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Research Article

Genetics of major biochemical components in groundnut (*Arachis hypogaea* L.)

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Abstract
Nine groundnut genotypes were crossed in half diallel fashion to study the combining ability and gene action in respect of oil, protein and total soluble sugar content. The magnitudes of general combining ability (GCA) variances were higher than specific combining ability (SCA) variances in F_1 and F_2 generations indicating that additive effects were more pronounced than non-additive effects. The parent TPG 41 was a good general combiner for high oil content, but poor combiner for protein and sugar content. The genotype NRCG 10389 was a good general combiner for protein content, while parent NRCG 201 was a good general combiner for protein and total soluble sugar content. A number of cross combinations involving theses genotypes indicated high positive effects for oil, protein and total soluble sugars, but none of the crosses showed consistently significant *sca* effects over generations. The ratios of average degree of dominance were also in the range of over dominance for all the traits. Dominant and recessive alleles were not equally distributed among the parents with respect to all the traits. The ratio of dominance to recessive alleles for oil and protein content showed that the dominant genes were less than the recessive ones, while for the total soluble sugar, dominant genes were in excess. Moderate narrow-sense heritability was recorded in both F_1 and in F_2 generations for all three traits.

Keywords: Groundnut, gene action, oil content, protein content, soluble sugar

Introduction:

Oil content is of primary importance in groundnut, and in Indian cultivated groundnut varieties it ranges from 47 to 54.6% (Bishi *et al.*, 2013). Likewise, the protein content in groundnut kernels varies from 22-36% depending on cultivar, location, season, seed maturity and agronomic practices. Average protein content is higher than that of eggs, dairy products, meat and fish and the digestibility of groundnut protein is very high (Singh and Singh, 1991). The soluble sugars content in groundnut varies from 9.2 to 13.3% (Asibuo *et al.*, 2008)These three biochemical components have greater dietary importance, and groundnut is of much relevance particularly in vegetarian diet. However, except oil content to some extent, the work to improve these biochemical components through breeding is limited in groundnut. Information on the genetic control of these traits is important for initiating a breeding programme. Therefore, the present investigation was taken up to study the genetic nature of oil, protein and total soluble sugar content in groundnut.

Material and methods

The experimental materials for the present study comprised of nine parental lines, 36 F_1s and 36 F_2s. The parental lines comprised of cultivated varieties (GG 5, TPG 41, J 11 and AK 303); germplasm lines (NRCG 115, NRCG 201 and NRCG 10389) and elite advanced breeding lines (J 71 and JB HPS K 08-1). These lines were crossed in a half-diallel fashion to develop 36 F_1s (excluding reciprocals) and their 36 F_2s, which were evaluated along with the parental lines in a randomized block design with three replications during summer 2010 at the Instructional Farm, Junagadh Agricultural University, Junagadh. Each entry consisted of a single row of 2 m length for each of parents and F_1s, two rows each of F_2 progenies. Inter- and intra-row spacing adopted was 45 and 10 cm, respectively. Recommended agronomic package of practices were followed to raise the crop. The observations on oil and protein contents were recorded from the thoroughly crushed seed-mixture by using Near Infra Red Spectroscopy (N.I.R. DICKOY-JOHNY INSTALAB600) instrument and the same set of material was used for evaluating the total soluble sugars by using Phenol Sulphuric Acid (Colorimetric) method suggested by Dubois *et al.* (1956). The replicated data were subjected to analysis of variance for mean performance (Panse and Sukhatme, 1985) and combining ability analysis was carried out according to Model-I (Fixed effect), Method-2 (Parents and one set of F_1's or F_2's without reciprocals) of Griffing (1956).

Results and discussion

Analysis of variance revealed significant differences due to genotypes, which was highly

significant for all three traits. Highly significant variance was found due to parents for all the traits indicating substantial amount of genetic variability among the parents for the traits studied. Mean sum of squares due to hybrids (F_1) were also highly significant for all three traits revealing the existence of potential variability in the parental material used in the present study. The variances due to F_2s were also highly significant for all the traits studied. The mean squares due to F_1s Vs F_2s revealed that the F_1s differed significantly from their F_2s for all the traits (Table 1).

When combining ability analysis was performed, significant differences due to general combining ability (GCA) and specific combining ability (SCA) were observed for all the traits studied in both the generations (F_1 and F_2) (Table 2). The magnitudes of GCA variances were larger than SCA variances in both the generations for soluble sugars, and in F_2 generation for oil and protein contents, indicating that additive genetic variance is largely responsible in the expression of these traits. In F_1 generation non-additive genetic variances were observed for oil and protein contents; however, in F_2 generation additive variances were more important for these traits. It may be ascribed to the fact that non-additive gene action observed for a trait tends to be converted into additive in the later generations (Fasoulas, 1981).

General combining ability: Identification of parents for improvement of a trait in question necessitates the assessment of general combining ability effects (*gca*). General combining ability effects for the traits studied are presented in Table 3. For oil and protein contents, out of nine parents, five parents in F_1 and six parents in F_2 expressed significant *gca* effects, while for total soluble sugars eight parents each in F_1 and F_2 generations showed significant gca effects. TPG 41 showed significant and positive *gca* effects consistently in both the generations for oil content, while two parents, JB HPS K 08-1 and NRCG 115 showed consistently significant and negative gca effects over the generations for this trait. For protein content over both the generations, two parents, NRCG 201 and NRCG 10389 showed significant and positive gca effects, while two parents, TPG 41 and JB HPS K 08-1 recorded significant and negative gca effects in both the generations. Five parents *viz*., GG 5, NRCG 115, NRCG 201, J 71 and J 11 had significant and positive gca effects in F_1 and F_2 generations and are good general combiners for increasing total soluble sugars content, whereas, AK 303, JB HPS K 08-1 and TPG 41 had significant and negative gca effects in both the generations for this trait.

The parent, TPG 41 was good general combiner for high oil content, but poor combiner for protein and sugar contents, therefore, if the breeding objective is to tailor a groundnut genotype with enhanced oil productivity, the TPG 41 can be used as one of the donor parents. However, if the breeding objective is to develop groundnut genotypes for confectionery types, where high values for sugar and protein are required, and on the other hand reduced contents of oil are preferred, the parental line NRCG 201, which has been identified as good general combiner for protein and total soluble sugars contents, is recommended for use in such hybridization programmes as donor parent for these two attributes. Another line NRCG 10389 has been identified as good general combiner for protein content. This line may act as a good source for developing groundnut genotypes with enhanced protein content, which is an essential requirement of groundnut varieties use for peanut-butter.

Specific combining ability**:** Specific combining ability (*sca*) effects calculated are presented in Table 4. Only limited number of crosses exhibited high *sca* effects for different quality traits. For oil content, six and three crosses showed significant and positive *sca* effects in F_1 and F_2 generations, respectively. For protein content two crosses in F_1 generation and five crosses in F_2 generation showed significant and positive *sca* effects. Significant and positive *sca* effects were observed for total soluble sugars content in 12 and 13 crosses in F_1 and F_2 generation, respectively.

None of the crosses showed consistently significantly positive *sca* effects over generations for these three traits. Based on the results of F_1 generation, the crosses, TPG 41 × JB HPS K 08-1, NRCG 115 × TPG 41 and J 11 × AK 303 were the good specific combiners for oil, protein and total soluble sugars, respectively. While in F_2 generation the crosses, JB HPS K 08-1 × AK 303, NRCG 201 × NRCG 10389 and TPG 41 × AK 303 showed good *sca* for oil, protein and total soluble sugars content, respectively. Significant *sca* effects were not observed in F_1 generation in cross NRCG 201 × J 11 for any of the three traits studied, however, in F_2 generation this cross exhibited significant and positive sca effects for all these traits. This inconsistency in the expression of crosses in F_1 and F_2 generations may be attributed to new reconciliation of genes in later generations.

Genetic components of variation**:** The genetic components of variations are presented in Table 5. The additive dominance model was adequate for oil, protein and total soluble sugars contents. For all the three traits, additive (D) and non-additive (H_1 and H_2) components of genetic variance were significant in both F_1 and F_2 generations suggesting the importance of additive and non-additive gene actions in the expression of these traits. Further, the magnitudes of non-additive

components were higher than additive component indicating the preponderance of dominant genetic component in the inheritance of these traits. For oil content, the overall effects of heterozygote loci (h^2) were non-significant in both F_1 and F_2, while for protein and total soluble sugar contents, the overall effects of heterozygote loci (h^2) were highly significant. The environmental components (E) were non-significant in both the F_1 and F_2 generations for these traits. The estimates of degree of dominance $(H_1/D)^{1/2}$ exhibited over dominance, as it was greater than unity for all the three traits in both the generations. The estimates of $H_2/4H_1$ deviated from the theoretical value 0.25 for all the three traits in both the generations, indicating that distribution of negative and positive genes controlling these traits was asymmetrical in the parents used for the study. The ratio of h^2/H_2 was less than unity in both the generations for all the three traits, which indicated that only one dominant gene group governed these traits. These results are in accordance with Basu *et al*. (1988), Parmar *et al*. (2002) and Jivani *et al.* (2009).

Based on the two generations, the less than unity ratio of dominance to recessive alleles (K_D/K_R) and the negative 'F' value observed for oil and protein contents indicates that the proportion of dominant genes was less than the recessive ones, while results on K_D/K_R in case of total soluble sugars revealed excess of dominant genes than recessive ones, and this was also confirmed from the positive 'F' value observed for this trait. The narrow sense heritability was recorded moderate in both the F_1 and F_2 generations for all the three traits.

Present study revealed inconsistency in the F_1 and F_2 generations for combining ability effects and the gene action. Further, results suggested that the selection of potential crosses for throwing transgressive segregants, should be made not only on the basis of F_1 evaluation but on the basis of the evaluation of F_2 also with respect to residual heterosis and combining ability of the parents of crosses as reported earlier in gram by Chaudhary *et al*. (1978) and also theoretically proposed by Fasoulas (1981).

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Table 1 Analysis of variance for the oil, protein and total soluble sugar content in groundnut

Source	d. f.	Mean Squares		
		Oil content (%)	Protein content (%)	Total soluble sugar (%)
Replications	2	0.31	1.22	0.06
Genotypes	80	5.06**	4.56**	4.57**
Parents	8	3.00**	3.59**	6.68**
F_1's	35	6.37**	3.46**	2.86**
F_2's	35	4.17**	3.96**	5.51**
Parents vs crosses	1	7.07*	52.04**	12.44**
F_1's vs F_2's	1	4.65*	24.18**	7.10**
Error	160	1.10	1.01	0.13

*, ** Significant at 5% and 1% levels, respectively

Table 2. Analysis of variance for combining ability in F_1 and F_2 generation for oil, protein and total soluble sugar content in groundnut

Source	d. f.	Mean squares					
		Oil (%)		Protein (%)		Total soluble sugar (%)	
		F_1	F_2	F_1	F_2	F_1	F_2
gca	8	6.063**	4.891**	4.301**	4.317**	5.248**	8.677**
sca	36	0.941**	0.496*	0.914**	0.665**	0371**	0.365**
Error	88	0.374	0.319	0.333	0.320	0.033	0.048
σ^2g		0.517	0.416	0.361	0.363	0.474	0.784
σ^2s		0.567	0.177	0.581	0.346	0.338	0.317
σ^2g/σ^2s		0.912	2.345	0.621	1.052	1.402	2.473

*, ** Significant at 5% and 1% levels, respectively

Table 3. General combining ability (gca) effects of the parents for oil, protein and total soluble sugar content in groundnut.

Parents	Oil content (%)		Protein content (%)		Total soluble sugar (%)	
	F_1	F_2	F_1	F_2	F_1	F_2
GG 5	0.56**	-0.03	0.65**	0.15	0.22**	0.23**
NRCG 115	-1.20**	-0.67**	0.23	0.47**	1.13**	0.72**
NRCG 201	-0.48**	-0.08	0.41*	0.60**	0.23**	0.21**
NRCG 10389	0.24	0.50**	0.80**	0.41*	0.09	0.05
TPG 41	1.45**	1.13**	-1.11**	-1.32**	-0.89**	-0.87**
J 71	-0.11	-0.03	0.20	0.46**	0.33**	0.65**
JB HPS K 08-1	-0.49**	-0.96**	-0.64**	-0.62**	-0.85**	-1.01**
J 11	-0.07	-0.51**	-0.31	0.02	0.50**	1.34**
AK 303	0.09	0.64**	-0.24	-0.17	-0.76**	-1.31**
S. E. (gi) ±	0.174	0.161	0.164	0.161	0.052	0.062

*, ** Significant at 5% and 1% levels, respectively

Table 4. Estimation of specific combining ability (sca) effects of hybrids for oil, protein and total soluble sugar content in groundnut.

Crosses	Oil content (%)		Protein content (%)		Total Soluble Sugar (%)	
	F_1	F_2	F_1	F_2	F_1	F_2
GG 5 x NRCG 115	1.21*	-0.87	0.10	1.03*	0.06	0.90**
GG 5 x NRCG 201	-0.06	-0.72	0.71	-0.26	-0.09	0.63**
GG 5 x NRCG 10389	-0.45	0.14	0.23	-0.48	0.06	0.05
GG 5 x TPG 41	-0.58	0.63	0.78	-0.60	0.72**	-0.50*
GG 5 x J 71	0.16	0.37	0.11	0.38	-0.09	0.41*
GG 5 x JB HPS K 08-1	0.61	-0.74	0.79	0.35	0.67**	-0.35
GG 5 x J 11	-0.21	-0.83	0.86	0.20	0.05	0.02
GG 5 x AK 303	-1.01	-0.22	0.43	-0.14	-0.04	-0.57**
NRCG 115 x NRCG 201	0.61	-0.17	0.24	0.74	0.26	0.47*
NRCG 115 x NRCG 10389	-0.54	0.35	-0.04	0.62	0.61**	-0.32
NRCG 115 x TPG 41	-2.31**	0.40	1.52**	0.10	0.85**	-0.97**
NRCG 115 x J 71	-0.26	0.01	0.14	0.68	0.02	0.13
NRCG 115 x JB HPS K 08-1	0.47	0.50	0.65	-0.57	-0.55**	-0.83**
NRCG 115 x J 11	-0.25	0.16	-0.17	-0.41	0.19	0.58**
NRCG 115 x AK 303	-1.24*	-0.12	1.00	0.70	0.41*	-0.55**
NRCG 201 x NRCG 10389	0.25	0.20	-0.89	1.70**	-0.06	-0.02
NRCG 201 x TPG 41	-0.55	0.11	0.80	-0.23	0.92**	-0.68**
NRCG 201 x J 71	-0.50	0.72	0.30	-0.06	-0.30	0.00
NRCG 201 x JB HPS K 08-1	-1.05	-0.44	0.64	-0.61	0.77**	-0.12
NRCG 201 x J 11	0.32	1.15*	0.75	1.13*	-0.27	0.58**
NRCG 201 x AK 303	0.05	0.28	0.50	-0.16	0.37*	-0.14
NRCG 10389 x TPG 41	-0.38	0.88	0.88	-2.07**	0.64**	-0.10
NRCG 10389 x J 71	0.05	1.15*	0.64	-0.24	-0.06	0.49*
NRCG 10389 x JB HPS K 08-1	-0.65	-0.68	0.61	-0.54	0.49**	-0.16
NRCG 10389 x J 11	0.37	-1.08*	0.53	0.21	-0.33*	0.52**
NRCG 10389 x AK 303	1.10*	0.33	0.00	-0.27	0.09	0.02
TPG 41 x J 71	1.31*	-0.10	-1.07*	1.36**	-0.55**	0.98**
TPG 41 x JB HPS K 08-1	2.20**	0.23	0.54	1.08*	0.00	0.54**
TPG 41 x J 11	1.25*	-0.22	-1.26*	-0.46	-0.52**	0.49*
TPG 41 x AK 303	2.12**	0.30	-0.27	0.40	-0.51**	1.05**
J 71 x JB HPS K 08-1	-0.30	-0.21	-0.09	-0.58	0.79**	-0.56**
J 71 x J 11	-0.58	-0.80	0.72	0.13	0.25	0.24
J 71 x AK 303	-0.17	-0.65	1.10*	-0.29	0.68**	-0.48*
JB HPS K 08-1 x J 11	0.20	-0.38	-0.08	0.78	-0.87**	0.64**
JB HPS K 08-1 x AK 303	-0.60	1.18*	-1.16*	0.58	-0.23	0.46*
J 11 x AK 303	-0.99	0.80	0.64	0.19	1.03**	-0.95**
S. E. (s_{ij}) ±	0.56	0.52	0.53	0.52	0.17	0.20
S. E. (s_{ij} - s_{ik}) ±	0.83	0.76	0.78	0.76	0.25	0.25
S. E. (s_{ij} - s_{lk}) ±	0.78	0.72	0.74	0.72	0.23	0.30

*, ** Significant at 5% and 1% levels, respectively

Table 5. Estimation of genetic components of variance with their standard errors and ratios for oil, protein and total soluble sugar content in groundnut

Genetic components	Oil content (%)		Protein content (%)		Total soluble sugar (%)	
	F_1	F_2	F_1	F_2	F_1	F_2
D	0.63** ±0.24	0.68** ±0.15	0.87** ±0.19	0.88** ±0.32	2.20** ±0.10	2.18** ±0.10
H_1	3.25** ±1.24	6.37** ±1.34	2.34** ±0.43	8.11** ±2.79	4.31** ±0.23	10.15** ±0.88
H_2	2.74** ±1.03	4.12** ±1.15	2.05** ±0.36	6.71** ±2.40	3.15** ±0.20	7.82** ±0.79
h^2	0.13 ±0.82	0.18 ±0.77	1.48** ±0.25	4.16** ±1.61	1.81** ±0.33	1.71** ±0.53
F	-1.39 ±1.51	-1.57 ±0.71	-0.77 ±0.45	-0.92 ±1.47	0.50** ±0.18	0.89** ±0.31
E	0.37 ±0.21	0.32 ±0.24	0.33 ±0.26	0.32 ±0.21	0.03 ±0.03	0.05 ±0.03
$(H_1/D)^{1/2}$	2.27	1.53	1.64	1.52	1.40	1.08
$H_2/4\ H_1$	0.21	0.16	0.22	0.21	0.18	0.19
K_D/K_R	0.35	0.14	0.58	0.49	1.18	1.46
h^2/H_2	0.05	0.04	0.72	0.62	0.57	0.22
Heritability (ns)%	54.70	62.50	48.90	44.50	64.50	58.70

*, ** Significant at 5% and 1% levels, respectively