A Note On Broad-Sense Heritability of Selected Sensory Descriptors in Virginia-Type Arachis Hypogaea L.¹

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ABSTRACT

Improvement of flavor quality is a breeding objective that merits increased attention. To obtain further information on broad-sense heritability of selected sensory attributes, 30 virginia-type genotypes sources were grown in replicated experiments at two locations during 1988 for evaluation. Roasted peanut paste samples were evaluated for 14 sensory attributes. Fruity attribute was confirmed as having a significant suppressive effect on roasted peanut attribute. Session-to-session variation was significant and use of an incomplete block design provided for control of panel variation in the experimental error. Broad-sense heritability estimates for roasted peanut, sweet, and nutty sensory attributes were higher than previously reported, 0.31 vs. 0.24; 0.68 vs. 0.14; 0.37 vs. 0.05, respectively. Nine genotypes were found to have statistically significant higher roasted peanut intensity than the industry accepted standard Florigiant. Further calculations showed that experiments with two replications at each of four locations should have an 80% chance of detecting statistical significance for roasted peanut attribute differences of 0.5 units among genotypes when testing at the 5% level. A similar experiment with two replications at two locations should have a 40% chance of detecting statistical significance.

Key Words: Arachis hypogaea, genotype, broad-sense heritability, sensory attributes

Enhancement of roasted peanut flavor has been a longstanding objective of the peanut industry. Recent documentation of broad-sense heritability of the roasted peanut sensory attribute suggests that improvement can be obtained through breeding strategies (Pattee and Giesbrecht, 1990). The broad survey and limited replication of the genotype entries in our previous study suggested the need for a more specific confirmation of this observation of broad-

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sense heritability. The objectives of this study were to (a) determine broad-sense heritability of selected peanut sensory descriptors in virginia market-type peanut (*Arachis hypogaea* L.), (b) investigate sources of statistical variation which could be controlled, and (c) determine the statistical design needed to have an 80% chance of detecting statistically significant differences among genotypes sources.

Materials and Methods

Thirty virginia market-type genotypes, consisting of cultivars and advanced breeding lines, were grown in randomized complete block experiments at two locations, Northampton County, NC and Suffolk, VA with two replications in 1988 using recommended cultural, harvesting, and handling practices. A 1,000-g sample of the sound mature kernel (SMK) fraction from each replication of each location-entry was shipped to Raleigh, NC in February, 1989 and placed in controlled storage at 5 C and 60% RH until roasted. The peanut samples were roasted during May, 1989 using a Blue M "Power-O-Matic 60" laboratory oven, ground into a paste, and stored in glass jars at -20 C until evaluated. The roasting, grinding, and color measurement protocols were as described by Pattee and Giesbrecht (1990).

Sensory Evaluation

An eight-member trained roasted peanut flavor profile panel at the Food Science Department, North Carolina State University, Raleigh, NC evaluated all peanut-paste samples using a 14-point intensity scale. An orientation session was conducted in which the panel reviewed the definition of the following roasted peanut sensory attributes: painty, stale, roasted peanut, overroast, underroast, sweet, fruity, mold, petroleum, bitter, astringent, throat/tongue burn and nutty. Then they compared selected experimental peanut paste samples to a peanut butter control. A handout containing the defined roasted peanut sensory attributes and the control sample with ratings was presented to the panel at each session. Two sessions were conducted weekly but never on consecutive days. Samples were presented in a incomplete block design with four samples tasted in each session. Sensory evaluation was conducted on the samples from June 20 through October 2, 1989.

Statistical Analysis

Statistical analysis in this study was performed using procedures in the SAS (1987) system, version 6 and Giesbrecht's (1985) procedure for analysis of mixed models to estimate the components of variance. It should be noted that the incomplete block design of the study enables estimates of variation between and within sensory panel sessions.

Broad-sense heritability estimates for the sensory attributes were obtained by computing the ratio of the estimated variance components for differences among genotypes to the sum of all components. The equation used to calculate broad-sense heritability was:

$$\frac{S_{\rm C}^2}{S_{\rm C}^2 + S_{\rm L}^2 + S_{\rm CL}^2 + S_{\rm R}^2 + S_{\rm P}^2 + S_{\rm V}^2}$$

where S_{G}^{2} , S_{L}^{2} , S_{GL}^{2} , S_{R}^{2} , S_{P}^{2} , and S_{w}^{2} are estimates of variance components for genotype, locations, genotype by location interaction, replicates, panels, and within-panel error, respectively.

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Results and Discussion

An understanding of the capability to control sources of variation are major factors in obtaining best estimates of broad-sense heritability. Two major sources of variance in the roasted peanut attribute response have been shown to be paste color, i.e., degree of lightness or darkness, (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1990; Pattee *et al.*, 1991) and intensity of the fruity attribute response (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1990; Sanders *et al.*, 1989).

For this study a specific effort was made to control the paste color between the suggested limits of CIELAB L* color values <56 to >62. However, three of the samples exceeded these limits (Table 1) and when the above limits were applied to the data a decrease in the coefficient of variability was observed, confirming the need to control the limits of peanut paste color. The second factor, excessive level of fruity response, cannot be controlled by laboratory protocols. The intensity of this attribute is related to interactions of maturity of the sample, environmental factors, and improper practices during curing of the peanuts (Pattee et al., 1989, Sanders et al., 1989; Pattee et al., 1991). Thus, within a given data set selected constraining limits for the fruity intensity need to be set. In this study we chose to eliminate all fruity values with an intensity level 3 or above when constraining limits were applied. The inclusion of this limit also reduced the coefficient of variability (Table 1). However, an additive effect when constraining both variables was not observed. This probably results from the limited improvement when constraining CIELAB L* alone. In general, these data support the concept that peanut paste color and the fruity attribute intensity must be constrained to minimize the coefficient of variability.

Using the constrained data set, board-sense heritability estimates were obtained for the six peanut sensory attributes evaluated which have the potential to be inherited traits. The three sensory attributes with the highest broad-sense heritability estimates were roasted peanut (0.31), sweet (0.68), and nutty (0.37). These were even higher than previously reported, 0.24, 0.14, and 0.05, respectively (Pattee and Giesbrecht, 1990). The broad-sense heritability estimate for roasted peanut compares favorably with the estimate obtained by Pattee and Giesbrecht (1990), confirming the potential to improve the roasted peanut attribute intensity with appropriate selection techniques in a breeding program. The estimates for the other sensory attributes, bitter, throat/ tongue-burn, and astringent were 0.02, 0.12, and 0.00, respectively.

The use of an incomplete block statistical design in the sensory analysis portion of this study permitted an analysis of the variation sources influencing the sensory panel data.

Table 1. Coefficient of variability values for roasted peanut attribute using selectively constrained variables.

Constrained Variable	No. Obs.	Genotype Entries	Coeff. of Variability	
None	120	30	11.88	
CIELAB L	117	30	11.77	
Fruity	87	30	11.24	
L + Fruity	85	29	11.32	

Because the roasted peanut attribute is the component of principal interest, we will now limit our data and discussion to that component. The sources of variation were genotype, location, genotype X location, replication, session to session (panel), and within a session (panel). We also investigated the effect of the model assumptions used on the variance component (Table 2). The variance component for genotype, location, genotype X location, replication, and session to session (panel) were the same magnitude regardless of the model assumptions used for determination of the variance component. In contrast, the use of various model assumptions with the within session (panel) variance component showed a significant change in the magnitude when the fruity attribute is controlled. This decrease in magnitude indicated that the individual panel members within a session had difficulty in judging the effect of the fruity attribute on the roasted peanut attribute as the intensity of the fruity attribute increases above three (Table 2). However, the variation between panel members is shown to be consistent for the individual panel members as the session to session variance magnitude did not change significantly. The above data on statistical variation also suggest that use of the slightly more complex incomplete block statistical design for presentation of the samples to the panel may not be justified in these studies using this particular set of panelists (Table 2).

Table 2. Components of variance for rasted peanut attribute obtained from the complete data set and sub-sets conforming to limits on CIELAB L* color values and fruity attribute.

	Source of Variation					
Model Assumptions	Geno- type	Loc	GXL	Rep	Panel	Within Panel
All Data	.040	0	.043	.168	.092	.106
Reject L* <56 & >62	.040	0	.038	.167	.087	.113
Reject Fruity Attribute >3	.044	0	.051	.160	.104	.046
Reject L* + Fruity	.044	0	.048	.170	.102	.049

Evaluation of the 30 virginia-type genotypes for intensity of the roasted peanut attribute showed that nine of the 30 entries had an intensity rating significantly higher than that found for Florigiant (Table 3). These comparative flavor improvements over Florigiant taken in concert with the previously published flavor comparisons of virginia, runner, and spanish-type germplasm (Pattee *et al.*, 1990) suggest that the roasted flavor intensity of virginia market-type peanuts can be increased with selective breeding techniques to levels approaching that of the industry standard Florunner.

In conducting comparative genotype flavor studies it is imperative, because of the costs involved, that these studies be conducted as economically as possible, yet be large enough to give a reasonable expectation of finding significant differences if they exist. Calculations using formula 5.34 in Steel and Torrie (1980):

$$n = \frac{(z (\alpha/2) + z (\beta))^2 \sigma_D^2}{\delta^2}$$

and assuming among panel variance equal to 0.1, show that experiments with two replications at each of four locations should have an 80% chance of statistical significance

Table 3. Comparison of roasted peanut attribute intensity across genotype sources and the intensity difference when compared to Florigiant.

	Attribute	Difference from
Genotype	Intensity	Florigiant
VA830516	5.6	1.0-/
NC18460	5.5	0.9*
VC-1	5.4	0.8*
NC18431	5.4	0.8
NC18455	5.3	0.7*
NC18456	5.3	0.7
NC 7	5.3	0.7
NC18457	5.2	0.6
NC 9	5.2	0.6
VP8420	5.1	0.5
NC18423	5.1	0.5
VP8407	5.1	0.5
NC18464	4.9	0.3
VP8417	4.9	0.3
NC-V 11	4.9	0.3
NC18449	4.9	0.3
NC18459	4.8	0.2
NC18462	4.8	0.2
NC18424	4.8	0.2
NC18426	4.8	0.2
NC18452	4.8	0.2
NC18454	4.8	0.2
NC18463	4.7	0.1
NC18451	4.7	0.1
VNC 851	4.7	0.1
NC18450	4.6	0
VA830416	4.6	0
Florigiant	4.6	
NC 10C	4.5	-0.1

 $^{*'}$ LSD = 0.6 p=0.05.

testing at the 5% level of significance $(z(\alpha/2) = 1.96, z(\beta) = 0.84, \sigma_D^2 = 0.2, \delta = 0.5)$. A similar experiment with two replications at two locations should certainly be adequate to have a 40% chance $(z(\beta) = -0.25)$ of detecting statistical significance under the same conditions.

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