

Recurrent selection progress in a population derived from an interspecific peanut cross*

T.M. Halward, J.C. Wynne & H.T. Stalker

Dept. of Crop Science, N.C. State University, Raleigh, North Carolina 27695-7629, USA

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Summary

Two cycles of recurrent selection for yield were previously conducted using a population of *Arachis hypogaea* L.-like tetraploid hybrid derivatives selected from among the progeny of a cross between *A. hypogaea* and *A. cardenasii* Krap. et Greg. nom. nud., a diploid species with resistance to late leafspot (*Cercosporidium personatum* (Burk. and Curt.) Deighton). Using the 10 highest yielding parents from each of the above cycles of recurrent selection, a study was conducted for 12 morphological traits and susceptibility to leafspot infection in a replicated test at a single location. The two parents used to initiate the interspecific hybrid population (PI 261942-3 and *A. cardenasii*) as well as two adapted cultivars (Florigiant and NC 7) were included as checks. The objectives of the study were to determine the amount of genetic variation remaining in the population after two cycles of recurrent selection in order to predict whether further progress from selection could be expected and determine the potential for utilizing wild species for the improvement of quantitative traits in peanut. The results indicate that significant levels of genetic variation remain in the population after two cycles of recurrent selection for all traits measured, including several components of yield and leafspot resistance. This suggests that continued progress in population improvement from further cycles of selection should be possible while enhancing the genetic diversity of cultivated peanut germplasm.

Introduction

Recurrent selection is an effective method to use for simultaneously improving a population and broadening its genetic base. The inclusion of wild species germplasm in a recurrent selection program for population improvement in peanut (*Arachis hypogaea* L.) could serve to further broaden the genetic base of the cultivated crop. Wild species of *Arachis* have long been advocated for utilization in a breeding program aimed at transferring qual-

itative traits such as disease and insect resistance to certain diseases and insects to the cultivated peanut. More recently, these species have come under investigation for their potential to improve quantitatively inherited traits, including yield. The utilization of desirable germplasm from related wild and weedy species for the improvement of quantitative traits in cultivated species has recently been reported for a number of crops including oat (*Avena sativa* L.) (Lawrence & Frey, 1975), barley (*Hordeum vulgare* L.) (Rodgers, 1982), and tobac-

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co (*Nicotiana tabacum* L.) (Wernsman et al., 1976). Guok et al. (1986) showed that recurrent selection effectively increased yield and leafspot resistance in a population derived from selected progeny of an interspecific peanut hybrid. However, the amount of genetic variation remaining in the population for yield components, morphological traits, and leafspot resistance was not estimated.

The present study was conducted to determine (1) the amount of genetic variation remaining in the population after two cycles of recurrent selection; (2) whether a genetic shift had occurred among progeny selections, based on principal component analyses, relative to the original parents of the recurrent selection population, or the two commercial cultivar checks; and (3) the relative success with which interspecific *A. hypogaea*-like lines are recovered which appear to have retained at least some wild *Arachis* germplasm.

Materials and methods

Development of recurrent selection population. The original cross between *A. hypogaea* subsp. *fastigiata* Waldron (PI 261942-3), a small-seeded Valencia-type line collected in Paraguay, and *A. cardenasii* Krap. et Greg. nom. nud. (GKP 10017), a small-seeded diploid species with resistance to late leafspot (*Cercosporidium personatum* (Berk. & Curt.) Deighton), was made by Smartt & Gregory (1967). The sterile triploid hybrid ($2n = 3x = 30$) was colchicine-treated to restore fertility at the hexaploid ($2n = 6x = 60$) level. After five generations of self-pollination, all cytologically observed plants from a morphologically variable population of hybrid derivatives had undergone spontaneous chromosome loss to the tetraploid level ($2n = 4x = 40$) (Stalker et al., 1979). Using this as a base population, $S_{7,x}$ (S_7 selections in the S_8 generation) progenies from 24 selected S_7 plants were tested for yield in 1975 (Guok et al., 1986). The 10 highest yielding families were crossed in partial diallel to initiate the recurrent selection program, and two cycles of recurrent selection have thus far been completed (Table 1).

Table 1. Recurrent selection procedure (Guok et al., 1986)

Cycle 0	10	parents: Greenhouse (random-paired matings)
	42	S_0 rows: Field nursery (bulk harvest)
	42	$S_{0,1}$ families: Yield test (selection among and within families)
Cycle 1	10	$C_1S_{0,2}$ selections: Greenhouse (random-paired matings)
	60	S_0 rows: Field nursery (bulk harvest)
	60	$S_{0,1}$ families: Yield test (selection among and within families)
Cycle 2	10	$C_1S_{0,2}$ selections: Greenhouse (random-paired matings)
	30	S_0 rows: Field nursery (bulk harvest)
	30	$S_{0,1}$ families: Yield test

Genetic variation field study. The 10 highest yielding selections from each of the two cycles of recurrent selection were evaluated for yield and morphological traits at the Upper Coastal Plain Research Station, Rocky Mount, NC. Entries 1–10 represented parental selections from cycle 0, entries 11–20 represented parental selections from cycle 1, and entries 21–30 represented parental selections from cycle 2. A randomized complete block design with two replications was used for these estimates. Each plot consisted of two 10-seed rows, with 91 cm between rows. The two parents used to initiate the interspecific hybrid population (PI 261942-3 and *A. cardenasii*) – entries 31 and 34, respectively – as well as two commercial cultivars (Florigiant and NC 7) – entries 32 and 33, respectively – were included as checks. A single location was deemed adequate for use in this study because the traits measured are highly heritable in peanut and the objective was to observe relative levels of variation among entries – not to make selections based on estimates of genetic parameters.

The following 12 morphological traits were measured on two sub-samples per plot to estimate the amount of genetic variation retained in the population:

- Leaflet length (LL), in mm;
- Leaflet width (LW), in mm;
- Plant height (PH), in cm;
- Plant color (CR), 1 = yellow, 2 = light green, 3 = dark green;
- Petiole length, of leaf on lateral branch (PLL), in cm;

Petiole length, of leaf on main stem (PLM), in cm;
 Length of longest lateral (LLL), in cm;
 Pod length (10 pods)⁻¹ (PL), in cm;
 Seed length (10 seeds)⁻¹ (SDL), in cm;
 Seed width (10 seeds)⁻¹ (SDW), in cm;
 Number of seed pod⁻¹ (SP), average of 10 pods;
 Percent pod constriction (PC), average of 10 pods.

In addition, the percentage natural leafspot infection per plot (% LS) was estimated using a visual rating scale. Estimates of genetic variance were obtained from the analysis of variance. Broad-sense heritability estimates were calculated as the ratio of genotypic to phenotypic variance for each trait measured.

Principal component analyses were conducted and two biplots – using the biplot program (FORTRAN) written by Ted Emigh, Dept. of Genetics, North Carolina State Univ. and Ann Antlfinger, Dept. of Biology, Univ. of Nebraska – were generated to estimate changes in the genetic composition of the population over cycles of selection and to determine whether a genetic shift toward either of the original parents had occurred. The first included all traits measured; however, since the *A. cardenasii* parent failed to produce fruit in the field, it could not be included in the analysis. A second principal component analysis was run and a second

biplot generated using only the nonfruit traits but including the *A. cardenasii* parent as an entry.

Results and discussion

Significant levels of genetic variation for all morphological traits measured including several components of yield, as well as variation for susceptibility to leafspot infection, remained in the population after two cycles of recurrent selection (Table 2). Thus, variation introduced to *A. hypogaea* through the use of wild species germplasm appears to have been maintained through two cycles of recurrent selection. This suggests that recombination in future cycles of selection has the potential for producing additional progress in population improvement.

For each trait measured, there were several selections within each cycle that had means superior to the *A. hypogaea* parent and/or the commercial cultivars included as checks. This suggests that the inclusion of introgressed wild *Arachis* germplasm in a recurrent selection program may allow improvements in both qualitative and quantitative traits while broadening the genetic base of the cultivated peanut.

Guok et al. (1986) evaluated the same three sets

Table 2. Mean squares and variance component estimates for 14 morphological traits among lines representing the parental selections from the first two cycles of recurrent selection in a population derived from an interspecific peanut cross^a

Source	Mean squares													
	df	LL	LW	PH	% LS	CR	PLL	PLM	LLL	PL	PC	SDL	SW	SP
Rep	1	9.53	24.74	0.89	3011.76	0.03	0.82	0.13	166.41	0.06	126.46	0.01	0.89	0.03
Entries	33	187.68**	21.33*	214.91**	832.53**	1.02**	1.60**	1.63**	236.17**	0.24**	681.88**	0.09**	0.09**	0.03**
Error	101	40.84	12.99	19.33	74.64	0.11	0.36	0.69	83.40	0.09	104.97	0.02	0.04	0.01
Variance component est. ^b														
σ_g^2		73.42	4.17	97.79	378.95	0.46	0.62	0.47	76.39	0.08	288.46	0.04	0.03	0.01
σ_{ph}^2		93.84	10.67	107.45	416.27	0.51	0.80	0.82	118.08	0.12	340.94	0.05	0.05	0.02
H		0.78	0.39	0.91	0.91	0.39	0.78	0.57	0.65	0.67	0.85	0.70	0.60	0.50

^a LL = leaflet length; LW = leaflet width; PH = plant height; LS = % leafspot infection; CR = plant color; PLL = petiole length, lateral; PLM = petiole length, mainstem; LLL = length of longest lateral; PL = pod length; PC = % pod constriction; SDL = seed length; SW = seed width; and SP = no. seed/pod.

^b σ_g^2 , σ_{ph}^2 , H represent estimates of genotypic and phenotypic variances and broad-sense heritability (σ_g^2/σ_{ph}^2), respectively.

*, ** Indicate significance at the 0.05 and 0.01 probability levels, respectively.

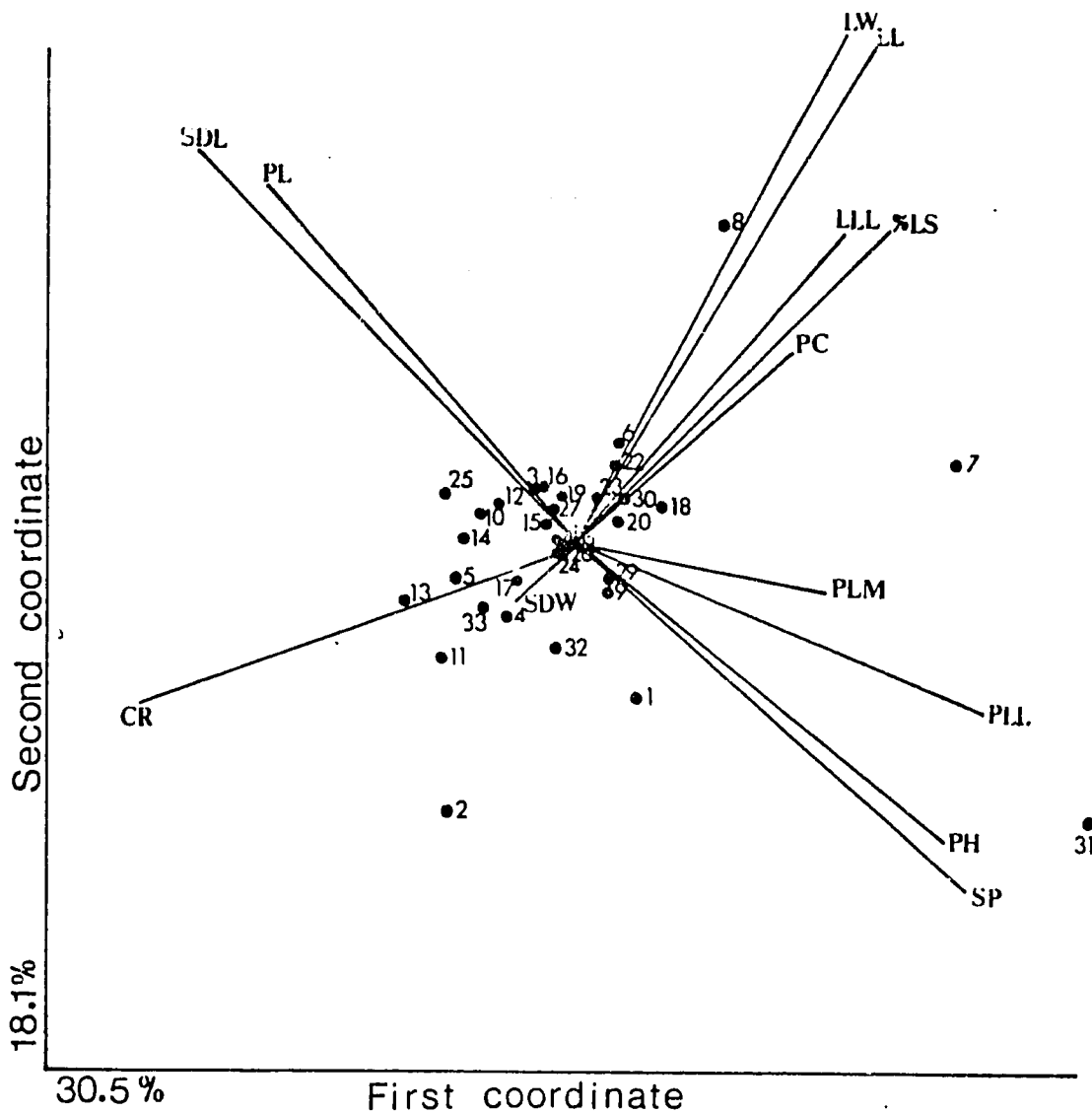


Fig. 1. Biplot display of first and second principal components for all traits measured for the parental selections from the first two cycles of a recurrent selection population derived from an interspecific peanut cross. Vector label abbreviations are as described in Table 2. Number represent entries in the field study: 1-10, cycle 0 selections; 11-20, cycle 1 selections; 21-30, cycle 2 selections; 31, *A. hypogaea fastigiata* (PI 261942-3); 32, NC 7; 33, Florigiant

of parental selections from cycles 0, 1, and 2 in replicated yield trials at two locations in 1982 and 1983. They found that mean fruit yield increased significantly from 3670 kg ha⁻¹ for the C₀ parents to 4050 kg ha⁻¹ for the C₁ parents and 4090 kg ha⁻¹ for the C₂ parents. In addition, they observed a greater number of high yielding families in the C₁ and C₂ populations than in the C₀; as well as lines from each cycle with yields that were not significantly

different from those of the commercial cultivars included as checks. Families from each cycle of the recurrent selection program were found to produce yields equivalent to those of commercial cultivars and, as the results from the present study indicate, these families are still heterogeneous. Thus, additional selection within families should lead to further yield increases in the population.

From the biplot analysis of all traits, the first and

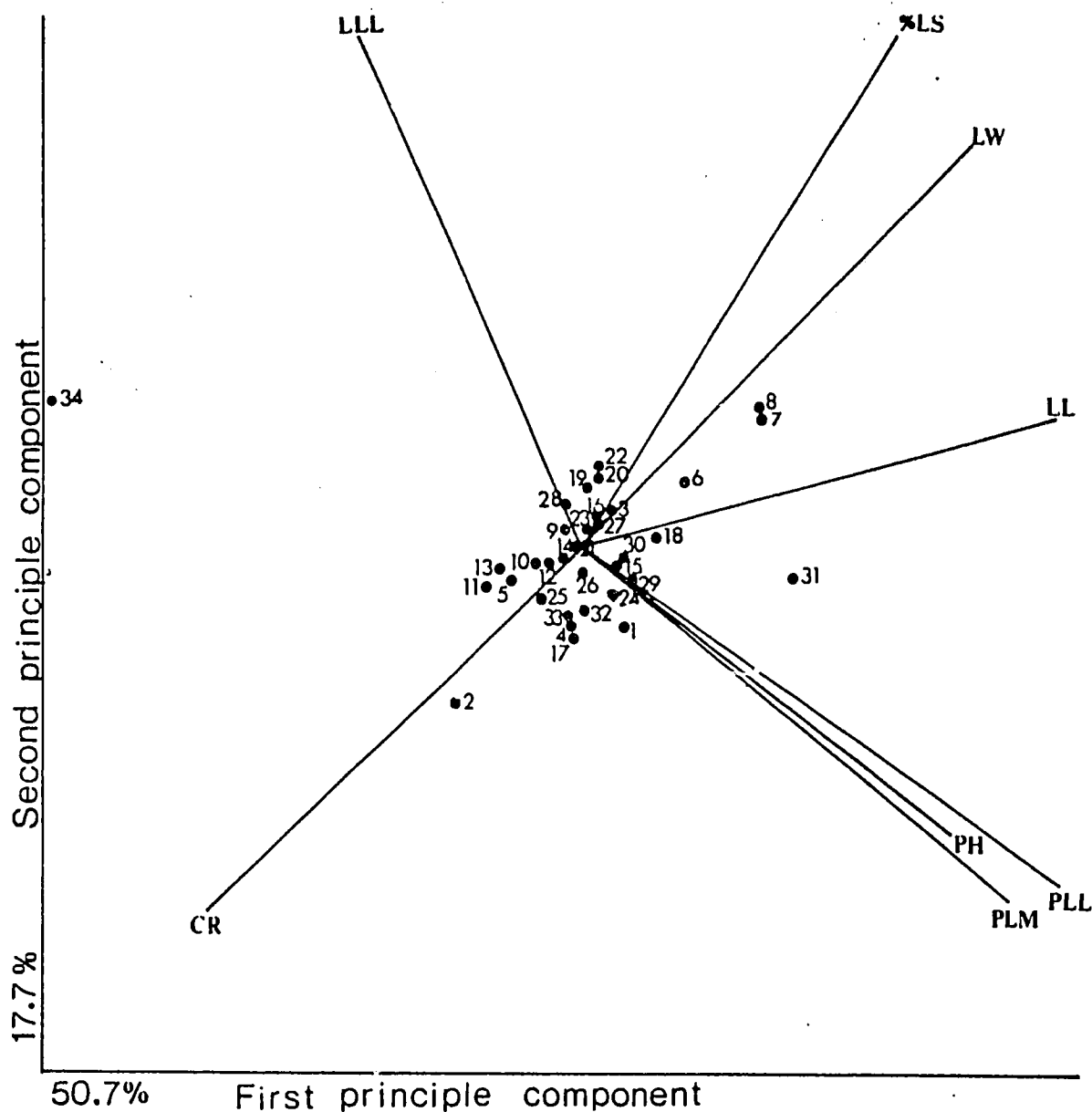


Fig. 2. Biplot display of first and second principal components for nonfruit traits for the parental selections from the first two cycles of a recurrent selection population derived from an interspecific peanut cross. Vector label abbreviations are as described in Table 2. Numbers represent entries in the field study: 1-10, cycle 0 selections; 11-20, cycle 1 selections; 21-30, cycle 2 selections, 31, *A. hypogaea fastigiata* (PI 261942-3); 32, NC 7; 33, Florigiant; 34, *A. cardenasii*

second principal components accounted for 48.6% of the dispersion in the population (Fig. 1). Most traits were well represented except seed width, pod constriction, and main stem petiole length, all of which exhibited relatively short vectors as projected in the defined X-space.

When fruit traits were omitted and *A. cardenasii*

was included in the analysis, the biplot generated using the first and second principal components accounted for 68.4% of the dispersion in the population and all variables were well represented as evidenced by the length of the vectors projected in the defined X-space (Fig. 2).

In both biplot analyses, the *A. hypogaea* parent

(# 31) fell out as a unique data point, as did the *A. cardenasii* parent (# 34) in the second analysis. Entries 2, 7, and 8 also fell outside the main cluster as unique points in both biplots, while the remaining entries formed a rather tight cluster around the two cultivated checks (# 32 and # 33), indicating similarities among these data points for the variables measured.

Two cycles of recurrent selection for yield and agronomic characters have shifted the population away from either of the original parents—*A. cardenasii*, the wild species (# 34) and Pi 261942-3, a small-seeded relatively low yielding valencia type (# 31) — and toward the commercial cultivars (# 32 and # 33). This was to be expected since selection was practiced in each cycle for yield, seed size and shape, and other desirable agronomic qualities associated with virginia market-type cultivars grown commercially. However, even with a shift in the genetic composition of the population toward that of the commercial cultivars, significant levels of variation remain in the population for a number of traits (Table 2). Thus, it appears that through a recurrent selection program improvements can be made in a population originating from an interspecific peanut hybrid while maintaining adequate levels of variation for broadening the germplasm base of the cultivated peanut. This is especially important for the transfer of resistance to important diseases and insects (e.g., late leaf-spot resistance in this population) as well as for developing a breeding population with greater

adaptability to a wide range of environments, including those areas in developing nations where high input agriculture is not feasible.

In summary, recurrent selection appears to have been effective in improving this interspecific hybrid population with the recovery of a number of *A. hypogaea*-like hybrid derivatives. Thus, wild *Arachis* species can be considered useful as parents when initiating a recurrent selection program aimed at improving both qualitative and quantitative traits, as well as for broadening the genetic base of cultivated peanut germplasm.

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