia Blight

Sclerotinia blight of peanuts (Arachis hypogaea L.) in Virginia and North Carolina is caused by Sclerotinia minor Jagger, a soil-borne fungus (14). Symptoms of Sclerotinia blight first appear as wilted lateral branches with white mycelium growing on the branches, especially where they are in contact with the ground. Sclerotinia can eventually cause death of the plant and/or rotting of pegs and pods. The best way to positively identify Sclerotinia blight is the presence of a white mold and small irregularly shaped black fruiting structures (sclerotia) inside diseased pod and stem tissues or on the surface of diseased stems and pods or soil under the plants.

Porter et al. (15) were the first to report screening results for resistance to Sclerotinia blight. They found Florigiant to be the most resistant of the cultivars tested and suggested breeding lines with Spanish or Valencia parental lines may be more resistant than those without. More recently, Coffelt and Porter (7) have reported that two genotypes, Chico and VA 71-347, have been consistently more resistant than Florigiant and other current cultivars as well as other breeding material screened. The two germplasm lines (NC 3033 and VGP 1) released for CBR resistance have also shown appreciable resistance to Sclerotinia blight.

In 1979, a breeding program for resistance to Sclerotinia blight was initiated in Virginia. Crosses were made between resistant, moderately resistant and susceptible genotypes. These crosses also included backcrosses with a resistant parent.

As with CBR, the development of races of Sclerotinia minor appears to be a possibility, making future development of resistant varieties more difficult. Resistance to Sclerotinia blight appears to be quantitatively inherited in addition to the cytoplasmic factors indicated in crosses with Chico and Florigiant (7).

In summary, the development of CBR and Sclerotinia blight-resistant cultivars that are commercially acceptable appears promising. However, the possibility of race development in both causal fungi indicates that
a continuous breeding program searching for new sources of resistance and incorporating this resistance into additional acceptable cultivars will be necessary to maintain resistant cultivars.

Literature Cited


BREEDING FOR RESISTANCE TO POD ROT AND LESION NEMATODES

O. D. Smith and T. E. Boswell

Texas Agricultural Experiment Station, Texas A&M University, College Station 77843

Abstract

Adapted cultivars were crossed and backcrossed with Plant Introductions 341885 and 365553 for pod rot resistance, and 295233 and 290606 for lesion nematode resistance. Segregating populations were screened in field tests where pod rot or lesion nematodes were expected based on site history. Repeated evaluations were necessary because of mid-classifications resulting from escape and micro-environmental variability. Pod rot and nematode evaluations on a plant progeny basis were used where variability in disease incidence was pronounced. Moderately rot-resistant Spanish x PI 341885 F6 and F9 lines yielded equal to the commercial Spanish and runner checks. In lesion nematode-infested areas the lesion nematode resistance of PI 365553, which has a higher level of pod rot resistance than PI 341885, was equal to that of I 295233 and PI 290606. Multiple resistance in PI 365553 should increase its potential usefulness as a parent. F6 lines derived from PI 365553 are now in yield tests.

Pod Rot Resistance

Pod rot caused by Pythium myriotylum Drechsler and Rhizoctonia solani annually lowers the yield and grade of peanuts in Texas. Early symptoms of P. myriotylum infection in root and pod tissue are small, dark brown to black, sunken, necrotic spots which rapidly spread and coalesce, often encompassing the total pod tissue. The rotted pods remain black in appearance when dried. Infected kernels become watery and may be totally destroyed. Losses from this organism are greatest in fields with high moisture and high temperature. Poor quality (salty) irrigation water tends to increase the severity of the disease.

R. solani infection of roots and pods produces symptoms which may resemble those of P. myriotylum (3), but the lesion margins are more delineated and decayed pods are generally medium to dark brown in color compared to a darker black coloration with Pythium. Kernels from infected pods are initially buff in color, later darken, and in time become totally rotted. These diseased kernels are covered by buff-colored mycelia with masses of brown sclerotia. The decay produced by R. solani is a drier type of rot than that which is produced by P. myriotylum.

PI 341885, 'Toalson', and PI 365553 have shown resistance to these rotting organisms during several years of testing in Texas (2). PI 41885 and Toalson are of the vulgaris subspecies with the latter being well adapted to Texas. However, in the absence of severe pod disease,
Toalson is usually exceeded by 'Florunner' in yield and grade. PI 365553 is of the subspecies *hypogaea*, is late maturing with a red testa, and has shown a higher level of pod rot resistance than the other genotypes.

PI 341884 and PI 365553 have been crossed and backcrossed with adapted commercial Spanish and runner cultivars and selected progeny advanced to the F₈ generation. Selection has been effected in field tests for disease reaction and agronomic traits during successive generations. Pod disease ratings were visually assigned on a 0 (no disease) to 10 (totally discolored pod tissue) basis. Field sites were chosen on the basis of pod disease history: *Pythium* being the primary pod-rotting pathogen at one location and *Rhizoctonia* at the other. The major emphasis for selection has been the disease and agronomic response of plant rows as a whole (families) with only superior plants taken from the 20+ plants within the selected, thinly planted rows. The emphasis on the family was aimed at reducing the number of erroneous selections resulting from escape.

Lines with yield potential equal or superior to the Spanish commercial checks and pod disease ratings equal or superior to PI 341885 have been selected according to data from 1978 and 1979 yield tests in both *Pythium* and *Rhizoctonia*-infested soils. Additional testing will be required to evaluate the performance of these lines in a variety of disease pressures and management systems. Spanish and runner entries containing PI 365553 parentage are entered in 1980 preliminary yield tests.

**Lesion Nematode Resistance**

The lesion nematode, *Pratylenchus brachyurus* (Godfrey) Felip & Sch. Stek causes erratic but significant losses in peanut yield and grade (1). The penetration sites of the pathogen also serve as entry sites and infection courts for other destructive microorganisms (5). PI 295233 and PI 290606, two late maturing strains of the *hypogaea* subspecies, were reported earlier by the authors to resist lesion nematode damage (4). These have been crossed and backcrossed with Spanish and runner-type cultivars, and segregating F₂ to F₆ generation populations have been grown in a producer's field with recurring nematode problems. Inadequate population development and non-uniform distribution within test sites have slowed progress over the years, and selection has often, by necessity, been primarily on agronomic traits. However, the nematode population pressure and uniformity were highly favorable in 1979. These and previous results have shown that the trait is heritable. Semi-adapted lines tentatively classified as resistant have been selected.

PI 365553 was included among the replicated checks in the 1979 nematode tests to assess the lesion nematode reaction of this line. The pod discoloration from lesion nematode infection of this line was no greater than that of PI 295233 and markedly less than that of the cultivars 'Tamnut 74' and Florunner. Nematode extractions were made using a modified mist chamber technique for confirmation of the visual differences in infection on 10 g fresh pod and root tissue samples. The means and standard errors for the number of nematodes recovered, for the three replications were as follows:
<table>
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<th>Entry</th>
<th>Pod tissue</th>
<th>Root tissue</th>
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<tr>
<td>PI 365553</td>
<td>40±9</td>
<td>147±119</td>
</tr>
<tr>
<td>PI 295233</td>
<td>165±136</td>
<td>150±108</td>
</tr>
<tr>
<td>Florunner</td>
<td>1570±1446</td>
<td>1430±531</td>
</tr>
<tr>
<td>Tamnut 74</td>
<td>3917±2567</td>
<td>2117±1334</td>
</tr>
</tbody>
</table>

The average nematode recovery from PI 365553 was similar to that of PI 295233, and markedly less than that of the susceptible checks in both pod and root tissue. This strong indication of lesion nematode resistance, led to the previous results on *Pythium* and *Rhizoctonia*, increases are 51

in this introduction as a parent. Lines selected for pod rot resistance derived from this PI are also included in 1980 nematode tests search of multiple disease resistance.

**Literature Cited**


BREEDING PEANUTS FOR DISEASE RESISTANCE: RUST AND LEAFSPOT

Ray O. Hammons

Crops Research, AR-SEA-USDA, Coastal Plain Experiment Station, Tifton, GA 31794

Rust

Peanut rust (causal agent Puccinia arachidis Speg.) has been known to mycologists since 1884 from specimens collected on cultivated peanuts (Arachis hypogaea L.) in Paraguay (Spegazzini, 1884). After Mazzani and Hinojosa (1961) observed resistance in the 'Tarapoto' cultivar and some resistance in 12 other lines, the Venezuelan collection was added to the USDA plant introduction germplasm pool. About 1,500 accessions from this pool were exposed to natural rust infection in Puerto Rico in 1964 to initiate the USDA investigations for resistant germplasm. Only Tarapoto was markedly resistant.

In the late 1960's, Bromfield and Cevario (1970) added PI 314817 ('DHT 200') and PI 315608 ('Israel 136') to the list of resistant genotypes.

Seed of the Tarapoto, DHT 200 and Israel 136 peanuts were distributed widely by the USDA. Various U.S. plant introduction numbers for these three distinct genotypes were documented by Hammons (1977).

Since 1970 peanut rust has become established throughout Asia and Oceania, in Australia, and in much of Africa (Commonw. Mycol. Inst., 1980).

The U.S. Department of Agriculture and the Virginia Agricultural Experiment Station in 1973 released 14 breeding lines selected as resistant in the progeny of a single natural hybrid between Israel 136 (PI 298115) and an unknown pollen donor (Bailey et al., 1973). These "FESR" lines have been disseminated worldwide.

A small collection of cultivars by Leland D. Tripp in Peru was added to the U.S. germplasm resources in 1974. Rust occurred widely in the Southeast in 1975. Peanut genotypes previously reported to have moderate or higher resistance and those collected by Tripp were increased in a one-replicate nursery at Tifton in 1976 for evaluation of rust reaction in the winter nursery at Isabella, PR.

By chance rust was epidemic at Tifton. Nearly 700 genotypes were evaluated (scale: 0 = highly resistant to 4 = highly susceptible). Eighteen entries had few pustules, mainly on the older leaves (Table 1).

These lines were evaluated in Puerto Rico, where rust is endemic (Hammons, 1977), in the winter nurseries harvested in the springs of 1977, 1978 and 1979. Variation in scores (Table 1) probably reflect
Table 1. Rust reactions of some peanut genotypes in field screening trials at Tifton, GA, Isabella, PR, and ICRISAT, Hyderabad, India.

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<td>Romero</td>
<td>Honduras</td>
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<sup>a</sup> Evaluations at Tifton and Isabella by R. O. Hammons or A. C. Mixon, ISDA-SEA-AR, Tifton, GA. Data for ICRISAT by D. McDonald and P. Subrahmanyam, ICRISAT, A.P., India.

Continued
Assessments in Georgia and Puerto Rico on a 5-point field scale, where 0 = no disease or highly resistant, 1 = few postules, etc. to 4 = highly susceptible.

Assessments at ICRISAT on the 9-point field scale where 1 = no disease; 2 = few, very small pustules on some older leaves; 3 = few pustules mainly on older leaves; some ruptured; poor sporulation; 4 = pustules small or big, mostly on lower or middle leaves; disease evident; 5 = many pustules mostly on lower and middle leaves; yellowing and necrosis of some lower and middle leaves; moderately sporulating; 6 = like score 5, but spots heavily sporulating; 7 = pustules all over the plant; lower and middle leaves withering; 8 = like score 7, but withering is heavy; and 9 = plants severely affected: 50-100% leaves withering. (Scale courtesy of ICRISAT groundnut pathologists.)

Trivial names applied by R. O. Hammons from plant introduction records and personal communications with collectors.

differences in the onset of diseases, in plot orientation to prevailing winds, and/or in classifiers, rather than differences in the pathogen, or genotypes.

Twelve new sources of resistance were found: PI's 215696, 390593, 390595, 393516, 393526, 393527, 393531, 393641, 393643, 393646 and 407454 (Table 1). Eight are from the Tripp collection and some of these are possibly duplications of genotypes in the same or previous collections from Peru. Others are obviously different phenotypes and/or variations in their reaction to rust or other diseases.

Two additional peanuts, PI 414331 ('Resistente Corto') and PI 414332 ('Resistente Largo') with resistance to rust, are documented in Table 1. Both are derivatives from the cross 'Florispan Runner' x Tarapoto, and were bred by Julio Romero in Honduras. Both lines have moderate resistance to leafspot and good resistance to rust in Honduras (Romero, pers. comm.).

The 22 USDA PI accessions exhibiting the most resistance to rust in Georgia and in Puerto Rico were sent to ICRISAT in September 1978 for cooperative research evaluation. The entries were grown in unreplicated single rows adjacent to susceptible genotypes in the Post-Entry Plant Quarantine area and scored for rust reaction in July 1979.

The trial was repeated in the 1979-80 post-rainy season with these and other entries in a 11 x 11 triple lattice design. Infector rows were inoculated and the field irrigated as described by Subrahmanyam et al. (1980).

Disease assessment was on a 9-point field scale (see footnote, Table 1). Eighteen of the 22 entries were scored "3" for one or both of the seasons. Material in this class had "few postules, mainly on older leaves; some ruptured; poor sporulation" (P. Subrahmanyam, pers. comm.). Three entries--PI's 298115, 393516, and 393526--were somewhat less
resistant at ICRISAT than in Puerto Rico or Georgia. Resistente Largo had the lowest rust index (Table 1).

Most of the resistant genotypes appear unsuited for agronomic production other than in subsistence agriculture. In contrast to the other entries, Israel 136 (PI's 298115 and 315608) is a 'Virginia' type with a white testa and should offer greater selection opportunities in crossing program.

Romero's Resistente Corto and Resistente Largo show that improved lines combining adequate yield with good resistance to rust can be obtained through breeding.

The entries described in this report are available for distribution by the USDA to the peanut scientific community.

Leafspot

The leafspots, caused by Cercospora arachidicola Hori and "Cercosporidium personatum" (Berk. & Curt.) Deighton, are the most widely distributed and destructive foliar diseases of the peanut (Smith and Jittrell, 1980). Breeding resistant cultivars would be a powerful means of controlling these fungi. Research to find and incorporate resistances is underway in State AES and/or cooperating USDA/SAES laboratories in Florida, Georgia, North Carolina, Oklahoma, Texas and Virginia and at other locations throughout the world. This report focuses on the status of the cooperative USDA/Georgia projects at Tifton.

Beginning in 1968, Grover Sowell, Jr., and Don Smith developed methods for evaluation and screened more than 1,400 peanut plant introductions for reaction to the early leafspot pathogen. They detected 22 lines that were below the arbitrarily selected maximum levels of infection. Seven of these--PI's 109839, 162857, 259639, 259679, 259747, 170806, and 350680--exhibited the greatest amount of resistance in three field tests (Sowell et al., 1976).

During five subsequent years, 1975-79, PI 109839 had consistently less leafspot invasion and defoliation than other 'A. hypogaea' genotypes in unsprayed nurseries of the USDA-Georgia breeding projects. This peanut was released in October 1979 and registered as Cercospora arachidicola-resistant germplasm with its PI number formalized as a name (Hammons et al., 1980).

Low yield, small seed and late maturity make PI 109839 unacceptable for commercial production.

Two of the other six leafspot-resistant PI's were different accessions, 259747 and 350680, of the 'Tarapoto' cultivar, originally from the Tarapoto (Peru) Experiment Station (Hammons, 1977). PI 341879, a shorter-podded selection from Tarapoto with similar resistance to leafspot (and rust), was used with PI 109839 as parents in our leafspot resistance breeding program.

In 1976, we made 11 crosses involving PI 109839 and PI 341879, reciprocally or with three adapted peanuts (GA 194R-44, F 439-16-10-3,
and Tennessee Red). The F1 generation (16 plants) were grown in the USDA winter nursery, 1976-77, at Isabella, PR. Subsequent generations for this study were grown at Tifton. The unsprayed F2 nursery was surrounded with infector rows. From six to 41 selected plants per cross were bulked to form 16 spaced F3 populations with 1,000 seed each driller in a 4-row bed.

The 186 selected F4 progenies were sown in the 1979 unsprayed field nursery where both leafspot diseases defoliated the interspersed susceptible parents.

Progeny-row performances will be evaluated for 40 selections in the F5, 1980 nursery, with susceptible Florunner as the border (Table 2). Mass selection can be used to produce adequate seed for a preliminary yield trial in the F6.

**Table 2. Breeding peanuts for leafspot resistance: Cross and F5 progeny record. Tifton, GA. 1980.**

<table>
<thead>
<tr>
<th>Cross</th>
<th>Pedigree</th>
<th>Sel. (no.)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Φ</td>
<td></td>
</tr>
<tr>
<td></td>
<td>σ</td>
<td></td>
</tr>
<tr>
<td>C 324</td>
<td>Ga. 194-44 x PI 341879</td>
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</tr>
<tr>
<td>C 326</td>
<td>Ga. 194-44 x PI 109839</td>
<td>4</td>
</tr>
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<td>PI 109839 x Ga. 194-44</td>
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<tr>
<td>C 331</td>
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<td>PI 341879 x PI 109839</td>
<td>4</td>
</tr>
<tr>
<td>C 333</td>
<td>PI 109839 x F 439-16-10-3</td>
<td>6</td>
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<td>C 334</td>
<td>F 439-16-10-3 x PI 109839</td>
<td>13</td>
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<td>PI 341879 x F 439-16-10-3</td>
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<td>C 337</td>
<td>PI 341879 x Tenn. Red</td>
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<tr>
<td>C 338</td>
<td>Tenn. Red x PI 341879</td>
<td>2</td>
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</tbody>
</table>

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*a*Cooperative projects of USDA-SEA-AR and the Univ. Ga. Col. Agr. Coastal Plain Sta. The assistance of Peter Y. P. Tai is gratefully acknowledged.

*b*Ga. 194-44 = sister sel. of the Tifrun cultivar; PI 341879 = short-podded sel. from Tarapoto; PI 109839 is a leafspot-resistant germplasm line; F 439-16-10-3 = a component line of Florunner cultivar; Tenn. Red = a Valencia cultivar.

In addition, the F1's were double-crossed and this population advanced six generations in 3 years, 1977-79, by single seed descent.
SSD) and alternating plantings at Tifton and Isabella. The F7 is in preliminary yield trial in 1980.

Although the experiment is still in progress and any conclusions must be tentative, some of our observations, however, should be of interest. First, the leafspot resistance(s) in PI 109839 and PI 341879 is amenable to selection in cross-progeny populations. Nearly all of the 86 progenies in our F4 nursery exhibited significantly less defoliation than their susceptible parents where natural infection by leafspot pathogens was uncontrolled.

Second, a linkage group for several undesirable characters may be present in the leafspot-resistant parents. For example, resistant selections from the PI 109839 crosses are usually late-maturing, have small seeds in pods with elongated constrictions, and are prostrate.

Finally, a back-crossing program, transferring leafspot resistance to high-yielding, adapted cultivars (the recurrent parent), should have good chance of succeeding.

The benefits to be derived from developing a resistant peanut cultivar include reduced losses in yield and quality, improved production management, lower energy requirements and environmental pollution, and enhanced food safety.

Acknowledgments

Appreciation is expressed to Peter Tai and Bill Branch for their cooperation in the project work; to Ziv Frank, Bruno Mazzani, Julio Mero and Leland Tripp for rust-resistant genotypes; to Aubrey Mixon for evaluating rust in the Puerto Rican winter nurseries, 1978 and 1979; to P. Subrahmanyan and D. McDonald for scoring rust in the 1979 rainy and the 1979-80 post-rainy seasons at ICRISAT.

Literature Cited


