Flavor Profiles of Wild Species-Derived Peanut Breeding Lines

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ABSTRACT

Several diploid wild species of the genus *Arachis* L. have been used as sources of resistance to common diseases of cultivated peanut (*Arachis hypogaea* L.). Because flavor is among the most important quality attributes for commercial acceptance of roasted peanuts, sensory attributes of interspecific hybrid derived breeding lines were evaluated to determine if transfer of disease resistance from wild species is associated with concomitant changes in flavor. Sixteen interspecific hybrid derivatives with five diploid species in their ancestries and the commercial flavor standard, NC 7 were evaluated for sensory quality. Significant variation among entries was found for the roasted peanut, sweet, and bitter sensory attributes, but not for the overall contrast between NC 7 and the wild species-derived breeding lines. The variation was either between two groups of wild species-derived breeding lines or within one or both groups. Introduction of disease and pest resistance traits from *Arachis* species did not result in degradation or improvement of the flavor profile. This suggests that flavor of wild species-derived germplasm will not prevent its use either as parents in peanut breeding programs or as cultivars.

Key Words: *Arachis hypogaea* L., *Arachis* spp., wild species, sensory quality, roasted peanut.

Flavor is among the most important quality attributes for commercial acceptance of roasted peanuts (*Arachis hypogaea* L.) as snacks or peanut butter. Relatively little research has been published on flavor and other sensory attributes of peanut cultivars under development in the USA, mainly because breeding efforts have been directed at developing cultivars with increased yield, grade and disease resistance, the traits with the most economic impact on peanut production. Traits such as peanut flavor, an important attribute for consumers, but one with little direct and measurable economic value, have received little weight in selecting lines for release to commercial producers. Isleib *et al.* (2001) suggested that there is greater variation in peanut flavor among cultivars and breeding lines developed and/or released during the past 10 years than there was in cultivars released earlier, in part due to the incorporation of exotic parents into breeding programs in order to introduce genes for disease resistance. Recently manufacturers of products such as snack foods or peanut butter have demanded increased emphasis on maintenance or improvement of peanut flavor in new releases.

To date, only two cultivars have been released that trace their immediate ancestry to diploid wild species of genus *Arachis*: COAN and NemaTAM (Simpson and Starr, 2001; Simpson *et al.*, 2003). Because of changes in the U.S. peanut price support program, growers are demanding greater levels of host plant resistance in new cultivar releases, and use of wild species-derived resistances is likely to become more common in the future. The peanut genetics program at N.C. State Univ. has been actively developing peanut lines with multiple disease resistance using diploid *Arachis* species as sources of resistance. Several germplasm lines derived from crosses between *A. hypogaea* ($2n = 4x = 40$) and *A. cardenasii* Krap. & Greg. ($2n = 2x = 20$), a species with high levels of resistance to several pathogens and insect pests of peanut, have been released (Stalker and Beute, 1993; Stalker and Lynch, 2002; Stalker *et al.*, 2002a,b). These germplasm lines are being used as parents in several U.S. peanut breeding programs. At N.C. State and Texas A&M Univ., additional populations have been derived from the diploid species *A. diogoi* Hoehne, *A. correntina* (Burk.) Krap. & Greg., *A. stenosperma* Greg. & Greg., and *A. batizocoi* Krap. & Greg. (Tallury and Stalker, unpublished data; Simpson *et al.*, 1993). These new germplasm lines and other interspecific hybrid selections have been hybridized with commercial cultivars. Several advanced populations are being evaluated in field tests for yield, grade, and resistance to the diseases tomato spotted wilt virus (TSWV), leaf spots [caused by *Cercospora arachidicola* Hori and *Cercosporidium personatum* (Berk. & Curt.) Deighton], Cylindrocladium black rot (CBR) (caused by *Cylindrocladium parasiticum* Crous, Wingfield, & Alfenas), and Sclerotinia blight (caused by *Sclerotinia minor* Jagger). Preliminary yield and disease resistance data suggest that several lines are promising candidates for commercial cultivation in the Virginia-Carolina

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Table 1. Wild species-derived lines for sensory evaluation using the notation Purdy *et al.*, (1968).

NC Ac	Identity or Parentage*
HTS 00-02	NC 7 /3/ 90 APS 47, NC 6 // PI 270806 / GP-NC WS 4
HTS 02-01	NC 6*2 // 4x Plot 18C Plant 2-2, PI 338280 (*A. stenosperma* HLK 410) / PI 276235 (*A. diogoi* GK 10602)
HTS 02-03	PI 261942 / PI 262141 (*A. cardenasii* GKP 10017)
HTS 02-05	PI 298639 (*A. batizocoi* K 9484) / C2
HTS 02-06	Florigiant / PI 337396, NC Ac 18000 // PI 262881 (*A. correntina* GKP 9548)
HTS 02-07	NC 6 /3/ F1 A, NC 3033 / GP-NC WS 4, 82 F2LS 201-1 // 82 F2LS 215-1, PI 109839 / GP-NC WS 3
HTS 02-08	NC 6 /3/ 90 APS 15, NC 6 // NC 3033 / GP-NC WS 1
HTS 02-09	NC 6 /3/ 90 APS 25, NC 5 // PI 270806 / GP-NC WS 4
HTS 02-10	NC 6 /3/ 90 APS 25, NC 5 // PI 270806 / GP-NC WS 4
SPT 04-01	Perry / GP-NC WS 11
SPT 04-03	NC 12C / GP-NC WS 15
SPT 04-05	NC 12C / GP-NC WS 15
SPT 04-06	Southern Runner /4/ 95 LBCF4-139, NC 6 /3/ 90 APS 25, NC 5 // PI 270806 / GP-NC WS 4
SPT 04-08	Southern Runner /4/ 95 LBCF4-139, NC 6 /3/ 90 APS 25, NC 5 // PI 270806 / GP-NC WS 4
SPT 04-10	NC 12C / GP-NC WS 13
SPT 04-12	NC 12C / GP-NC WS 13
17209	NC 7

*GP-NC WS 1, WS 3 and WS 4 were selected from the cross PI 261942 / PI 262141 (*A. cardenasii* GKP 10017), GP-NC WS 11 from the cross NC 6 // NC 3033 / GP-NC WS 1, GP-NC WS 13 from the cross NC 5 // PI 270806 / GP-NC WS 4, and GP-NC WS 15 from the cross NC 6 // PI 270806 / GP-NC WS 4.

production area (Tallury *et al.*, unpublished). However, no sensory evaluations have been made on these materials. The overall objective of this research was to evaluate sensory attributes of interspecific hybrid-derived breeding lines for peanut flavor to determine if transfer of disease resistance from wild species was associated with concomitant changes in flavor.

Materials and Methods

Plant material

An array of 16 wild species-derived breeding lines (Table 1) were grown as entries in the Leafspot Advanced Test during 2005 (Sprayed) and 2006 (Sprayed and Unsprayed) at the Peanut Belt Research Station at Lewiston, NC. The lines traced to five *Arachis* species: *A. batizocoi*, *A. cardenasii*, *A. correntina*, *A. diogoi*, and *A. stenosperma*. Lines designated "HTS" were developed by H.T. Stalker; those designated "SPT" were developed by S.P. Tallury. Parentage of the wild species-derived lines was complex and included U.S. virginia-type parents Florigiant (Carver, 1969), NC 5 (Emery and Gregory, 1970), NC 6 (Campbell *et al.*, 1977), NC 7 (Wynne *et al.*, 1979), NC 12C (Isleib *et al.*, 1997), Perry (Isleib *et al.*, 2003), runner-type parents Southern Runner (Gorbet *et al.*, 1987) and NC 3033 (Beute *et al.*, 1976), and *A. hypogaea* plant introductions PI 261942, PI 270806, and PI 337396 (USDA-ARS, Nat. Genetic Resources Program. *Germplasm Resources Information Network*). The virginia-type cultivar NC 7 was included as a performance and flavor standard. The tests were conducted in a randomized complete block design with 2 replications. Each plot was comprised of two rows 7.3 m in length spaced 91 cm apart. Seed spacing at planting was 25 cm. Plots were planted on 11 May 2005 and 11 May 2006, dug 30 Sept. 2005 and 2 Oct. 2006, and harvested by combine on 5 Oct. 2005 and 5 Oct. 2006. Standard cultural practices, including irrigation and a full program of chemical control of leaf spots, were applied to the plots except that leaf spot fungicides were not applied to the "unsprayed" test in 2006.

Sample handling, roasting and preparation

Pods were sized on a rolling grader and shelled with a standard reciprocating grading sheller (Georgia Federal-State Inspection Service, Albany, GA). Seeds were screened over a 6.0 × 25.4 mm (15/64 × 1 in) grading screen. Samples from the 2005 sprayed test and from both 2006 tests were retained for sensory analysis. The shelled peanuts were stored at 5 C and 60% RH. Samples were roasted in March, 2006 and June, 2007 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). Roast color of the peanut paste was evaluated as CIELAB L*. Six samples failed to produce paste within two color units of the target value (58 CIELAB L*), so duplicate samples were processed to produce paste within the desired color range.

Sensory evaluation

An eight-member, trained, roasted peanut profile panel at the Food Science Dept. at N.C. State Univ., Raleigh, NC, conducted a descriptive sensory analysis of 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). Sensory evaluation commenced on 20 March 2006 and 3 July 2007 and continued until all samples were evaluated. The averages of individual panelists' scores on sensory attributes were used in all analyses.

Statistical analysis

Flavor data were analyzed using a linear model for a randomized complete block design (RCBD) repeated across three environments with each test (the 2005 sprayed and the 2006 sprayed and unsprayed tests) being considered a separate environment using the general linear models procedure (PROC GLM) of SAS statistical software (SAS Institute, Cary, NC). Data from all samples (including re-roasted samples) were included in the analysis. The sum of squares for variation among environments was partitioned into two orthogonal contrasts each with a single degree of freedom, one between the 2 test years and the other between the sprayed and unsprayed tests grown in 2006. The sum of squares for variation among entries was partitioned into two parts, one comparing NC 7 to all wild species-derived lines, the other reflecting variation among wild species-derived lines. The latter sum of squares was further partitioned into a contrast between HTS and SPT lines, and two contrasts of means reflecting the variation within the two groups of wild species-derived lines. An analogous partition was made of the sum of squares for variation due to environment-by-entry interaction. Variation between initial and re-roasted samples was partitioned from the experimental error. Fruity attribute intensity and linear and quadratic effects of roast color were applied as covariates in the initial analysis. Covariates that did not significantly reduce the experimental error were dropped from the model. Means were adjusted to a common environmental effect and to the mean level for any covariates applied in ANOVA. Because the standard errors and covariances of the genotypic means were not constant, mean separation was by individual t-tests.

Results and Discussion

Variation among environments was primarily attributable to the difference between the 2005 and 2006 seasons (Table 2). This observation is consistent with earlier studies where year-to-year variation was shown to be a major part of the total variation in peanut sensory quality (Pattee *et al*., 1994, 1997, 1998, 2004). Although significant variation among entries was found for the roasted peanut, sweet, and bitter sensory attributes, in no case was the contrast between NC 7 and the mean of wild species-derived lines significant (Tables 2, 3). There was a difference between the means of the HTS and SPT lines for roasted peanut [4.62 vs. 4.35 flavor intensity units (fiu), $P=0.0038$] and sweet attributes (3.57 vs. 3.80 fiu, $P=0.0041$), but not for bitter (2.45 vs. 2.49 fiu, $P=0.5924$). Significant variation was also observed among the HTS lines for sweet and among the SPT lines for bitter (Table 2). For roasted peanut, five of the 16 species-derived lines scored as great as or numerically greater than NC 7 for sensory intensity, although none was significantly greater (Table 3). Two lines, SPT 04-01 and SPT 04-12, had significantly lower roasted peanut intensity scores than NC 7. For sweet attribute intensity, the mean of SPT lines was significantly greater than that for NC 7 (3.80 vs. 3.42 fiu, $P=0.0264$), and four individual SPT lines scored significantly greater than NC 7. One line, SPT 04-06, also scored significantly less in the bitter attribute. There was very little environment-by-genotype interaction (Table 2).

These results are positive in the sense that, except in two cases, introduction of disease and pest resistance traits from the *Arachis* species did not result in degradation of the flavor profile relative to NC 7, the long-time flavor standard for the virginia market-type. This has not always been the case in breeding for disease resistance because large-seeded virginia-type cultivars developed for resistance to CBR (NC 8C, NC 10C, NC 12C, and Perry) had inferior flavor profiles (Isleib *et al*., 2001). In the case of those cultivars, their resistance to CBR was derived from sources within *A. hypogaea*. As a result of these observations, it appears that flavor of wild species-derived germplasm will not prevent its use either as parents in peanut breeding programs or as cultivars. Variation observed among wild species-derived lines for sensory quality is consonant with the variation observed among lines derived exclusively from *A. hypogaea* ancestry. However, with these lines and as additional *Arachis* species are utilized for germplasm enhancement, it will be necessary to monitor flavor profiles in lines deriving resistance from them.

Table 2. Mean squares from analysis of variance of sensory attributes measured on wild species-derived peanut breeding lines developed by H.T. Stalker ("HTS" lines) and S.P. Tallury ("SPT" lines) and on virginia market-type flavor standard NC 7.

Source	Roasted peanut		Sweet		Bitter	
	df	Partial MS	df	Partial MS	df	Partial MS
	flavor intensity units(1–14)					
Total	115	–	115	–	115	–
Environments	2	0.8246^{ns}	2	4.7395*	2	6.2358**
2005 vs. 2006	1	1.1826†	1	9.2022*	1	12.3749**
Sprayed vs. unsprayed in 2006	1	0.4665^{ns}	1	0.4064^{ns}	1	0.1033^{ns}
Reps in environments	3	0.1704^{ns}	3	0.4613*	3	0.2021^{ns}
Genotypes	16	0.4382^{ns}	16	0.7727**	16	0.3230*
NC 7 vs. species-derived lines	1	0.2871^{ns}	1	0.3589^{ns}	1	0.0725^{ns}
Among species-derived lines	15	0.4471*	15	0.7971^{ns}	15	0.3388**
HTS vs. SPT lines	1	1.8223**	1	1.3369**	1	0.0349^{ns}
Among HTS lines	8	0.3410^{ns}	8	0.3356*	8	0.1852^{ns}
Among SPT lines	6	0.3132^{ns}	6	1.1432^{ns}	6	0.5691**
Environment × genotype	32	0.1688^{ns}	32	0.2430^{ns}	32	0.1238^{ns}
Environment × (NC 7 vs. species-derived lines)	2	0.0703^{ns}	2	0.0931^{ns}	2	0.5632*
Environment × (Among species-derived lines)	30	0.1753^{ns}	30	0.2556*	30	0.0990^{ns}
Environment × (HTS vs. SPT lines)	2	0.0507^{ns}	2	0.2639^{ns}	2	0.0042^{ns}
Environment × (Among HTS lines)	16	0.1303^{ns}	16	0.2648†	16	0.1140^{ns}
Environment × (Among SPT lines)	12	0.2608^{ns}	12	0.2254^{ns}	12	0.0962^{ns}
Error	48	0.1973^{ns}	48	0.1467^{ns}	48	0.1201^{ns}
Between re-roasted samples	14	0.2745	13	0.1331	13	0.1183
Covariates						
Roast color, linear	–	–	1	1.5605**	1	1.8427**

ns, †, *, ** Denote mean squares found to be not significant and significant by F-test at P<0.10, P<0.05, and P<0.01, respectively.

Table 3. Adjusted means of sensory attributes measured on wild species-derived peanut breeding lines developed by H.T. Stalker ("HTS" lines) and S.P. Tallury ("SPT" lines) and on virginia market-type flavor standard NC 7.

	Roasted peanut	Sweet	Bitter
	flavor intensity units (1–14)		
HTS 00-02	4.58±0.17^{a-d}	3.57±0.15^{d-g}	2.48±0.14^{b-e}
HTS 02-01	4.83±0.18^{ab}	3.50±0.16^{d-h}	2.62±0.14^{a-d}
HTS 02-03	4.85±0.18^{a}	3.79±0.17^{b-f}	2.40±0.15^{c-f}
HTS 02-05	4.83±0.16^{ab}	3.84±0.14^{b-e}	2.33±0.13^{def}
HTS 02-06	4.33±0.18^{bcd}	3.45±0.17^{d-h}	2.40±0.15^{c-f}
HTS 02-07	4.39±0.17^{a-d}	3.07±0.15^{h}	2.77±0.14^{abc}
HTS 02-08	4.31±0.18^{cd}	3.61±0.16^{c-g}	2.32±0.14^{def}
HTS 02-09	4.60±0.18^{a-d}	3.69±0.16^{b-f}	2.21±0.14^{ef}
HTS 02-10	4.85±0.18^{a}	3.60±0.16^{c-g}	2.56±0.14^{a-e}
SPT 04-01	4.13±0.16^{d}	3.99±0.14^{bc}	2.20±0.13^{ef}
SPT 04-03	4.25±0.18^{cd}	3.22±0.17^{gh}	2.94±0.15^{a}
SPT 04-05	4.58±0.18^{a-d}	3.36±0.16^{fgh}	2.88±0.15^{ab}
SPT 04-06	4.33±0.16^{cd}	4.60±0.15^{a}	1.97±0.14^{f}
SPT 04-08	4.73±0.18^{abc}	3.89±0.16^{bcd}	2.47±0.14^{cde}
SPT 04-10	4.28±0.17^{cd}	3.43±0.16^{d-h}	2.58±0.15^{a-e}
SPT 04-12	4.18±0.17^{d}	4.11±0.15^{b}	2.39±0.14^{c-f}
NC 7	4.73±0.18^{abc}	3.42±0.16^{e-h}	2.58±0.14^{a-e}
Species-derived lines	**4.50±0.04**‡	**3.67±0.04**‡	**2.47±0.03**‡
HTS lines	**4.62±0.06**$^{\alpha}$	**3.57±0.05**$^{\beta}$	**2.45±0.05**^{ns}
SPT lines	**4.35±0.07**$^{\beta}$	**3.80±0.06**$^{\alpha}$	**2.49±0.05**^{ns}

[a,b,c]Line means followed by the same Roman letter are not different by t-test (P<0.05).
‡Denotes means across species-derived lines that are not different from the mean for NC 7 by t-test (P<0.05).
[a,β]Group means followed by the same Greek letter are not different by t-test (P<0.05).

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