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Research Note

Combining ability analysis for yield, yield attributes and quality traits in groundnut (*Arachis hypogaea* L.)

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Abstract

Line × Tester analysis was carried out in a set of 20 crosses developed using five lines and four testers to ascertain the nature of gene action and combining ability of parents for yield, yield attributes and quality traits in groundnut. The estimates of GCA and SCA variance indicated the predominance of non-additive gene action for the inheritance of all the traits except SCMR at 60 DAS. The parents TCGS 1694, TCGS 1862, Kadiri-6 and TCGS 2251 were identified as good general combiners which could be further used in breeding programmes for yield improvement. The cross, Kadiri-6 × TCGS 1862 exhibited desirable *sca* effects for days to maturity, number of secondary branches plant⁻¹, number of pods plant⁻¹, number of mature pods plant⁻¹ and kernel yield plant⁻¹, while the cross Narayani × TCGS 2251 was found to be a good combiner with high *sca* effects for earliness (days to flowering and days to maturity). These two combinations had either low × high or high × medium *gca* parents indicating the involvement of both additive and non-additive gene action.

Keywords: Groundnut, Combining ability, Non-additive gene action

Groundnut (*Arachis hypogaea* L.) is a unique leguminous crop called the “wonder legume” as it can be used in diverse ways due to its nutritional, medical and fodder values. It is an annual self pollinated leguminous oilseed crop. It is a segmental allotetraploid with two genomes, AABB with a chromosome number of $2n = 4x = 40$ and belongs to the family *Fabaceae*. It is native to South America, grown throughout the tropical and sub-tropical regions of the world between the latitudes of 40°N to 40°S. In India, it is cultivated in an area of 57 lakh hectares with production of 101.13 Mt and productivity of 1776.59 kg/ha (Directorate of Economics and Statistics, 2022-2023).

So far, groundnut is considered as a crop of drylands grown in marginal lands of poor fertility. With increase

in demand for groundnut, it is no more a dryland crop and is cultivated in irrigated conditions and has attained commercial crop status. In this changed scenario, it is essential to develop varieties with high yield potential along with improved quality traits *i.e.*, confectionary as well as oil purpose. In this context, the information on the combining ability of parents and nature of gene action of yield and its components, would help in understanding the inheritance of characters, selection of suitable parents for hybridization and identification of promising crosses in early generation. Among the different methodologies available to assess the nature of gene action and also combining ability effects of genotypes, the Line × Tester analysis is most widely used because of its ease and simplicity. Hence, the present study was taken up

to determine the combining ability of five lines and four testers in groundnut.

The base material for the present study comprised of nine groundnut genotypes which include five lines (TCGS 1694, TCGS 2245, Dheeraj, Kadiri-6, Narayani) and four testers (TCGS 1862, TCGS 2251, ICGR 161930 and NRCG-CS19) along with their 20F₁s derived through hybridization in a L×T mating fashion (Kharif, 2021). The twenty F₁s along with their parents were sown in RBD with two replications during, 2020-21 at dry land farm of S.V. Agriculture college, Tirupati, ANGRAU. Each genotypewas sown in 2 rows plots of 3m length with a spacing of 30 cm between the rows and 10cm between the plants. Recommended crop production and protection measures were followed to maintain good crop growth.

Observations were recorded on five randomly tagged competitive plants from the centre of the row in each cross in each replication for all the physiological, yield, yield components and quality traits viz. days to 50% flowering, days to maturity, relative water content, SPAD chlorophyll meter reading at 60 DAS, plant height, specific leaf area at 60 DAS, number of primary branches plant⁻¹, number of secondary braches plant⁻¹, number of pods plant⁻¹, number of mature pods plant⁻¹, 100 pod weight,shelling per cent (SP), 100 kernel weight, sound mature kernel per cent, dry haulms yield plant⁻¹, pod yield plant⁻¹, kernel yield plant⁻¹, oil content, protein content, oleic acid content, linoleic acid content and O/L ratio expect days to 50% to flowering and maturity that were noted on per plot basis. Statistical analysis was done as per Kempthorne (1957) for combining ability analysis using the software TNAU STAT statistical package. Near Infrared Reflectance Spectroscopy (NIRS) was done for non destructive estimation of fatty acid composition, oil content, protein content, oleic and linoleic acid content in large populations (Velasco and Becker, 1998; Biskupeck-Korell and Moschner, 2007).

Analysis of variance revealed highly significant differences for all the characters studied except harvest index among the crosses (Table 1).The parents differed significantly for all the characters except specific leaf area at 60 DAS, number of primary branches plant⁻¹, hundred pod weight, dry haulms yield plant⁻¹, harvest index and oil content. The variance due to crosses was partitioned into lines, testers and their interaction. Among the lines, differences were not significant for three traits i.e., days to flowering, pod yield plant⁻¹ and harvest index. Among testers, differences were not significant for specific leaf area at 60 DAS, sound mature kernel per cent, 100 pod weight, dry haulms yield plant⁻¹, harvest index, oil content, linoleic acid content and O/L ratio. The mean squares due to Line × Tester component were significant for the characters days to maturity,plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹, 100 pod weight,kernel yield plant⁻¹, oleic acid content and not significant for days to 50 % flowering, SCMR at 60 DAS, SLA at 60 DAS, relative water content, number of mature pods plant⁻¹, pod yield plant⁻¹, shelling per cent, 100 kernel weight, harvest index, dry haulms yield plant⁻¹, oil content, protein content linoleic acid content and O/L ratio.

The magnitude of specific combining ability (SCA) variances was much greater than general combining ability variances (GCA) for all the characters except SCMR at 60 DAS which indicated major role of non additive gene action in their genetics (Table 2). Hence improvement of these traits could be accomplished by selection in later filial generations. Earlier,non-additive gene action for number of pods plant⁻¹, number of mature pods plant⁻¹, and number of primary branches plant⁻¹wasdocumented by Mathur *et al.* (2003), Ganesan*etal.* (2010),John*etal.* (2014),Pavithradevi(2013). Similarly the results are in line with Prabhu *et al.* (2014), Boraiah *et al.* (2015), Vaithiyalingan (2015), Pramesh *et al.* (2017), Shaibu *et al.* (2018), Sowmya *et al.* (2018),

Table 1. Analysis of variance for combining ability in Line × Tester analysis for yield, yield attributes and quality traits groundnut

Source of Variation	df	MEAN SUM OF SQUARES											
		DFF	DM	SCMR	SLA (cm ² g ⁻¹)	RWC	PH (cm)	NPB	NSB	NPP	NMP	100PW (g)	SP (%)
Replications	1	3.38	1.72	0.32	45.37	106.79*	0.86	0.28	0.15	20.4	6.42	6.69	1.97
Entries	28	4.17**	3.11**	17.20**	2283.68**	94.20**	61.91**	14.77**	2.05**	145.71**	526.39**	113.92**	122.05**
Crosses	19	2.90**	2.77**	13.46*	2694.18**	85.32**	57.85**	9.24**	2.00**	142.72**	678.98**	106.99**	150.42**
Lines	4	1.96	4.09**	19.68*	4991.99**	88.65**	148.60**	23.34**	2.76**	333.82**	909.95**	213.26**	76.17**
Testers	3	9.84**	3.33**	34.44**	446.62	97.76**	56.51**	5.58*	3.07**	108.96**	373.03	107.70**	30.42**
Parents	8	7.51**	3.34**	25.55**	1441.44	95.54**	79.59**	1.81	2.41**	169.29**	214.22	144.50**	16.35**
L vs T	1	42.71	17.78**	6.48	0.86	34.78	246.68**	6.24*	1.73**	448.90**	542.68	355.61**	0.01
Parents vs Crosses	1	1.54	7.73**	21.38*	1222.08	252.23**	0.00	223.82**	0.10	13.86	124.46	0.89	423.83**
Error	28	0.92	0.74	6.2	647.22	19.75	8.05	1.41	0.19	22.6	179.43	19.51	61.05

Table 1. Continued..

Source of Variation	df	MEAN SUM OF SQUARES										
		100KW (g)	SMK (%)	DHY (g)	HI (%)	KYP (g)	OIL (%)	PRO (%)	OA (%)	LLA (%)	O/L	PYP (g)
Replications	1	0.62	68.54**	6.45	32.03	1.76	0.15	0	24.62	46.01	0.51	1.49
Entries	28	90.32**	91.69**	66.60**	36.23	24.49**	7.72**	21.72**	182.26**	127.85**	1.83**	36.51**
Crosses	19	95.75**	117.86**	64.70**	23.74	23.24**	9.32**	20.67**	106.81**	111.03**	1.60**	37.25*
Lines	4	161.60**	98.18**	193.49**	32.61	22.34**	14.12**	38.64**	207.36**	226.06**	3.75**	35.08
Testers	3	138.83**	12.31	33.49	5.08	31.72**	0.61	13.75**	229.05**	30.11	0.89	58.61*
Parents	8	71.38**	39.88*	22.28	57.71	25.66**	4.04	5.44*	70.91**	182.98**	2.16**	35.45*
L vs T	1	36.1	0.00	42.26	26.62	16.55**	6.74	5.48	67.50**	57.45	0.16	29.01
Parents vs Crosses	1	138.62**	9.05	457.30**	101.79	0.08	6.63	171.99**	2506.50**	6.45	3.47**	29.01
Error	28	13.19	14.77	18.86	228.26	8.23	3.1	1.99	7.58	41.00	0.38	14.75

*Significant at 5% and **Significant at 1%

DF : Days to 50% flowering; DM : Days to maturity; SCMR : SPAD chlorophyll meter reading at 60 DAS ; SLA : Specific leaf area at 60 DAS (cm² g⁻¹); RWC: Relative water Content(%);PH : Plant height (cm); NPB : No of Primary branches plant⁻¹; NPB : No of Secondary branches plant⁻¹ NPP: No of pods plant⁻¹;NMP: No of mature pods plant⁻¹;100-PW : 100 Pod weight (g); SP: Shelling Per cent; 100-KW : 100 Kernel weight (g);); SMK: Sound mature kernel (%); DHY: Dry haulms yield plant⁻¹ (g); HI : Harvest index (%);KYP : Kernel yield plant⁻¹ (g);OIL: Oil content (%); PRO: Protein content (%);OA: Oleic acid (%); LLA: Linoleic acid (%); O/L: Oleic to Linoleic ratio ; PYP: Pod yield plant⁻¹ (g).

Table 2. Estimates of components of genetic variance for yield, yield attributes and quality traits in groundnut.

S. No.	Character	GCA variance	SCA variance	GCA variance/ SCA variance	σ^2A	σ^2D	$\sigma^2A: \sigma^2D$
1	Days to 50% flowering	0.062	0.245	0.254	0.249	0.981	0.254
2	Days to maturity	0.025	1.015	0.025	0.102	4.059	0.025
3	SCMR at 60 days after sowing	0.320	0.149	2.157	1.281	0.594	2.157
4	Specific leaf areaat 60 DAS (cm ² g ⁻¹)	8.933	984.584	0.009	35.732	3938.336	0.009
5	Relative water content (%)	0.185	30.980	0.006	0.739	123.921	0.006
6	Plant height (cm)	1.310	8.468	0.155	5.239	33.871	0.155
7	Number of primary branches plant ⁻¹	0.166	1.795	0.092	0.663	7.182	0.092
8	Number of secondary branches plant ⁻¹	0.023	0.636	0.036	0.091	2.544	0.036
9	Number of pods plant ⁻¹	2.419	33.039	0.073	9.677	132.155	0.073
10	Number of mature pods plant ⁻¹	1.559	26.239	0.059	6.234	101.955	0.061
11	Hundred pod weight (g)	0.022	221.296	0.000	0.088	885.183	0.000
12	Shelling per cent	-2.397	72.392	-0.033	-9.587	289.566	-0.033
13	Hundred kernel weight (g)	1.432	24.504	0.058	5.729	98.017	0.058
14	Sound mature kernel per cent	-1.442	71.911	-0.020	-5.769	287.644	-0.020
15	Dry haulms yield plant ⁻¹ (g)	1.538	1.910	0.805	6.152	7.640	0.805
16	Harvest index (%)	-0.075	-133.571	0.001	-0.299	-534.282	0.001
17	Kernel yield plant ⁻¹ (g)	-0.048	9.861	-0.005	-0.192	39.443	-0.005
18	Oil content (%)	-0.025	2.877	-0.009	-0.102	11.502	-0.009
19	Protein content (%)	0.187	0.870	0.215	0.746	27.478	0.027
20	Oleic acid content (%)	2.805	16.243	0.173	11.221	64.989	0.173
21	Linoleic content (%)	0.793	19.461	0.041	3.171	77.843	0.041
22	Oleic to linoleic Ratio	0.024	0.266	0.088	0.094	1.063	0.088
23	Pod yield plant ⁻¹ (g)	0.202	7.117	0.028	0.808	28.469	0.028

Table 3 Mean performance of nine parents and 20F₁s for yield, yield attributes and quality traits in groundnut

Table with 33 columns: LINES, DFF, DM, SCMR, SLA (cm² g⁻¹), RWC, PH (cm), NPB, NSB, NPP, NMP, 100PW (g), SP (%), 100KW (g), SMK (%), DHY (g), HI (%), KYP (g), OIL (%), PRO (%), OA (%), LLA (%), O/L, PYP (g). The table lists various groundnut lines and their performance metrics, including parent lines, F1s, and a mean of testers section.

DF : Days to 50% flowering; DM : Days to maturity; SCMR : SPAD chlorophyll meter reading at 60 DAS ; SLA : Specific leaf area at 60 DAS (cm² g⁻¹); RWC: Relative water Content(%);PH : Plant height (cm); NPB : No of Primary branches plant⁻¹; NSB : No of Secondary branches plant⁻¹ NPP: No of pods plant⁻¹;NMP: No of mature pods plant⁻¹;100-PW : 100 Pod weight (g); SP : Shelling Per cent; 100-KW : 100 Kernel weight (g); SMK: Sound mature kernel (%); DHY: Dry haulms yield plant⁻¹ (g); HI : Harvest index (%);KYP : Kernel yield plant⁻¹ (g);OIL: Oil content

Kakeeto *et al.* (2020), Gonya Nayak *et al.* (2020), Abady *et al.* (2021) and Vishnuprabha *et al.* (2021) for pod yield plant⁻¹ and kernel yield plant⁻¹; Lal *et al.* (2014) for sound mature kernel (%) and shelling per cent; Neya *et al.* (2017), Waghmode *et al.* (2017a) for days to maturity, plant height, 100 pod weight and 100 kernel weight.

Among the lines, TCGS 1694 recorded significant *gca* effects for SCMR at 60 DAS, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of pods plant⁻¹, sound mature kernel %, hundred kernel weight and linoleic acid content. The line-Kadiri-6 was a good general combiner as it exhibited desirable significant positive *gca* effects for number of pods plant⁻¹, dry haulms yield plant⁻¹, number of mature pods plant⁻¹, 100 pod weight, protein content and negative significant *gca* effects for days 50% flowering. Among the testers, TCGS-1862 exhibited positive and significant *gca* effects for SCMR at 60 DAS, relative water content, number primary branches plant⁻¹, number secondary branches plant⁻¹, number of pods plant⁻¹, number of mature pods plant⁻¹, 100 kernel weight, oleic acid content and recorded negative significant *gca* effects for days to 50% flowering and plant height. While, TCGS 2251 was the next best tester as it showed positive and negative significant *gca* effect for 100 kernel weight and days to maturity, respectively. Since high *gca* effect is attributed to additive and additive × additive type of gene action, the lines and testers with high *gca* *i.e.*, TCGS 1694, Kadiri-6, TCGS 1862 and TCGS 2251 could be used in groundnut breeding programmes for yield improvement through pedigree breeding.

Cross combinations with high mean, favourable *sca* effects and involving at least one parent with desirable *gca* effect would enhance the concentration of favourable alleles to improve target traits (Tables 3 and 4). None of the cross combinations was found desirable simultaneously for all the characters *i.e.*, different crosses expressed significant *sca* effects for different characters. However, the cross Kadiri-6 × TCGS 1862 was found to be the best specific combination as it showed highly significant *sca* effects in the desirable direction for five characters *viz.*, days to maturity, number of secondary branches plant⁻¹, number of mature pods plant⁻¹, kernel yield plant⁻¹ and protein content. Dheeraj × NRCG CS 19 was identified as next best cross combination as it exhibited significant positive *sca* effects for number of secondary branches plant⁻¹, 100 kernel weight and sound mature kernel per cent. For shelling per cent and sound mature kernel per cent, the best cross combination with significant positive *sca* effects was Kadiri-6 × TCGS 2251. Earlier John *et al.* (2016) reported significant negative *sca* effects for days to 50% flowering, days to maturity, specific leaf area and positive significant *sca* effects for relative water content, dry haulms yield plant⁻¹ and harvest index. Patil (2017) reported positive *sca* effects for 100 kernel weight, sound mature kernel (%) and dry haulm weight plant⁻¹. The hybrids with high *per se* performance and *sca* effects

for pod yield and yield related characters were earlier reported by Manivanannan *et al.* (2008). Mothilal and Ezhil (2010), Vishnuprabha *et al.* (2021), Amarnath *et al.* (2022a) and Archana *et al.* (2023). Gaurav *et al.* (2010), Gor *et al.* (2013) and Sun zi *et al.* (2021) for oil and protein content.

Most of the traits - yield and yield components are governed by non-additive gene action predominantly as SCA variance was far greater than GCA variance. Only SCMR at 60 DAS is predominantly influenced by **additive** gene action. Majority of the crosses with high *sca* effects involved poor × good, good × poor and poor × poor *gca* groups indicating the role of non-additive gene action. Hence the selection has to be postponed to later filial generations as the effects of non-additive gene action *i.e.*, dominance and epistasis would get dissipated in later generations. Biparental mating or reciprocal recurrent selection followed by single plant selection is the best breeding strategy to handle these crosses. However, in groundnut it is not feasible due to difficulties in hybridization because of its near cleistogamous flower structure. The crosses *i.e.*, Kadiri-6 × TCGS 1862 and Narayani × TCGS 2251 with high *sca* effects arising from parents with good × good *gca* values might be a result of the cumulative effect of high combining loci and no mutual annulment of gene effects between high general combining loci. Hence, these crosses can be handled through pedigree breeding and selection would be effective in early generations.

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