Lokendra Singh Rajput
Ph.D., Scholar,
Department of Genetics and
Plant Breeding, College of
Agriculture, Rajmata Vijayaraje
Scindia, Agricultural University,
Gwalior, Madhya Pradesh, India

RS Sikarwar
Scientist, Department of
Genetics and Plant Breeding,
College of Agriculture, Rajmata
Vijayaraje Scindia, Agricultural
University, Gwalior, Madhya
Pradesh, India

MK Tripathi
Principal Scientist,
Department of Genetics and
Plant Breeding, College of
Agriculture, Rajmata Vijayaraje
Scindia, Agricultural University,
Gwalior, Madhya Pradesh, India

Sushma Tiwari
Scientist, Department of
Genetics and Plant Breeding,
College of Agriculture, Rajmata
Vijayaraje Scindia, Agricultural
University, Gwalior, Madhya
Pradesh, India

PK Prajapati
Ph.D., Scholar,
Department of Genetics and
Plant Breeding, College of
Agriculture, Rajmata Vijayaraje
Scindia, Agricultural University,
Gwalior, Madhya Pradesh, India

RK Yadav
Ph.D., Scholar,
Department of Genetics and
Plant Breeding, College of
Agriculture, Rajmata Vijayaraje
Scindia, Agricultural University,
Gwalior, Madhya Pradesh, India

Corresponding Author:
Lokendra Singh Rajput
Ph.D., Scholar,
Department of Genetics and
Plant Breeding, College of
Agriculture, Rajmata Vijayaraje
Scindia, Agricultural University,
Gwalior, Madhya Pradesh, India

Assessment of variability, heritability and genetic advance in peanut [*Arachis hypogaea* (L.)]

Lokendra Singh Rajput, RS Sikarwar, MK Tripathi, Sushma Tiwari, PK Prajapati and RK Yadav

DOI: https://doi.org/10.33545/26174693.2024.v8.i5l.1235

Abstract
The present investigation of experimental yield trial on genetic variability involving 56 genotypes of groundnut were carried out in kharif season 2022-23 at Research farm, Department of genetics and plant breeding, college of agriculture, RVSKVV, Gwalior (M.P.). The 13 traits were recorded and genetic parameters *viz*., PCV, GCV, heritability and genetic advance as percent of mean were studied. Based on the analysis of variance, it was determined that there were significant differences in genotypes for every character, demonstrating variability across the traits. High PCV and GCV estimates were identified for pod yield per plant had the highest GCV followed by kernel yield per plant, kernel number per plant and number of pods per plant. Moderate PCV and GCV values observed number of branches per plant, plant height, 100 kernel weight, 100 pod weight and harvest index, whereas low PCV and GCV values were observed days to 50% flowering, days to maturity, sound mature kernel and shell outturn. The estimation of high heritability value coupled with high genetic advance was recorded for pod yield per plant followed by kernel yield per plant, kernel number per plant, number of pods per plant, plant height, number of branches per plant, 100 kernel weight, 100 pod weight and harvest index indicating that direct selection for these traits would be more successful in achieving the intended genetic improvement and that the inheritance of these attributes was more likely the result of additive gene effects.

Keywords: Groundnut, genetic variability, heritability, genetic advance, peanut

1. Introduction
The peanut, *Arachis hypogaea* L., is a member of the Fabaceae family's Papilionaceae subfamily. It is regarded as the king of oilseed crops because of the edible oil it contains. Groundnuts are currently grown in tropical, subtropical, and warm temperate temperatures around the world, with Brazil in South America being their primary site of origin. Pod formation in the soil is promoted by the crop species' cleistogamous flower, which is extremely self-pollinating and has a geotropic inclination toward light following fertilization. Because of a wide variety of adaptations in different agro-climatic conditions and soils, it might be grown at latitudes of 40°N and 40°S. Grains legumes, groundnuts are classified as allotetraploid (2n=4x=40), diploid (2n=20), and aneuploid (2n=18) (Poojitha *et al*., 2024) [1]. India's most well-known state for groundnut cultivation is Gujarat; Andhra Pradesh, Tamil Nadu, Rajasthan, and Karnataka are closely behind. In India, groundnut is cultivated on 57.45 lakh hectare along production and productivity levels for 2021–22 are 1759 kg/ha and 101.06 lakh tonnes (Department of Agriculture & Farmers Welfare, GOI 2021-22), respectively. With 3.91 lakh hectares of growing land, Madhya Pradesh is expected to produce 6.73 lakh tonnes of groundnuts and produce 1722 kg/ha in the 2021–2022 growing season. A sizable portion of high-quality edible oil (50%) as well as quickly assimilated protein (25%) and carbohydrates (20%) can be found in groundnut seeds. It also contains minerals such as phosphorus, calcium, and zinc and vitamins such as A, C, E, K, thiamine and niacin. Meat, eggs, and other veggies are all lower in protein than groundnuts (Gummadala *et al*., 2022) [3]. For growing children, pregnant women, and nursing mothers, freshly roasted peanuts with jaggery and goat milk are extremely beneficial. It strengthens the body's defenses against hepatitis and TB.

The first step in improving a crop is to look into the genetic variability of the crop species. This is because the degree of genetic variability in genotypes dictates the effectiveness of a crop improvement program. Genetic advancement and heritability estimates combined provide insight into the type of character that can be enhanced through selection. Therefore, the current study examined Variability, Heritability and Genetic Advance in several peanut populations.

2. Materials and Methods

The experiment consisting of 56 groundnut genotypes for 13 traits was conducted in a randomized block design (RBD) with three replications at Research Farm, Department of Genetics and Plant Breeding, RVSKVV, College of Agriculture, Gwalior (M.P.) during the Kharif season 2022-23. In each replication each genotype was sown in one rows of 5m length with a spacing of 30 cm x 10 cm. The 13 quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, kernel number per plant, kernel yield per plant, 100 kernel weight, sound mature kernel, 100

pod weight, shelling outturn, harvest index and pod yield per plant were recorded on five randomly selected plants from each genotype in each replication. The mean values were used for analysis for variance. The statistical analysis for variance was worked out according to Panse and Sukhatme (1985) [11]. The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton (1952) [4]. Heritability in broad sense was estimated by using the formula given by Hanson *et al*. (1956) [5] and was expressed in percentage. Genetic advance and genetic advance as percent of mean were computed and categorized as low (< 10%), moderate (10 - 20%) and high (> 20%) according to the method suggested by Johnson *et al*. (1955) [6].

3. Results and Discussion
3.1 Analysis of variance
Based on the analysis of variance, it was determined that there were significant differences in genotypes for all the thirteen traits, demonstrating variability across the traits. (Table 1). To begin the selecting process, these differences alone are adequate.

Table 1: ANOVA for various quantitative traits of peanut

Source of Var.	D.F.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	Kernel no. per plant	Kernel yield per plant (gm)
Replications	2	4.84	2.54	2.49	0.32	3.76	2.68	0.03
Treatments	55	16.44***	154.70***	128.97***	1.96	58.57***	95.83***	8.35***
Error	110	0.8	0.96	2.34	0.2	0.79	1.15	0.5
Source of Var.	D.F.	100 kernel weight (gm)	Sound mature kernel (%)	100 pod weight (gm)	Shell Outturn (%)	Harvest index (%)	Pod yield per plant (gm)	
Replications	2	4.43	0.188	4.95	1.64	3.03	0.16	
Treatments	55	55.03***	54.82***	315.78***	31.26***	67.76***	18.92***	
Error	110	1.94	1.95	4.15	2.21	2.52	1.67	

3.2 Per se Performance and Range
The days to 50% recorded least value of RVGN-69 (24 days) and maximum of RVGN-9 (33 days) with mean value of 28.64 days. The days to maturity fluctuated from RVGN-64(99 days) to RVGN-22(126 days) with mean value of 108.27days. The average plant height was 46.03cm while minimum plant height for RVGN-83 (33.33) and maximum in RVGN-91(61). The average number of branches per plant was 5.32 while minimum number of branches per plant for RVGN-97 (3.8) and maximum in RVGN- 115 (7.15). The number of pods per plant ranged from RVGN-12(9.73) to RVGN-17(28.1) whereas, the mean average value recorded for number of was 19.05. The kernel number per plant ranged from RVGN-110 (11.37) to RVGN-83 (32.9) whereas, the mean average value 23.66. The average kernel yield per plant was 6.32 gm while minimum kernel yield per

plant for RVGN-110 (2.98) and maximum in RVGN-114(10.12). The average 100 kernel weight was 34.44 gm while minimum 100 kernel weight for RVGN-52 (21.7) and maximum in RVGN-4 (42.8). The Sound mature kernel fluctuated from 74.47 (RVGN-13) to 93.5 (RVGN-4) with mean value of 87.41. The average 100 pod weight was 93.86 gm while minimum 100 pod weight for RVGN-13 (73.67) and maximum in RVGN-36 (118.67). The average shell outturn was 66.78 while minimum shell outturn for RVGN-52 (59.97) and maximum in RVGN-49 (71.99). The harvest index ranged from RVGN-78 (33.9) to RVGN-79 (53.27) whereas, the mean average value recorded was 43.35. The pod yield per plant fluctuated from RVGN-110 (4.71) to RVGN-114 (16.15) with mean value of 9.47 gm. The mean performance according to attributes is shown in Table 2.

Table 2: Genetic variability parameters for yield and its constituent traits

S. No.	Traits	Range			Coefficient of variation		h² (bs)	Genetic	Gen. Adv as % of Mean
		Min	Max	Grand Mean	GCV %	PCV %	%	Advance	
1.	Days to 50% flowering	24	33	29	7.98	8.18	95.2	4.59	16.03
2.	Days to maturity	99	126	108	6.61	6.63	99.4	14.7	13.58
3.	Plant height (cm)	33.33	61	46.03	14.11	14.25	98.1	13.26	28.8
4.	No. of branches per plant	3.8	7.15	5.32	14.43	15.22	89.9	1.5	28.18
5.	No. of pods per plant	9.73	28.1	19.05	23.04	23.2	98.7	8.98	47.15
6.	Kernel no. per plant	11.37	32.9	23.66	23.75	23.89	98.8	11.5	48.63
7.	Kernel yield per plant (gm)	2.98	10.12	6.32	25.61	26.41	94	3.23	51.15
8.	100 kernel weight (gm)	21.7	42.8	34.44	12.21	12.44	96.4	8.51	24.7
9.	Sound mature kernel (%)	74.47	93.5	87.41	4.8	4.89	96.4	8.49	9.72
10.	100 pod weight (gm)	73.67	118.67	93.86	10.86	10.93	98.7	20.86	22.22
11.	Shell Outturn (%)	59.97	71.99	66.78	4.66	4.83	92.9	6.18	9.25
12.	Harvest index (%)	33.9	53.27	43.35	10.76	10.96	96.3	9.43	21.74
13.	Pod yield per plant (gm)	4.71	16.15	9.47	25.68	26.51	93.8	4.85	51.24

3.3 Coefficient of Variation

The reliable measures that will enable us to evaluate the amount of variability and comprehend its heritable and non-heritable components are the genotypic and phenotypic coefficient of variations. The difference between the phenotypic and genotypic coefficient of variations indicates the percentage of environmental effect on the variability presented by the genotypes. The environment affects all biometrical aspects, as evidenced by the fact that PCV levels in this study are higher than GCV values. Table 2 presented the coefficients of variation. Pod yield per plant (26.51%) had the highest PCV followed by kernel yield per plant (26.41%), kernel number per plant (23.89%), number of pods per plant (23.2%), moderate PCV was for number of branches per plant (15.22%), plant height (14.25%), 100 kernel weight (12.44%), harvest index (10.96%),100 pod weight (10.93%) and low PCV was for phenological traits i.e., days to 50% flowering (8.18%), days to maturity (6.63%), sound mature kernel (4.89%) and shell outturn (4.83%) respectively. In general, phenotypic coefficients of variation (PCV) values were higher than the genotypic coefficients of variation (GCV) for the respected characters. Pod yield per plant (25.68%) had the highest GCV followed by kernel yield per plant (25.61%), kernel number per plant (23.75%), number of pods per plant (23.04%), moderate GCV was for number of branches per plant (14.43%), plant height (14.11%), 100 kernel weight (12.21%), 100 pod weight (10.86%), harvest index (10.76%) and low PCV was for phenological traits i.e., days to 50% flowering (7.98%), days to maturity (6.61%), sound mature kernel (4.8%) and shell outturn (4.66%). These observations are in agreement with the findings of Kumari and Sashidharan (2020) [10], Kulheri *et al*. (2022) [7], Singh *et al*. (2022) [8] and Yadav *et al*. (2023) [9].

High coefficients of variation were identified for pod yield per plant followed by kernel yield per plant, kernel number per plant and number of pods per plant. This indicates that effective selection may improve these parameters. In order to maximize yield, these attributes might be taken into account at every stage of the selection process.

3.4 Heritability (broad sense) and genetic advance as percent of mean (GAM)

Estimation of high heritability value coupled with high genetic advance was recorded for pod yield per plant followed by kernel yield per plant, kernel number per plant, number of pods per plant, plant height, number of branches per plant, 100 kernel weight, 100 pod weight and harvest index indicating that direct selection for these traits would be more successful in achieving the intended genetic improvement and that the inheritance of these attributes was more likely the result of additive gene effects. High heritability with moderate to low genetic advance was observed for days to 50% flowering, days to maturity, sound mature kernel, shelling outturn demonstrating that the limited potential for improvement of these traits and the likelihood that their heredity resulted from a non-additive gene effect. The similar kind of results were also reported by Kulheri *et al*. (2022) [7], Singh *et al*. (2022) [8] and Yadav *et al*. (2023) [9].

4. Conclusion

Significant mean sums of squares due to genotypes were observed for all the traits through analysis of variance. It was discovered that traits among genotypes can be distinguished using genetic variability analysis. The estimation of high heritability value coupled with high genetic advance was recorded for pod yield per plant followed by kernel yield per plant, kernel number per plant, number of pods per plant, plant height, number of branches per plant, 100 kernel weight, 100 pod weight, harvest index. To maximize the crop's genetic yield potential, high yielding breeding traits may be chosen based on traits that have been found to have higher heritability and high genetic advance as a percentage of mean. A methodical hybridization program may also be developed, accounting for traits with higher heritability and high genetic advancement as a percentage of mean, in order to choose transgressive segregants in the segregating generations.

5. Competing interests

Authors have declared that no competing interests exist.

6. References

1. Poojitha P, Singh L, Gummadala K, Nath R, Perli H, Bacham S, *et al*. Assessment of variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). Environ Ecol.; c2024. p. 42.
2. Panse VG, Sukhatme PV. Statistical methodology for agricultural workers. New Delhi: ICAR Publications; c1978.
3. Gummadala KR, Tomar SS, Perli VH, Kaushik M. Agronomical performance of black gram (*Vigna mungo* L.) in the presence of organic manures and bio-fertilizers in typic haplustalf. Pharma Innov. 2022;11(6):1927-1931.
4. Burton GW. Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress; c1952. p. 277-83.
5. Hanson GH, Robinson HF, Comstock RE. Biometrical studies on yield in segregating population. Agron. J. 1956;48:268-272.
6. Johnson HW, Robinson HF, Comstock HS. Estimation of genetic and environmental variability in soybean. Agron. J. 1955;47:314-8.
7. Kulheri A, Sikarwar RS, Rajput SS. Genetic variability studies for yield and yield related traits in groundnut (*Arachis hypogaea* L.). Pharma Innov. J. 2022;11(6):315-317.
8. Singh P, Sikarwar RS, Barela A. Study of genetic variability parameter and correlation in groundnut. Pharma Innov. J; c2022. p. 10.
9. Yadav GL, Rajput SS, Gothwal DK, Jakhar ML. Genetic variability, character association and path analysis for pod yield and its component characters in groundnut [*Arachis hypogaea* (L.)]. Legume Res. 2023;46(6):678-683.
10. Kumari K, Sashidharan N. Studies on genetic variability, correlation and path coefficient analysis for morphological and yield traits in different *Arachis* spp. Int. J Curr. Microbiol. App Sci. 2020;9(11):1030-1039.
11. Panse VG, Sukhatme PV. Stlltistical MelhodsJor Agricultural Workers. Indian Council of Agricultural Research, New Delhi; c1985.