International Journal of Advanced Biochemistry Research 2025; 9(7): 540-544

International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating: 5.29
IJABR 2025; 9(7): 540-544
www.biochemjournal.com
Received: 05-05-2025
Accepted: 09-06-2025

Rajanna B
Head & Senior Scientist,
Department of Plant Breeding,
AICRP on Groundnut, MARS,
Raichur, Karnataka, India

Raghavendra BT
Scientist, Department of Plant
Pathology, AICRP on
Groundnut, MARS, Raichur,
Karnataka, India

Shivakumar K
Scientist, Department of Plant
Breeding, AICRP on Linseed,
MARS, Raichur, Karnataka,
India

Lokesh GY
Associate Professor,
Department of Plant Breeding,
College of Agriculture,
Raichur, Karnataka, India

Corresponding Author:
Rajanna B
Head & Senior Scientist,
Department of Plant Breeding,
AICRP on Groundnut, MARS,
Raichur, Karnataka, India

Exploring genetic variation In F_2 population of groundnut using quantitative traits

Rajanna B, Raghavendra BT, Shivakumar K and Lokesh GY

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i7g.4788

Abstract

An investigation was conducted during the *Rabi*/summer 2023-24 at the University of Agricultural Sciences, Raichur to assess the extent of variability generated by hybridization and to estimate the heritability and genetic advance as a per cent of mean for pod yield and its attributing traits in F_2 generation of the cross TMV-2 × K-1812. Genetic variability is essential for enhancing crops as it allows for a broader range of selection options. Hence, the success of selection relies on the type, amount and degree of genetic variability in the material, as well as how much of it is inherited. The segregating population thus obtained was evaluated for ten quantitative traits, revealing significant variability due to genetic segregation. The F_2 population showed significant genetic variability for ten traits including pod yield and yield-contributing traits. Traits like the number of branches per plant, number of matured pods, dry pod yield, kernel yield, biological yield and harvest index exhibited higher GCV and PCV coupled with high heritability and GAM values indicating sufficient variability for selection. The phenotypic co-efficient of variation (PCV) was slightly higher than the genotypic co-efficient (GCV), indicates minimal environmental influence.

Keywords: Genetic variability, F_2 population, genetic co-efficient of variation, phenotypic co-efficient of variation, broad sense heritability, and genetic advance

1. Introduction

The cultivated peanut (*Arachis hypogaea* L.) is a significant crop in many tropical and subtropical regions and is the leading edible oilseed in India. Peanut seeds are particularly valuable due to their high oil content (43-54 per cent) and protein content (25-30 per cent). It belongs to the Fabaceae family and is classified into two subspecies, *hypogaea* and *fastigiata*, with various botanical varieties. Groundnut grows well in semi-arid areas situated between 40° N and 40° S latitudes, with its centre of origin located in the eastern foothills of the Andes (Southern Bolivia and Northern Argentina). In India, groundnut is primarily cultivated under rainfed conditions, making it crucial for crop diversification. The country has the largest groundnut area globally, covering 8.5 million hectares, but ranks second in production with 8.4 million tonnes, trailing behind China. Indian groundnut productivity is relatively low at an average of 988 kg/ha, compared to 2,995 kg/ha in the USA and 2,688 kg/ha in China. Cultivation occurs over three seasons—*Kharif*, *Rabi* and summer—mainly in Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka and Maharashtra, which together account for 80 per cent of the total area and production. Karnataka ranks fourth in production, yielding 1.167 million tonnes annually from 1.22 million hectares (Anon. 2023) [2].

Genetic variability is the basic requirement for crop improvement as this provides a wider scope for selection. Thus, the effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in materials and the extent to which it is heritable. Despite being developed and released in 1940, TMV-2 continues to dominate the market, even though there are other varieties with higher pod yields. Oil mills prefer TMV-2 for oil extraction due to its uniformly sized pods and attractive kernels. However, since the government has officially withdrawn TMV-2, it is no longer available through the official seed distribution system. There is a pressing need to create a new variety that surpasses TMV-2 in yield but retains its desirable pod and kernel characteristics. This is essential to bridge the productivity gap between groundnut cultivation in Karnataka and the national average. For crop improvement, it is crucial to have access to genetic variability, as this offers a broader selection and heritability. Given that the existing variability has been maximized through selection, generating new variability in segregating populations by crossing top genotypes is necessary (Byadagi *et al*. 2018) [6]. In this study, we sought to assess the variation in key traits associated with pod yield and the factors influencing it. We also determined variability indices, including the genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), broad-sense heritability (h²bs) and genetic advance as a per cent of mean (GAM).

2. Materials and Methods

In the present investigation, F_2 population of cross TMV-2 × K-1812 consisting of 109 plants and seven checks namely R-8808, TMV-2, K-9, ICRC-1, Dh-256, Dh-257 and K-1812 belonging to both Virginia and Spanish habit groups were evaluated for genetic variability for pod yield and its attributing traits at All India Co-ordinated Research Project on groundnut research block, Main Agricultural Research Station (MARS), UAS, Raichur during *Rabi*/summer, 2023-24. The F_2 plants were planted in unreplicated block (Kempton and Gleeson 1997) [17] with 8 rows of F_2 population followed by two rows of each check planted with the a spacing of 30 cm between rows and 10 cm between plants respectively. The crop was raised by following all the agronomic practices as per the package of practices recommended for groundnuts in the North-eastern dry zone of Karnataka (Zone 2).

Observations were recorded for ten quantitative characters *viz.* days to flowering, days to maturity, number of branches per plant, number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), shelling percentage (%), sound mature kernel (%), biological yield per plant (g) and harvest index (%). Observations on yield and yield-associated traits were recorded from individual plants since the F_2 population exhibits significant variability due to the segregation of genes at each locus where the parents differed. The mean and range were calculated as per Sunderaraj *et al.* (1972) [29], while genotypic co-efficient of variance (GCV), and phenotypic co-efficient of variance (PCV) were computed for the F_2 population for each character as per the method suggested by Burton and Devane (1953) [5]. Heritability (%) in the broad sense was determined according to Lush's (1949) method, while genetic advance as a per cent of mean was estimated by using the formula of Johnson *et al.* (1955) [16].

3. Results and Discussion

3.1 Genotypic and phenotypic co-efficient of variance

The studies on the co-efficient of variation use percentage of the mean to represent variance. The findings related to phenotypic co-efficient of variance (PCV), genotypic co-efficient of variance (GCV), heritability, and genetic advance expressed as a percentage of the mean are detailed by trait in Table 1. The outcomes of PCV and GCV are depicted in fig. 1, further heritability and GAM in Fig. 2. These statistical values offer insights into the existing variability, gene action, and the potential for enhancing these traits through selective breeding or other genetic strategies.

The phenotypic co-efficient of variation (PCV) ranged from 3.19 per cent (Sound matured kernels) to 40.25 per cent (biological yield per plant). The genotypic co-efficient of variation (GCV) ranged from 3.10 per cent (days to maturity) to 40.22 per cent (biological yield per plant). The slightly higher PCV compared to GCV indicates that environmental influences are minimal on these traits.

An estimate of GCV and PCV for all characters studied revealed that the phenotypic co-efficient of variation (PCV) is slightly greater than the genotypic co-efficient of variation (GCV), it indicates minimal environmental influence on the traits studied.

Table 1: Estimates of genetic variability parameters for yield and its attributing traits in F_2 generation of cross TMV-2 × K-1812

Sr. No.	Characters	Co-efficient of variation		h^2 Broad sense (%)	GAM (%)
		PCV (%)	GCV (%)		
1	Days to flowering	8.14	6.82	70.23	11.78
2	Days to maturity	3.31	3.10	87.65	5.99
3	No of branches per plant	31.22	28.19	81.48	52.41
4	No. of mature pods per plant	39.10	38.30	95.97	77.30
5	Dry pod yield per plant (g)	38.07	37.53	97.22	76.24
6	Kernel weight per plant (g)	37.82	37.46	98.09	76.43
7	Sound matured kernels (%)	3.19	3.14	97.02	6.38
8	Shelling (%)	5.93	5.90	98.99	12.10
9	Biological yield per plant (g)	40.25	40.22	99.85	82.80
10	Harvest index (%)	27.21	27.20	99.99	56.05

- **PCV (%):** Phenotypic coefficient of variation
- **GAM:** Genetic advance as percent means
- **GCV (%):** Genotypic coefficient of variation
- **h^2bs:** Broad sense Heritability

Higher magnitude of GCV and PCV were recorded for biological yield per plant (g) followed by number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), number of branches per plant and harvest index (%), suggesting sufficient amount of variability and thus offer better scope for genetic improvement through selection of these traits.

The results are in agreement with the findings of Ajith *et al.* (2023) [1] for number of branches per plant; Makhan *et al.* (2003) for number of matured pods per plant; Hiremath *et al*. (2011) [12] for dry pod yield per plant (g); Shobha *et al.* (2010) [27] for kernel weight per plant (g); Yadav *et al.* (2023) [33] for biological yield per plant (g); Vasanthi and Reddy (2002) [31] for harvest index (%), who similarly reported that high PCV and GCV values are indicative of traits with a strong genetic basis and reduced environmental variability.

Sound matured kernels (%), days to maturity, shelling percentage (%) and days to flowering recorded a low GCV as well as PCV values suggesting minimal genetic variability within these traits for selection. The results were in agreement with the findings of Zaman *et al*. (2011) [34] and Chavadhari *et al*. (2017) [27] for days to flowering, John *et al*. (2008) [11] and Meta and Monpara (2010) [20] for days to maturity, Vishnuvardhan *et al*. (2012) [32] and John *et al*. (2011) [13] for sound matured kernels and Prasad *et al*. (2002) [25] and Bhagat *et al*. (1986) [4] for shelling percentage.

3.2 Heritability and genetic advance

Broad-sense heritability varied from 70.23 per cent for days to flowering to 99.99 per cent for harvest index. The genetic advance as a per cent of mean ranged from 5.99 per cent for days to maturity to 82.80 per cent for biological yield per plant.

Higher estimates of broad sense heritability (bs) coupled with high genetic advance as per cent of mean were observed for number of branches per plant, number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), biological yield per plant (g) and harvest index (%) revealing that these traits are governed by additive gene action and direct selection for the higher phenotypic value of this trait will be effective.

These results were on par with the findings of Sridevi *et al.* (2022) [28] for number of branches per plant; Aparna *et al.* (2018) [3] for number of matured pods per plant; Gowda (2021) [9] for dry pod yield per plant (g); Patidar and Nadaf (2017) [22] for kernel weight per plant (g); Gupta *et al.* (2015) for biological yield per plant (g); Patil *et al*. (2014) [23] for harvest index (%) who observed that traits with high heritability and genetic advance are primarily governed by additive genetic effects, making them highly amenable to selection.

Days to flowering and shelling percentage recorded high heritability values but moderate GAM values, while sound matured kernels and days to maturity exhibited high heritability but low GAM values. These results reveals the prevalence of both additive and non-additive gene actions in these traits. Enhancing these traits can be accomplished through straightforward selection, progeny selection, or adjusted selection methods that emphasize stabilizing additive gene effects rather than depending exclusively on traditional selection. These results were on par with the findings of Mahalakshmi *et al*. (2005) [19] and Hampannavar *et al*. (2018) [11] for days to flowering, Gali *et al*. (2021) [8] and Savaliya *et al*. (2009) [26] for days to maturity, Narasimhulu *et al*. (2012) [21] and John *et al*. (2005) [15] for sound matured kernels and Prabhu *et al*. (2015) [24] and Suthar *et al*. (2023) [30] for shelling percentage.

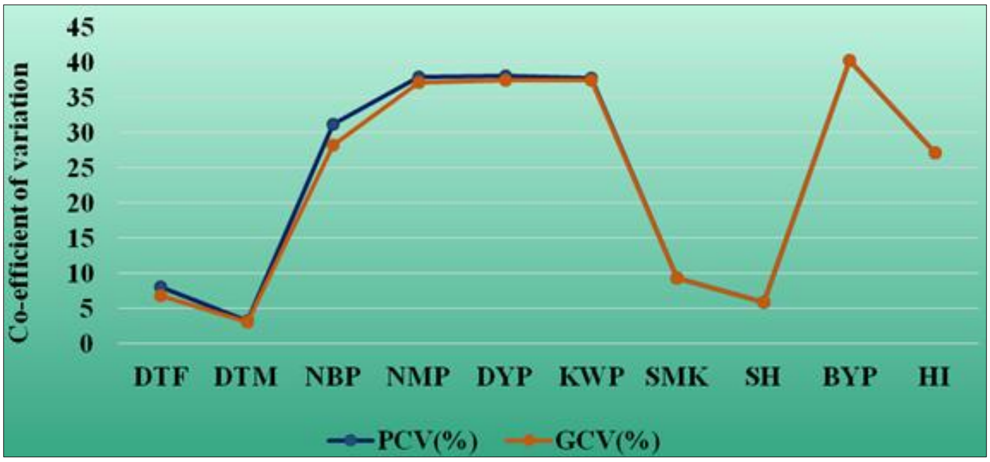

Fig 1: Phenotypic coefficient of variation (PCV) and Genotypic coefficient variation of (GCV) for yield and yield attributing traits in F_2 population of cross TMV-2× K-1812

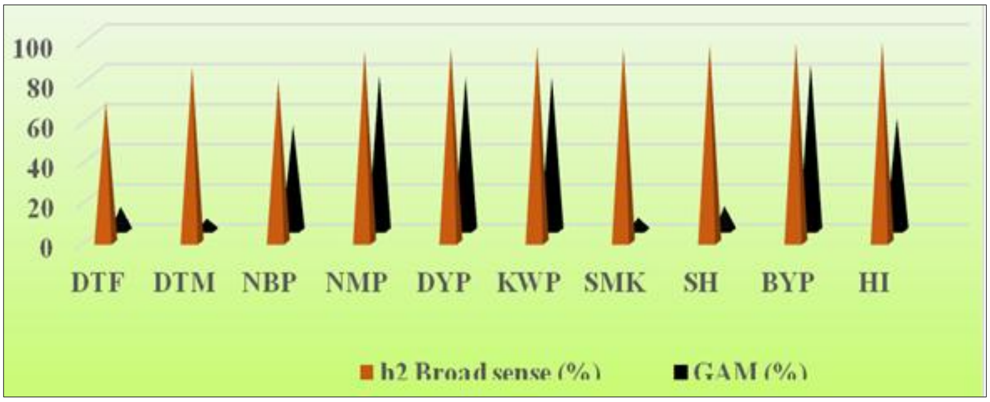

Fig 2: Broad sense heritability (h^2 bs) and genetic advance as per cent of mean (GAM) for yield and yield attributing traits in F_2 population of cross TMV-2 × K-1812.

4. Conclusion

The study revealed that most of the traits studied had sufficient genetic variability which shows its potential to be improved though selection. Phenotypic selection would be more effective for enhancing for number of branches per plant, number of matured pods per plant, dry pod yield per plant (g), kernel weight per plant (g), biological yield per plant (g) and harvest index (%) as these traits exhibited high genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance over mean (GAM).

5. References

1. Ajith P, Rani RK, Kumar M, Brindavathy R, Thiruvarassan S. Variability and association analyses in F2 populations of groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2023;14(3):948-953.
2. Anonymous. Indiastat, Area, Yield and Production for the year 2022-23. 2023. https://www.indiastat.com
3. Aparna P, Shanthi MP, Reddy DM, Latha P. Estimation of genetic parameters in groundnut (*Arachis hypogaea* L.) for yield and its contributing characters under inorganic fertilizer managements. Int J Curr Microbiol Appl Sci. 2018;7(4):1559-1565.
4. Bhagat NR, Taslim, Ahmed, Lalwani HB, Nagraj G. Variation, character association and path analysis in improved groundnut varieties. Indian J Agric Sci. 1986;56(8):300-302.
5. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agron J. 1953;45(10):478-481.
6. Byadagi UR, Venkataravana P, Priyadarshini SK. Genetic variability studies in F2 and F3 populations of three crosses of groundnut (*Arachis hypogaea* L.). J Pharmacogn Phytochem. 2018;7(5):3139-3143.
7. Chavadhari RM, Kachhadia VH, Vachhani JH, Virani MB. Genetic variability studies in groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2017;8(4):1288-1292.
8. Gali S, Reddy DL, Rajesh AP, John K, Sudhakar P, Rao VS. Genetic variability studies in large seeded peanut (*Arachis hypogaea* L.). Pharma Innov J. 2021;10(9):2065-9.
9. Gowda DP. Genetics of late leaf spot disease resistance, pod yield and its component traits in groundnut (*Arachis hypogaea* L.) [MSc thesis]. Bangalore: Univ. of Agril. Sci.; 2021.
10. Gupta RP, Vachhani JH, Kachhadia VH, Vaddoria MA, Reddy P. Genetic variability and heritability studies in virginia groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2015;6(1):253-256.
11. Hampannavar MR, Khan H, Temburne BV, Janila P, Amaregouda A. Genetic variability, correlation and path analysis studies for yield and yield attributes in groundnut (*Arachis hypogaea* L.). Int J Pharmacogn Phytochem. 2018;7(1):870-874.
12. Hiremath CP, Nadaf HL, Keerthi CM. Induced genetic variability and correlation studies for yield and its component traits in groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2011;2(1):135-1342.
13. John K, Reddy PR, Reddy PH, Sudhakar P, Reddy NE. Genetic variability for morphological, physiological, yield and yield traits in F2 population of groundnut (*Arachis hypogaea* L.). Int J Appl Biol Pharm Technol. 2011;2(4):463-469.
14. John K, Vasanthi RP, Venkateswarlu O. Variability and correlation studies for pod yield and its attributes in F2 generation of six Virginia × Spanish crosses of groundnut (*Arachis hypogaea* L.). Leg Res. 2008;31(3):210-3.
15. John K, Vasanthi RP, Venkateswarlu O, Naidu PH. Variability and correlation studies for quantitative traits in spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. Leg Res. 2005;28(3):189-193.
16. Johnson HW, Robinson HI, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron J. 1955;47(7):314-318.
17. Kempton RA, Gleeson AC. Unreplicated trials. In: Statistical methods for plant variety evaluation. Dordrecht: Springer Netherlands; 1997. p. 86-100.
18. Lush JL. Heritability of quantitative characters in farm animals. Proc 8th Cong Genet Heriditas. 1945;35(9):356-75.
19. Mahalakshmi P, Manivannan N, Muralidharan V. Variability and correlation studies in groundnut (*Arachis hypogaea* L.). Leg Res. 2005;28(3):194-197.
20. Meta HR, Monpara BA. Genetic variation and trait relationship in summer groundnut (*Arachis hypogaea* L.). J Oilseeds Res. 2010;27(1):8-11.
21. Narasimhulu R, Kenchanagoudar PV, Gowda MVC. Study of genetic variability and correlations in selected groundnut genotypes. Int J Appl Biol Pharm Technol. 2012;3(1):355-358.
22. Patidar OP, Nadaf HL. An assessment of genetic variability and traits association among high oleic advanced breeding lines for yield and quality traits in groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2017;8(1):201-205.
23. Patil AS, Punewar AA, Nandanwar HR, Shah KP. Estimation of variability parameters for yield and its component traits in groundnut (*Arachis hypogaea* L.). Bioscan. 2014;9(2):749-754.
24. Prabhu R, Manivannan N, Mothilal A, Ibrahim SM. Estimates of genetic variability parameters for yield and yield attributes in groundnut (*Arachis hypogaea* L.). Int J Agric Environ Biotechnol. 2015;8(3):551-559.
25. Prasad YAK, Verma ZA, Haider, Jayalal Mahto. Correlation and path analysis in spanish bunch groundnut (*Arachis hypogaea* L.). J Res. 2002;14(2):91-93.
26. Savaliya JJ, Pansuriya AG, Sodavadiya PR, Leva RL. Evaluation of inter and interspecific hybrid derivatives of groundnut (*Arachis hypogaea* L.) for yield and its components. Leg Res. 2009;32(2):129-132.
27. Shoba D, Manivannan N, Vindhiyavarman P. Gene effects of pod yield and its components in three crosses of groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2010;1(6):1415-1419.
28. Sridevi S, Meenakumari B, Manivannan N, Ravichandran V. Assessment of genetic variability, character association and path analysis of kernel yield and yield components in groundnut (*Arachis hypogaea* L.). Electron J Plant Breed. 2022;13(2):476-481.
29. Sunderaraj N, Nagaraju S, Venkara RMN, Jagannath MK. Designs and analysis of field experiments [MSc thesis]. Bangalore: Univ. Agril. Sci.; 1972.

30. Suthar DM, Patel DG, Patel PR, Soni NV. Studies on variability for yield and yield attributing traits in groundnut (*Arachis hypogaea* L.). Biol Forum. 2023;15(11):520-525.
31. Vasanthi RP, Reddy RC. Variability in F2 generation of five groundnuts crosses involving foliar disease resistant genotypes. J Res. 2002;30(2):137-142.
32. Vishnuvardhan KM, Vasanthi RP, Reddy PKH, Reddy BV. Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). Int J Appl Pharm. 2012;3(1):976-455.
33. 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.). Leg Res. 2023;46(6):678-683.
34. Zaman MA, Tuhina-Kahatun M, Ullah MZ, Moniruzzamn M, Alam KH. Genetic variability and path analysis of groundnut (*Arachis hypogaea* L.). J Sci Krishi Found. 2011;9(2):29-36.