Parent Selection in Breeding for Roasted Peanut Flavor Quality

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ABSTRACT

The sensory attributes that make up roasted peanut flavor quality are important traits to evaluate in the development of new cultivars. Recent publications have characterized the variation in sensory attributes in U.S. peanuts (*Arachis hypogaea* L.), however, no estimates of the effects of lines as parents in a breeding program have been calculated. Best linear unbiased prediction (BLUP) is a method for predicting the breeding value of a parent based on the performance of its relatives. Commonly used in animal and tree breeding, the method is rarely applied in annual crop species. The method was applied to a set of data collected on the three sensory attributes roasted peanut, sweet, and bitter for 250 peanut genotypes evaluated in 53 environments. BLUP solutions computed using different estimates of narrow-sense heritability (h^2) were highly correlated ($r > 0.9$), suggesting that precise estimates of h^2 are not necessary. Correlations of values predicted by BLUP with observed values were moderate ($0.63 < r < 0.71$) for individual lines, but strong ($0.85 < r < 0.92$) for means of crosses. BLUPs of breeding value can be used to predict means of crosses, but segregation within crosses affords additional opportunity for progress from selection. BLUPs of breeding value were superior to midparent values in predicting cross means. The previously reported flavor relationships between the runner and virginia market types were predicted by the breeding values of some commonly used parents. Specific lines with superior breeding values for flavor quality included runner-types Florunner, its components and sibling lines, and high-oleic derivatives of Sunrunner; virginia-types Altika, White's Runner, NC Ac 18457, and X90053; and spanish-type Pearl. Jenkins Jumbo, Florigiant, NC 7, and CBR-resistant lines had inferior breeding values for flavor quality.

Key Words: *Arachis hypogaea* L., BLUP, breeding value, sweet, bitter.

Parent selection for the development of new cultivars is primarily based upon those heritable characteristics impacting agronomic value because of their direct, measureable effect on the producer's profit margin. Heritable characteristics, which do not have a directly measureable economic value, can sometimes be overlooked or forgotten as new cultivars are developed. Roasted flavor quality is one such set of characteristics. Isleib *et al.* (1995, 2000) have shown that failure to monitor and evaluate these characteristics can lead to serious quality defects in new breeding lines and cultivars.

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It is important to understand the potential of the proposed parents to transfer these quality characteristics to their progeny Hence, the selection of those genotypes which are to serve as the progenitors of future breeding lines and cultivars must be undertaken with as much insight as possible.

In a self-pollinating crop such as peanut (*Arachis hypogaea* L.), the value of the best-inbred line that can be selected from a population is a function of two population parameters--the mean and the variance. Because the numbers of segregating loci in the population determines both parameters, the selection of potential parents is especially critical. Best Linear Unbiased Prediction (BLUP) is a procedure described by Henderson (1975) to calculate the best linear unbiased predictors of breeding values of dairy cattle based on observed data and the known variance-covariance structure among fixed and random effects in a mixed linear model. In general, the genetic effects in the model are considered to be random while the environmental effects are considered to be fixed. The variance-covariance matrix of additive genetic effects is calculated using standard quantitative genetic theory and is based upon the matrix of coancestries among related lines (Malécot, 1948). BLUP is used widely in animal parent selection and is beginning to be used for tree improvement and in annual crop species. It has been found useful for identifying superior single crosses in maize (*Zea mays* L.) prior to field testing (Bernardo, 1994, 1995, 1996a,b). Panter and Allen (1995a,b) found BLUP to be superior to midparent value in selecting cross combinations in soybean (*Glycine max* L.).

Enhancement of roasted peanut flavor has been a long-standing objective of the peanut industry. Certain roasted peanut quality sensory attributes have been shown to be heritable traits (Pattee *et al.*, 1993, 1994, 1995, 1998; Isleib *et al.*, 1995), and highly significant correlations have been found among least square means for the attributes, particularly of bitter with sweet and of roasted peanut with sweet and bitter (Pattee *et al.*, 1997, 1998). Although there have been recent efforts to characterize the variation in sensory attributes in the overall U.S. peanut breeding population, the literature is lacking entirely in estimates of the effects of lines as parents in a breeding program. It would be beneficial to the peanut industry to increase the desirable quality attributes, roasted peanut and sweet, while decreasing the undesirable attribute bitter. Although no optimum levels of these attributes have been identified, the highest individual panelist scores that have been recorded for roasted peanut are in the range of 7-8 flavor intensity units (fiu), with a panel mean score of 7.25 fiu on a scale of 1-14 with 14 being the most intense. The highest individual panelist scores for sweet are in the 5-6 range, with a panel mean score of 5.16 fiu. These means represent realistic breeding goals for these attributes. Elimination of any bitter attribute would enhance the perception of roasted peanut and sweet.

The objective of this work is to determine whether BLUP is a superior procedure for identifying parents that could be used by peanut breeders to develop new breeding lines and cultivars while still maintaining or enhancing the flavor profile of the germplasm.

Materials and Methods

Genotype Resources and Evaluations. From 1986 to 1997, 1822 roasted peanut samples were tested from the Southeast, Southwest, and Virginia-Carolina peanut production regions. Represented within these samples were 250 genotypes (Table 1), including the most common peanut cultivars in the runner and virginia market types, and 53 year-by-location combinations. Components of the multiline cultivars were identified in Pattee *et al.* (1998). All samples were obtained from plants grown and harvested under standard recommended procedures for the specific location.

Each year samples were shipped to Raleigh, NC in February following harvest and placed in controlled storage at 5 C and 60% RH until analyzed. All samples were roasted between May and June using a Blue M "Power-O-Matic 60" laboratory oven, ground into a paste, and stored in glass jars at -10 C until evaluated. The roasting, grinding, and color measurement protocols were as described by Pattee and Giesbrecht (1990). A long-standing, six- to eight-member trained roasted peanut profile panel at the Food Science Dept., North Carolina State Univ., Raleigh, NC, evaluated all peanut paste samples using a 14-point intensity scale. Panel orientation and reference control were as described by Pattee and Giesbrecht (1990) and Pattee *et al.* (1993). Two sessions were conducted each week on nonconsecutive days. Panelists evaluated four samples per session. Sensory evaluation commenced mid-July and continued until all samples were evaluated. The averages of individual panelists' scores on sensory attributes were used in all analyses in this study.

Statistical Analysis. PROC MIXED in SAS (SAS Inst., 1997) was used for analysis of the unbalanced data set to estimate the sensory attribute least square means for genotypes. Covariates fruity and roast color were used, as needed, based upon the findings of Pattee *et al.* (1991, 1997) and Pattee and Giesbrecht (1994). The fixed effects were genotype, region, genotype-by-region, and covariates fruity and roast color. Each genotype effect was partitioned to reflect the effects of market type and genotype within market types. Classification of lines into market types was based upon branching pattern, pod type, and seed size.

PROC IML in SAS was used to perform the calculations to compute BLUP estimates according to Harville (1977). The mixed model (Eq. 1) includes a mean (μ), a set of fixed effects (β) with a corresponding incidence matrix (X), a set of random additive genetic effects (a) with its incidence matrix (Z), and a vector of error terms:

$$Y = \mu + X\beta + Za + \varepsilon \qquad \text{[Eq. 1]}$$

The variance-covariance matrix for the random effects and error terms is

$$\mathrm{Var}\left(\begin{bmatrix} a \\ \varepsilon \end{bmatrix}\right) = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}\sigma^2 \qquad \text{[Eq. 2]}$$

where σ^2 is the error variance and a = $G\sigma^2$ is the additive genetic variance-covariance matrix for the lines. G is therefore $2Ch^2/(1-h^2)$ where C is the coancestry matrix and h^2 is the narrow-sense heritability of the trait. Pedigree information on the lines was obtained from published records and from

Table 1. Cultivars and breeding lines with their predicted breeding values for roasted peanut, sweet, and bitter sensory attributes.

Germplasm	Roasted peanut	Sweet	Bitter
Runner-type lines			
AT 127	+0.02	-0.06	-0.13
Andru 93	+0.18	+0.12	-0.10
Basse	+0.09	+0.15	-0.09
Bradford Runner	+0.05	-0.19	+0.05
Dixie Runner	-0.09	-0.28	+0.13
Early Runner	+0.14	-0.11	-0.27
Early Runner Comp. 1	+0.13	-0.10	-0.26
Early Runner Comp. 2	+0.13	-0.12	-0.27
Early Runner Comp. 3	+0.14	-0.11	-0.27
Early Runner Comp. 4	+0.14	-0.12	-0.27
Early Runner Comp. 5	+0.15	-0.11	-0.27
F1315	+0.43	+0.04	-0.09
F1316	+0.45	+0.05	-0.10
Florispan Comp. 1	+0.17	-0.06	-0.24
Florispan Comp. 2	+0.13	-0.04	-0.22
Florispan Comp. 3	-0.00	-0.21	-0.18
Florispan Comp. 4	+0.07	-0.01	-0.22
Florispan Comp. 5	+0.15	-0.03	-0.16
F439-1-4-4-2-1-2	+0.31	+0.24	-0.29
F439-16-4	+0.27	+0.35	-0.34
F439-16-6-3	+0.23	+0.35	-0.35
F439-17-2-1-1	+0.24	+0.18	-0.35
F439-2-3-2-1	+0.28	+0.35	-0.36
F439-3-1-1-3-3-B3	+0.19	+0.27	-0.29
Florunner	+0.28	+0.26	-0.31
Florunner Comp. 1	+0.28	+0.29	-0.31
Florunner Comp. 2	+0.30	+0.28	-0.31
Florunner Comp. 3	+0.28	+0.29	-0.31
Florunner Comp. 4	+0.26	+0.19	-0.30
GA 207-2	-0.02	-0.18	+0.10
GA 207-3-4	+0.04	-0.30	+0.17
Georgia Runner	+0.08	-0.11	-0.12
GK-7	-0.01	+0.10	-0.25
Langley	+0.28	+0.01	-0.03
MARC I	+0.25	+0.32	-0.16
NC 3033	-0.24	-0.38	+0.17
Okrun	+0.10	+0.21	-0.10
PI 109839	+0.11	-0.18	+0.14
S.E. Runner 56-15	-0.12	-0.42	+0.05
Southern Runner	-0.11	+0.07	+0.01
Spannette	-0.16	-0.38	+0.22
Sunbelt Runner	-0.14	-0.24	+0.13
SunOleic 95R	+0.41	+0.01	-0.09
SunOleic 97R	+0.45	+0.05	-0.08
Sunrunner	+0.23	-0.04	-0.12
Tamrun 88	+0.11	+0.06	-0.13
TP107-11	+0.24	+0.04	-0.11
UF81206-2	+0.08	+0.12	-0.01
UF90106	+0.29	+0.21	-0.26
UF91108	+0.11	+0.17	+0.04
UGA-3-5	+0.14	-0.04	-0.15
UGA-3-6	+0.08	+0.02	-0.16
UGA-3-7	+0.10	-0.17	-0.18
UGA-3-8	+0.07	-0.12	-0.08
UGA-3-9	+0.11	-0.07	-0.19
UGA-3-10	+0.19	-0.05	-0.12
UGA-3-11	+0.10	-0.10	-0.05
Spanish- and valencia-type lines			
Comet	-0.14	-0.03	-0.14
Improved Spanish 2B	-0.17	-0.55	+0.32
N.M. Valencia C	+0.00	+0.68	-0.19
Pearl	+0.35	+0.54	-0.23
PI 337396	+0.05	+0.21	+0.03
Pronto	-0.04	+0.34	-0.41
Small White Spanish	+0.08	-0.09	+0.10
Spanish- and valencia-type lines (cont.)			
Spanco	-0.04	+0.14	-0.25
Starr	-0.14	-0.03	-0.14
Tamspan 90	+0.06	+0.31	-0.21
Virginia-type lines			
86X45B-10-1-2-2-b2-B	+0.04	-0.10	+0.11
86X45B-8-1-1-b3-B	+0.08	-0.05	+0.10
AT VC-1	+0.14	+0.20	-0.05
Dixie Giant	-0.07	+0.08	-0.19
Early Bunch	-0.12	-0.34	+0.30
F393-7-1-b4-B	-0.02	-0.15	-0.02
Early Bunch Comp. 1	-0.12	-0.35	+0.29
Early Bunch Comp. 2	-0.12	-0.33	+0.30
Early Bunch Comp. 3	-0.11	-0.34	+0.30
Early Bunch Comp. 4	-0.12	-0.34	+0.30
Early Bunch Comp. 5	-0.12	-0.34	+0.30
Florigiant	-0.27	-0.45	+0.24
GA 119-20	-0.02	+0.07	-0.20
Gregory	-0.02	-0.24	+0.24
Holland Va. Jumbo	+0.07	+0.06	+0.04
Jenkins Jumbo	-0.26	+0.01	+0.09
N88003	-0.10	-0.12	-0.03
N90002	-0.16	-0.42	+0.23
N90010	+0.00	-0.16	+0.26
N90016	-0.14	-0.17	+0.20
N90017	-0.12	-0.04	+0.09
N91003	-0.24	-0.35	+0.26
N91045	-0.15	-0.28	+0.18
N91047	-0.08	-0.10	+0.11
N91048	-0.08	-0.11	+0.14
N93112C	-0.15	-0.40	+0.26
NC-V 11	-0.10	-0.38	+0.14
NC 10C	-0.31	-0.44	+0.30
NC 12C	-0.28	-0.38	+0.29
NC 2	+0.13	-0.02	+0.12
NC 4	+0.04	+0.13	+0.03
NC 6	-0.12	+0.06	-0.11
NC 7	-0.18	-0.24	+0.19
NC 8C	-0.24	-0.42	+0.28
NC 9	-0.05	-0.21	+0.16
NC Ac 17921	-0.01	-0.17	+0.02
NC Ac 18016	-0.24	-0.51	+0.14
NC Ac 18423	+0.03	-0.06	+0.15
NC Ac 18424	-0.12	-0.40	+0.19
NC Ac 18431	-0.03	-0.17	+0.08
NC Ac 18449	-0.02	-0.29	-0.02
NC Ac 18450	-0.08	-0.41	+0.02
NC Ac 18451	-0.08	-0.26	+0.11
NC Ac 18452	-0.12	-0.18	+0.07
NC Ac 18454	-0.14	-0.34	+0.11
NC Ac 18455	-0.05	-0.35	+0.11
NC Ac 18456	+0.03	-0.13	-0.05
NC Ac 18457	+0.15	+0.42	-0.05
NC Ac 18459	-0.16	-0.02	+0.18
NC Ac 18460	+0.02	-0.09	+0.06
NC Ac 18462	-0.08	-0.05	+0.00
NC Ac 18463	-0.11	+0.08	+0.05
NC Ac 18464	-0.05	+0.08	+0.00
Altika (UF 714021)	+0.18	+0.37	-0.22
UF 87118	-0.51	-0.65	+0.40
VA-C 92R	-0.13	-0.30	+0.11
VA 93B	-0.09	-0.20	+0.05
VP 8407	+0.04	+0.10	-0.19
VP 8417	-0.16	-0.04	-0.05
White's Runner	+0.21	+0.18	-0.02
X90037	+0.03	-0.10	-0.07
Virginia-type lines (cont.)			
X90042	-0.21	-0.51	+0.27
X90053	+0.08	+0.32	-0.22
Progeny of NC 7 / NC Ac 18431			
X90023-01-01 & -02	-0.10	-0.28	+0.21
X90023-02-01 & -02	-0.11	-0.25	+0.21
X90023-03-01 & -02	-0.13	-0.39	+0.29
X90023-04-01 & -02	-0.08	-0.17	+0.23
X90023-05-01 & -02	-0.16	-0.36	+0.23
X90023-06-01 & -02	-0.11	-0.23	+0.18
X90023-07-01 & -02	-0.11	-0.19	+0.19
X90023-08-01 & -02	-0.08	-0.27	+0.20
X90023-09-01 & -02	-0.10	-0.44	+0.21
X90023-10-01 & -02	-0.16	-0.35	+0.24
X90023-11-01 & -02	-0.09	-0.37	+0.22
X90023-12-01 & -02	-0.07	-0.25	+0.21
X90023-13-01 & -02	-0.10	-0.25	+0.18
X90023-14-01 & -02	-0.11	-0.28	+0.22
X90023-15-01 & -02	-0.06	-0.14	+0.21
X90023-16-01 & -02	-0.08	-0.16	+0.23
X90023-17-01 & -02	-0.17	-0.36	+0.31
X90023-18-01 & -02	-0.10	-0.13	+0.24
X90023-19-01 & -02	-0.12	-0.26	+0.24
X90023-20-01 & -02	-0.12	-0.23	+0.26
X90023-21-01 & -02	-0.15	-0.22	+0.25
X90023-22-01 & -02	-0.13	-0.46	+0.27
X90023-23-01 & -02	-0.05	-0.08	+0.20
X90023-24-01 & -02	-0.19	-0.29	+0.28
X90023-25-01 & -02	-0.13	-0.20	+0.21
X90023-26-01 & -02	-0.17	-0.26	+0.21
X90023-27-01 & -02	-0.13	-0.40	+0.22
X90023-28-01 & -02	-0.10	-0.22	+0.22
X90023-29-01 & -02	-0.11	-0.10	+0.22
X90023-30-01 & -02	-0.15	-0.21	+0.25
X90023-31-01 & -02	-0.12	-0.23	+0.24
X90023-32-01 & -02	-0.06	-0.05	+0.24
X90023-33-01 & -02	-0.08	-0.15	+0.22
X90023-34-01 & -02	-0.05	+0.13	+0.30
X90023-35-01 & -02	-0.12	-0.16	+0.22
X90023-36-01 & -02	-0.13	-0.20	+0.22
X90023-37-01 & -02	-0.12	-0.24	+0.24
X90023-38-01 & -02	-0.09	-0.27	+0.24
X90023-39-01 & -02	-0.06	-0.25	+0.24
X90023-40-01 & -02	-0.14	-0.25	+0.22
X90023-41-01 & -02	-0.18	-0.36	+0.26
X90023-42-01 & -02	-0.08	-0.24	+0.22
X90023-43-01 & -02	-0.13	-0.05	+0.20
X90023-44-01 & -02	-0.11	-0.21	+0.23
X90023-45-01 & -02	-0.09	-0.15	+0.25
X90023-46-01 & -02	-0.06	-0.22	+0.24
X90023-47-01 & -02	-0.14	-0.12	+0.23
X90023-48-01 & -02	-0.07	-0.14	+0.23
X90023-49-01 & -02	-0.09	-0.26	+0.26
X90023-50-01 & -02	-0.07	-0.22	+0.25
X90023-51-01 & -02	-0.12	-0.16	+0.28
X90023-52-01 & -02	-0.13	-0.16	+0.25
X90023-53-01 & -02	-0.14	-0.22	+0.27
X90023-54-01 & -02	-0.15	-0.31	+0.28
X90023-55-01 & -02	-0.10	+0.00	+0.24
X90023-56-01 & -02	-0.11	-0.22	+0.24
X90023-57-01 & -02	-0.11	-0.27	+0.24
X90023-58-01 & -02	-0.12	-0.08	+0.24
X90023-59-01 & -02	-0.09	-0.21	+0.21
X90023-60-01 & -02	-0.09	-0.18	+0.24

the individual breeders. Coancestries among lines were calculated using standard computational techniques incorporated into the computer program of Delannay *et al.* (1983). Modifications described by Cockerham (1983) were required to calculate coancestries among lines derived from the same cross. Lines tracing to different F_2 plants had the same coancestry as full sibs, while pairs tracing to the same F_3 or later generation selection were more closely related than full sibs. When no information was available on the commonality of two lines derived from the same cross, it was assumed that the lines traced to different F_2 selections.

The standard BLUP solutions (Eq. 3) can be obtained only when the genetic variance-covariance matrix is nonsingular.

$$\begin{bmatrix}\hat{\beta}\\ \hat{a}\end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z+G^{-1}\end{bmatrix}^{-1}\begin{bmatrix}X'R^{-1}Y\\ Z'R^{-1}Y\end{bmatrix} \qquad \text{[Eq. 3]}$$

Because of the inclusion of multiline cultivars and their component pure lines in the study, there were collinearities in the coancestry matrix, the G matrix was singular, and the BLUP solutions were obtained using Equation 4.

$$\begin{bmatrix}\hat{\beta}\\ \hat{v}\end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}ZG+I\end{bmatrix}^{-1}\begin{bmatrix}X'R^{-1}Y\\ Z'R^{-1}Y\end{bmatrix} \qquad \text{[Eq. 4]}$$

where $v = G^{-1}a$.

Results and Discussion

Broad-sense Heritability Estimate Effects on BLUP Values. The variance-covariance matrix for random effects given by Harville (1977) is based upon narrow-sense heritability estimates. Because only broad-sense heritability (H) estimates are available for the sensory attributes (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1993, 1995, 1998), we investigated the effect of variability in the narrow-sense heritability estimate on computation of BLUPs. BLUPs were computed for each sensory attribute more than once using a slightly different estimate of narrow-sense heritability (h^2) each time (Table 2). The estimates of h^2 bracketed the range of published estimates of H for each trait. Correlations among BLUPs obtained using these heritability values were examined as indicators of BLUPs sensitivity to variation in the heritability estimate. In all cases, the correlations and rank correlations among the BLUPs were highly significant ($r \geq 094$, $P < 0.01$), indicating that the method is relatively insensitive to lack of precision in the estimate of narrow-sense heritability. We thus conclude that broad-sense heritability estimates can be substituted for narrow-sense heritability estimates in the BLUPs calculations and have made the appropriate substitutions in the data calculations presented in this study.

Correlation Among BLUP Values for Sensory Attributes. Pattee *et al.* (1997, 1998) have shown roasted peanut and sweet sensory attribute intensity scores to be positively correlated overall across peanut genotypes, while both roasted peanut and sweet attribute scores were negatively correlated with bitter sensory attribute intensity. The degree of correlation, however, varied widely between market-types. These same relationships are found to exist between these heritable sensory attributes and their BLUPs breeding values (Table 3). The correlations were highly significant over all genotypes and for the runner and virginia market-types ($P < 0.01$), but their magnitudes varied. Within the spanish-valencia market-type there were only 10 lines, and only the BLUPs for sweet and bitter were significantly correlated ($P < 0.01$). Runner and virginia market-types have similar correlation values for all three sensory attributes. It is of interest to note that all three market-types have the strongest relationships between the sweet and bitter attributes and the weakest relationships between bitter and roasted peanut attributes. These correlation values demonstrate the complexity of the interrelationships among these sensory attributes and the challenges facing peanut breeders in developing new cultivars while maintaining or improving flavor quality.

Variation of BLUP Values in Peanut Germplasm. Over all market-types, the range in breeding values for the roasted peanut attribute was 0.96 fiu (Table 4), nearly twice the magnitude detectable to the human palate. The ranges for the individual market-types were less than 0.75 fiu, so reflected in this overall range were differences in the mean values associated with different market types.

Table 2. Correlations among BLUPs of breeding value for the roasted peanut, sweet, and bitter attributes estimated at selected heritabilities.

Heritability estimate	Correlation			Rank correlation		
Roasted peanut	$h^2 = 0.05$	$h^2 = 0.10$	$h^2 = 0.15$	$h^2 = 0.05$	$h^2 = 0.10$	$h^2 = 0.15$
$h^2 = 0.05$	1.0000	0.9879**	0.9690**	1.0000	0.9720**	0.9454**
$h^2 = 0.10$	0.9879**	1.0000	0.9954**	0.9720**	1.0000	0.9933**
$h^2 = 0.15$	0.9690**	0.9954**	1.0000	0.9454**	0.9933**	1.0000
Sweet heritability estimate	$h^2 = 0.15$	$h^2 = 0.20$	$h^2 = 0.25$	$h^2 = 0.15$	$h^2 = 0.20$	$h^2 = 0.25$
$h^2 = 0.15$	1.0000	0.9972**	0.9911**	1.0000	0.9997**	0.9980**
$h^2 = 0.20$	0.9972**	1.0000	0.9983**	0.9997**	1.0000	0.9980**
$h^2 = 0.25$	0.9911**	0.9983**	1.0000	0.9980**	0.9980**	1.0000
Bitter heritability estimate	$h^2 = 0.05$	$h^2 = 0.10$		$h^2 = 0.05$	$h^2 = 0.10$	
$h^2 = 0.05$	1.0000	0.9918**		1.0000	0.9908**	
$h^2 = 0.10$	0.9918**	1.0000		0.9908**	1.0000	

**Denotes significance at the 1% level of probability.

The runner market-type had the highest average breeding value for roasted peanut, followed by the fastigiate market-type that had a neutral average effect, and the virginia market-type with a negative average breeding value. There was little effect of market-type on the variance observed for breeding values of roasted peanut.

For the sweet attribute, the overall range was 1.33 fiu. The fastigiate market-type alone had a range of 1.23 fiu, while the runner and virginia market-types had narrower ranges. All three market-types had similar standard deviations for the breeding value of sweet. The fastigiate types had the highest average breeding value for sweet followed by the runners which were neutral on average and the virginias which had an average negative breeding value. For bitter, the overall range was 0.81 fiu, with the runner and fastigiate market-types having negative average breeding values and the virginia market-type a positive average breeding value. The ranges and standard deviations were consistent across market-types. These differences in the breeding values associated with market-types are similar to the variation observed in mean flavor scores.

It is clear that the runner market-type has the best general effect on flavor profile, followed by the fastigiate market-type. Used as a parent, the virginia market-type is associated with decreased roasted peanut and sweet attributes and increased bitter attribute. Improvement of the flavor of virginia cultivars may require introgression of genes from the runner or fastigiate groups.

Examination of the estimates of individual breeding values (Table 1; Figs. 1 and 2) reveals some interesting exceptions to the general findings as well as confirmation of some findings from earlier work with peanut flavor. In spite of the generally inferior predicted effect of virginia-type parents on flavor, there were a few lines with positive effects on roasted peanut and sweet attributes. Agratech VC-1, Altika, NC Ac 18457, White's Runner, and large-seeded line X90053 all were predicted to improve flavor when used as parents. Agratech VC-1 was selected from a breeding population more closely related to the runner than to the virginia market type. Altika's ancestry would not lead one to expect a beneficial effect on flavor because it traces to Jenkins Jumbo as a grandparent. As has been reported previously using less sophisticated predictive methodology (Isleib *et al.*, 1995), the ancestral virginia-type line Jenkins Jumbo has a large negative effect on roasted peanut intensity. However, Altika also traces to GA 119-20, a line that derived its large seed size from Dixie Giant rather than Jenkins Jumbo. When used as a parent, Dixie Giant tends to reduce bitterness while having little effect on roasted peanut and sweet intensities. White's Runner was one of the seven parents used by W.C. Gregory to establish the breeding program in North Carolina, and it is a parent of NC 2, a virginia-type cultivar that also had a weakly positive effect on roasted peanut and sweet. The existence of large-seeded lines with superior effects on flavor illustrates the possibility of improving flavor in the virginia market type without sacrificing large seed size.

There were 120 F_3-derived lines included in this study that were developed without selection from a single cross NC 7/NC Ac 18431 originating from 60 F_2 plants selected at random and two F_3 plants selected at random within each F_2-derived family. These lines were tested for sensory attributes as $F_{3:5}$ families and afford an opportunity to examine the relationship between two specific parents and a large array of their progeny. For roasted peanut, the BLUP values for the families were all intermediate to the extremes represented by the two parents (Fig. 1). For sweet, the BLUP values of the two parents were very close, and the progeny exhibited a wide degree of variation around the narrow parental range. For bitter, the mean BLUP value of the progeny fell outside the range defined by the two parents. Based on these results, there appears to be little opportunity for improvement of roasted peanut attribute in this population, while there is an opportunity to improve the sweet attribute. The entire hybrid population appeared to have regressed in terms of the bitter attribute.

There appears to be an association of low breeding value for sweetness with resistance to Cylindrocladium black rot (CBR) caused by *Cylindrocladium parasiticum* Crous, Wingfield, & Alfenas. All three of the resistant cultivars available to growers—NC 10C, NC 12C, and Perry—have negative effects on sweet and roasted peanut and positive effects on bitter. To prevent degradation of the general flavor profile of the virginia market type, it will be important to include CBR-resistant parents in crosses with parents

Table 3. Correlations among BLUPs of breeding value for the roasted peanut, sweet, and bitter attributes at their estimated heritabilities.

	Roasted peanut $h^2 = 0.10$	Sweet $h^2 = 0.25$	Bitter $h^2 = 0.05$	Roasted peanut $h^2 = 0.10$	Sweet $h^2 = 0.25$	Bitter $h^2 = 0.05$
	-------------	Overall	-------------	------------	Spanish-Valencia	-------------
Roasted peanut, $h^2 = 0.10$	1.0000	0.7098**	-0.7717**	1.0000	0.5742^{ns}	-0.2603^{ns}
Sweet, $h^2 = 0.25$	0.7098**	1.0000	-0.7345**	0.5742^{ns}	1.0000	-0.7898**
Bitter, $h^2 = 0.05$	-0.7717**	-0.7345**	1.0000	-0.2603^{ns}	-0.7898**	1.0000
	--------------	Runner	---------------	-----------------	Virginia	------------------
Roasted peanut, $h^2 = 0.10$	1.0000	0.6457**	-0.5499**	1.0000	0.7426**	-0.6321**
Sweet, $h^2 = 0.25$	0.6457**	1.0000	-0.6620**	0.7426**	1.0000	-0.7764**
Bitter, $h^2 = 0.05$	-0.5499**	-0.6620**	1.0000	-0.6321**	-0.7764**	1.0000

^{ns},** Denote nonsignificance and significance at the 1% level of probability, respectively.

Table 4. Summary statistics for BLUPs of breeding value for the roasted peanut, sweet, and bitter attributes at their estimated heritabilities.

	Roasted peanut $h^2 = 0.10$	Sweet $h^2 = 0.25$	Bitter $h^2 = 0.05$	Roasted peanut $h^2 = 0.10$	Sweet $h^2 = 0.25$	Bitter $h^2 = 0.05$
	flavor intensity units					
	Overall			Spanish-Valencia		
Mean	+0.02	-0.06	-0.02	+0.00	+0.15	-0.11
Minimum	-0.51	-0.65	-0.41	-0.17	-0.55	-0.41
Maximum	+0.45	+0.68	+0.40	+0.35	+0.68	+0.32
Range	0.96	1.33	0.81	0.52	1.23	0.74
Std. dev.	0.17	0.25	0.20	0.16	0.25	0.20
	Runner			Virginia		
Mean	+0.14	+0.01	-0.14	-0.08	-0.16	+0.10
Minimum	-0.24	-0.42	-0.36	-0.51	-0.65	-0.22
Maximum	+0.45	+0.35	+0.22	+0.21	+0.42	+0.40
Range	0.69	0.78	0.58	0.72	1.07	0.62
Std. dev.	0.18	0.25	0.20	0.16	0.26	0.20

conveying superior flavor attributes such as Altika or NC Ac 18457. This negative association between two desirable traits illustrates the need to monitor flavor attributes as an adjunct to resistance breeding. Although its sweet scores are still low, Perry represents an improvement in roasted peanut attribute over NC 10C and NC 12C. Perry's flavor scores were monitored as part of the North Carolina breeding program, and they were weighed against its array of agronomic traits and disease resistances. Monitoring also has helped in the runner market type. Florida breeding line UF87118 was developed to have resistance to late leaf spot caused by *Cercosporidium personatum* Berk. & Curtis, but its use as a parent could have a highly negative impact on flavor of its progeny. This line was not released to growers.

Among the runner-type lines, Florunner and its component and sibling lines had positive effects on roasted peanut and sweet. Because Florunner has been used widely as a parent in development of new runner-type cultivars, the runner market type should have generally superior flavor profiles. Another interesting set of runner-type lines is the

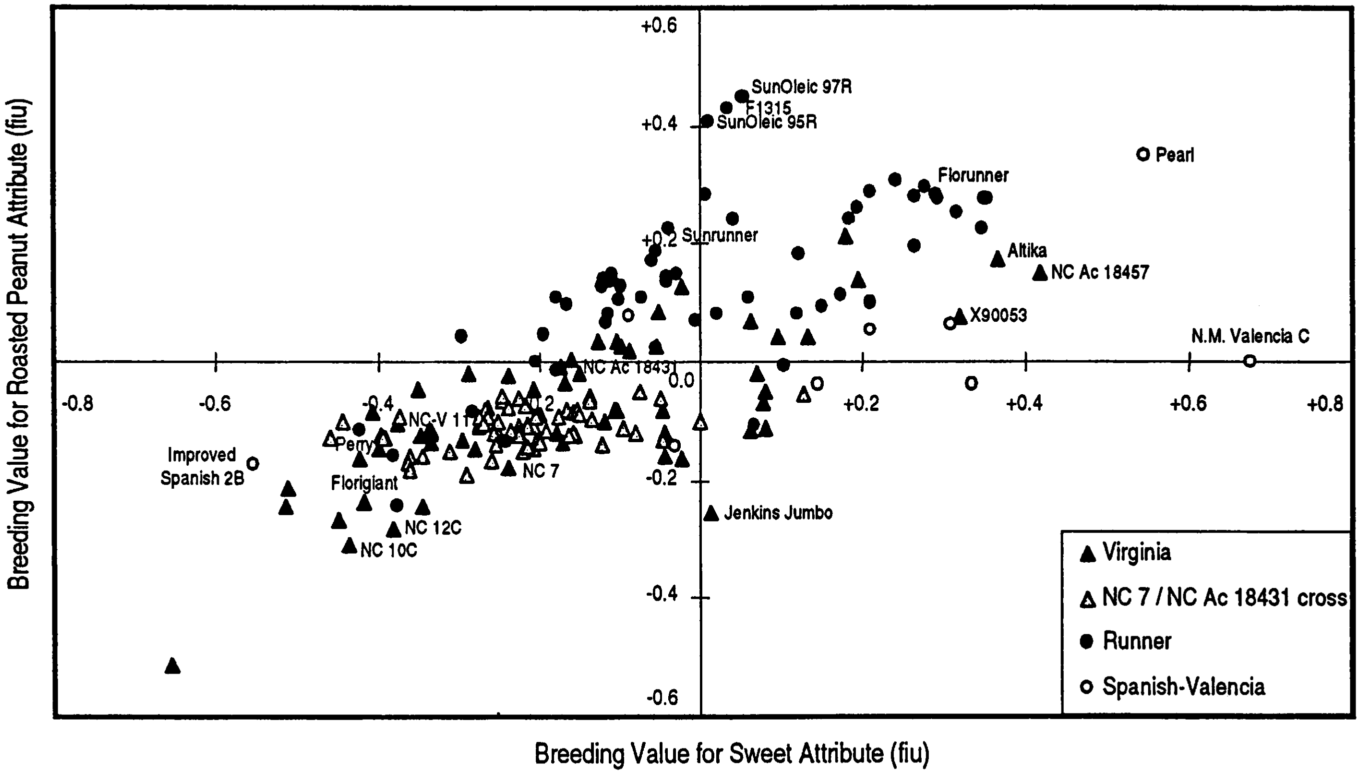

Fig. 1. Best linear unbiased predictors (BLUPs) of breeding values for roasted peanut attribute intensity vs. sweet attribute intensity for 250 peanut genotypes.

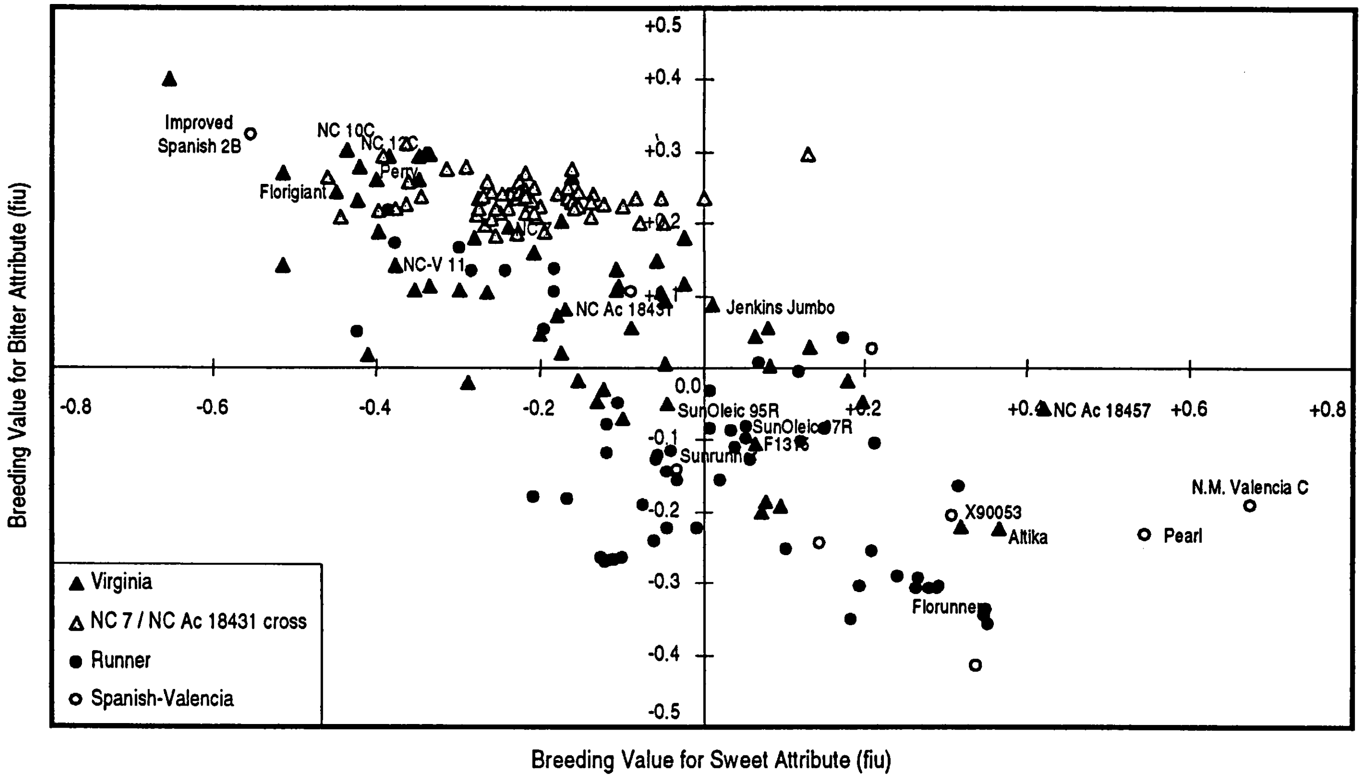

Fig. 2. Best linear unbiased predictors (BLUPs) of breeding values for bitter attribute intensity vs. sweet attribute intensity for 250 peanut genotypes.

group of high-oleic cultivars and breeding lines derived from the Sunrunner cultivar. The high-oleic derivatives have approximately the same BLUPs for breeding value of the sweet attribute, but they are consistently higher in breeding value for roasted peanut. They had the greatest positive effects on roasted peanut of any of the lines tested. It remains to be seen whether the difference is real or an artifact of the sensory evaluation. The protocol requires a storage period prior to roasting and tasting during which oxidation of linoleic acid in the Sunrunner might produce off-flavors that could mask the roasted peanut.

New Mexico Valencia C, a valencia-type cultivar, had the highest scores for sweet attribute of any line tested to date (Pattee *et al.*, 1998); it also had the greatest positive predicted parental effect on sweetness but was neutral for roasted peanut. Pronto, a spanish-type cultivar, had the lowest predicted breeding value for bitter attribute. It also had a strong positive effect on sweet and a weakly positive effect on roasted peanut. Pearl, a spanish-type cultivar, had a strong positive effect in both roasted peanut and sweet and a negative effect on bitter. Improved Spanish 2B, a spanish-type line used to establish the breeding program in North Carolina, was a very poor choice of lines from the standpoint of flavor.

Validation of BLUP Predictors and Comparison of Midparent and BLUP Values for Parent Selection. To validate the BLUP procedure, the BLUPs can be used to predict the sensory attribute values of lines actually evaluated. This is akin to the coefficient of multiple determination in multiple regression, i.e., the correlation between the predicted and observed values of the data. Because the BLUPs of breeding value of two parents predict the mean value of the progeny derived from the cross between them, it is worth considering not only the correlation of the predicted values with the individual observed values, but also the correlation between the predicted and observed cross means. There were 231 lines derived from 53 crosses for which predicted and observed values could be compared (Table 5). For all three sensory attributes, the correlation of predicted with observed cross means was greater in magnitude than the correlation with individual values. The agreement between predicted and observed cross means was close, r > 0.85 for each

Table 5. Correlation of observed values with values predicted by BLUPs of breeding value or by midparent value.

	Roasted Peanut	Sweet	Bitter
Observed value vs.			
value predicted by BLUP			
231 observations on lines[a]	0.6335	0.6520	0.7046
53 cross means	0.8839	0.9152	0.8588
Observed value vs.			
value predicted by BLUP or MP			
143 observations on lines, BLUP[b]	0.3325	0.2610	0.2675
143 observations on lines, MP	0.2729	0.1788	0.2470
13 cross means, BLUP	0.8220	0.7743	0.6189
13 cross means, MP	0.6803	0.6025	0.5771

[a] 231 lines from 53 crosses had BLUP estimates for both parents, permitting prediction of the cross mean from the BLUPs of the parents.

[b] 143 lines from 13 crosses had both parents or all four grandparents included in the genotype sample, permitting prediction of the cross mean by the midparent value.

attribute, indicating that the BLUPs were good predictors of mean cross performance.

Before the advent of the BLUP procedure, plant breeders could estimate breeding value or combining ability only by empirical production of hybrid populations followed by progeny testing. The method most commonly used to predict breeding value was to compute the midparent value (i.e., the arithmetic mean of the phenotypic values of the two parents) or to conduct empirical experiments. Because BLUP uses information from all relatives, it should provide superior predictors of breeding value. The data provided an opportunity to compare BLUP estimates with midparent values for 143 lines derived from 13 crosses whose parents or grandparents were included in the study (Table 5). In all cases, the correlation between observed and predicted values by BLUPs was greater in magnitude than the correlation of observed values with values predicted by midparent. The increase in correlation was most pronounced for roasted peanut and sweet, especially when examining cross means rather than values of individual lines. These results indicate that the BLUP procedure is at least as good as the midparent method for predicting cross performance, and may be sub-stantially better for some traits.

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