

Genotype-by-Environment Interaction in Sweet and Bitter Sensory Attributes of Peanut

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ABSTRACT

Although there have been recent studies of the roasted peanut sensory attribute of roasted peanut (*Arachis hypogaea* L.), there is little information on the factors influencing the sweet and bitter attributes. A study was conducted to test the significance of the effects of genotype, environment, and their interaction on the sweet and bitter attributes, to estimate genotypic means of these sensory attributes, and to determine an efficient scheme of resource allocation for multiple-site testing of breeding lines for sweet and bitter attributes. Samples of sound mature kernels from 17 genotypes grown at 42 different location-year combinations were stored under 5 C and 60% RH, roasted to nearly common color, ground into paste, and tasted by a trained sensory evaluation panel. Results for the roasted peanut attribute were similar to those found in previous studies. Significant variation among years was observed for bitter but not for sweet. There were no consistent differences among the three main peanut production regions for either attribute, but there was significant year-by-region interaction for sweet. Variation among locations within years and regions was significant for both attributes as was variation among genotypes. The mean flavor profile for the runner market class was significantly better than the mean for the virginia class in sweet, bitter and roasted peanut, but the distributions of the two classes did overlap. Significant correlations of genotypic means for the three attributes indicated that chemical assays for currently unidentified sweet or bitter principles could be used for indirect selection to improve roasted peanut attribute without the need for expensive and time-consuming sensory evaluation. Significant genotype-by-year interaction for bitter makes it necessary to acquire sensory data from 2 yr with three replications at each of four locations or two replications at each of five locations to differentiate statistically between means differing by half a flavor intensity unit. The precision of comparisons for sweet and roasted peanut will be more precise than that for bitter at a given arrangement of testing resources.

Key Words: *Arachis hypogaea* L., flavor, quality, resource allocation.

Several factors may significantly influence the economic traits of crop species. With sufficient knowledge about the genetic and environmental sources of variation

on characteristics of interest to a breeding program, field experiments can be designed to efficiently separate genotypes. This sort of investigation is common for agronomic and horticultural traits, including chemical and physical aspects of crop quality. Several such studies have been published for peanut (*Arachis hypogaea* L.) yield and grade (Norden *et al.*, 1982; Wynne and Coffelt, 1982; Knauff and Ozias-Akins, 1995). However, similar reports for sensory aspects of crop quality, which are perhaps more important to the consumer, are limited (Zanon, 1978; True and Work, 1981; Crisosto *et al.*, 1984).

Significant heritable variation was found consistently for some components of roasted peanut flavor, namely the roasted peanut and sweet attributes, while the nutty attribute exhibited significant genetic variation in some studies and not in others (Pattee and Giesbrecht, 1990; Pattee *et al.*, 1993, 1995). Breeding programs have been undertaken to modify these inherited characteristics to enhance the flavor of roasted peanuts. Although some aspects of the variation in these flavor components have been investigated—such as roast color and fruity attribute (Pattee *et al.*, 1991; Pattee and Giesbrecht, 1994), genotype-by-environment (G×E) interaction on roasted peanut attribute (Pattee *et al.*, 1994), ancestral effects on roasted peanut attribute (Isleib *et al.*, 1995) and high oleic acid content (Pattee and Knauff, 1995)—other aspects have not been reported. Little is known about the influence of genotype (cultivar or breeding line), environment, and their interaction on the sweet and bitter sensory attributes. Documentation of these sources of variation is important for the efficient allocation of resources to measure sweet and bitter attributes values to be used in comparing genotypes. The specific objectives of this study were to (a) test the significance of the effects of genotype, environment, and their interaction on the sweet and bitter attributes, (b) estimate the means of these sensory attributes for a set of genotypes, and (c) determine an efficient scheme of resource allocation for multiple-site testing of breeding lines for sweet and bitter attributes.

Materials and Methods

Genotype Resources. From 1986 to 1994, 480 peanut samples were obtained from the Southeast, Southwest, and Virginia-Carolina regions. The data set contained 17 genotypes, including the most common peanut cultivars in the runner and virginia market types and 42 year-location combinations. All samples were obtained from plants grown and harvested under standard recommended procedures for the specific location. Replicate samples for each genotype were obtained from a given site when available.

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

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C and 60% RH until roasted. SMK fractions were separated using official grading standards for each market type.

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 -20 C until evaluated. The roasting, grinding, and color measurement protocols were described by Pattee and Giesbrecht (1990). In 1991, a controlled 60-min cooling period was added between grinding and final color measurement to ensure the stability of the color measurement.

Sensory Evaluation. A 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. Only two panelists were changed on the panel across years. 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 six samples per session in 1986, five samples per session in 1987-88, and four samples per session in subsequent years. Sensory evaluation commenced mid-June and continued until all samples were evaluated. The average scores on individual sensory attributes across panelists were used in all statistical analyses in this study.

Statistical Analysis. Variation in sensory attribute scores was partitioned into parts due to environment, genotype, G×E interaction, and error. Error sums of squares were reduced further by the application where appropriate of paste color (linear and quadratic effects) and fruity attribute (linear effect only) as covariates. Paste color was selected as a covariate to correct for the unavoidable sample-to-sample variation in degree of roast. Fruity attribute reflects a combination of immaturity and improper handling after harvesting. While it can be argued that the frequency of immature kernels may have a genetic component, the importance of cultural practices such as time of harvest and handling of the crop justify the use of fruity attribute as a covariate (Pattee and Giesbrecht, 1994). All three covariate effects were initially included in the linear model for each attribute, then effects that did not significantly reduce the error sum of squares were eliminated from the model for final analysis.

Environmental effects were further divided into portions due to region, year, region-by-year interaction, and location within region and year. The sum of squares for G×E interaction was divided in an analogous manner. The effects of genotype, region, and their interaction were considered fixed, and the effects of year, year-by-region interaction, location, genotype-by-year interaction, genotype-by-year-by-region interactions, and genotype-by-location interactions were assumed to be random. Significance of effects was tested by constructing Satterthwaite approximate F-ratios with partial means squares for effects in the numerator and the approximate error mean square in the denominator. Least squares means for genotypes were estimated. These analyses were performed using the general linear models (GLM) procedure in SAS (1987).

A second analysis was performed to obtain estimates of the standard errors of differences between genotype means. The MIXED procedure in SAS (1992) was used to compute modified or residual maximum likelihood (MML or REML) estimates of the variance components corresponding to the random effects in the overall data set. These estimates

differ from the conventional maximum likelihood estimates in that the likelihood is based on the error contrasts remaining after fitting the fixed effects of the model (Patterson and Thompson, 1971).

For a balanced test of genotypes across a number of years (*y*), regions (*r*), and locations (*l*) in each year-region combination, and with the same number of observations (*n*) obtained from a completely random design at each location, the expected mean squares from the analysis of variance are presented in Table 1 and the standard error of the difference between two genotype means was estimated as:

$$s_{\text{Diff}} = \sqrt{2 \left(\frac{\hat{\sigma}_{\text{GY}}^2}{y} + \frac{\hat{\sigma}_{\text{GL(YR)}}^2}{yl} + \frac{\hat{\sigma}^2}{yln} \right)} \quad [\text{Eq. 1}]$$

where $\hat{\sigma}_{\text{GY}}^2$ is the estimate of genotype-by-year interaction, $\hat{\sigma}_{\text{GL(YR)}}^2$ is the estimate of genotype-by-location interaction within year and region, and $\hat{\sigma}^2$ is the estimate of experimental error variance. Because most cultivars are grown in only one production region, breeders are concerned more about the flavor of genotypes when grown in their particular regions rather than in others. As a rule, they will be testing in a single region only (*r*=1), so that the standard error of a difference actually used by the breeder will be

$$s_{\text{Diff}} = \sqrt{2 \left(\frac{\hat{\sigma}_{\text{GY}}^2}{y} + \frac{\hat{\sigma}_{\text{GL(YR)}}^2}{yl} + \frac{\hat{\sigma}^2}{yln} \right)} \quad [\text{Eq. 2}]$$

Note that the limit of s_{Diff} as the number of locations per year increases is

$$\lim_{l \rightarrow \infty} (s_{\text{Diff}}) = \sqrt{2 \left(\frac{\hat{\sigma}_{\text{GY}}^2}{y} \right)} \quad [\text{Eq. 3}]$$

Results and Discussion

The coefficients of variation for sweet, bitter, and roasted peanut attributes were 9.4, 10.4, and 9.4%, respectively. Results of the analysis of variance for roasted peanut (Table 2) were very similar to those obtained earlier (Pattee *et al.*, 1994) with one noticeable exception. Use of the random model and Satterthwaite approximate F-tests resulted in less precision in testing the effects of locations in years and regions, which were a highly significant source of variation in a fixed-effect model but not significant in the mixed model. Year remained a highly significant source of environmental variation. Results for the sweet and bitter attributes were somewhat different from those for roasted peanut. For sweet and bitter, the effect of location in year and region was highly significant. Year had a significant effect on bitter but not on sweet. The sorts of environmental factors associated with production regions in particular years would be related to general temperature and rainfall. The exact nature of the influence of these two general factors on the bitter and roasted peanut attributes is not clear. As was found previously for roasted peanut attribute, the effect of production region was not consistent enough to have statistical significance across years, although in the case of sweet, one could expect to see regional differences in a given year. Varia-

Table 1. Expected mean squares from analysis of variance of flavor scores of samples from g genotypes, y years, r regions, l locations per year-region combination, and n samples per test.

Source	df	Expected mean square
Year	y-1	$\sigma^2 + ng\sigma_{L(YR)}^2 + nglr\sigma_Y^2$
Region	r-1	$\sigma^2 + ng\sigma_{L(YR)}^2 + ngl\sigma_{YR}^2 + ngly\theta_R^2$
Year × region	(y-1)(r-1)	$\sigma^2 + ng\sigma_{L(YR)}^2 + ngl\sigma_{YR}^2$
Location in year, region	yl(r-1)	$\sigma^2 + ng\sigma_{L(YR)}^2$
Genotype	g-1	$\sigma^2 + n\sigma_{GL(YR)}^2 + nlr\sigma_{CY}^2 + nly\theta_C^2$
Genotype × year	(g-1)(y-1)	$\sigma^2 + n\sigma_{GL(YR)}^2 + nlr\sigma_{CY}^2$
Genotype × region	(g-1)(r-1)	$\sigma^2 + n\sigma_{GL(YR)}^2 + nlr\sigma_{CYR}^2 + nly\theta_{CR}^2$
Genotype × year × region	(g-1)(y-1)(r-1)	$\sigma^2 + n\sigma_{GL(YR)}^2 + nlr\sigma_{CYR}^2$
Genotype × location in year, region	yr(g-1)(l-1)	$\sigma^2 + n\sigma_{GL(YR)}^2$
Error	yr(lg(n-1))	σ^2

where σ_Y^2 is the component of variance associated with years,
 θ_R^2 is the variance of region effects,
 σ_{YR}^2 is the component of variance associated with year-by-region interaction,
 $\sigma_{L(YR)}^2$ is the component of variance associated with locations in year and region,
 θ_C^2 is the variance of genotype effects,
 σ_{CY}^2 is the component of variance associated with genotype-by-year interaction,
 θ_{CR}^2 is the variance of genotype-by-region interaction effects,
 σ_{CYR}^2 is the component of variance associated with genotype-by-year-by-region interaction,
 $\sigma_{GL(YR)}^2$ is the component of variance associated with genotype-by-location interaction in year and region, and
 σ^2 is the component of variance associated with experimental error.

Table 2. Mean squares from analyses of variance of the sweet, bitter, and roasted peanut attributes of flavor.

Source	Sweet		Bitter		Roasted peanut	
	df	MS	df	MS	df	MS
		fiu ^a		fiu		fiu
Total	462	0.2246	462	1.4564	479	0.6011
Genotype	16	1.7211**	16	2.8423**	16	1.3959**
Environment	41	0.6902**	41	8.0559**	41	1.9122**
Year	7	1.1737	7	37.9682**	7	7.7001**
Region	2	0.0063	2	0.0253	2	0.3763
Year × region	9	0.7800*	9	0.6277	9	0.2305
Location in year and region	22	0.2715**	22	0.5575**	22	0.3335
Genotype × environment	155	0.1155*	155	0.2206**	155	0.2374**
Genotype × year	57	0.1258	57	0.2747*	57	0.1964
Genotype × region	18	0.1106	18	0.2420†	18	0.2440
Genotype × year × region	20	0.1231	20	0.1163	20	0.1605
Genotype × location in year, region	57	0.0970	57	0.1633	57	0.3096**
Covariates	2	0.5265**	3	7.9975**	3	9.2664**
Roast color (linear)	1	0.7498**	1	1.7373**	1	7.7367**
Roast color (quadratic)	--	--	1	1.3501**	1	7.5408**
Fruity	1	0.4748*	1	1.4532**	1	14.9629**
Error	248	0.0842	247	0.1556	264	0.1703

^aFlavor intensity units.

†, *, ** Denote significance at the 10, 5, and 1% levels of probability, respectively.

tion among genotypes for sweet and bitter was highly significant as it was for roasted peanut.

A major difference between the results for sweet and bitter compared with those for roasted peanut was in the main source of G×E interaction. For roasted peanut, the

G×E interaction was due largely to the interaction between genotype and specific location within year and region. For bitter, the main source of G×E interaction was genotype-by-year, and genotype-by-region interaction bordered on significance (P ≤ 0.10). None of the

partitioned G×E effects for sweet were significant, although the aggregate G×E variation was significant.

The relative magnitudes of the variance components for the random effects of environment and genotype-by-environment interaction on flavor attributes generally reflected the F-tests of significance with significant effects having larger variance component estimates (Table 3). The only notable exception to this trend was the large variance component of year-by-region interaction for the bitter attribute. Year-by-region interaction was not significant in the analysis of variance (Table 2), and the standard error of the variance component for the effect was practically identical to the estimate itself (Table 3).

as compared with the virginia class, yet it was low in roasted peanut attribute compared with runner cultivars of similar sweet and bitter scores.

Overall, there was significant correlation among the three sensory attributes across the 17 genotypes (Fig. 1). The correlation between roasted peanut and sweet scores was 0.76 ($P \leq 0.01$) overall and 0.88 ($P \leq 0.01$) for the virginia class (Fig. 1a). Although positive, the correlation was not significant for the runner class ($r = 0.54$) due in large part to two cultivars, Southern Runner and GK 7, which were low in roasted peanut attribute considering their high sweet and low bitter scores. Likewise, Pronto reduced the overall correlation by lying outside the

Table 3. Estimates of variance components and their standard errors for the sweet, bitter, and roasted peanut attributes of flavor.

Source	Variance component estimate \pm standard error		
	Sweet	Bitter	Roasted peanut
	----- flavor intensity units -----		
Year	0.0142 \pm 0.0238	1.1195 \pm 0.6239	0.1759 \pm 0.0993
Year \times region	0.0393 \pm 0.0301	0.0575 \pm 0.0572	0.0000
Location in year and region	0.0248 \pm 0.0128	0.0578 \pm 0.0268	0.0135 \pm 0.0135
Genotype \times year	0.0042 \pm 0.0064	0.0243 \pm 0.0136	0.0005 \pm 0.0005
Genotype \times year \times region	0.0006 \pm 0.0092	0.0000	0.0000
Genotype \times location in year, region	0.0115 \pm 0.0092	0.0050 \pm 0.0126	0.0199 \pm 0.0145
Error	0.0835 \pm 0.0073	0.1541 \pm 0.0133	0.1770 \pm 0.0152

Generally, if the variance component estimate was larger than the standard error by 20 to 30%, the F-test in the analysis of variance was significant at the 5% level of probability. If the estimate was more than twice as large as its standard error, the F-test was significant at the 1% level. Experimental error was the largest component of variance for the sweet and roasted peanut attributes and the second largest for bitter. The variance component of year-by-region interaction was negligible for roasted peanut attribute, and that of genotype-by-year-by-region was negligible for all three attributes.

The least squares means for the 17 genotypes tested (Table 4) showed that the ranges of sweet, bitter, and roasted peanut attributes for runner and virginia peanuts were overlapping with the runner class showing a significantly ($P \leq 0.01$) higher mean than the virginia types for sweet (3.25 vs. 2.85 intensity units) and roasted peanut (4.65 vs. 4.37) and a significantly ($P \leq 0.01$) lower mean for bitter (3.21 vs. 3.78). MARC I and Florunner were the runner cultivars with the best sensory attributes in the runner class while the proprietary cultivar VC-1 was the best-tasting virginia-type cultivar. The ancestry of VC-1 is much closer to runner cultivars than to virginias, and the cultivar is characterized by somewhat small seed size compared with other virginia-type cultivars. Among the large-seeded virginia genotypes, the breeding lines NC Ac 18431 and N90010E had the best sensory attributes. Because there was only one spanish-type cultivar among the 17 genotypes tested, no generalizations can be made about the spanish class as a whole. However, cultivar Pronto exhibited high sweet and low bitter

Table 4. Mean sensory attribute scores for runner, spanish, and virginia-type peanut genotypes.

Genotypes	Sweet	Bitter	Roasted peanut
	----- flavor intensity units -----		
Runner			
ANDRU 93	3.18 bed ^a	3.40 c	4.76 ab
Florunner	3.35 b	3.06 b	4.80 a
GK 7	3.24 bc	2.96 ab	4.51 bed
MARC I	3.55 a	2.87 ab	4.88 a
Southern Runner	3.14 cde	3.60 cd	4.26 def
Sunrunner	3.05 def	3.36 c	4.71 ab
Spanish			
Pronto	3.50 a	2.74 a	4.48 bed
Virginia			
Agratech VC 1	3.36 ab	3.39 c	4.72 ab
Florigiant	2.66 h	3.85 de	4.21 ef
N90010E	2.97 defg	3.94 de	4.54 bcd
N90013E	2.68 h	4.09 e	4.11 f
NC 10C	2.61 h	4.24 e	4.07 f
NC 7	2.85 g	3.72 d	4.27 ef
NC 9	2.92 fg	3.64 d	4.45 cd
NC Ac 18431	2.95 efg	3.60 cd	4.60 abc
NC-V 11	2.71 h	3.64 d	4.36 cde
VA-C 92R	2.76 gh	3.70 cd	4.40 cde

^aMeans within a column followed by the same letter are not significantly different by t-test ($P < 0.05$).

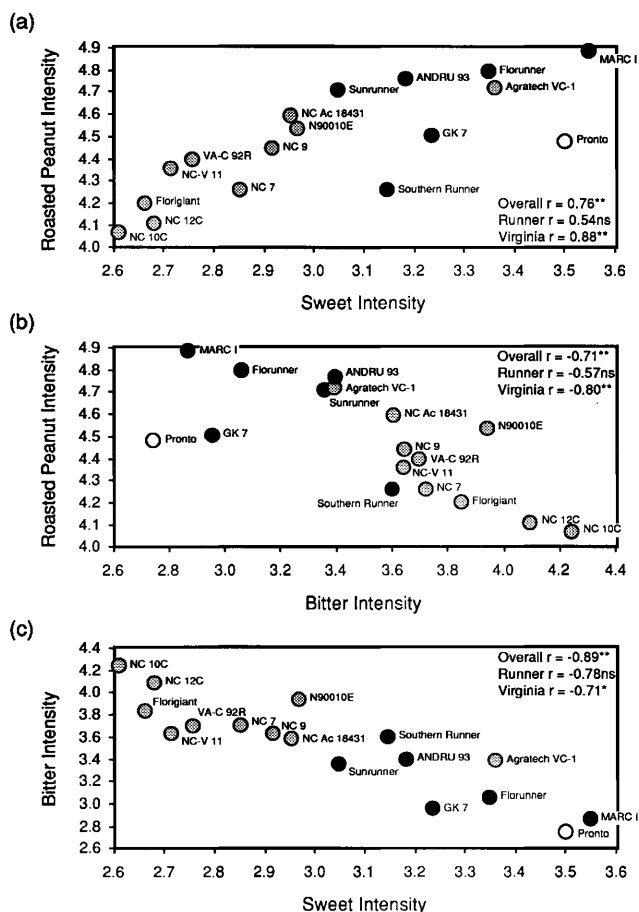


Fig. 1. Relationships between sweet, bitter, and roasted peanut attributes of runner (●), spanish (○), and virginia-type (●), cultivars. (a) Roasted peanut versus sweet. (b) Roasted peanut versus bitter. (c) Bitter versus sweet. ns, *, ** denote correlation values that are not significant, significant at the 5% level of probability, and significant at the 1% level, respectively.

general bivariate distribution. Because of the generally positive correlation, it might be possible to select for greater roasted peanut attribute by selecting for sugar content if the correlation between sugar content and sweet attribute is sufficiently high. This would permit a great reduction in the cost and time required for sensory evaluation of flavor. Similarly, the generally strong negative correlations of the bitter attribute with the roast peanut and sweet attributes (Fig. 1b,c) indicates the possibility of improving flavor by selecting against the bitter principles if they can be identified chemically.

Predicted values of the standard error of the difference between genotype means estimated from a common, balanced set of field trials in a single production region follow the usual pattern (Table 5). For the sweet and roasted peanut attributes, which had little genotype-by-year interaction, the breeder could achieve the same level of precision by obtaining the same number of observations in a single year at more locations rather than by testing at fewer locations across more years. Although this would allow more rapid breeding progress, it also

would increase the annual cost of flavor evaluation because the cost would be incurred in a single year rather than being spread out over two or more. Because genotype-by-year interaction was the dominant component of overall G × E interaction for the bitter attribute, testing for bitter at fewer locations across more years is clearly superior to testing at more locations across fewer years. For example, the breeder might obtain 24 observations from tests with two replications at 12 locations in a single year ($s_{Diff} = 0.25$), six locations in 2 yr ($s_{Diff} = 0.19$), four locations in 3 yr ($s_{Diff} = 0.17$), and so on to a single location in 12 yr ($s_{Diff} = 0.13$). There is a clear advantage in testing across at least 2 yr, then the improvement in precision is less for each additional year of testing. There is no such trend for roasted peanut attribute, and the trend is present but much weaker for sweet. The precision of comparison of bitter attribute is the worst of the three for a given pattern of testing. The breeder could set the allocation of resources for flavor evaluation by choosing a desired level of precision for bitter, knowing that the precision for sweet and roasted peanut will be better. If a difference of half a flavor intensity unit is desired to be significant by t-test, then assuming the critical value of t to be 2.0 to 2.5, a standard error of no more than 0.20 units is required. This precision can be achieved for the bitter attribute by sampling from three replications at a single location in each of 4 yr, three replications at two locations in each of 3 yr, or three replications in four locations in 2 yr. The desired level of precision cannot be reached with only 1 yr of testing because the limit of s_{Diff} for bitter with $\gamma = 1$ of testing is 0.22. If only two replications are sampled in each test, then the alternatives are two replications at a single location in each of 6 yr, two replications at two locations in 4 yr, two replications in three locations in 3 yr, or two replications in five locations in 2 yr. In each case described, the precision of comparisons between genotypes for sweet and roasted peanut is better than that for bitter. Because most breeders need to make decisions on retention or discarding of breeding lines after one or two years at the preliminary or intermediate stages of testing, the 2-yr scenario with three-replication tests at four locations or with two-replication tests at five locations would be the most viable options.

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Table 5. Standard error of the difference in sensory attribute between the means of two breeding lines grown in a single region.

No. environments (yl)	Years (y)	Locations (l)	Sweet			Bitter			Roasted peanut		
			n=1 ^a	n=2	n=3	n=1	n=2	n=3	n=1	n=2	n=3
----- flavor intensity units -----											
1	1	1	.45	.34	.30	.61	.46	.40	.63	.47	.40
2	1	2	.32	.25	.22	.46	.36	.32	.44	.33	.28
2	2	1	.32	.24	.21	.43	.33	.28	.44	.33	.28
3	1	3	.27	.21	.19	.39	.32	.29	.36	.27	.23
3	3	1	.26	.20	.17	.35	.27	.23	.36	.27	.23
4	1	4	.24	.19	.17	.36	.30	.28	.32	.23	.20
4	2	2	.23	.18	.16	.32	.26	.23	.31	.23	.20
4	4	1	.22	.17	.15	.30	.23	.20	.31	.23	.20
5	1	5	.22	.18	.16	.34	.29	.27	.28	.21	.18
5	5	1	.20	.15	.13	.27	.21	.18	.28	.21	.18
6	1	6	.20	.17	.15	.32	.28	.26	.26	.19	.17
6	2	3	.19	.15	.13	.28	.23	.21	.26	.19	.16
6	3	2	.19	.14	.13	.26	.21	.19	.26	.19	.16
6	6	1	.18	.14	.12	.25	.19	.16	.26	.19	.16
7	1	7	.19	.16	.14	.31	.27	.25	.24	.18	.15
7	7	1	.17	.13	.11	.23	.17	.15	.24	.18	.15
8	1	8	.18	.15	.14	.30	.26	.25	.22	.17	.14
8	2	4	.17	.13	.12	.25	.21	.20	.22	.17	.14
8	4	2	.16	.13	.11	.23	.18	.16	.22	.17	.14
8	8	1	.16	.12	.10	.21	.16	.14	.22	.16	.14
9	1	9	.17	.15	.14	.29	.26	.25	.21	.16	.14
9	3	3	.16	.12	.11	.23	.19	.17	.21	.16	.13
9	9	1	.15	.11	.10	.20	.15	.13	.21	.16	.13
10	1	10	.17	.14	.13	.28	.26	.24	.20	.15	.13
10	2	5	.15	.12	.11	.24	.20	.19	.20	.15	.13
10	5	2	.14	.11	.10	.20	.16	.14	.20	.15	.13
10	10	1	.14	.11	.09	.19	.15	.13	.20	.15	.13
11	1	11	.16	.14	.13	.28	.25	.24	.19	.14	.12
11	11	1	.13	.10	.09	.18	.14	.12	.19	.14	.12
12	1	12	.16	.14	.13	.27	.25	.24	.18	.14	.12
12	2	6	.14	.12	.11	.23	.19	.18	.18	.14	.12
12	3	4	.14	.11	.10	.21	.17	.16	.18	.14	.12
12	4	3	.13	.11	.09	.20	.16	.15	.18	.14	.12
12	6	2	.13	.10	.09	.19	.15	.13	.18	.14	.12
12	12	1	.13	.10	.09	.17	.13	.12	.18	.13	.12
∞	1	∞	.10	.10	.10	.22	.22	.22	.03	.03	.03
∞	2	∞	.07	.07	.07	.16	.16	.16	.02	.02	.02
∞	3	∞	.06	.06	.06	.13	.13	.13	.02	.02	.02
∞	4	∞	.05	.05	.05	.11	.11	.11	.02	.02	.02
∞	5	∞	.04	.04	.04	.10	.10	.10	.01	.01	.01
∞	6	∞	.04	.04	.04	.09	.09	.09	.01	.01	.01

^aNumber of replicates per environment.

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