

Original Research Article

GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR YIELD AND RELATED ATTRIBUTES IN GROUNDNUT (*Arachis hypogaea* L.)

ABSTRACT

The present study was designed to assess the extent of variability, genetic advance, heritability and correlation of different traits of 20 groundnut genotypes using randomized block design with three replications. The observations were recorded on five randomly selected plants from each treatment and replication for 15 different quantitative traits. Based on the mean performance, high pod yield per plant were identified for the genotype SC-28, VG-17 (CHECK). High estimates of GCV and PCV were recorded for number of branches per plant followed by days to germination, number of pegs per plant, plant height. Genetic parameters revealed that heritability and genetic advance as % mean values are high were recorded for number of pegs per plant followed by plant height, biological yield per plant, 100 kernel weight. Correlation coefficient analysis revealed that pod yield per plant exhibited positive and significant association with number of branches and days to germination at genotypic and phenotypic levels. Path coefficient analysis revealed that character's harvest index, biological yield per plant, number of branches per plant, number of pods per plant, kernel yield per plant have positive direct effect on pod yield per plant at genotypic and phenotypic levels.

Keywords: Variability, Genetic advance, Heritability, correlation, coefficient, GCV, PCV, Path coefficient.

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the most important legume crops of the world which is native to Brazil in the South American leguminous oilseed (Hammons 1982). Groundnut (*Arachis hypogaea* L.) is a vital oil seed crop. It is an annual, herbaceous, and self-pollinated legume that is classified under the sub-family Papilionaceae and family Fabaceae.

Groundnut covers 31.3% of the total cropped area under oilseeds and accounts for 36.1% of the overall oilseed production in the world. The maximum share of groundnut production is contributed by China, India and USA. According to latest available data (2016-17), groundnut cultivation occupies ~27.6 million ha in the world, with an annual production of 43.9 million tons (with shell). The average worldwide yield is 1590 kg/ha (with shell) Food and Agriculture Organization Corporate Statistical Database (**FAOSTAT**).

Genetic variability is important indices for plant breeders because it provides a source of variation as well as raw material for yield enhancement (Gaur *et al.*, 2020; Verma *et al.*, 2018). The selection of yield contributing characters is important for crop improvement and the selection of such characters depends mainly on heritable variation as well as the heritability of the trait concerned.

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For improvement of yield in groundnut direct selection is often misleading. The knowledge of existing variability and degree of association between yield contributing characters and their relative contribution in yield is essential for developing high yielding genotypes in groundnut. The observed variability is a combined measure of genetic and environmental causes (Patel *et al.* 2009). The genetic variability is heritable from generation to generation. Heritability and genetic advance is a useful tool for breeders in determining the direction and magnitude of selection. Correlation studies provide an opportunity to study the magnitude and direction of association of

yield with its components and also among various components. Path coefficient is essential to accumulate optimum combination of yield contributing characters and to know the implication of the interrelationships of various characters in a single genotype. Considering the above points, the present study was undertaken to evaluate the genotypes for yield and its components and to estimate the inter-relationship among the agronomic traits in groundnut. The present investigation has been made with the following objectives:-

1. To estimate genetic parameters for genetic variability in groundnut crop.
2. To study the correlation in groundnut germplasm to obtain high yield.
3. To study direct and indirect effect of yield contributing character on seed yield.

2. MATERIALS AND METHODS

2.1. Description of study area

The experiment was conducted during *Kharif* season of 2022. The experiment was conducted using Randomized Block Design consisting of 15 treatments with three replication in field condition at the department of Genetics & Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh. Prayagraj is located in the south eastern part of Uttar Pradesh, India. This region has subtropical Climate with extreme of summer and winter. The temperature falls to as low as 2-3⁰c during winter season especially in the month of December and January.

2.2 Experimental design and treatment details

Experimental material, for the present study consists of groundnut, 20 genotypes was received from Department of genetics and Plant Breeding, SHUATS, during Kharif-2022 and experiment will be carried out in Randomized block design with 3 replications was conducted at the Experimental Farm of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh during *Kharif, 2022*.

Table 1. List of genotypes used for the study

SL.NO	GENOTYPES	SL.NO	GENOTYPES
1	FSICC-37AxCS-319	11	SC-28
2	NRCG-12177	12	TMV-10
3	LGN-184	13	RG-614
4	LGN-01	14	ICGV-7247
5	JL-1186	15	TG-37A
6	NRCG-1374	16	AVK-4
7	ICGV-98170	17	IVK-2013-23
8	JL-27	18	RG-562
9	NARAYANI	19	GG-21
10	RG-638	20	VG-17(CHECK)

RESULTS AND DISCUSSION

Analysis of variance shows that every treatment is differ from each other so genetic variability exists. 1% level of significance is highest Number of Branches per plant (144.12**) and lowest for Pod yield per plant (2.15**).

Table 2. Analysis of Variance of 20 genotype for 15 characters

Sl.No	Source	Mean Sum of Squares (MSS)		
		Replication	Treatment	Error
	Degrees of freedom	2	19	38
1	Days to Germination	0.1920	2.15**	0.096
2	Days to initial flowering	0.3640	5.56**	0.677
3	Days to 50% flowering	1.4010	16.559**	2.048
4	Plant height (cm)	2.8750	77.101**	5.811
5	Number of Branches per plant	0.790	10.792**	0.396
6	Number of pegs per plant	25.5860	144.12**	10.551
7	Number of pods per plant	8.3690	27.768**	4.202
8	100 pod weight	31.0430	37.705**	15.567
9	Kernel yield per plant	5.3860	7.993**	2.698
10	100 kernel weight	25.5170	46.635**	8.254
11	Shelling (%)	8.7550	10.537**	4.351
12	Sound Mature Kernels (%)	5.2170	27.67*	12.146
13	Harvest Index (%)	30.2310	36.492*	15.117
14	Biological yield per plant	4.0370	70.17**	12.253
15	Pod yield per plant	10.3780	16.546**	5.16

*** 5% Level of Significance**

**** 1% Level of Significance**

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Table 3. Mean table of 20 genotype for 15 characters

Sl. No	Variety Name	Days to Germination	Days to initial flowering	Days to 50% flowering	Plant height (cm)	Number of Branches per plant	Number of pegs per plant	Number of pods per plant	100 pod weight	Kernel yield per plant	100 kernel weight	Shelling (%)	Sound Mature Kernels (%)	Harvest Index (%)	Biological yield per plant	Pod yield per plant
1	FSICC-37AxCS-319	5.6	14.133	24.667	39.6	6.4	43.333	23.6	78.997	21.27	44	71	70.667	43.327	39.81	30.4
2	LGN-184	5.467	15.667	25.997	39.6	9.133	53.533	23.8	83	22.997	40	68.333	65	45.317	40.66	33.4
3	LGN-01	5.533	14.4	24.667	40.933	9.867	54.797	30.133	81.663	22.27	41	71.667	65.667	48.433	34.71	32.733
4	JL-1186	5.667	14.53	25.667	40.737	11.4	60.933	28.267	78.667	19.333	40	67.67	67.333	46.097	41.42	34.933
5	NRCG-1374	4.547	14.467	24.667	49.267	8.2	61.397	26.6	81.333	22.067	39.667	70.67	65.667	48.19	34.383	32
6	ICGV-98170	5.13	14.6	26.333	54.933	10.533	57.863	27.267	79.333	20.663	40.333	67.333	69	43.78	40.913	31.667
7	JL-27	5	14.667	24.333	52.133	8	63.93	28.4	78.333	22.933	40.333	70.333	71.333	47.18	36.457	32.867
8	NARAYANI	6.467	16.267	26.997	43.133	11.267	64.133	27.133	89.667	20.867	45.333	67	67.667	38.983	48.053	30.67
9	RG-638	4.533	15.133	25.333	38.933	9.003	45.403	23.333	79.337	21.733	39	65.333	64.333	45.297	40.297	33.6
10	SC-28	5.6	14.93	24.333	43.53	5.733	54.067	33.597	78.667	25.2	43	69.337	67	43.503	49.247	37.933
11	TMV-10	5.6	16.067	27.67	43.6	8.2	66.867	27.933	78.997	21.867	44	71.667	70.333	43.707	40.257	31.137
12	RG-614	6.6	18	30.333	45.4	10.667	53.063	27	84	19.463	36.667	67.333	68.667	38.233	46.73	28.867
13	ICGV-7247	6.733	17.667	29.667	49.933	11	61.4	28.67	78.333	20.67	42	70	69.667	38.93	47.21	30.333
14	TG-37A	4.467	14.8	25.667	52.333	6.8	55	33.733	80.333	24.663	44.333	70.67	70.667	42.37	47.82	35.47
15	AVK-4	5.333	18.2	30.997	51.267	10.667	66.333	33.533	82	19.867	40	68.67	73.667	42.883	46.857	35.2
16	IVK-2013-23	5.597	15.067	25.333	43.93	7.397	55.403	28.003	77.667	19.867	47.333	67.333	72.667	36.957	49.32	29.533
17	RG-562	7.4	17.733	30.667	42.467	10.667	63.197	30.533	85.003	22.13	50	69.667	74	42.883	42.973	32.2
18	GG-21	5.533	15.6	28.333	39.4	6.13	66.6	29.8	85	21	40.333	69	74	39.42	47.643	31.337
19	NRCG-12177	7.4	17.6	30.667	40	11.6	50.067	30.797	89.333	22.867	52.667	72	66.667	43.43	41.693	32.467
20	VG-17 (CHECK)	5.937	16.263	27.667	43.2	8.933	64.067	29.4	79.667	23.6	45.333	67.333	67.333	48.75	37.967	36.067

Mean	5.71	15.79	27	44.72	9.08	58.07	28.58	81.47	21.77	42.77	69.12	69.07	43.38	42.72	32.64
CV	5.43	5.21	5.3	5.39	6.93	5.59	7.17	4.84	7.55	6.72	3.02	5.05	8.96	8.19	6.96
SEm	0.18	0.47	0.83	1.39	0.36	1.88	1.18	2.28	0.95	1.66	1.2	2.01	2.24	2.02	1.31
CD at 5%	0.51	1.36	2.37	3.98	1.04	5.37	3.39	6.52	2.71	4.75	3.45	5.76	6.43	5.79	3.75
Minimum	4.47	14.13	24.33	38.93	5.73	43.33	23.33	77.67	19.33	36.67	65.33	64.33	36.96	34.38	28.87
Maximum	7.4	18.2	31	54.93	11.6	66.87	33.73	89.67	25.2	52.67	72	74	48.75	49.32	37.93

Table 4. Estimates of PCV, GCV, Heritability, and Genetic Advance & Genetic Advance as percent of mean for 15 characters

Sl.No.	Parameters	GCV	PCV	h ² (Broad Sense) %	Genetic Advancement 5%	Gen. Adv as % of Mean 5%
1	Days to Germination	14.497	15.479	87.713	1.596	27.97
2	Days to initial flowering	8.08	9.614	70.639	2.209	13.99
3	Days to 50% flowering	8.146	9.718	70.251	3.797	14.064
4	Plant height (cm)	10.901	12.162	80.35	9.001	20.13
5	Number of Branches per plant	20.502	21.64	89.755	3.633	40.012
6	Number of pegs per plant	11.491	12.78	80.843	12.359	21.283
7	Number of pods per plant	9.808	12.151	65.148	4.66	16.307
8	100 pod weight	3.334	5.88	32.159	3.173	3.895
9	Kernel yield per plant	6.104	9.705	39.55	1.721	7.907
10	100 kernel weight	8.364	10.727	60.786	5.745	13.433
11	Shelling (%)	2.078	3.664	32.155	1.677	2.427
12	Sound Mature Kernels (%)	3.294	6.026	29.874	2.561	3.708
13	Harvest Index (%)	6.153	10.871	32.035	3.112	7.174
14	Biological yield per plant	10.285	13.15	61.175	7.079	16.571
15	Pod yield per plant	5.968	9.168	42.379	2.613	8.004

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Experimental Findings & Discussion

The analysis of variance for all characters revealed highly significant difference among all fifteen genotype for all the characters Pod yield, Shelling percentage, Kernel yield, Days to Maturity, 100 Kernel weight, Sound mature Kernel percentage and oil percentage, indicating the existence of considerable genetic variation among the genotypes (Table 1).

Days to Germination the Genotype TG- 37A exhibited significantly least days (4.47) followed by NRCG-1374 (4.55) while significantly highest days (7.40) were shown by genotype that NRCG-12177. The variation in days to initial flowering ranged between 14.13 to 18.20. Genotype FSICC- 37AxCS-319 (14.13) exhibited significantly least days followed by LGN-01 (14.40), NRCG-1374 (14.47) while significantly highest days AVK-4 (18.20). days to 50% flowering the Genotype JL- 27 and SC-28 exhibited significantly least number of days (24.33) followed by FSICC- 37AxCS-319, NRCG-1374 (24.67). The genotypes ICGV-98170 (54.93), TG-37A (52.33), JL- 27 (52.13) were the longest plant height. The results are the agreement with Sarvamangla (2009), John et al. (2011), Thakur et al. (2011), Vishnuvardhan et al. (2012) and Mahalakshmi et al. (2018) in groundnut.

The genotypes TG-37A (33.73), AVK-4 (33.53) were recorded highest number of pods per plant. The genotypes SC- 28 (25.20), TG-37A (24.66), VG-17 (CHECK) (23.60) were recorded highest kernel yield compared to the other genotypes. The genotypes RG-614 (36.67), RG-638 (39.00), NRCG-1374 (39.67) recorded 100 kernel weight compared to other genotypes.

The genotypes NRCG-12177 (72.00), TMV-10 (71.67), FSICC- 37AxCS-319 (71.00) were recorded higher shelling %. The genotypes RG-562, GG-21 (74.00), AVK-4 (73.67), IVK-2013-23 (72.67) were recorded higher sound mature kernel %. The genotypes UDAY (check) (54.6), ICC-13348 (52.15), ILC-59468 (50.3), ICC-20-08 (50.51), were recorded highest grain yield compared to the other genotypes. Similar findings reported by Vishnuvardhan et al. (2012) and Gupta et al. (2015)

The genotypes SC-28, VG-17 (CHECK) were recorded higher pod yield per plant were found significantly superior over check and the genotypes IPC-08-69 (57.6), ICC-13348 (45.333), GNG-469 (42.733) were recorded higher biological yield per plant. Similar results were obtained by Kumar and Rajamani (2004), Ravi Kumar (2005), John et al. (2007), Rout et al. (2010), Rao et al. (2012), Zaman et al. (2011) and Mahalakshmi et al. (2018).

The component of variance revealed that the phenotypic coefficient of variance were higher than the genotypic coefficient of variance for all the character studied indicating the role of environmental variance in the total variance. The magnitude of PCV and GCV was high for the characters number of branches per plant followed by days to germination, number of pegs per plant, biological yield per plant, number of pods per plant. Similar findings were reported by Zaman *et al.* (2011), John *et al.* (2007). In the present investigation it is depicted that in general, estimates of phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the influence of environment on the expression of these characters.

High heritability along with high genetic advance percent was observed for the character Highest heritability in genetic parameters ranged number of branches per plant followed by days to germination, number of pegs per plant, plant height, days to initial flowering, days to 50% flowering, number of pods per plant, biological yield per plant. The same trend was also observed by Zaman *et al.* (2011), John *et al.* (2007) and Narsimula *et al.* (2012). High heritability with high genetic advance and high genetic advance in percentage of mean could be further improved through individual plant selection.

The results of correlation studies indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients analysis revealed that pod yield per plant exhibited positive and significant association with harvest index followed by biological yield at genotypic and phenotypic levels. For maximizing the Pod yield per plant, emphasis should be given in selection of characters such as biological yield, sound mature kernel, kernel yield, Shelling percentage and 100 kernel weight for further improvement of groundnut crop. Path Analysis is used to partition contributing character to yield through direct and indirect effect. As evident from the table that maximum direct positive effect on pod yield per plant was observed in biological yield per plant followed by harvest index, 100 kernel weight, kernel yield per plant and number of pegs per plant, days to flowering, days to initial flowering, number of pods per plant at genotypic and phenotypic levels. Maximum negative direct effect on pod yield per plant was observed from days to germination followed by plant height, 100 pod weight, shelling, sound mature kernel. Hence utmost importance should be given to these characters during selection for pod yield per plant. The result were comparable to the result reported by (Paven *et al.*, 2014)

CONCLUSION

From the present investigation it is concluded that among 20 genotypes of groundnut on the basis of mean performance SC-28 was found to be superior in seed yield over the check followed by VG-17 (CHECK), The early days to flowering was recorded by FSICC- 37AxCS-319 that may fit for multiple cropping system. High estimates of GCV and PCV were recorded for number of branches per plant, days to germination, number of pegs per plant. Genetic parameters revealed that heritability and genetic advance as % mean values are high were recorded for plant height, biological yield per plant. Correlation coefficient analysis revealed that seed yield per plant exhibited positive and significant association with harvest index followed by biological yield at genotypic and phenotypic levels. Hence these characters may be effective for selection of high pod yield genotypes. Highly significant correlation was observed for the character pod yield. Path coefficient analysis revealed that characters harvest index, biological yield have positive direct effect on pod yield per plant at genotypic and phenotypic levels.

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