

Research Note

Studies on genetic variability for important traits in F₂ generations of groundnut (*Arachis hypogaea* L.)

C. K. Patel, J. H. Vachhani, V. H. Kachadia and R. K. Jalu

Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh-36200, Gujarat

E-Mail: chiragp762@gmail.com

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Abstract

Six crosses of F₂ population and nine parental lines were evaluated for variability, heritability and genetic advance during summer, 2016. Observations on nine characters recorded. Analysis of variance revealed highly significant differences among the genotypes, parents as well as crosses for all the characters thereby indicating sufficient variability in the material studied. The range of variation was maximum for plant height, number of matured pods per plant, shelling outturn, kernel yield per plant and pod yield per plant in most of the crosses. Moderate to high values of GCV and PCV observed for most of the character except for days to appearance of flower and days to maturity in most of the crosses. Moderate to high heritability estimates were found for most of the characters. The expression of moderate to high heritability coupled with moderate to high genetic advance and moderate to high values of GCV and PCV for pod yield per plant for above characters indicating that F₂ generation as mainly under the influence of additive gene action and scope for improvement through simple selection.

Key words

Variability, Genetic coefficient of variation

Groundnut (*Arachis hypogaea* L.) is a highly self-pollinated crop and can be grown successfully in tropical and subtropical areas. The crop has a narrow genetic base therefore, it is essential to create more variability in the segregating materials. The F₂ generation in which segregation and recombination are of maximum, which makes this generation ideal for imposing selection. The knowledge of nature and magnitude of genetic variability is of great importance to a breeder for planning efficient breeding programme and selecting desirable segregants. Hence, an attempt was made to study the genotypic variability and direct selections for important traits in the segregating materials of groundnut.

Cultivated groundnut is a self-pollinated, auto tetraploid legume crop with $2n=4x=40$ chromosomes and belong to the family *Fabaceae*. Botanically, cultivated groundnut can be classified into two sub-species, which mainly differed in their branching pattern. Each sub-species is again divided into two botanical varieties, sub-species *hypogaea* into var. *hypogaea* (Virginia) and var. *hirsuta* as well as sub-species *fastigiata* into var. *fastigiata* (Valencia) and var. *vulgaris* (Spanish).

Groundnut is a rich source of edible oil (47-54%), high quality protein (22-30%), starch (6-24%),

cellulose (1-2 %), minerals (2-3 %) and calories (5-6%). It has a distinct position among the oilseeds, as it can be consumed and utilized in diverse ways. India is the largest producer of groundnut. Despite of this fact, it is facing a serious shortage at present in the indigenous supply of vegetable oils. Oil is the component of yield available from groundnut. As indicated above the main use of groundnut is for oil extracting hence, the object of increasing in oil yield. To make the nation self-sufficient in vegetable oil, the oil content in groundnut should be brought to a higher level than the existing one.

The experimental material consisted of F₂ generation of six crosses derived from crossing among eleven parents. Six F₂ populations and eleven parental lines were sown during summer, 2016 at the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh, in Randomized Block Design with three replications. Each F₂ generation was planted in 3 rows of 5 m length and parents were planted in a single row of the same length at the spacing of 60 cm between rows and 15 cm between the plants. Observations on nine characters (Table 1) were recorded on randomly selected five plants from each parent and eighty plants from each F₂ generation per replication. The data subjected to different statistical analysis *viz.*, analysis of variance, the magnitude of genetic variability, the

phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability and genetic advance were performed following the standard procedures.

Analysis of variance revealed highly significant differences among the genotypes, parents as well as crosses for all the characters thereby indicating sufficient variability in the material studied. Mean squares due to parents vs crosses were also highly significant for all the characters indicating the significant deviation of F₂ populations from the parents (Table 1). Similar findings were recorded by Jayalakshmi *et al.* (2001), John *et al.* (2007), Khote *et al.* (2009), Ladole *et al.* (2009) and Ramana *et al.* (2015). The mean, range, GCV, PCV, heritability and genetic advance as a percentage of the mean for different characters in six crosses of F₂ generation are given in Table 2. The range of variation was maximum for plant height, number of matured pods per plant, shelling outturn, kernel yield per plant and pod yield per plant in most of the crosses indicated a better scope for selection and improvement of these characters. John *et al.* (2007) and Ladole *et al.* (2009) also reported similar results. The estimates of GCV were quite close to the PCV for the characters *viz.*, days to appearance of first flower and days to maturity indicating the least influence of environmental variation. This suggested that phenotypic variation can be used reliably to judge genetic variation. Moderate to high values of GCV and PCV were obtained for all the character except for days to appearance of first flower and days to maturity in most of the crosses indicating that these characters were under influence of genetic control. Hence, simple selection can be practised for further improvement. These results are in agreement with the earlier findings of Kadam *et al.* (2007) and Khote *et al.* (2009). They reported high GCV and PCV for number of pods per plant, kernel yield per plant and pod yield per plant. High GCV and PCV for plant height and number of pods per plant were observed by Ladole *et al.* (2009). However, high variance values alone were not the determining factors of the expected progress that could be made in respect of quantitative traits (Falconer, 1981). It was suggested that the GCV together with the high heritability estimates would give a better picture of the extent of genetic gain to be expected under selection. Genetic advance expressed as a percentage of the mean was high for number of primary branches per plant, number matured pods per plant, number immature pods per plant, kernel yield per

plant and pod yield per plant. High value of genetic advance is helpful in identifying the appropriate character for selection and enabling the breeder to apply selection pressure. Khote *et al.* (2009) observed high heritability for days to flowering and Ladole *et al.* (2009) for plant height. Genetic advance expressed as a percentage of the mean was high for number of primary branches per plant, number matured pods per plant, number immature pods per plant, kernel yield per plant and pod yield per plant. These results are in conformity with the findings of Khote *et al.* (2009).

Thus, from the present investigation, it can be concluded that these crosses were mainly under the influence of additive gene action and improvement of these traits would be possible through individual plant selection in the subsequent generations to isolate high yielding genotypes with desirable characteristics.

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Table 1. Analysis of variance showing mean square for nine characters in parents and F₂ generation of six groundnut crosses

Sources	d. f.	Days to appearance of first flowering	Days to maturity	No. of primary branches/Plant	Plant height (cm)	No. of matured pods/plant	No. of immature pods/plant	Kernel yield/plant (g)	Shelling outturn (%)	Pod yield/plant (g)
Replications	2	32.05	2.85	0.21	12.95	1.34	0.04	2.68	11.94	2.77
Genotypes	17	43.82**	9.66**	0.67**	57.32**	17.28**	1.32**	6.85**	45.51**	6.68**
Parents	11	34.79**	2.56**	0.80**	13.00**	20.93**	2.36**	5.64**	59.25**	7.55**
Crosses	5	49.81**	13.45**	0.57**	82.66**	13.95**	0.89**	7.29**	14.99**	6.16**
Parents vs Crosses	1	23.11**	3.40**	1.05**	0.16**	35.59**	0.85**	7.98**	37.24**	8.01**
Error	34	4.86	0.53	0.18	3.81	2.64	0.15	0.88	4.20	0.57

*, ** Significant at p=0.05 and 0.01 levels, respectively

Table 2. Mean, range, genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense heritability (h^2) and genetic advance (GA as % of mean) for different characters in six crosses of F_2 generation of groundnut

Cross	Mean	Range	GCV (%)	PCV (%)	h^2 (%)	GA % of Mean
Days to appearance of first flowering						
Cross 1	50.25	42.67-55.33	4.68	6.60	50.30	6.84
Cross 2	51.18	42.00-56.33	5.15	7.37	48.80	7.41
Cross 3	52.05	43.67-56.67	4.94	7.08	48.64	7.09
Cross 4	52.18	42.67-56.00	5.34	7.42	51.95	7.94
Cross 5	51.27	44.33-55.33	4.62	6.92	44.56	6.35
Cross 6	50.23	43.00-54.00	4.67	7.03	44.22	6.40
Days to maturity						
Cross 1	110.13	105.00-114.67	2.06	2.85	52.44	3.08
Cross 2	109.93	104.33-114.67	2.11	3.03	48.53	3.03
Cross 3	110.58	106.67-114.67	2.11	2.94	51.58	3.12
Cross 4	110.55	105.67-115.00	2.15	3.03	50.43	3.14
Cross 5	112.70	106.00-114.67	2.00	3.07	42.76	2.70
Cross 6	110.06	105.33-115.67	2.06	2.93	49.39	2.98
No. of primary branches/plant						
Cross 1	3.71	1.67-5.00	20.33	28.82	49.76	29.54
Cross 2	3.38	1.33-5.67	18.86	29.73	40.24	24.65
Cross 3	4.02	2.00-5.67	19.75	28.50	48.04	28.20
Cross 4	3.94	1.67-5.67	21.08	31.08	45.99	29.45
Cross 5	3.60	1.67-5.00	20.22	30.57	43.76	27.56
Cross 6	4.01	2.33-5.33	15.32	23.32	43.17	20.73
Plant height (cm)						
Cross 1	14.90	10.67-21.00	13.40	18.76	51.00	19.71
Cross 2	16.19	12.33-23.33	14.50	21.60	45.06	20.05
Cross 3	15.65	10.67-23.33	18.32	24.79	54.61	27.88
Cross 4	19.60	12.67-29.33	17.10	25.59	44.68	23.55
Cross 5	17.78	11.00-30.00	17.88	27.27	43.02	24.16
Cross 6	17.60	12.00-25.67	17.03	25.22	45.59	23.69
No. of matured pods/ plant						
Cross 1	7.75	3.00-19.67	39.96	56.02	50.89	58.73
Cross 2	8.97	4.00-25.33	42.05	58.65	51.41	62.11
Cross 3	11.62	4.67-26.33	39.11	57.50	46.27	54.81
Cross 4	7.85	2.33-28.00	44.79	66.57	45.28	62.09
Cross 5	5.92	2.00-13.00	39.86	58.27	46.78	56.16
Cross 6	9.14	3.67-25.33	42.51	62.65	46.05	59.42
No. of immature pods/ plant						
Cross 1	4.23	1.67-7.00	24.70	37.21	44.09	33.79
Cross 2	3.52	1.67-5.67	26.20	37.78	48.11	37.44
Cross 3	4.12	1.33-6.67	27.78	43.11	41.53	36.88
Cross 4	3.92	2.00-7.67	24.80	39.09	40.25	32.41
Cross 5	4.06	2.33-7.33	27.27	40.57	45.18	37.76
Cross 6	3.99	2.00-6.00	26.10	39.70	43.22	35.35

(Contd.)



Table 2. (Contd.)

Cross	Mean	Range	GCV (%)	PCV (%)	h ² (%)	GA % of Mean
Kernel yield/plant (g)						
Cross 1	5.62	1.00-21.00	48.47	70.78	46.89	68.37
Cross 2	3.90	1.33-9.67	44.85	62.18	52.03	66.65
Cross 3	7.20	1.67-16.00	47.49	65.08	53.24	71.38
Cross 4	5.38	1.33-23.33	59.70	88.16	45.86	83.29
Cross 5	5.14	1.67-16.33	44.97	66.83	45.28	62.34
Cross 6	5.41	1.33-22.33	70.37	88.89	62.67	90.26
Shelling outturn (%)						
Cross 1	68.05	38.89-89.19	12.50	18.92	43.67	17.03
Cross 2	70.25	51.67-85.46	11.52	15.61	54.47	17.52
Cross 3	74.35	51.67-93.04	11.68	17.28	45.69	16.27
Cross 4	71.32	51.67-92.56	11.55	17.14	45.37	16.02
Cross 5	71.98	46.11-91.78	11.81	17.87	43.68	16.08
Cross 6	70.46	51.67-92.00	11.89	18.09	43.23	16.11
Pod yield/plant (g)						
Cross 1	7.42	1.67-18.33	12.50	18.92	43.67	17.03
Cross 2	5.87	2.33-14.67	11.52	15.61	54.47	17.52
Cross 3	8.70	3.00-18.00	11.68	17.28	45.69	16.27
Cross 4	6.99	2.33-24.67	11.55	17.14	45.37	16.02
Cross 5	6.86	3.33-15.00	11.81	17.87	43.68	16.08
Cross 6	6.88	2.33-23.33	11.89	18.09	43.23	16.11

Cross 1 = NRCG - C5 - 253 x TPG - 41

Cross 2 = TG - 71 x SB - XI

Cross 3 = TG - 26 x GJG - 22

Cross 4 = JB - 1296 x RG - 425

Cross 5 = GJG - 9 x JUN - 27

Cross 6 = CTMG - 9 x GJG - 22