The Pharma Innovation Journal 2021; 10(11): 1008-1012

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(11): 1008-1012

www.thepharmajournal.com
Received: 12-08-2021
Accepted: 19-09-2021

Shrotri SM
Department of genetics and plant breeding, College of Agriculture, Latur. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

MV Dhuppe
Associate professor, College of Agriculture, Ambajogai. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

PR Sargar
Department of genetics and plant breeding, College of Agriculture, Latur. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

SS Gavade
Department of genetics and plant breeding, College of Agriculture, Latur. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

BN Ralebhat
Department of genetics and plant breeding, College of Agriculture, Latur. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

Corresponding Author:
Shrotri SM
Department of genetics and plant breeding, College of Agriculture, Latur. Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India

Assessment of genetic variability, heritability and genetic advance for yield and yield contributing traits in groundnut (*Arachis hypogaea* L.)

Shrotri SM, MV Dhuppe, PR Sargar, SS Gavade and BN Ralebhat

Abstract
Background: Genetic variability is a necessary requirement for crop improvement programmes in order to generate high yielding varieties by estimating various genetic parameters such as components of variances, genotype and phenotype coefficients of variability, heritability, and genetic advance. The present investigation was aimed to estimate genetic variability in terms of variance components, heritability and genetic advance in the groundnut genotypes.
Methods: During *kharif* 2020 thirty groundnut genotypes for ten characters were investigated to estimate genetic variability for pod yield and component characteristics. The investigation conducted at Oilseed Research Station, Latur.
Results: Analysis of variance revealed existence of quite substantial differences among the genotypes for all the characters examined. The genotypes *viz.,* ICGV00189, ICGV0213 and ICGV00202 demonstrated high mean performance for pod yield and its element features *viz.,* number of mature pods per plant, kernel yield per plant, hundred kernel weight and sound mature kernel. High heritability coupled with high genetic advance as per cent of mean was recorded by the kernel yield per plant, pod yield per plant, number of mature pods per plant and hundred kernel weight making sure that these characters are under additive genetic control and consideration of these traits for the improvement will be lucrative and may rapidly contribute to increase pod yield in groundnut cultivars.

Keywords: Groundnut, genetic variability, heritability and genetic advance

Introduction
Groundnut (*Arachis hypogaea* L.) is highly self-pollinated monoecious annual leguminous oilseed crop originated in Bolivia cultivated commercially in over 100 countries between the latitudes of 40°N and 40°S extensively grown in the tropics and subtropics under rainfed conditions including both small and large commercial farmers relying on it. The economic and nutrient attraction of the groundnut has increased in popularity as it contains a lot of edible oil (45 to 54 per cent), protein and carbohydrates (22-32 per cent) (8-14 percent). It also supplies carbohydrates (10–25%), vitamins (E, K and B complexes), minerals (Ca, P, Mg, Zn and Fe) and fibre, in addition to oil and protein. The shell of the ground-nut is used as fuel, animal feeds, livestock litters, feed and fertiliser fillings, transhumance (vegetable parts above ground) used as animal feed and legume roots adding nitrogen (100-152 kg/ha) and soil organic substances to help improve the fertility of soil. While India is the world's leading producer of groundnuts, its productivity is much lower than others. As a result, breeds with high genetic potential must be developed for rainfed conditions in order to increase productivity. The selection of superior genotypes is therefore essential to enhance yields and to reduce the gap in economic performance which can only be achieved via genetic studies of the yield and the element features.
Genetic variability is an essential prerequisite for crop improvement programmes for obtaining high yielding varieties, through the estimation of different genetic parameters like components of variances, genotype and phenotype coefficients of variability, heritability and genetic advance. Genetic variability is an essential precursor for crop development programmes to attain high yield varieties by estimating several genetic characteristics such as variance components, genotype and phenotype variability coefficients, inheritance and genetic progression. The production of cultivars via selection and hybridization demands a large quantity of resources for the use of available genetic diversity to adapt to diverse environmental circumstances. The efficiency of the breeding material for the desired characteristic depends on the type, size and amplitude of its genetic variability. Genotypical

variability estimate coefficient delivers strong implication for genetic potential enhancement of crops through selection (Johnson *et al*., 1955) [8].

Heritability is the square connection between expected value (phenotypes) and true genetic or genotypes. Heritability (h^2) may be used to predict selection response (R) as $R=h^2S$, where S is the differential of selection (Falconer and Mackay, 1996) [5]. Patrimony is an essential parameter since it impacts the selection response. It is defined as the percentage of phenotypic variance between people in a group due to heritage genetic effects known as narrow sense patrimony (heritability), while the percentage of phenotypical variance attributable to the whole genotype, comprises the sum of additives, dominance and epistatic effects known as broad sense heritability. Heritability and genetic advance for breeders are highly helpful biometric tools to determine the selection's direction and extent. High heritability alone is insufficient for effective selection in advanced generations and without significant genetic advance. The high heritability and genetic advance of a given characteristic display that it is driven by additive gene action and, accordingly, the most efficient selection condition. It is important to identify plant characteristics that affect productivity for reproductive programmes to boost groundnut production. In order to improve the efficiency of seed-selection and pod yield, knowledge on the type and scale of genetic variability and transmission of characteristics is of crucial relevance. In this study, the genetic variability, heritability and genetic advance of groundnut were investigated.

Materials and Methods

The present the experiment entitled "Genetic variability studies for yield, yield contributing traits and oil content in groundnut (Arachis hypogea)." was undertaken at Oilseed Research Station, Latur during *kharif*, 2020. The experimental material encompassed thirty genotypes of groundnut. The experiment was configured in a Randomized Block Design with two replications having each and every genotype sown in row of 5meter length at spacing of 45cm in rows and 10cm in plants under rainfed conditions. The method of sowing followed was dibbling. One plant per hill was maintained by thinning 15 days after sowing. At planting, the necessary 25 kg N + 50 kg P_20_5 per hectare was applied to sustain healthy crops as well as to exploit full potential, together with all other cultural techniques and plant protection measures. Comments have been recorded in each genotype on randomly selected five competing plants for the all characters *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of mature pods per plant, pod yield per plant (g), kernel yield per plant (g), Shelling percentage (%), hundred kernel weight(g), sound mature kernel (%), and oil content (%). Sound mature kernel were recorded as proportion of yield fully developed kernels to yield of total kernel multiplied by 100. Fifty grams of seeds were taken and dried to estimate oil content in percentage using NMR (Nuclear Magnetic Resonance) spectrometer. The data were analysed using descriptive statistics and analysis of variance was performed (Cocheran and Cox 1957) [3] and following genetic parameters were computed for the character having significant mean square due to the genotypes. Phenotypic and genotypic coefficient of variation was estimated as recommended by Burton (1952) [2], heritability (broad sense) by lush (1949) [11] and Hanson *et al.* (1956) [6], genetic advance by Johnson *et al.* (1955) [8]. Table 3 decodes the categorization of genetic estimates *viz.,* Sivasubramanian and Madhavamenon (1973) [20] categorized GCV and PCV as less than 10% as low, 10-20% as moderate and higher than 20% as high. As suggested by Robinson H. F. *et al.* (1949) [6] heritability was categorized as less than 30% as low, 30%-60% as moderate and more than 60% as high. GAM was categorized by Johnson *et al.,* (1955) [8] less than 10% as low, 10-20% as moderate and more than 20% as high.

Results and Discussion

The analysis of variance recorded for all the characters presented in Table 1. The figures recorded for pod yield and the contributing traits demonstrated highly significant genotypic effects for agronomic characters, consequently displayed that the groundnut accessions were highly variable in performance for agronomic characters. The occurrence of variability across genotypes is significant for genetic investigations and, as a result, for improvement and selection. The large variation between pod yield and the contributing traits among the accessions allows for the selection of superior ones. Range of mean pod yield varied from 8.66g to 25.07g. ICGV00189, ICGV0213 and ICGV00202 revealed strange hegemony in terms of pod yield per plant and contributing attributes except days to 50% flowering and days to maturity. ICGV00189 displayed legitimacy in terms of number of mature pods per plant, pod yield per plant and kernel yield plant (Table 2). Subsequently, ICGV0213 recorded superiority in terms of number of mature pods per plant, pod yield per plant and kernel yield per plant. Afterwards, IVT-2019-25 ranked highest in terms of kernel yield per plant and shelling percentage as well as it shows supremacy in terms of sound mature kernel. Hundred kernel weight recorded highest for the genotypes ICGV00213, ICGV00189 followed by IVT-2019-25. The highest oil content was observed in the genotypes ICGV07235 followed by ICGV0211, ICGV02125 and ICGV07408. Likewise, ICGV07408 and ICGV02005 had highest plant height. Earliness in days to 50% flowering was observed in ICGV07408 and ICGV0705 followed by ICGV07214, ICGV07270 and ICGV06285. Interestingly, GPBD-4, ICGV07270 and ICGV98170 showcased the earliness in days to maturity. Table 4 displays the parameters of genetic variability *viz.,* range, mean performance, estimates of variance, phenotypic and genotypic coefficient of variation, estimates of broad sense heritability, genetic advance and genetic advance as per cent of mean for each character under investigation. Shelling percentage ranked highest in variance estimate followed by hundred kernel weight and pod yield per plant, these outcomes demonstrate conformity with Mohammad Raza *et al.* (2018) [16].

Table 4 witnessed that phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits flashing out influence of genotypic x environmental interaction in the expression of characters decoded by Uguru (1955) [24]. Coefficient of variation in terms of GCV and PCV values observed highest in the traits kernel yield per plant followed by pod yield plant and number of mature pods per plant whereas, days to 50% flowering, days to maturity, plant height, sound mature kernel and oil content recorded lower values for GCV and PCV. The findings are in agreement with Dake A. D. *et al.* (2018) [4] and Kadmani S. *et al.* (2017) [9] for lower estimates of GCV and PCV for the traits days to 50% flowering, days to maturity, plant height, sound mature kernel and oil content also the results reveal a resemblance to Sima

Sinha *et al.* (2020) [19], Mahalaxmi *et al.* (2005) [12], and Zaman *et al.* (2011) [26] for higher estimates of kernel yield per plant, pod yield plant and number of mature pods per plant.

Table 1: Analysis of variance (ANOVA) for yield and yield component traits studied in groundnut Mean sum of squares

Sr. No.	Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of mature pods per plant	Pod yield per plant (g)	Kernel yield per plant (g)	Shelling percentage (%)	100kernel weight (g)	Sound mature kernel (%)	Oil content (%)
1	Replication	1	0.600	5.400	0.480	0.051	0.086	0.108	1.734	0.379	0.428	0.223
2	Treatment	29	22.783**	37.813**	37.110**	36.347**	53.914**	28.218**	70.927**	55.431**	37.508**	4.420**
3	Error	29	9.324	15.572	15.216	5.959	5.340	2.353	9.825	5.246	15.105	0.642

*Indicates significance at 5% level
**Indicates significance at 1% level

Table 2: Mean performance between the treatments for yield and yield contributing traits in groundnut

Sr. No.	Genotypes	Days to 50 % flowering	Days to Maturity	Plant height (cm)	No. of mature pods / plant	Pod yield per plant (g)	Kernel yield per plant (g)	Shelling percentage %)	100 kernel weight (g)	Sound mature kernel (%)	Oil content (%)
1	ICGV00318	37.00	112.00	39.81	18.08	16.22	11.12	68.28	36.59	79.05	44.85
2	ICGV06279	40.00	114.50	35.76	22.63	20.63	12.96	62.84	39.27	81.73	43.20
3	ICGV06319	38.00	113.00	38.60	20.70	19.09	11.63	60.94	37.23	80.29	44.25
4	ICGV07213	42.00	117.00	41.87	17.95	16.07	10.49	66.13	36.80	76.57	44.99
5	ICGV07217	39.00	114.00	39.04	18.41	16.70	10.18	61.54	36.52	77.94	44.90
6	ICGV07210	38.00	113.00	34.93	22.18	20.46	14.70	71.99	40.84	83.27	44.01
7	ICGV02038	42.00	116.00	45.59	13.53	11.07	7.23	65.39	30.28	73.35	46.87
8	ICGV02005	41.00	116.50	47.33	11.35	9.43	7.01	74.18	29.24	70.93	46.45
9	ICGV07214	35.00	111.00	37.33	20.21	18.68	11.46	61.22	38.37	80.02	44.38
10	ICGV02125	41.00	117.00	46.22	12.23	10.28	6.99	67.73	29.42	71.57	47.11
11	ICGV07405	34.00	109.00	39.41	18.79	17.76	11.30	63.54	38.35	79.26	44.53
12	ICGV07406	40.00	114.00	34.83	22.32	23.30	16.48	70.82	42.83	83.21	43.13
13	ICGV07392	43.00	117.50	45.27	14.25	12.54	8.79	69.80	31.86	73.28	46.64
14	ICGV07404	36.00	111.00	44.90	13.55	12.29	8.03	65.45	31.19	73.80	46.53
15	ICGV07235	42.00	116.50	45.33	12.57	8.66	6.30	73.01	28.33	73.20	47.72
16	ICGV07408	34.00	108.50	47.63	10.18	8.81	7.47	72.24	30.52	69.38	47.00
17	GPBD-4	36.50	104.00	43.63	13.60	11.20	7.92	61.09	31.84	72.62	45.14
18	ICGV07270	35.00	104.50	45.60	12.97	10.55	6.85	65.72	30.95	72.81	45.49
19	ICGV7403	43.00	111.50	35.76	21.50	22.17	14.89	67.19	41.96	81.47	43.40
20	ICGV00211	35.50	107.00	46.78	11.39	9.09	6.18	68.76	28.28	70.41	47.46
21	ICGV00189	40.00	109.00	33.74	24.22	25.07	18.69	74.52	44.40	83.38	42.78
22	ICGV00191	44.00	108.50	41.02	14.80	13.62	8.59	63.37	34.01	75.24	45.13
23	ICGV0296	37.50	107.00	37.62	16.22	14.82	7.75	52.25	31.21	76.41	45.69
24	ICGV00202	43.50	113.00	42.33	22.23	23.49	13.71	58.37	40.14	80.49	43.05
25	ICGV0213	43.00	113.00	36.08	23.88	24.78	17.99	71.51	45.09	81.49	42.63
26	ICGV98170	34.50	104.50	40.25	16.33	14.60	7.63	53.20	31.19	76.44	45.80
27	ICGV99072	36.00	106.00	37.70	20.57	21.28	15.56	73.05	41.73	80.22	43.80
28	ICGV06285	35.00	105.00	42.40	14.98	15.04	9.17	60.77	35.73	76.01	45.27
29	LGN-1	43.00	106.00	39.57	18.83	17.45	11.36	64.72	38.13	78.22	44.85
30	IVT-2019-25	43.50	116.50	35.42	22.46	22.57	16.82	74.60	43.92	83.96	43.33
	Grand Mean	39.06	111.20	40.72	17.43	16.25	10.84	66.14	35.87	77.20	45.01
	SE	2.15	2.79	2.75	1.72	1.63	1.08	2.21	1.61	2.74	0.56
	CD at 5%	6.24	8.07	7.97	4.99	4.72	3.13	6.41	4.68	7.94	1.63
	CV (%)	7.81	3.54	9.57	14.00	14.21	14.14	4.73	6.38	5.03	1.78

Table 3: Categorization of genetic estimates

Estimates	GCV&PCV (%)	Heritability (h^2) (%)	GAM (%)
Low	0 to 10	0 to 30	0 to 10
Moderate	10 to 20	30 to 60	10 to 20
High	More than 20	More than 60	More than 20

Table 4: Parameters of genetic variability for yield and yield contributing traits in groundnut

Sr. No.	Name of the Character	Range	Mean	GV (σ^2g)	PV (σ^2p)	GCV (%)	PCV (%)	Heritability B.S. (%)	Genetic advance	GAM (%)
1	Days to 50% flowering	34-44	39.06	6.73	16.05	6.64	10.25	41.9	3.46	8.85
2	Days to maturity	104-117.5	111.20	11.12	26.69	2.99	4.64	41.7	4.43	3.98
3	Plant height(cm)	33.74-47.63	40.72	10.94	26.16	8.12	12.55	41.8	4.40	10.82

4	No. of mature pods per plant	10.18-24.22	17.43	15.19	21.15	22.36	26.38	71.8	6.80	39.03
5	Pod yield per plant (g)	8.66-25.07	16.25	24.28	29.62	30.30	33.47	82.0	9.19	56.53
6	Kernel yield per plant (g)	6.18-18.69	10.84	12.93	15.28	33.16	36.05	84.6	6.81	62.83
7	Shelling percentage (%)	52.25-74.60	66.14	30.55	40.37	8.35	9.60	75.7	9.90	14.97
8	100 kernel weight (g)	28.28-45.09	35.87	25.09	30.33	13.96	15.35	82.7	9.38	26.15
9	Sound mature kernel (%)	69.38-83.96	77.20	11.20	26.30	4.33	6.64	42.6	4.49	5.82
10	Oil content (%)	42.63-47.72	45.01	1.88	2.53	3.05	3.53	74.6	2.24	5.43

GV - Genotypic variance, PV - Phenotypic variance, GCV- Genotypic coefficient of variation, PCV- phenotypic coefficient of variation, GAM- Genetic advance as % mean.

Days to 50% flowering, days to maturity, plant height and sound mature kernel displayed moderate heritability. High heritability recorded for kernel yield per plant pod yield per plant Dake A. D. *et al.* (2019), John *et al.* (2007) [7] published comparable results. Also, findings reveled the high heritability for hundred kernel weight, number of mature pods per plant and hundred kernel weight these findings demonstrate congruence with Gonya Nayak P. *et al*. (2018), and Tirkey S. K. (2015) [23] and Thirumala Rao *et al.* (2012) [22].

High genetic advance as per cent of mean recorded for the traits number of mature pods per plant, pod yield per plant, kernel yield per plant and hundred kernel weight. Plant height and shelling percentage recorded moderate genetic advance as per cent of mean inversely, days to 50% flowering, days to maturity, sound mature kernel and oil content had low genetic advance as per cent of mean.

High heritability coupled with genetic advance as per cent of mean indicates presence of lesser environmental influence and prevalence of additive gene action in their expression displays that selection through these traits would be worthwhile. In present investigation this fortunate combination observed in traits kernel yield per plant, pod yield per plant, number of mature pods per plant and hundred kernel weight matches with earlier reports published by Sawargaonkar *et al.* (2010), Shukla *et al.* (2014), Mukesh Bhakal *et al.* (2017) and Solanki S. M. *et al.* (2019) [17, 18, 1, 21]. However moderate to high heritability paired with low or moderate genetic advance as per cent of mean observed for the traits days to 50% flowering, days to maturity, pant height, sound mature kernel and oil content indicates need to create variability either by hybridization or mutation followed by selection these findings are in agreement with Narsimhulu (2012), Varman and Raveendran (1996) and Korat V. P. *et al.* (2009) [13, 25, 10].

References

1. Bhakal M, Lal GM. Estimation of genetic variability, correlation and path analysis in groundnut (*Arachis hypogaea* L.) Germplasm Chemical Science Review and Letters Chem. Sci. Rev. Lett 2017;6(22):1107-1112.
2. Burton GW. Quantitative inheritance in grasses. Proc. Sixth International Grassland Congress. Pennsylvania State College, PA, US 1952,1:24.
3. Cochran WG, Cox GM. Experimental designs. 2nd ed. John Wiley and Sons., Inc., New York 1957.
4. Dake AD, Chavan MV, Thorat GS. Character association and variability studies of yield and its attributing character in groundnut (*Arachis hypogea* L.) International Journal of Current Microbiology and Applied Sciences 2018;6:924-929.
5. Falconer DS, Trudy Mackay FC. Introduction to Quantitative Genetics 4th ed. Longman Group Limited Malaysia 1996.
6. Hanson CH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population of Korean lespedesa. Agronomy Journal 1956;48:268-272.
7. John K, Vasanthi RP, Venkateswarlu O, Sudhakar P. Variability and correlation studies for quantitative traits in Spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. Legume Res 2007;28(3):189-193.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability of Soybeans. Agronomy Journal 1955;47:314-318.
9. Kademani S, Herakal R. Genetic variability parameters for yield and yield component traits in the mapping population of groundnut (*Arachis hypogea*) International Journal of Current Microbiology and Applied Sciences 2017;6(12):3321-3325.
10. Korat VP, Pithia MS, Savaliya JJ, Pansuriya AG, Sodavadiya PR. Studies on genetic variablity in different genotypes of groundnut. Agriculture communication centre. Legume Res 2009;32(3):224-226.
11. Lush JL. Heritability of quantitative characters in farm animals. Heriditas 1949;35:256-261.
12. Mahalaxmi P, Manivannan N, Murlidharan V. Variability and correlation studies in groundnut (*Arachis hypogaea* L.). Legume Res 2005;28(4):194-197.
13. Narasimhulu R, Kenchanagoudar PV, Gowda MVC. Study of genetic variability and correlation in selected groundnut genotypes. International journal of applied biology and pharmaceutical technology 2012;3:353-358
14. Pathulothu GN, Venkataiah M, Revathi P, Sukumar K. Genetic variability and correlation studies for yield and yield contributing characters in groundnut (*Arachis hypogaea* L.) International Journal of Current Microbiology and Applied Sciences 2018;10:354-356.
15. Robinson HF, Comstock RE, Harvey VH. Estimates of heritability and degree of dominance in corn. Agron. J 1949;41:353-359.
16. Raza M, Reddi Sekhar M, Shanthi Priya M, Prasad TNVKV, Rajarajeswari V. Genetic variability studies for pod yield and component traits in groundnut. Electronic Journal of Plant Breeding 2018;9(4):1436-1442.
17. Sawargaonkar SL, Giri RR, Hudge BV. Character association and path analysis of yield component traits and late leaf spot disease traits in groundnut (*Arachis hypogaea* L.). Agricultural Science Digest 2010;30(2):115-119.
18. Shukla AK, Rai PK. Evaluation of groundnut genotypes

for yield and quality traits. Annals of Plant and Soil Research 2014;16(1):41-44.
19. Sinha Sima, Rahman MH, Verma AK, Kishore C. Genetic variability, correlation and path analysis in fastigiata and hypogaea sub-species of groundnut (*Arachis hypogaea* L.) J. Oilseeds Re 2019;36(3):134-140.
20. Sivasubramanian S, Madhavamenon P. Combining ability in rice. Madras Agricultural Journal 1973;60:419-421.
21. Solanki SM, Chaudhari SB, Sapovadiya MH, Damor V. Genetic variability, correlation and path analysis for yield and its contributing traits in virginia groundnut (*Arachis hypogaea* L.) Ind. J. Pure App. Biosci 2019;7(6):226-233.
22. Thirumala Rao V, Bhadru D, Murthy KGK, Bharathi D. Genetic variability and association among the various characters in groundnut (*Arachis hypogaea* L.) International journal of applied biology and pharmaceutical technology 2012;3:337-341
23. Tirkey SK, Ekhlaque A, Mahto CS. Genetic variability and character association for yield and related attributes in groundnut Journal of Pharmacognosy and Phytochemistry (*Arachis hypogaea* L.) 2015;1:2487-2489.
24. Uguru MI. Heritable relationships and variability of yield and yield components in vegetable, cowpeas, African Crop Science Journal 1995;3(1):23-28.
25. Varman PV, Raveendran TS. Genetic variability and causal relationship in groundnut. Madras Agric. J 1996;83(12):784-786.
26. Zaman MA, Khatun MT, Ullah MZ, Moniruzzamn M, Alam KH. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). The Agriculturists 9(1&2):29-36.