

# Genetic analysis for yield, nutritional and oil quality traits in RIL population of groundnut (*Arachis hypogaea* L.)

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## Abstract

**A total of 268 recombinant inbred lines (RILs) were evaluated for genetic variability for yield, nutritional and oil quality traits under two consecutive seasons at two locations. Analysis showed that variability exists in the population for the nutritional and oil quality as well as for yield component traits. Majority of the yield components and oil quality traits were governed by additive effects. The nutritional and oil quality traits were not affected by environmental factors and simple phenotypic selection ensures increased performance of the genotypes. Yield components showed moderate to high heritability but with great influence of environment.**

**Key words:** Groundnut, oleic acid, oil quality, RILs, genetic variability

## Introduction

Cultivated groundnut (*Arachis hypogaea* L.), also known as peanut is one of the most important oilseed crop of the world and has a distinct position among the oil seed crops grown in India. In addition to being a source of edible oil and food, groundnut and its products are used in variety of ways. Groundnut seeds contain 44 to 56 % oil and 22 to 30 % protein on a dry weight basis and is a rich source of minerals and vitamins. The value and utility of an oilseed crop for both nutritional and industrial purpose primarily depends upon oil quality which is determined by the fatty acid composition of the oil [1]. Groundnut with high oleic acid and linoleic acid intern high O/L ratio have long product stability with better shelf life and command a premium price as compared to those with

products of low O/L ratio when traded internationally [2].

The basic key to bring about the genetic upgrading to a crop is to utilize the available genetic variability [3]. It is imperative to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters like genetic coefficient of variation, heritability and genetic advance. Thus the present study was undertaken to estimate genetic variability and their possible implications on yield, nutritional and oil quality improvement in groundnut (*Arachis hypogaea* L.).

## Materials and methods

Recombinant inbred lines were derived from a cross, TAG 24 x GPBD 4. The TAG 24, a Spanish bunch type variety derived from TGE-2 x TGE-1 [4] and GPBD4 (D-39d), an improved Spanish bunch groundnut variety derived from KRG-1 x CS16 (ICGV-86855). The cross was generated at University of Agricultural Sciences, Dharwad [5]. GPBD4 is a second cycle product of interspecific hybridization with desirable combination of early maturity, high yield and resistance to late leaf spot (LLS) and rust. Besides, it has high oil and protein contents and better O/L ratio. The other genotype TAG 24 was contrast to GPBD4 with comparatively late in maturity, low yielding, susceptible to LLS and rust, poor in oil quality with low O/L ratio. The objective of developing recombining

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inbred lines (RIL) population was to get all the recombinants which segregate for all possible gene combinations and utilization of those in mapping molecular marker linked to LLS, rust and oil quality parameters. A single seed descent method was followed for the development of RILs. The RIL population contained 268 genotypes which were evaluated in RCBD design with two replications in rainy and post rainy seasons (2008-09) at UAS, Dharwad, Karnataka, in vertisol field and one rainy season (year 2008) at ICRISAT Hyderabad. Each genotype was sown in 2.5 m bed with spacing of 30 cm inter row and 10 cm inter plant. Blocking of experimental area was followed to reduce soil heterogeneity. All recommended package of practices were followed to raise successful crop. Data were recorded on a plot basis for days to 50% flowering (days after emergence to the stage when 50% of the plant had begun flowering), pod yield (Kg/ha), shelling percentage and 100- seed weight (g). The pods from entire plot were harvested (immature pods were removed), air dried, cleaned and weighed. The yield of five randomly selected plants was added to determine total plot yield. A 200g matured pod sample was used to estimate shelling percentage. The seeds and shells were separated and shelling percentage was computed as follows.

$$\text{Shelling per cent (\%)} = \frac{\text{Kernel weight (g)}}{\text{Pod weight (g)}} \times 100$$

A random sample was used to record 100 seed weight, protein and oil contents and fatty acid composition. The traits were measured from five individual seeds from each sample that were of same size and of similar maturity with Near Infra Red spectroscopy [6, 7] and the average of five consistent scan results were taken for analysis. Data on seven yield and yield component traits and fourteen nutritional and oil quality traits were analyzed to find out genetic component of variation using WINDOSTAT software. Genotypic and Phenotypic coefficient of variation [8], broad sense heritability based on the ratio of genotypic variation to phenotypic variation in per cent [9], and genetic advance (GA) [10] were computed as per standard procedure.

## Results and discussion

The recombinant inbred lines (RILs) recorded significant variation for all the traits studied in both rainy and post rainy seasons except for few minor fatty acids. Across the seasons also, RILs recorded

significant variation for all the other traits studied (Tables 1 and 2). From the frequency distribution of the genotype for protein (%), oil (%) and oleic acid (%) contents, it was indicated that population do contain transgressive segregants, which over performed both the parents (Fig. 1). With increased variability for the targeted traits there is a scope to isolate better genotypes for future use. Since groundnut is a tetraploid species, there is more chance of accumulating desirable gene combination in positive direction upon inter-mating and selfing of two tetraploid species. This makes high probability of getting transgressive segregants in segregating generations. Years (seasons) had no significant effect on expression of all the traits except kernel yield/plant and oil content.

Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for all the traits studied are presented in Tables 3 and 4. Low GCV, PCV and GAM were recorded with medium to high heritability for days to 50 % flowering in both the seasons and across the seasons. There was not much of variation for days to 50 % flowering between the seasons, For plant height, RILs recorded moderate GCV, high PCV and GAM but heritability estimates were low. Moderate GCV, GAM and high PCV were recorded with moderate to high heritability for number of matured pods/plant in each season. For hundred seed weight low to moderate GCV and moderate PCV coupled with high genetic advance as per cent mean and heritability were estimated. In general, RILs had low GCV, PCV, GAM and moderate heritability for shelling percentage. Heritability was low across seasons but shelling per cent was not affected much by the seasons. For kernel yield, moderate GCV and high PCV were recorded in both the seasons, whereas, low to moderate heritability with high GAM was estimated. Moderate GCV, heritability coupled with high PCV and GAM were estimated for pod yield in each season. The kernel and pod yield were affected by the season. The differences between PCV and GCV was more for yield and yield component traits in each season and across the seasons at UAS, Dharwad. This indicated the prevalence of the environmental influence on the expression of these traits.

Among the RILs there was low GCV and PCV, but high heritability, moderate GAM in each season and across the seasons were recorded for protein and oil content, oleic acid, linoleic and other minor fatty acids in in both rainy and post rainy seasons at UAS, Dharwad and ICRISAT, Hyderabad. The RILs grown

**Table 1.** Mean, range and estimates of genotypic and phenotypic coefficient of variability, heritability and genetic advance for agronomic traits in RILS population

Parameters	Location/ season	Days to 50% flowering	Plant height (cm)	No. of matured pods/plant	100 kernel weight (g)	Shelling %	Kernel yield (g/plant)	Pod yield (g/plant)
Mean	E <sub>1</sub> S <sub>1</sub>	32.31	20.75	29.35	36.93	71.69	16.00	22.27
	E <sub>1</sub> S <sub>2</sub>	33.66	20.71	17.64	45.64	74.04	14.40	19.36
	Pooled	32.98	20.73	23.49	41.29	72.86	15.20	20.81
Range	E <sub>1</sub> S <sub>1</sub>	30-35	12.75-37.0	14-45.75	26-54.5	57.5-79.75	7.4-28.80	9.6-37.93
	E <sub>1</sub> S <sub>2</sub>	29-35.5	12.75-32.5	7-31.0	29.5-66.0	52.25-83.0	7.37-23.70	10.79-29.46
	Pooled	30.25-35.5	15.87-45.37	11.25-39.12	29.5-57.5	61.5-81.12	7.63-24.71	9-33.37
GCV (%)	E <sub>1</sub> S <sub>1</sub>	2.28	16.09	11.53	11.36	3.54	17.87	17.23
	E <sub>1</sub> S <sub>2</sub>	3.70	15.49	10.44	8.75	2.19	13.41	13.15
	Pooled	3.32	11.07	26.28	12.69	3.19	14.86	239.46
PCV (%)	E <sub>1</sub> S <sub>1</sub>	5.42	29.89	24.55	14.09	6.40	32.32	31.19
	E <sub>1</sub> S <sub>2</sub>	4.76	29.57	27.94	15.38	9.20	26.39	23.47
	Pooled	5.53	29.67	36.23	18.32	8.14	30.04	247.37
h <sup>2</sup> (%) (broad Sense)	E <sub>1</sub> S <sub>1</sub>	17.80	29.00	22.10	65.00	30.50	30.60	30.50
	E <sub>1</sub> S <sub>2</sub>	60.30	27.40	14.00	32.40	25.70	25.80	31.40
	Pooled	36.10	13.90	52.60	48.00	15.30	24.50	93.70
Genetic advance (% of mean)	E <sub>1</sub> S <sub>1</sub>	2.54	22.87	14.30	24.20	5.16	26.08	25.13
	E <sub>1</sub> S <sub>2</sub>	7.59	21.42	10.31	13.14	1.38	17.98	19.46
	Pooled	5.27	10.91	50.32	23.21	3.30	19.40	611.98

E<sub>1</sub>S<sub>1</sub> – UAS, Dharwad (kharif2008); E<sub>1</sub>S<sub>2</sub> – UAS, Dharwad (summer 2008-09)

at ICRISAT recorded less differences between PCV and GCV for all traits studied indicating the reliability of phenotypic variation for the selection. This kind of discrimination between different characters from being influenced by external factors may be attributed to the difference in their genetic effects. Those RILs, which showed more difference at phenotypic and genotypic level may have more of additive effects than dominance and epistatic effects [11-13]. The difference between phenotypic coefficient of variation and genotypic coefficient of variation are minimal which indicated the less influence of environment on the expression of these nutritional and oil quality traits. Variations do exist in the given population as it is indicated in Table 3, which depicts the mean and range for nutritional and oil quality traits. Protein content ranged from 21.40-32.81 %, whereas the range for oil content was 37.07-54.85% in the population. Also a wide range was observed for oleic acid (38.13-57.84%) and linoleic acid (24.11-38.2 %) content. Similarly, for other traits, a wide range of variations was observed as compared to parents. This gives a scope to isolate the genotype for better protein, oil content and oleic acid content as range for these traits are larger than the others but across the seasons their mean and range are not showing significant difference. Hence, it supports the fact that traits under investigations are not affected much by environment and whatever the variability exist in the population are mostly due to genetic constitution of the plant.

Since the genotypes consisted recombinant inbred lines advanced to F<sub>11</sub> generation, the population were expected to be homozygous. Thus, for the prediction of response to selection, it is apt to use broad sense heritability because the entire genotypic value is transmitted to the progeny when any selection is advanced through selfing. The results of genetic advance hold well as long as selection is practiced between the lines. The results of present study suggested that except days to 50 % flowering in rainy season and number of pods/plant in post rainy season,

**Table 2.** Genotypic and phenotypic coefficient of variability, heritability and genetic advance for quality traits in RILs

Sources	Location/ season	Protein (%)	Oil (%)	Palmitic acid (%)	Stearic acid (%)	Oleic acid (%)	Linoleic acid (%)	Arachidic acid (%)	Eicosenoic acid (%)	Behenic acid (%)	Lignoceric acid (%)	O/L ratio
GCV (%)	E <sub>1</sub> S <sub>1</sub>	6.72	3.87	3.70	10.50	5.61	6.77	9.34	4.86	5.24	5.90	12.46
	E <sub>1</sub> S <sub>2</sub>	5.31	2.48	1.35	2.54	5.76	6.77	2.44	2.36	1.83	3.02	12.36
	Pooled	5.17	2.45	2.36	6.76	3.75	4.23	9.07	2.23	3.32	3.88	7.73
PCV (%)	E <sub>2</sub> S <sub>1</sub>	8.26	6.24	4.42	5.07	7.89	8.67	5.40	5.09	4.52	5.34	14.97
	E <sub>1</sub> S <sub>1</sub>	7.31	4.25	3.89	11.01	5.83	7.06	9.63	5.14	5.43	6.19	12.92
	E <sub>1</sub> S <sub>2</sub>	6.37	4.33	3.67	7.72	6.13	7.26	6.08	4.57	4.32	5.20	12.95
h <sup>2</sup> (%) (broad Sense)	Pooled	5.99	3.33	3.22	8.35	4.52	5.25	11.26	3.46	4.08	5.38	9.48
	E <sub>2</sub> S <sub>1</sub>	9.16	6.63	6.01	10.28	7.93	8.74	7.15	6.69	6.20	7.09	15.04
	E <sub>1</sub> S <sub>1</sub>	85.00	83.00	91.00	91.00	93.00	92.00	94.00	90.00	93.00	91.00	93.00
Genetic advance (% of mean)	E <sub>1</sub> S <sub>2</sub>	69.00	33.00	73.00	71.00	88.00	87.00	76.00	67.00	78.00	84.00	91.00
	Pooled	75.00	54.0	54.00	66.00	69.00	65.00	65.00	42.00	66.00	52.00	66.00
	E <sub>2</sub> S <sub>1</sub>	81.00	89.00	54.00	24.00	99.00	98.00	57.00	58.00	53.00	57.00	99.00
Genetic advance (% of mean)	E <sub>1</sub> S <sub>1</sub>	16.32	9.33	9.31	26.46	14.29	17.12	23.93	12.14	13.34	14.84	31.73
	E <sub>1</sub> S <sub>2</sub>	11.66	3.75	1.30	2.20	14.27	16.66	2.59	3.22	2.05	4.64	31.15
	Pooled	11.79	4.76	4.56	14.43	8.19	8.99	19.31	3.79	7.13	7.37	16.62
Genetic advance (% of mean)	E <sub>2</sub> S <sub>1</sub>	19.66	15.49	8.58	6.61	20.73	22.68	10.79	10.22	8.68	10.62	39.36

E<sub>1</sub>S<sub>1</sub> – UAS, Dhanwad (rainy2008); E<sub>2</sub>S<sub>1</sub> – ICRISAT, Hyderabad (rainy2008); E<sub>1</sub>S<sub>2</sub> – UAS, Dhanwad (post rainy 2008-09)

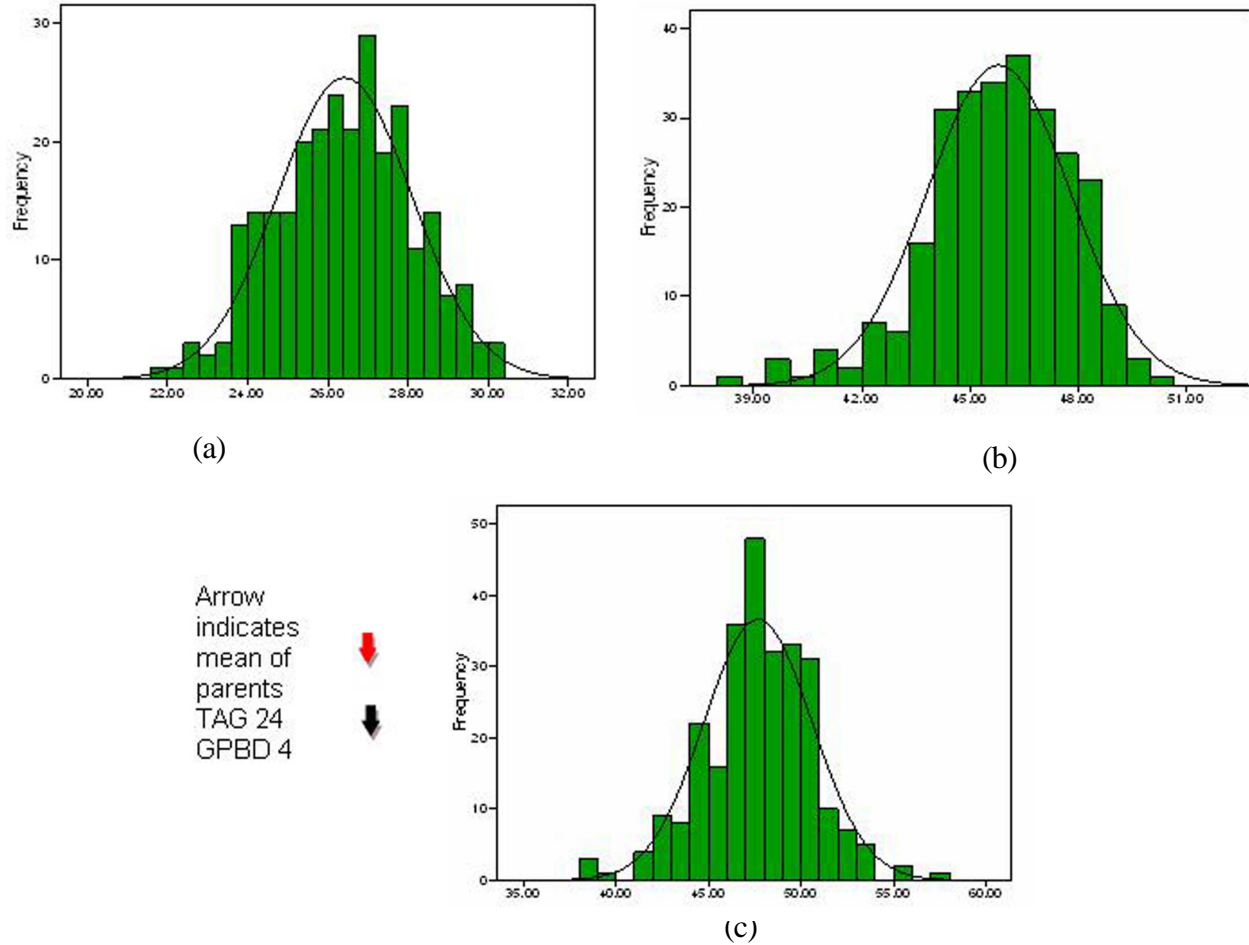
all the characters studied had moderate to high heritability. Whereas, nutritional quality traits recorded high heritability. The estimates of genetic advance over mean suggested that real progress could be made for plant height, 100 kernel yield, kernel yield/plant, pod yield/plant, protein content, oleic acid content, linoleic acid content, stearic acid, arachidic acid content and O/L ratio. This also indicated that these traits are mainly under the control of additive components of genetic variation. The traits like days to 50 % flowering, shelling percentage, oil content, palmitic acid content had profound influence of non-additive effects.

High heritability need not be necessarily associated with high genetic advance [14]. If heritability is mainly due to non additive effects (dominance and epistasis), the genetic advance will be low, whereas, if the heritability is due to additive effects it would be associated with high genetic advance [15]. Hence, it could be inferred that both the morphological as well as quality traits in groundnut are predominantly under the control of additive component of genetic variation [16-18]. Genotype with high heritability and high genetic advance in percentage of mean could be further improved through individual plant selection [19].

Nutritional and oil quality traits correlated negatively with yield component traits. Even within the nutritional traits, oleic acid negatively associated with linoleic acid, oil and protein contents. Protein content and oil content was negatively associated with

**Table 3.** Mean and range for nutritional and oil quality traits in RILs

Traits	Parental means		RILs	
	TAG 24	GPBD 4	Mean	Range
Protein (%)	25.88	28.73	26.35	21.40-32.81
Oil (%)	44.33	48.29	45.80	37.07-54.85
Palmitic acid (%)	10.85	9.99	10.31	9.23-11.53
Stearic acid (%)	2.96	2.43	2.99	2.09-3.66
Oleic acid (%)	45.04	51.24	47.23	38.13-57.84
Linoleic acid (%)	36.37	30.21	31.81	24.11-38.2
Arachidic acid (%)	1.31	1.35	1.36	0.87-1.55
Eicosenoic acid (%)	0.99	1.16	1.04	0.91-1.19
Behenic acid (%)	3.85	3.86	3.71	3.10-4.18
Lignoceric acid (%)	1.27	1.52	1.34	1.03-1.63
O/L ratio	1.24	1.70	1.50	1.11-2.35



**Fig. 1.** Frequency distribution of (a) protein content (%), (b) oil content (%) and (c) oleic acid content in the RIL population

**Table 4.** Genotypes with better nutritional quality traits and high pod yield/plant

Oleic acid (%)		Linoleic acid (%)		Protein (%)		Oil (%)		Pod yield (g/plant)	
RILs No.	Mean	RILs No.	Mean	RILs No.	Mean	RILs No.	Mean	RILs No.	Mean
252	54.12	73	25.65	185	30.33	33	48.53	132	446.50
193	53.81	252	27.71	90	30.51	140	48.59	68	448.00
191	52.88	123	27.76	267	30.55	74	48.60	268	448.00
166	52.81	187	27.85	62	30.58	57	48.71	85	454.75
31	52.37	193	27.88	85	30.66	219	48.72	177	455.75
234	52.22	234	28.32	86	30.90	81	48.77	88	466.25
158	51.8	95	28.37	25	30.90	174	48.98	197	466.25
187	51.7	3	28.65	28	31.03	185	49.23	243	467.75
136	51.6	2	28.82	102	31.09	267	49.62	110	479.25
146	51.49	145	28.86	81	31.31	168	49.96	201	491.25
GPBD4	51.24	GPBD4	30.21	GPBD4	29.09	GPBD4	48.28	GPBD4	508.00
TAG24	45.04	TAG24	36.37	TAG24	25.90	TAG24	44.39	TAG24	202.50
47.23		31.81		27.02		45.67		336.36	



each other (Data not shown). Hence, isolating genotype with all desirable traits like, increased oleic acid content, protein content with high pod yielding genotype is difficult. Therefore, from the RILs population selection of genotypes were independently done for oleic acid, linoleic acid, oil content, protein content and pod yield. Top ten best genotypes were selected for each above said traits (Table 4). For oleic acid RIL No. 252 ranked first having 54.12% oleic acid and 27.71% linoleic acid accumulating 19% more oleic acid in comparison with population mean, but this genotype didn't show high oil, protein and pod yield. The RILs No. 28, 81 and 102 recorded high protein (7.31%), oil (>49 %) and pod yield (446.50 g/plant). The one genotype, RILs No. 267 showed high protein (30.55%) as well as oil content (49.62%) among 10 selected genotypes. But no other genotypes had combinations of two or more desirable traits. Hence selected genotypes can be utilized as donor for different desired traits based on the objectives in groundnut improvement program.

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