

Variation in Intensity of Sweet and Bitter Sensory Attributes Across Peanut Genotypes¹

H. E. Pattee*, T. G. Isleib, and F. G. Giesbrecht²

ABSTRACT

Genetic improvement of sweet, bitter and roasted peanut attributes of peanut (*Arachis hypogaea* L.) flavor is predicated on the existence of genetic variation for the attributes. A total of 1136 SMK samples representing 122 cultivars and breeding lines and 42 year-by-location combinations from three major peanut-producing regions were roasted, ground to paste, and submitted to a trained sensory panel for evaluation of flavor attributes. Data were subjected to analysis of variance to separate genetic, environmental and G×E interaction effects following adjustment for roast color and intensity of the fruity attribute. Genotypic variation was significant for all three attributes as was location-to-location variation within year and region. Large year effects were observed for bitter and roasted peanut attributes. Estimates of broad-sense heritability (H) among inbred lines and cultivars were 0.28 for sweet, 0.06 for bitter, and 0.06 for roasted peanut attributes, indicating that selection for sweetness should result in relatively rapid genetic gain. The ranges of genotypic means were 2.33-4.12 flavor intensity units (fiu) for sweet, 2.43-4.46 fiu for bitter, and 3.75-5.22 fiu for roasted peanut. Correlations among least squares means for the three attributes were highly significant ($r = -0.80$ for bitter and sweet, $r = 0.59$ for roasted peanut and sweet, and $r = -0.59$ for roasted peanut and bitter), indicating that indirect selection based on the more highly heritable sweet attribute could be more effective than direct selection for increased intensity of the roasted peanut and decreased intensity of the bitter attribute. Specific genotypes with superior aspects of roasted peanut flavor were identified.

Key Words: *Arachis hypogaea* L., flavor, genetic variation, roasted peanut.

Sweet and bitter are two of the four basic tastes (Amerine *et al.*, 1965) and are defined in the sensory attribute lexicons for roasted peanuts (*Arachis hypogaea* L.) (Sanders *et al.*, 1995), yet there is little direct research in roasted peanut quality. Sanders *et al.* (1989a,b) found a varying influence of maturity on sweet and bitter intensities. They also found that increased curing tem-

peratures decreased bitterness in more mature peanuts. Curing temperatures had no effect on sweet attribute intensity across maturities. Muego-Gnanasekharan and Resurreccion (1992) found that sweet and bitter intensities did not change during storage at varying elevated temperatures over storage times up to 1 yr. Earlier, Oupadissakoon and Young (1984) modeled roasted peanut flavor and found that the best 10-variable model for predicting roasted peanut flavor used the concentrations of eight different amino acids, sucrose, and total sugar from raw peanuts. However, sucrose and total sugar contents were negatively correlated with the desirability of the roasted peanuts. They reported the sweet attribute to be significantly correlated with maturity and total sugars. Bitter attribute was not considered to be a significant contributor to the roasted peanut flavor because of its low intensity, but statistical analysis showed a significant negative correlation between the bitter and roasted peanut attributes. That both the bitter and sweet attributes arise from non-volatile constituents can be inferred from the headspace analysis work of Young and Hovis (1990) in which no relationship was found between the peaks of the headspace volatile chromatograms and sweet and bitter intensity scores.

The carbohydrates of peanuts have been identified and quantitated (Newell *et al.*, 1967; Holley and Hammons, 1968; Tharanathan *et al.*, 1975, 1976). They have been shown to be precursors of compounds imparting the roast peanut characteristic (Newell *et al.*, 1967; Mason *et al.*, 1969). They change over storage time (Pattee *et al.*, 1981) and vary across genotypes (Basha *et al.*, 1976; Oupadissakoon *et al.*, 1980). However, little information is available on the variation of the flavor attribute sweet across peanut genotypes or on which germplasm might serve as parents in breeding programs to enhance this characteristic.

Recent papers have described the variation in the sensory descriptors of roasted peanut (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1993, 1994, 1995; Isleib *et al.*, 1995). These reports have included estimates of broad-sense heritability of sufficient magnitude to warrant improving the roasted peanut attribute level through breeding. Estimates of broad-sense heritability for five additional sensory attributes (sweet, bitter, tongue/throat burn, astringent, and nutty) were also reported, but at that time, only sweet showed sufficient heritability for its improvement to be considered a realistic breeding objective. Roasted peanut, sweet and bitter sensory attribute data have been shown to require covariate adjustment for sample-to-sample variation in roast color and fruity attribute before the data can be properly interpreted (Pattee *et al.*, 1991, 1997; Pattee and Giesbrecht, 1994).

The objectives of this report are (a) to document the variability in sweet and bitter attributes across peanut cultivars and breeding lines in the runner, spanish, and

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²Res. Chem., U.S. Dept. of Agriculture, Agric. Res. Serv., Dept. of Botany, Box 7625; Prof., Dept. of Crop Science; and Prof., Dept. of Statistics, respectively, North Carolina State Univ., Raleigh, NC 27695.

*Corresponding author.

virginia market types, and (b) to determine the interrelationships among sweet, bitter and roasted peanut attributes.

Materials and Methods

Genotype Resources. From 1986 to 1994, 1136 peanut samples were obtained from the Southeast, Southwest, and Virginia-Carolina peanut production regions. Represented within the samples were 122 genotypes, including the most common peanut cultivars in the runner and virginia market types, and 42 year-by-location combinations. Utilizing the findings of Pattee *et al.* (1994) on genotype-by-environmental interaction in roasted peanut attribute, genotypes having less than four observations and two locations were not included in this paper, thus providing reasonable estimates of the experimental error in the mean values. All samples were obtained from plants grown and harvested under standard recommended procedures for the specific location.

Sample Handling. Each year a 1000-g sample of the sound mature kernel (SMK) fraction from each replicate of each location-entry was shipped to Raleigh, NC in February following harvest and placed in controlled storage at 5 C and 60% relative humidity until roasted.

Sample Roasting and Preparation. The peanut samples from each year were roasted between May and July using a Blue M "Power-O-Matic 60" laboratory oven, ground into a paste, and stored in glass jars at -10 C until they were evaluated. The roasting, grinding, and color measurement protocols were as described by Pattee and Giesbrecht (1990).

Sensory Evaluation. 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. Across years, only two panelists were changed on the panel. 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 non-consecutive days. Panelists evaluated six samples per session in 1986, five samples per session in 1987-88, and four samples per session in all subsequent years. Sensory evaluation commenced mid-June 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 GLM in SAS (1997) was used for initial analysis of the unbalanced data set. Genotype, region, genotype-by-region interaction, and covariates fruity and roast color were considered to exert fixed effects on the sensory attributes. Random effects were year, year-by-region interaction, location within year and region, genotype-by-year interaction, genotype-by-year-by-region interaction, genotype-by-location interaction within year and region, and experimental error. In this analysis, least squares means of the individual genotypes were estimated for the purpose of identifying genotypes with superior or inferior flavor characteristics. Correlations were computed among the least squares means to illustrate the relationships among attributes.

To estimate broad-sense heritability, a second analysis was performed using PROC MIXED (SAS, 1997) with genotypes and genotype-by-region interaction as random effects. The broad-sense heritability of means calculated from n observations taken in n_Y years, n_R regions, n_{YR} year-region combinations, and a total of n_L

locations is:

$$H = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_Y^2}{n_Y} + \frac{\sigma_{YR}^2}{n_{YR}} + \frac{\sigma_{L(YR)}^2}{n_L} + \frac{\sigma_{YG}^2}{n_Y} + \frac{\sigma_{RG}^2}{n_R} + \frac{\sigma_{YRG}^2}{n_{YR}} + \frac{\sigma_{LG(YR)}^2}{n_L} + \frac{\sigma^2}{n}} \quad [\text{Eq. 1}]$$

where σ_G^2 , σ_Y^2 , σ_{YR}^2 , $\sigma_{L(YR)}^2$, σ_{YG}^2 , σ_{RG}^2 , σ_{YRG}^2 , $\sigma_{LG(YR)}^2$, and σ^2 are the variance components associated with genotypes, years, year-by-region interaction, locations within years and regions, year-by-genotype interaction, region-by-genotype interaction, year-by-region-by-genotype interaction, location-by-genotype interaction within years and regions, and experimental error, respectively.

Results and Discussion

Variation among genotypes was highly significant ($P < 0.01$) for all three sensory attributes as was the portion of the genotype sum of squares attributable to market types, indicating that the mean sensory attributes for market types vary significantly. The magnitude of the variance components associated with the sweet, bitter, and roasted peanut sensory attributes indicate that year effects are of major importance on the bitter attribute and important to a lesser extent on the roasted peanut attribute (Table 1). The causes of such year-to-year variation in the bitter attribute are unknown, while relative crop maturity is probably a primary source of yearly variation in the roasted peanut attribute. The magnitude of the year variance component for bitter makes it imperative that multiple years of data be collected before reasonable confidence can be placed in the representation of the mean value for a genotype. The variance components for locations within years and regions and that for genotypes of the bitter attribute also are large relative to the other attributes. These observations suggest that we have much to learn about the bitter attribute in roasted peanut products before we can fully control its presence. In contrast to bitter, the variance components for sweet attribute are relatively small with only the locations within years and regions and genotypes being statistically significant.

Genotypic means for sweet attribute (Fig. 1a,b) ranged from 2.33 to 4.12 flavor intensity units (fiu), nearly a twofold difference between the least sweet genotype, NC Ac 18450, and the sweetest genotype, New Mexico Valencia C. The valencia market type had the highest average sweet score (3.75 fiu), followed by the runner (3.16 fiu), spanish (3.13 fiu), and virginia types (2.95 fiu) (Tables 2-4). Although the differences among market types were significant, their ranges overlapped extensively so that one could find virginia-type lines with sweet scores within the range of the runner-type lines, for example.

The results for the bitter attribute inversely mirrored those for sweet, as could be expected given the strong negative correlation between the two attributes. The range of genotypic means for bitter ran from 2.43 fiu for the least bitter genotype, New Mexico Valencia C (Table 3), to 4.46 fiu for the most bitter genotype, Improved Spanish 2B (Table 3). The valencia market class had the lowest average bitter score (3.03 fiu), followed by runner (3.32 fiu), spanish (3.46 fiu) and

Table 1. Estimates of genotypic, environmental, and genotype-by-environmental components of variance and broad-sense heritability (H) of sweet, bitter, and roasted peanut attributes.

Source of variation	Variance component ± Standard error		
	Sweet	Bitter	Roasted peanut
Year	0.0098 ± 0.0193	1.1311 ± 0.6189	0.1998 ± 0.1110
Year x region	0.0262 ± 0.0309	0.0096 ± 0.0338	0.0035 ± 0.0096
Location in year, region	0.0486 ± 0.0204	0.0735 ± 0.0296	0.0177 ± 0.0094
Genotype	0.0729 ± 0.0128	0.0923 ± 0.0182	0.0260 ± 0.0077
Year x genotype	0.0000 ± 0.0000	0.0173 ± 0.0076	0.0008 ± 0.0087
Region x genotype	0.0019 ± 0.0042	0.0048 ± 0.0071	0.0000 ± 0.0000
Year x region x genotype	0.0060 ± 0.0078	0.0000 ± 0.0000	0.0000 ± 0.0000
Location x genotype in year, region	0.0128 ± 0.0075	0.0113 ± 0.0087	0.0355 ± 0.0109
Error	0.0801 ± 0.0047	0.1422 ± 0.0081	0.1611 ± 0.0090
Broad-sense heritability (H) ^a	0.282	0.062	0.059
Previous estimate 1 ^b	0.143	0.180	0.243
Previous estimate 2 ^c	0.370	0.020	0.106
Previous estimate 3 ^d	0.259		0.093

^aHeritability estimate for a single observation in a single environment.

^bEstimates obtained by Pattee and Giesbrecht (1990).

^cEstimates obtained by Pattee *et al.* (1993).

^dEstimates obtained by Pattee *et al.* (1995).

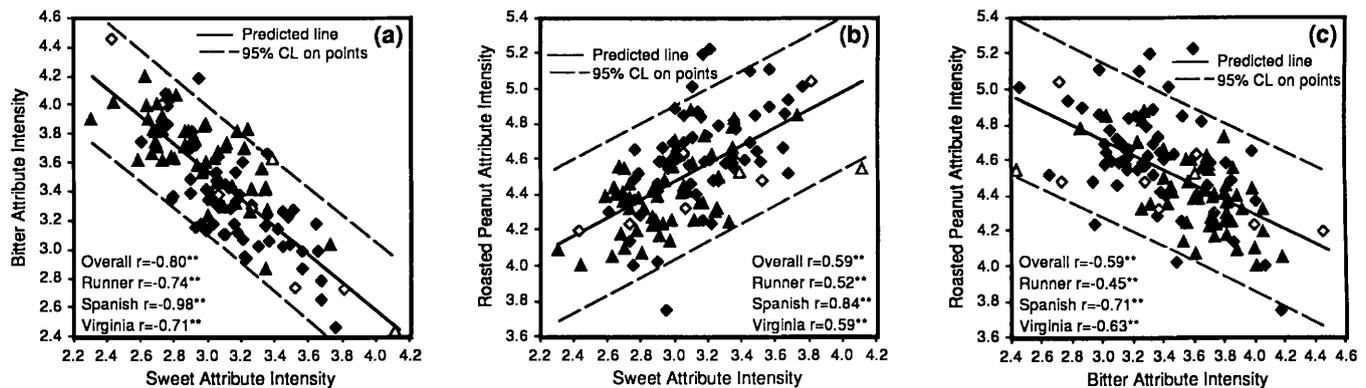


Fig. 1. Scatter diagrams of sweet, bitter, and roasted peanut attribute mean intensities for runner (▲), virginia (◆), spanish (△), and valencia (◇) peanut cultivars and breeding lines. (a) Bitter vs. sweet attribute intensity. (b) Roasted peanut vs. sweet attribute intensity. (c) Roasted peanut vs. bitter attribute intensity.

virginia types (3.66 fiu). Again, the ranges of the market types overlapped to a large extent.

Genotypic means for roasted peanut attribute have been published previously (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1993, 1995), each time with additional lines represented. The current estimates include additional data on common cultivars as well as data on new breeding lines and ancestral germplasm. The range of genotypic means for roasted peanut attribute was from 3.75 fiu for UGA-6 (Table 1), to 5.22 fiu for F1334 (Table 2), one of the components of the newly released cultivar, SunOleic 97R (D.W. Gorbet, pers. commun., 1997). The runner market class had the highest average roasted peanut score (4.62 fiu), followed by the valencia (4.53 fiu), spanish (4.48 fiu) and virginia types (4.40 fiu). In comparing the current estimates with earlier reports, it is immediately apparent that the newer estimates are substantially lower in many cases. These changes can be attributed to the inclusion of data

from additional years and locations in the newer estimates. Because the genotypic means are adjusted to a common average environmental effect, changes of this nature are to be expected. The standings of genotypes relative to each other are remarkably consistent from one set of estimates to another. Readers are cautioned that comparisons among genotypes should be made only within a particular set of least square means.

Previous study of the bitter and sweet attributes conducted on 17 cultivars and breeding lines indicated that there were significant correlations of bitter and sweet with each other and also with the roasted peanut attribute (Pattee *et al.*, 1997). In this study using 122 genotypes, the correlation between bitter and sweet was nearly identical to the earlier estimate ($r = -0.80$ over all genotypes in the current study vs. $r = -0.89$ in the previous study). Correlations between sweet and bitter within the runner and virginia market types were also

Table 2. Least squares means for sweet, bitter, and roasted peanut attributes of peanut breeding lines and cultivars of the runner market type.

Cultivar or breeding line	Sweet	Bitter	Roasted peanut	Cultivar or breeding line	Sweet	Bitter	Roasted peanut
----- flavor intensity units -----				----- flavor intensity units -----			
ANDRU 93	3.19±0.10	3.38±0.13	4.73±0.14	Florunner comp. 4	3.31±0.13	3.02±0.17	4.58±0.19
Basse (NCSU coll.)	3.42±0.13	3.13±0.17	4.59±0.17	GA 207-2	2.90±0.13 ^{2†}	3.69±0.17 ^a	4.45±0.19
Basse (PI 229553)	3.48±0.13	3.22±0.17	4.85±0.17 [†]	GA 207-3-4	2.76±0.13 ^{2†}	3.99±0.17 ^a	4.65±0.19
Basse (PI 237511)	3.35±0.13	3.16±0.17	4.57±0.18	Georgia Runner	2.99±0.12	3.41±0.16	4.60±0.18
Bradford Runner	2.91±0.13 ^{2†}	3.82±0.17 ^a	4.59±0.19	GK-7	3.24±0.09	2.94±0.11	4.48±0.12
Dixie Runner	2.76±0.13 ^{2†}	4.02±0.17 ^{a †}	4.37±0.18	Langley	3.14±0.12	3.29±0.16	4.86±0.17 ^{a †}
Early Runner	2.78±0.13 ^{2†}	3.34±0.17	4.52±0.19	MARC I	3.57±0.08	2.87±0.11 ^z	4.89±0.12 ^{a †}
E. Runner comp. 1	3.01±0.13	3.39±0.17	4.64±0.19	NC 3033	2.73±0.13 ^z	3.86±0.17 ^a	4.14±0.17 [†]
E. Runner comp. 2	2.93±0.13 ^{2†}	3.16±0.17	4.66±0.19	Okrun	3.35±0.10	3.24±0.14	4.55±0.15
E. Runner comp. 3	3.00±0.13	3.34±0.17	4.88±0.19 [†]	PI 109839	2.93±0.13 ^z	3.72±0.17 ^a	4.58±0.18
E. Runner comp. 4	3.13±0.13	3.43±0.17	4.40±0.19	S.E. Runner 56-15	2.61±0.13 ^{2††}	3.74±0.17 ^a	4.30±0.17
E. Runner comp. 5	2.90±0.13 ^{2†}	3.39±0.17	4.42±0.19	Sm.Wh.Span.(Aust.)	2.77±0.13 ^z	3.86±0.17 ^a	4.48±0.19
F1315	3.11±0.16	3.45±0.22	5.01±0.23 [†]	Southern Runner	3.17±0.08	3.53±0.10	4.26±0.11
F1316	3.17±0.16	3.32±0.22	5.19±0.23 [†]	Sunbelt Runner	2.75±0.15 ^z	4.08±0.20 [†]	4.00±0.21 [†]
F1334	3.21±0.13	3.61±0.17	5.22±0.19 ^{†§}	SunOleic 95R	3.05±0.13	3.53±0.17	4.85±0.19 [†]
F439-1-4-4-2-1-2	3.45±0.16 ^a	3.25±0.21	5.10±0.23 [†]	Sunrunner	3.06±0.08	3.35±0.10	4.69±0.11
F439-16-4	3.68±0.16 ^a	2.78±0.21 ^{2†}	4.93±0.23 [†]	Tamrun 88	3.18±0.10	3.11±0.13	4.59±0.14
F439-16-6-3	3.68±0.16 ^a	2.65±0.21 ^{2†}	4.52±0.23	TP107-11	3.16±0.17	3.18±0.22	4.84±0.24 [†]
F439-17-2-1-1	3.21±0.13	3.07±0.17	4.59±0.19	UF86107	3.08±0.13	3.29±0.17	4.56±0.18
F439-2-3-2-1	3.76±0.16 ^{a †§}	2.46±0.21 ^{2††}	5.01±0.23 [†]	UF90106	3.26±0.12	3.30±0.16	4.79±0.17 [†]
F439-3-1-1-3-3-B	3.51±0.16	3.27±0.21	4.58±0.23	UF91108	3.36±0.13	3.66±0.17	4.82±0.18 [†]
Florispan comp. 1	3.00±0.13	3.13±0.17	4.69±0.19	UGA-3-11*	3.06±0.17	3.31±0.22	4.62±0.24
Florispan comp. 2	3.03±0.13	3.17±0.17	4.61±0.19	UGA-3-5*	3.11±0.17	3.10±0.22	4.72±0.24 [†]
Florispan comp. 3	2.79±0.13 [†]	3.36±0.17	4.28±0.19	UGA-3-9*	2.96±0.17 ^z	3.17±0.22	4.54±0.24
Florispan comp. 4	3.09±0.13	3.10±0.17	4.46±0.19	UGA-4-1*	3.45±0.12 ^a	3.02±0.15	4.69±0.16
Florispan comp. 5	3.05±0.13	3.47±0.17	4.63±0.17	UGA-4-2*	3.49±0.10 ^a	3.03±0.14	4.65±0.15
Florunner	3.37±0.04	3.05±0.05	4.77±0.05	UGA-4-3*	3.22±0.14	2.95±0.18 ^{2†}	4.24±0.19
Florunner comp. 1	3.65±0.13 ^a	3.18±0.17	4.67±0.19	UGA-5*	2.89±0.12 ^z	3.49±0.15	4.02±0.16 ^{2†}
Florunner comp. 2	3.57±0.13 ^a	2.98±0.17	5.11±0.19 [†]	UGA-6*	2.95±0.14 ^z	4.18±0.19 ^{†§}	3.75±0.19 ^{2††}
Florunner comp. 3	3.65±0.13 ^a	2.99±0.17	4.85±0.19 [†]	Mean	3.16±0.03	3.32±0.04	4.62±0.04

^{a,z}Denote means not significantly different by t-test ($P < 0.05$) from the highest and lowest in the market class, respectively.

^{†,††}Denote means not significantly different by t-test ($P < 0.05$) from the highest and lowest in all classes, respectively.

^{§,§}Denote the highest and lowest means within a market class, respectively.

*Identities of Univ. of Georgia breeding lines were coded at the request of the breeder.

remarkably constant following expansion of the number of genotypes tested (Fig. 1a). The correlations of roasted peanut with sweet and bitter decreased markedly in the larger group although they were highly significant (Fig. 1b,c). These correlations confirm earlier conclusions that indirect selection for roasted peanut flavor could be based on chemical assays for as yet unidentified sweet and bitter principles. Even if selection must remain based on sensory data, the data indicate that directional selection to increase the intensity of the more highly heritable desirable attribute sweet would cause a correlated increase in roasted peanut and a decrease in the undesirable attribute bitter. It remains to be seen whether indirect selection for roasted peanut based on sweet would be more efficient than direct selection for roasted peanut.

The availability of flavor data on such a large number

of breeding lines and cultivars provides a unique opportunity to make comparisons to ancestral peanut lines, component lines within a cultivar, disease resistant lines, and currently available cultivars.

Ancestral Lines. Most modern runner- and virginia-type cultivars and breeding lines have in their ancestry one or more of four original lines (Small White Spanish, Dixie Giant, Basse, and Spanish 18-38) (Isleib and Wynne, 1992). Only one of these lines is directly identifiable today, Dixie Giant, and it was reclaimed from six viable seeds planted in 1992. Until 1996, it was not available in quantities sufficient for sensory evaluation. Thus, data on Dixie Giant were not available in this study. Spanish 18-38 is only available through a selection line released as the cultivar 'Spanette' (Spanish 18-38-42). The true Basse is not known but three Basse lines have been identified (Table 2). We believe the NCSU collection

Table 3. Least squares means for sweet, bitter, and roasted peanut attributes of peanut breeding lines and cultivars of the spanish and valencia market type.

Cultivar or breeding line	Sweet	Bitter	Roasted peanut
----- flavor intensity units -----			
Spanish types			
Impr. Spanish 2B	2.44±0.13 ^{a†¶}	4.46±0.17 ^{a†§}	4.19±0.17 ^{a†¶}
Pearl	3.81±0.13 ^{a†§}	2.73±0.18 ^{a†¶}	5.03±0.17 ^{a†§}
Pronto	3.52±0.07 ^a	2.74±0.10 ^{a†}	4.47±0.10 ^a
Sm. Wh. Span.	3.05±0.13	3.62±0.17 ^{a†}	4.63±0.18 ^{a†}
Spanco	3.27±0.11	3.28±0.15	4.47±0.16 ^a
Spanette	2.74±0.10 ^a	4.00±0.13	4.23±0.14 ^a
Starr	3.07±0.10	3.37±0.14	4.32±0.15 ^a
Valencia types			
N.M. Valencia C	4.12±0.15 ^{a†§}	2.43±0.19 ^{a†¶}	4.54±0.21 ^{a†§}
PI 337396	3.39±0.13 ^{a†¶}	3.62±0.17 ^{a†§}	4.53±0.17 ^{a†¶}
Mean of spanish	3.13±0.05	3.46±0.07	4.48±0.07
Mean of valencia	3.75±0.10	3.03±0.13	4.53±0.14

^{a,¶}Denote means not significantly different by t-test (P < 0.05) from the highest and lowest in the market class, respectively.

^{†,§}Denote means not significantly different by t-test (P < 0.05) from the highest and lowest in all classes, respectively.

^{§,¶}Denote the highest and lowest means within a market class, respectively.

Basse from W.C. Gregory's collection may be a selection or seed source from the original Basse. Two lines have been found identified as Small White Spanish, one a runner-type collection from Australia, which because of its market-type is not likely to be the true line, and an accession called Small White Spanish from W.C. Gregory's collection at NCSU. Again this spanish-type line is likely a selection or seed source from the original Small White Spanish. Comparison of these two spanish-type identified lines for sweet, bitter, and roasted peanut attributes provides the following: Spanette is not significantly different in sweet (2.74 fiu) and roasted peanut (4.23 fiu) than the lowest within its market class; Small White Spanish is not significantly different in roasted peanut (4.63 fiu) than the highest within its market class and all classes (Table 3). All other values for these lines fall within the mid-range for the spanish market-type.

Other lines that have ancestral importance, particularly to the virginia-type, are Improved Spanish 2B, Jenkins Jumbo, NC 4, and White's Runner. Improved Spanish 2B has the lowest sweet (2.44 fiu) and roasted peanut (4.19 fiu) and highest bitter (4.46 fiu) within its market class, and these values are not significantly different from the respective overall values (Table 3). Jenkins Jumbo is not significantly different in roasted peanut (4.24 fiu) than the lowest in its market class (Table 4). Conversely, White's Runner (4.82 fiu) is not significantly different from the highest overall value for roasted peanut and the lowest bitter (3.27 fiu) within its market class (Table 4). NC 4 (4.63 fiu) was not significantly different from the highest roasted peanut intensity within its market class (Table 4).

Expression of a positive or negative characteristic by a genotype and its ability to effectively pass the characteristic on to descendants are quite different factors. Preliminary work (Isleib *et al.*, 1995) in this area indicated that Jenkins Jumbo was the single most important ancestor of modern lines with respect to roasted peanut attribute, exerting a negative effect. In future work we shall explore in more detail this characteristic using our expanded data set through the use of best linear unbiased prediction procedures.

Cultivar Component Lines. Four multiline cultivars (Early Bunch, Early Runner, Florispan, and Florunner) were evaluated in this study along with their component lines (Table 5). The identity of individual components of these multilines were provided by D.W. Gorbet and D.A. Knauff (pers. commun., 1990). The Early Bunch composite line was very similar in all three flavor attributes to its five individual component lines (Table 4). Component 5 (4.06 fiu for bitter and 4.19 fiu for roasted peanut) did show some deviation from the other component lines by being not significantly different from the highest overall bitter intensity nor from the lowest roasted peanut intensity. The Early Runner composite was lower in sweet attribute than any of its component lines (Table 2), but its bitter and roasted peanut values were within the range defined by its components. The Florispan component lines were generally similar to each other except Component 3 which was lower in sweet (2.79 fiu) and roasted peanut (4.28 fiu) and higher in bitter (3.36 fiu) than the other components (Table 2). The Florunner composite presents a unique situation in that it has been the runner control line throughout this study and the observations came from many environment-by-year combinations, while the component line data came from a specific two-year ancestral study.

While breeder seed of Florunner is recomposited from the components every year in Florida, the releasing state, this may not be the case in other states where Florunner is propagated in seed certification programs by sampling from the composite. Even with annual recomposition, there are at least three generations in which natural selection can act upon the composite before the seed reaches the commercial peanut grower. Without annual recomposition, there is great opportunity for genetic shift to occur within the composite. Given this potential for deviation, the values for all three attributes were remarkably similar. Under very close scrutiny the Florunner control would appear to favor Component 4 in its characteristics (Table 2). In general it can be concluded from these limited observations from three cultivars that the component lines and the composited control line all have closely related sensory characteristics.

Disease-Resistant Lines. Only a limited number of lines are available for comparison and observation of any relationships that might exist between disease resistance characteristics and flavor quality. The first notable relationship is the standing of the cultivars (NC 10C and NC 12C) and breeding lines (NC 3033 and NC Ac 18016) with resistance to *Cylindrocladium* black rot

Table 4. Least squares means for sweet, bitter, and roasted peanut attributes of peanut breeding lines and cultivars of the virginia market type.

Cultivar or breeding line	Sweet	Bitter	Roasted peanut	Cultivar or breeding line	Sweet	Bitter	Roasted peanut
----- flavor intensity units -----				----- flavor intensity units -----			
AgraTech VC-1	3.35±0.09	3.41±0.12	4.66±0.12 ^a	NC Ac 18016	2.44±0.13 [†]	4.02±0.17 [†]	4.00±0.18 ^{††}
Early Bunch	2.89±0.13	3.81±0.17 ^a	4.25±0.17 ^z	NC Ac 18423	3.10±0.08	3.71±0.11	4.57±0.12 ^a
E. Bunch comp. 1	2.72±0.13	3.84±0.17 ^a	4.37±0.19 ^{az}	NC Ac 18424	2.65±0.15 [†]	3.89±0.19 ^a	4.40±0.21 ^{az}
E. Bunch comp. 2	2.87±0.13	3.81±0.17 ^a	4.42±0.19 ^{az}	NC Ac 18426	2.69±0.15 [†]	3.74±0.19	4.41±0.21 ^{az}
E. Bunch comp. 3	2.70±0.13 [†]	3.71±0.17	4.55±0.19 ^a	NC Ac 18431	2.99±0.09	3.55±0.11	4.60±0.12 ^a
E. Bunch comp. 4	2.73±0.13	3.82±0.17 ^a	4.46±0.19 ^{az}	NC Ac 18449	2.59±0.16 [†]	3.61±0.21	4.38±0.23 ^{az}
E. Bunch comp. 5	2.78±0.13	4.06±0.17 ^{a†}	4.19±0.19 [†]	NC Ac 18450	2.31±0.16 ^{††}	3.89±0.21 ^a	4.08±0.23 [†]
Florigiant	2.68±0.05	3.82±0.06	4.17±0.07 ^z	NC Ac 18451	2.73±0.16 [†]	3.93±0.21 [†]	4.33±0.23 ^{az†}
GA 119-20	3.17±0.13	3.32±0.17 ^z	4.35±0.19 ^{az}	NC Ac 18452	2.87±0.14	3.72±0.18	4.27±0.19 [†]
Holland Va. Jumbo	3.22±0.14	3.69±0.19	4.62±0.20 ^a	NC Ac 18454	2.69±0.15 [†]	3.82±0.19 ^a	4.36±0.21 ^{az}
Jenkins Jumbo	3.33±0.13	3.56±0.17	4.24±0.18 ^z	NC Ac 18455	2.67±0.14 [†]	3.66±0.18	4.55±0.19 ^a
N88003	2.93±0.17	3.76±0.23 ^a	4.23±0.24 [†]	NC Ac 18456	3.00±0.15	3.23±0.19 ^z	4.70±0.21 [†]
N90009 (Gregory)	2.64±0.17 [†]	4.00±0.23 [†]	4.44±0.24 ^{az}	NC Ac 18457	3.73±0.14 ^{a †§}	3.03±0.18 ^z	4.84±0.19 [†]
N90010E	2.99±0.09	3.86±0.13 ^a	4.55±0.13 ^a	NC Ac 18459	3.12±0.14	3.74±0.18	4.25±0.19 [†]
N90016	2.98±0.17	3.86±0.23 ^a	4.26±0.24 ^{az†}	NC Ac 18460	2.99±0.15	3.60±0.19	4.61±0.21 ^a
N90017	3.15±0.13	3.43±0.17	4.35±0.19 ^{az}	NC Ac 18462	3.08±0.15	3.47±0.19	4.42±0.21 ^{az}
N91047	3.04±0.12	3.62±0.16	4.40±0.17 ^{az}	NC Ac 18463	3.25±0.16	3.82±0.21 ^a	4.30±0.23 ^{az†}
N91048	3.06±0.14	3.68±0.18	4.43±0.20 ^{az}	NC Ac 18464	3.26±0.15	3.41±0.19	4.50±0.21 ^{az}
NC 2	3.18±0.14	3.81±0.19 ^a	4.73±0.19 [†]	UF82107	2.82±0.14	4.06±0.18 [†]	4.32±0.20 ^{az}
NC 4	3.35±0.13	3.43±0.17	4.63±0.19 ^a	VA-C 92R	2.79±0.09	3.64±0.12	4.38±0.13 ^z
NC 6	3.25±0.14	3.26±0.18 ^z	4.32±0.19 ^z	VA830215-1	2.91±0.15	3.74±0.19	4.17±0.21 [†]
NC 7	2.87±0.04	3.71±0.06	4.23±0.06 ^z	VA830416-1	2.81±0.16	3.62±0.21	4.07±0.23 [†]
NC 9	2.94±0.05	3.58±0.07	4.47±0.07 ^a	VA830516-1	3.09±0.15	3.29±0.19	4.88±0.21 ^{a†§}
NC-V 11	2.73±0.06	3.61±0.08	4.38±0.08 ^a	VP8407	3.35±0.16	2.87±0.21 ^{††}	4.78±0.23 [†]
NC 10C	2.63±0.10 [†]	4.19±0.13 ^{a§}	4.05±0.14 [†]	VP8417	2.98±0.15	3.53±0.19	4.14±0.21 [†]
NC 12C	2.70±0.08	4.01±0.11 ^a	4.10±0.11 [†]	VP8420	3.06±0.15	3.46±0.19	4.45±0.21 ^{az}
NC Ac 17921	2.90±0.13	3.73±0.17	4.38±0.19 ^z	White's Runner	3.36±0.13	3.27±0.17 ^z	4.82±0.19 [†]
				Mean	2.95±0.03	3.66±0.04	4.40±0.05

^{a, z}Denote means not significantly different by t-test (P < 0.05) from the highest and lowest in the market class, respectively.

^{†, ††}Denote means not significantly different by t-test (P < 0.05) from the highest and lowest in all classes, respectively.

^{§, †§}Denote the highest and lowest means within a market class, respectively.

Table 5. Identity of components of multi-line cultivars.

Multiline cultivar	Component	Identity
Early Bunch	1	F459B-3-2-4-6-3-1-1-b4-6-2-B
	2	F459B-3-2-4-6-2-2-1-1-2-2-1-B
	3	F459B-3-2-4-6-2-2-1-5-3-6-B
	4	F459B-3-2-4-6-2-2-1-5-5-1-1-B
	5	F459B-3-2-4-6-3-2-2-B
Early Runner	1	F230-118-B-8-1-B
	2	F230-118-B-8-1-1-B
	3	F230-118-B-8-1-2-B
	4	F230-118-B-8-1-3-B
	5	F230-118-B-8-1-5-B
Florispán	1	F334A-B-9-3-1-B
	2	F334A-B-11-7-1-B
	3	F334A-B-13-B
	4	F334A-B-14-B
	5	F334A-B-17-1-B
Florunner	1	F439-16-10-3
	2	F439-16-10-3-1
	3	F439-16-10-3-2
	4	F439-16-10-1-1

(CBR, *C. parasiticum* Crous, Wingfield & Alfenas) which rank among the lowest overall in roasted peanut and sweet and among the highest in bitter (Tables 2 and 4). It appears that the constituents responsible for CBR resistance may also be contributing to bitter flavor, although this apparent association may be spurious. The breeding line UGA-6 exhibits similar characteristics (Table 2), however, the no information about this line's ancestry or characteristics is available. No similar relationships are evident among the lines with resistance to other diseases (e.g., late leaf spot-resistant line Southern Runner and UF 91108) and flavor (Table 2).

Current Cultivars. There are many comparisons that might be of interest to the individual reader. However, among current cultivars, New Mexico Valencia C is the sweetest and least bitter, while F1334 (SunOleic 97R), MARC I, Langley, and SunOleic 95R are not significantly different from the highest roasted peanut intensity (Tables 2 and 3). While none of the virginia-type cultivars currently match these levels, breeding lines are available that do equal them (Table 4). Conversely it also can be observed that among the lowest roasted peanut intensities is Sunbelt Runner (4.00 fiu)

and several runner breeding lines (Table 2). These comparisons illustrate that with continued monitoring of flavor quality of breeding lines, the flavor quality of future peanut cultivars can be enhanced. However, without that vigilance it is readily apparent that the quality standard that we now enjoy can be lost.

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