

# Narrow-Sense Heritability of Selected Sensory Descriptors in Virginia-Type Peanut (*Arachis hypogaea* L.)<sup>1</sup>

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## ABSTRACT

The sweet, bitter and roasted peanut attributes of roasted peanut (*Arachis hypogaea* L.) flavor have been shown to be heritable traits. Previous research has estimated broad-sense heritability (H) and breeding values of numerous peanut cultivars and breeding lines for these attributes, but no study has estimated narrow-sense heritability ( $h^2$ ) in a specific population derived through hybridization and inbreeding. A population of 120  $F_3$ -derived families was developed without selection from the cross of NC 7 / NC Ac 18431, a virginia-type line identified in 1990 as having a good flavor profile. The parents and  $F_{3.5}$  families were grown at two locations in North Carolina in 1995. SMK samples from each plot were roasted, ground to paste, tasted by a sensory panel, and scored for roasted peanut, sweet, bitter and astringent attributes. Additive and nonadditive genetic variances were estimated by equating variances among  $F_2$ -derived families and among  $F_3$ -derived families within  $F_3$ -derived families to genetic covariances among inbred relatives. Regardless of whether the genetic model included dominance or additive-by-additive epistasis, the estimates of additive genetic variance for flavor attributes were small compared to those for nonadditive genetic variance. Narrow-sense heritability in the  $F_2$  generation was estimated at 0 for roasted peanut and astringent, 0.02 to 0.04 for sweet, and 0.01 to 0.03 for bitter, depending on the model used. Because of the low values of  $h^2$ , which are specific to this population, gain from selection in early generations is expected to be limited within this population. Selection in this population should be practiced in late generations. Other parents have been identified whose crosses should produce greater improvement in sensory quality than can be expected from the NC 7 / NC Ac 18431 population.

Key Words: Flavor, genetic gain, sensory attributes.

Enhancement of roasted peanut flavor has been a long-standing objective of the peanut industry. That this enhancement could be accomplished in part through appropriate breeding programs has been documented in wide ranging studies on

effects of genotype, environment, and their interaction (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1993, 1994, 1995, 1997); high oleic acid content (Pattee and Knauff, 1995); and roast color and fruity attribute (Pattee *et al.*, 1991; Pattee and Giesbrecht, 1994). 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. Hence, the selection of genotypes that are to serve as the progenitors of future breeding lines and cultivars must be undertaken with as much insight as possible. Understanding the potential of proposed parents to transfer these quality characteristics to their progeny has been discussed by Pattee *et al.* (2001). They proposed the use of Best Linear Unbiased Prediction (BLUP) procedures to estimate the breeding value of potential parents. Breeding programs have been undertaken to modify these inherited characteristics to enhance the roasted peanut flavor of *Arachis hypogaea* L. The BLUP procedure is useful in predicting the mean of the progeny derived from a cross between two parents. The total improvement in flavor is the sum of the shift in mean achieved by the choice of parents and the additional progress achieved by selection within the population. This additional progress is proportional to the narrow-sense heritability of the trait in the population. The objective of this study was to determine narrow-sense heritability of selected peanut sensory descriptors in a population of virginia-type peanut (*A. hypogaea*).

## Materials and Methods

**Genotype Resources.** In 1990, a cross between NC 7 and NC Ac 18431 was made based on the superior roast peanut attribute quality of NC Ac 18431 and the agronomic qualities of NC 7. The  $F_2$  generation was grown in 1992, and 60 plants were sampled at random from the population. In 1993, two  $F_3$  plants were harvested from each  $F_{2.3}$  family. In 1994,  $F_{3.4}$  families were harvested in bulk, and in 1995 the 120  $F_{3.5}$  families were grown with the two parents at two locations, the Upper Coastal Plains Res. Sta. at Rocky Mount, NC, and the Peanut Belt Res. Sta. at Lewiston, NC. All plots were irrigated and recommended procedures for weed and disease control, soil fertilization, digging and harvesting were followed.

**Sample Handling.** A 1000-g sample of the sound-mature-kernel (SMK) fraction from each location-entry was placed in controlled storage at 5 C and 60% RH in February following the 1995 crop harvest until roasted. SMK fractions were separated using official grading standards for each market type.

**Sample Roasting and Preparation.** The peanut samples were roasted in May and June 1996 using a Blue M "Power-O-Matic 60" laboratory oven, ground into a paste, and stored in jars at -20 C until evaluated. The roasting, grinding, and color measurement protocols were as described by Pattee and Giesbrecht (1990) and modified by Pattee *et al.* (1997).

**Sensory Evaluation.** A long-standing 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

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(1990) and Pattee *et al.* (1993). Two sessions were conducted each week on nonconsecutive days. Samples were presented in an incomplete block design with four per session. Sensory evaluation commenced 23 July 1996 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.** Statistical analysis in this study was performed using PROC MIXED in SAS (1992) to estimate the design components of variance using restricted maximum likelihood estimation. Covariates fruity and roast color were used, as needed, based upon the findings of Pattee *et al.* (1991, 1997) and Pattee and Giesbrecht (1994). It should be noted that the incomplete block design of the study enables estimates of variation between and within sensory panel sessions.

Genetic components of variance were obtained by equating the design components to a linear combination of genetic components, inverting the matrix of coefficients, and multiplying it by the vector of design variance components. The component of variance among  $F_{2.5}$  families was equated to the covariance between  $F_5$  ( $S_3$ ) plants derived from the same  $F_2$  ( $S_0$ ) plant,  $C_{033} = \sigma_A^2 + (1/64)\sigma_D^2 + \sigma_{AA}^2$ , where  $\sigma_A^2$  is the additive genetic variance,  $\sigma_D^2$  the dominance variance, and  $\sigma_{AA}^2$  the additive-by-additive ( $A \times A$ ) epistatic variance (Cockerham, 1983). The component of variance among  $F_{3.5}$  families within  $F_{3.5}$  families was equated to the difference between the covariance of  $F_5$  ( $S_3$ ) plants derived from the same  $F_3$  ( $S_1$ ) plant and  $C_{033}$ ,  $C_{133} - C_{033} = (1/2)\sigma_A^2 + (1/32)\sigma_D^2 + (5/4)\sigma_{AA}^2$ . The residual variance was equated to the difference between the variance of  $F_5$  plants and the covariance of  $F_5$  plants derived from the same  $F_3$  plant,  $C_{333} - C_{133} = (3/8)\sigma_A^2 + (3/16)\sigma_D^2 + (81/64)\sigma_{AA}^2$ . Because there were insufficient different family types to estimate three genetic variances simultaneously, alternative genetic models were fit separately: an additive-dominance model and an additive-  $A \times A$  epistatic model.

Narrow- and broad-sense heritability ratios for single-plot values were computed from estimates of genetic, environmen-

tal and genotype-by-environment interaction variances. Narrow-sense heritability was estimated as the ratio of additive genetic variance to phenotypic variance for a single plot. The equation used to estimate narrow-sense heritability was

$$\hat{h}^2 = \frac{\hat{\sigma}_A^2}{\hat{\sigma}_A^2 + \hat{\sigma}_{NA}^2 + \hat{\sigma}_{LA}^2 + \hat{\sigma}_{LNA}^2 + \hat{\sigma}_P^2 + \hat{\sigma}_W^2} \quad [\text{Eq. 1}]$$

and the equation used to estimate broad-sense heritability was

$$\hat{H}^2 = \frac{\hat{\sigma}_A^2 + \hat{\sigma}_{NA}^2}{\hat{\sigma}_A^2 + \hat{\sigma}_{NA}^2 + \hat{\sigma}_{LA}^2 + \hat{\sigma}_{LNA}^2 + \hat{\sigma}_P^2 + \hat{\sigma}_W^2} \quad [\text{Eq. 2}]$$

where  $\sigma_A^2$  was the estimate of additive genetic variance,  $\sigma_{NA}^2$  the estimate of nonadditive genetic variance due to dominance or epistasis,  $\sigma_{LA}^2$  the estimate of location-by-additive interaction variance,  $\sigma_{LNA}^2$  the estimate of location-by-nonadditive interaction variance,  $\sigma_P^2$  the estimate of panel-to-panel variance, and  $\sigma_W^2$  the estimate of plot-to-plot environmental variance.

## Results and Discussion

Estimates of genetic variance obtained by this method apply to the  $F_2$  ( $S_0$ ) generation. Regardless of whether the genetic model included dominance or  $A \times A$  epistasis, the estimates of additive genetic variance for flavor attributes roasted peanut, sweet, bitter, and astringent were very small (Table 1). The nonadditive component of genetic variance was substantially larger in either model. With only two family types included in the experiment, it was not possible to compare the goodness of fit of the additive-dominance and additive-epistasis models. The standard errors of estimation of dominance variance were somewhat less than the errors for estimates of epistatic variances. To some degree, the very large estimates of dominance variance may be artifacts due to the very small coefficients

**Table 1. Estimates of genetic variances, narrow- and broad-sense heritabilities in  $F_{3.5}$  families derived from a cross of NC 7 / NC Ac 18431.**

Model	Parameter estimated	Roasted peanut	Sweet	Bitter	Astringent
----- flavor intensity units -----					
Additive & dominance	$\sigma_A^2$	-0.0003±0.0063	0.0097±0.0095	0.0071±0.0102	0.0014±0.0060
	$\sigma_D^2$	0.1241±0.0032	0.3742±0.0048	0.2827±0.0051	0.1253±0.0030
	$\sigma_{LA}^2$	0.0000±0.0000	0.0000±0.0000	-0.0014±0.0098	-0.0054±0.0002
	$\sigma_{LD}^2$	0.0000±0.0000	0.0000±0.0000	0.2985±0.0049	0.3437±0.0004
	$\sigma_W^2$	0.0717±0.0107	0.0142±0.0102	-0.0406±0.0133	-0.0229±0.0102
	$\sigma_{panel}^2$	0.0127±0.0064	0.0008±0.0049	0.0147±0.0068	0.0072±0.0052
	$h^2$	0.0000	0.0243	0.0117	0.0029
Additive & $A \times A$ -epistasis	H	0.5953	0.9624	0.4805	0.2653
	$\sigma_A^2$	-0.0023±0.0108	0.0038±0.0138	0.0026±0.0151	-0.0006±0.0099
	$\sigma_{AA}^2$	0.0039±0.0114	0.0117±0.0134	0.0088±0.0149	0.0039±0.0103
	$\sigma_{LA}^2$	0.0000±0.0000	0.0000±0.0000	-0.0061±0.0192	-0.0107±0.0114
	$\sigma_{LAA}^2$	0.0000±0.0000	0.0000±0.0000	0.0093±0.0212	0.0107±0.0143
	$\sigma_W^2$	0.0908±0.0153	0.0717±0.0162	0.0488±0.0283	0.0492±0.0201
	$\sigma_{panel}^2$	0.0127±0.0064	0.0008±0.0049	0.0147±0.0068	0.0072±0.0052
	$h^2$	0.0000	0.0437	0.0313	0.0000
	H	0.0361	0.1764	0.1361	0.0551

associated with dominance variance in the covariances among the relatives tested in the experiment: 1/64 in the variance among  $F_{2.5}$  families and 1/32 in the variance among  $F_{3.5}$  families within  $F_{2.5}$  families. The coefficients on additive-by-additive epistasis in the same covariances were substantially larger: 1 and 5.4, respectively. The epistatic model is more likely to reflect the biological facts in an allotetraploid species such as peanut. The self-pollinated tetraploid peanut does not exhibit appreciable heterosis for agronomic traits, and therefore it would be surprising to see large dominance effects for flavor attributes. Again, regardless of the model used, the estimate of narrow-sense heritability was less than 5% for any of the four attributes, with sweet and bitter having the highest values among the four. While such low numbers were expected for roasted peanut and bitter, whose broad-sense heritabilities in a more genetically diverse population were estimated at  $H = 0.06$  (Pattee *et al.*, 1998), the previous estimate of  $H$  for sweet in the same population was  $H = 0.28$ .  $H$  for astringent can be estimated as 0.13 from variance component values published by Pattee and Giesbrecht (1990). Estimates of  $H$  for the NC 7/NC Ac 18431 population are similar to the values reported in the literature for the broad population. The narrow-sense heritability values estimated in this study suggest that gain from selection within the NC 7/NC Ac 18431 population would be limited. The preponderance of nonadditive variance, if due to  $A \times A$  epistasis, indicates that early generation selection would be ineffective.

The data from this study were included in a larger set that was subjected to a best linear unbiased prediction analysis of breeding value in a larger set of data (Pattee *et al.*, 2001). Although breeding values of the parents are predictive of the mean of the population rather than of the variance to be expected among their inbred progeny, the predicted breeding values of NC 7 and NC Ac 18431 were close for roasted peanut [-0.18 vs. -0.03 flavor intensity units (fiu)], sweet (-0.24 vs. -0.17 fiu), and bitter (0.08 vs. 0.19 fiu). Based on their breeding values, these two lines were not the best candidates for use as parents to improve flavor in virginia-type peanut in spite of the relatively good flavor profile of NC Ac 18431 compared with other lines evaluated by 1990 when the cross was made. Other virginia-type lines with positive breeding values for roasted peanut and sweet and negative values for bitter have been identified.

Some breeders use the coefficient of coancestry of two parents as an indicator of the amount of genetic variance there should be among their inbred progeny (Manjarrez-Sandoval *et al.*, 1997), with lower values being predictive of greater intra-

population variance. The coefficient of coancestry between NC 7 and NC Ac 18431 was  $\theta = 0.08$ , suggesting that the genetic variance among their inbred progeny should not be restricted due to close relationship of the parents. It is not clear why there is a paucity of additive genetic variation within this population. Possibly the genes affecting flavor in these two parents are identical in state without being identical by descent.

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