Plant Archives Vol. 26, Supplement 1, 2026 pp. 1816-1821 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.244

STUDY ON EXPLORING THE GENETIC VARIABILITY IN M_2 GENERATION OF GROUNDNUT (*ARACHIS HYPOGAEA* L.) FOR POD YIELD AND KERNEL TRAITS

Priyanka[1], H.C. Sowmya[2*], Hasan Khan[2], G.C. Shekar[3], Sheela. B. Patil[1], S.K. Jayalakshmi[4] and H. C. Latha[5]
[1]Department of Genetics and Plant Breeding, College of Agriculture, Raichur, Karnataka, India
[2]Department of Genetics and Plant Breeding, College of Agriculture, Kalaburagi, Karnataka, India
[3]Department of Genetics and Plant Breeding, College of Agriculture, Bheemarayanagudi, Karnataka
[4]Department of Plant Pathology, College of Agriculture, Kalaburagi, Karnataka, India
[5]Farm Superintendent, ARS, Madikeri, UAS, Mandya, Karnataka, India
*Corresponding author's email address: soumyahc@uasraichur.edu.in

(Date of Receiving : 02-10-2025; Date of Acceptance : 13-12-2025)

ABSTRACT

Groundnut (*Arachis hypogaea* L.) is a highly self-pollinated crop with limited genetic variation. Induced mutagenesis might serve as a potential tool in creating variability to supplement plant breeders in crop improvement. The current investigation emphasize on comprehending the gamut of genetic variation expressed for twelve traits in M_2 generation of groundnut variety Vijetha (R-2001-2) treated with four dosage of Gamma rays (150 Gy, 200 Gy, 250 Gy and 300 Gy) and three concentrations of Sodium azide (0.02%, 0.03% and 0.04%) during late *kharif* 2023. Analysis revealed the inheritance of wider genetic variation for the majority of traits under study as upheld by high values of mean, GCV and PCV. Key traits like the matured pods per plant, kernel yield per plant, pod yield per plant and shelling percentage registered elevated heritability and GAM indicating a plausible avenue of inducing desirable mutations in these traits. Further the effective selection of these promising traits in M_2 would yield genetic improvement and subsequent development of a superior variety.

***Keywords* :** Groundnut, M_2 generation, Gamma rays, Sodium azide, Variability

Introduction

Groundnut, known as *Arachis hypogaea* L., is predominantly a self-pollinating, oilseed and grain legume that thrives well in tropical and subtropical climates. In India, it is spread across the area (44.31 lakh hectares), production and productivity (86.54 lakh tonnes & 1,953 kg per hectare) respectively (Anon., 2023-24). Despite the crop being self-pollinated and possessing narrow genetic base, infusion of more genetic variations through creative breeding techniques is vital in crop improvement activity. The mutation breeding serves as one among the potential breeding methods to diversify the genetic variations and yield potentiality of crop plant (Raina & Khan, 2020). The intrinsic bottlenecks associated with crop, such as floral structure and the biology limiting intensive hybridization, interspecific cross-incompatibility, and polyploidy, limit the varietal improvement in groundnut (Gregory and Gregory, 1979). Although the traditional breeding techniques have greatly aided in developing superior types, induced mutagenesis might serve as a potential bridge to diversify genetic variability, a prerequisite in crop improvement. Consequently, the selection efficiency is largely impacted by the degree of variability residing in the material and its heritable nature.

Therefore, the current study was initiated in the light of exploiting genetic variability for promising traits related to yield. The variability indices like the genotypic and phenotypic co-efficient of variance (GCV & PCV), broad sense heritability (h^2_{bs}) and genetic advance as a percent of mean (GAM) were computed in M_2 generations following induced mutagenesis in groundnut variety (R-2001-2).

Materials and Methods

The M_2 population consisted of 1429 plants and control (R-2001-2) in plant to progeny row obtained from four dosage of gamma irradiation(150 Gy, 200 Gy, 250 Gy and 300 Gy) and three concentrations of Sodium azide (0.02%, 0.03% and 0.04%) and study was undertaken in experimental plot with 30cm x 15cm spacing for between rows and within plants at Zonal agricultural research station (ZARS), Kalaburagi during late *kharif* 2023 and agricultural practices as per package of practices were carried. Observations were documented from individual plants as the M_2 population is heterozygous. The twelve quantitative characters namely survival percentage, plant height, seedling height, number of branches per plant, days to first flowering, days to maturity, matured pods per plant, pod yield, kernel yield, 100-pod weight, 100-kernel weight and shelling percentage were recorded.

The mean and range were computed by following the method of Sunderaraj *et al.* (1972), the co-efficient of variance (PCV and GCV) as per Burton and De Vane (1953) while heritability and GAM using the formula given by Johnson *et al.,* (1955).

Results and Discussion

Genetic variability assessment

The research findings on variability parameters encompass co-efficient of variance that rely on the percentage of mean to express variance, phenotypic and genotypic co-efficient of variation (GCV and PCV), heritability in broad sense and GAM for traits under study and are executed in (Table 1 & 2), highlighting the existing variation, gene activity and potential for trait improvement by selective breeding methods.

The evaluated genetic variability across the treatments exhibited the PCV value in the gamma-irradiated population ranging from 1.83 per cent for trait days to maturity at 200 Gy to 63.61 per cent for trait kernel yield at 150 Gy. Similarly, GCV values range from 1.56 per cent for days to maturity at 200Gy to 53.78 per cent for kernel yield at 150 Gy. Meanwhile, in the sodium azide treated population, PCV ranged from 1.28 per cent for days to maturity at 0.02% to 56.56 per cent for kernel yield in 0.03% and GCV range from 0.85 per cent for days to maturity in 0.02% to 43.89 per cent in kernel yield at 0.02% mutagenic treatment.

Further PCV values are consistently high than the GCV values for all twelve traits under study. Elevated PCV values indicate environmental influence and thus reducing the efficiency of selection, in line with Vasanthi *et al.* (2015) in groundnut. A low marginal difference in PCV and GCV (< 3 %) was registered for four traits viz., Days to first flower, Days to maturity, 100- pod weight and shelling percentage in both the treated populations specifying minimal environmental influence and hence mere phenotypic selection could be duly considered (Jerish *et al*., 2024)

Traits like number of matured pods, pod yield and kernel yield exhibited higher value of GCV and PCV across every treatment of both gamma irradiated and sodium azide treated populations, displaying the greater scope in crop improvement. These findings were on par with earlier works of Shashikumara *et al.* (2016); Bharathi *et al.* (2005); Jerish *et al.* (2024); Mensah and Obadoni (2007) for pod yield per plant.

Traits *viz.,* shelling percentage, 100-pod weight and 100-kernel weight recorded low magnitude of GCV and PCV, suggesting the narrow variability induced for traits and limiting the scope of selection. These findings are in line with earlier reports of Channayya *et al.* (2011) for shelling percentage.

Heritability and genetic advance

The Broad sense heritability spanned from 37.62 per cent to 88.84 per cent for trait seedling height and survival per cent at harvest at 150 Gy and 300 Gy dose of mutagen respectively. Meanwhile, the sodium azide treated population displayed the heritability values varying from 34.10 per cent to 83.71 per cent for number of branches per plant and 100-pod weight respectively in 0.03% concentration of mutagen treatment.

In addition, the GAM values were between 2.76 per cent for days to maturity at 200 Gy to 103.77 per cent for trait number of mature pods per plant in 250Gy mutagenic dose. While the sodium azide treated population exhibited the GAM values between 1.17 per cent for Days to maturity at 0.02% to 86.00 per cent for number of mature pods at 0.03% concentration of mutagenic treatment.

The strong heritability was demonstrated for the majority of traits subjected to study in both of the treated populations. The traits survival percent at harvest, number of matured pods, pod yield per plant, kernel yield per plant, 100-pod weight, 100-kernel weight and shelling percentage have shown higher heritability across the treatments, while trait number of branches executed moderate heritability except at 150 Gy and 0.02% mutagenic treatments, which showed high heritability. The trait days to maturity has shown higher heritability except at 0.02% showing moderate heritability. Similarly, days to first flower has shown higher heritability except at 0.02% and 0.03% mutagen treatments displaying moderate heritability. Similar findings of higher heritability by Ittah *et al.* (2016) for pods per plant; by Jerish *et al.* (2024) for pod yield; by Bharathi *et al.* (2005) for kernel yield; by Channayya *et al.* (2011) for shelling percentage.

Higher GAM was registered for traits such as survival percent at harvest, matured pods per plant, pod yield per plant, 100-pod weight, 100-kernel weight, kernel yield per plant and shelling percentage across all the mutagic treatments. These outcomes are confirmed by Ittah *et al.* (2016) for kernel yield per plant, by Badigannavar and Murty (2007) for pod yield; by Jerish *et al.* (2024) for trait number of matured pods. Moderate GAM for trait number of branches per plant was documented at 300 Gy and 0.03% concentration of mutagen treatments. Similar outcomes of moderate GAM by Channayya *et al.* (2011); Kavera (2009) were noticed. Lower GAM was registered for days to first flower & days to maturity across all the treatments of the mutated populations.

Elevated heritability and GAM suggests the governance of additive genic action and the noticed variations are largely due to genetic factors and are least impacted by environmental factors. Therefore, selection of traits like the number of matured pods per plant, kernel yield per plant, pod yield per plant and 100- pod weight are beneficial, as changes induced through breeding efforts within traits are most likely to pass to the later generations. Similar outcomes of higher heritability and GAM by Ittah *et al.* (2016); Shashikumara *et al.* (2016); Jerish *et al.* (2024) in groundnut and Kishore *et al.* (2023) in chickpea for traits like the number of branches per plant, plant height, matured pods per plant, pod yield per plant were noticed.

Conclusion

These findings reveal the presence of ample genetic variations across various traits of both the treated populations, showcasing the potency of genetic improvement through effective selection of mutagen dose and desirable traits. Elevated GCV and PCV was noticed for promising traits like matured pods per plant, pod yield per plant and kernel yield per plant at 150 Gy, 0.02% and 0.03% suggesting maximum variability and effectiveness of dosage to selection. Higher estimate of heritability with GAM were documented for traits like the survival per cent at harvest matured pods per plant and 100-pod weight at 250 Gy, 300 Gy and 0.04% dose of mutagen, revealing the governance of additive genic action and the possibility of direct selection for yield enhancement.

Table 1: Estimates of Genetic variability parameters in M_2 generation of roundnut

Traits	Treatment	Mean	GCV (%)	PCV (%)	h2 (%)	GAM
Survival percentage at harvest	**T_1 (150 Gy)**	43.33	16.42	20.64	63.31	20.64
	T_2 (200 Gy)	42.8	25.31	28.1	81.07	46.94
	T_3 (250 Gy)	39.73	17.97	22.53	63.61	29.52
	T_4 (300 Gy)	37.71	40.6	43.08	88.84	78.83
	Control	71.23	-	-	-	-
	T_5 (0.02%)	42.8	19.73	23.44	70.83	34.2
	T_6 (0.03%)	41.86	26.5	29.56	80.39	48.95
	T_7 (0.04%)	41.55	17.52	21.83	64.35	28.94
Seedling Height (cm)	**T_1 (150 Gy)**	6.76	9.94	16.2	37.62	12.56
	T_2 (200 Gy)	6.52	16.84	21.44	61.72	27.26
	T_3 (250 Gy)	6.24	22.19	17.32	60.91	27.85
	T_4 (300 Gy)	6.12	14.99	20.6	52.98	22.49
	Control	6.75	-	-	-	-
	T_5 (0.02%)	6.3	14.26	19.8	51.84	21.15
	T_6 (0.03%)	6	16.5	21.92	56.71	25.61
	T_7 (0.04%)	5.98	16.8	22.18	57.39	26.23
Plant Height (cm)	**T_1 (150 Gy)**	15.04	12.36	16.22	58.06	19.41
	T_2 (200 Gy)	14.23	14.44	18.22	62.82	23.58
	T_3 (250 Gy)	13.81	21.79	24.61	78.37	39.74
	T_4 (300 Gy)	13.61	30.65	32.78	87.45	59.05
	Control	15.05	-	-	-	-
	T_5 (0.02%)	15.94	16.21	19	72.77	28.49
	T_6 (0.03%)	15.78	16.48	19.28	73.01	29
	T_7 (0.04%)	14.97	28.49	30.38	87.92	55.04
Days to First	**T_1 (150 Gy)**	29.27	4.24	4.83	77.03	7.66

Flower	**T_2 (200 Gy)**	29.94	3.97	4.56	75.76	7.12
	T_3 (250 Gy)	30.21	3.3	3.97	68.99	5.64
	T_4 (300 Gy)	31.75	4.77	5.24	82.93	8.95
	Control	30.64	-	-	-	-
	T_5 (0.02%)	28.83	2.12	3.1	46.91	3
	T_6 (0.03%)	30.05	2.36	3.27	52.31	3.52
	T_7 (0.04%)	31.76	3.22	3.88	68.92	5.52
Days to Maturity	**T_1 (150 Gy)**	107.07	1.62	1.88	74.22	2.88
	T_2 (200 Gy)	108.16	1.56	1.83	73.27	2.76
	T_3 (250 Gy)	110.08	1.79	2.02	78.78	3.27
	T_4 (300 Gy)	112.94	1.89	2.1	81.36	3.52
	Control	111.5	-	-	-	-
	T_5 (0.02%)	107.52	0.85	1.28	44.64	1.17
	T_6 (0.03%)	109.25	1.5	1.77	72.08	2.63
	T_7 (0.04%)	110.8	2.57	2.73	88.55	4.98
Number of primary branches per plant	**T_1 (150 Gy)**	6.15	29.48	35.96	67.22	49.8
	T_2 (200 Gy)	6.02	21.12	29.77	50.35	30.88
	T_3 (250 Gy)	5.7	27.38	35.88	58.2	43.03
	T_4 (300 Gy)	5.09	14.32	28.17	25.83	14.99
	Control	5.97	-	-	-	-
	T_5 (0.02%)	6.14	24.77	31.87	60.42	39.67
	T_6 (0.03%)	6.08	15.64	26.79	34.1	18.82
	T_7 (0.04%)	5.65	22.43	33.82	43.99	30.65

Table 2: Estimates of genetic variability parameters in M_2 generation of groundnut

Traits	Treatment	Mean	GCV (%)	PCV (%)	h^2 (%)	GAM
Number of pods per plant	**T_1 (150 Gy)**	27.75	49.48	53.75	84.74	93.84
	T_2 (200 Gy)	24.89	48.57	53.92	81.14	90.14
	T_3 (250 Gy)	24	55.05	60.17	83.71	103.77
	T_4 (300 Gy)	24.2	46.55	52.41	78.89	85.17
	Control	23.28	-	-	-	-
	T_5 (0.02%)	21.98	46.7	53.7	75.62	83.67
	T_6 (0.03%)	19.92	48.7	56.8	73.49	86
	T_7 (0.04%)	24.22	39.32	46.1	72.75	69.1
Pod yield per plant (g)	**T_1 (150 Gy)**	16.55	50.46	59.04	73.04	88.85
	T_2 (200 Gy)	15.94	44.51	54.72	66.17	74.6
	T_3 (250 Gy)	16.24	47.59	56.92	69.88	81.95
	T_4 (300 Gy)	17.16	46.72	55.29	71.41	81.34
	Control	16.87	-	-	-	-
	T_5 (0.02%)	15.72	46.05	56.23	67.07	77.69
	T_6 (0.03%)	14.07	43.19	56.26	58.94	68.32
	T_7 (0.04%)	17.28	36.42	46.77	60.62	58.41
Hundred pod weight (g)	**T_1 (150 Gy)**	59.62	19.69	23.35	71.09	43.95
	T_2 (200 Gy)	64.67	18.35	21.7	71.53	31.98
	T_3 (250 Gy)	69.14	20.15	22.87	77.59	36.56
	T_4 (300 Gy)	71.11	18.36	21.16	75.26	32.81
	Control	71.9	-	-	-	-
	T_5 (0.02%)	72.15	20.76	23.21	80.01	38.25
	T_6 (0.03%)	73.2	23.18	25.34	83.71	43.7
	T_7 (0.04%)	72.06	13.03	16.66	61.15	20.99
Kernel yield per plant (g)	**T_1 (150 Gy)**	10.42	53.78	63.61	71.49	93.69
	T_2 (200 Gy)	10.21	43.86	55.89	61.58	70.91
	T_3 (250 Gy)	11.15	49.02	58.39	70.5	84.8

	T_4 (300 Gy)	11.9	48.77	57.12	72.9	85.78
	Control	11.23	-	-	-	-
	T_5 (0.02%)	10.57	43.89	55.19	63.23	71.89
	T_6 (0.03%)	9.36	42.09	56.56	55.39	64.54
	T_7 (0.04%)	11.82	38.56	48.8	62.42	62.76
Hundred kernel weight (g)	**T_1 (150 Gy)**	30.81	12.52	17.76	71.39	26.12
	T_2 (200 Gy)	31.44	14.06	16.38	85.32	28.66
	T_3 (250 Gy)	33.46	13.44	16.13	83.15	24.5
	T_4 (300 Gy)	33.51	12.58	14.28	79.05	20.85
	Control	32.66	-	-	-	-
	T_5 (0.02%)	33.16	11.78	15.09	82.32	23.89
	T_6 (0.03%)	32.57	12.21	13.52	82.76	24.77
	T_7 (0.04%)	33.26	11.49	12.82	81.73	23.26
Shelling percentage	**T_1 (150 Gy)**	63.34	16.77	17.95	87.3	32.29
	T_2 (200 Gy)	64.8	15.06	16.3	85.29	28.65
	T_3 (250 Gy)	68.95	13.04	14.3	83.12	24.49
	T_4 (300 Gy)	69.06	11.38	12.8	79	20.84
	Control	66.6	-	-	-	-
	T_5 (0.02%)	68.33	12.78	14.09	82.29	23.89
	T_6 (0.03%)	67.12	13.21	14.52	82.73	24.76
	T_7 (0.04%)	68.53	12.49	13.82	81.69	23.25

Where, GCV- Genotypic co-efficient of variation, PCV- Phenotypic co-efficient of variation, h^2- Broadsense heritability, GAM- Genetic advance as percent of mean

Disclaimer (Artificial Intelligence)

Author(s) hereby declares that NO generative AI technologies such as Language Models (ChatGPT. COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

Acknowledgement

The current work has been undertaken as a part of the master's research program in ZARS, Kalaburagi, UAS Raichur, Karnataka, India. I am thankful to the advisory committee, Dean (PGS) and Head of the Department of Genetics and Plant Breeding, College of Agriculture, Kalaburagi for the necessary research facilities and for their support during the master's program.

References

Anonymous (2023-24). Area, yield, and production for the year 2023-24. *Indiastat.* Retrieved from https://www.indiastat.com.

Badigannavar, A. M. and Murty, G. S. S. (2007). Genetic enhancement of groundnut through gamma ray induced mutagenesis. *Plant Mutat. Rep*., **1(3)**, 16-21.

Bharathi, V. B., Prakash, M., Jagadeesan, S., Kavimani, S., Saravanan, K. and Ganesan, J. (2005). Variability studies in M_2 generation of groundnut (*Arachis hypogaea* L.) Var. VRI-2. *Legume Res*., **28(1)**, 68-70.

Burton, G.W. and De Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.,* **45(2)**, 478-481.

Channayya, H. P., Nadaf, H. L. and Keerthi, C. M. (2011). Induced genetic variability and correlation studies for yield and its component traits in groundnut (*Arachis hypogaea* L.). *Electron. J. Plant Breed.,* **2(1)**, 135-142.

Gregory, M. P. and Gregory, W. C. (1979). Exotic germplasm of *Arachis hypogaea* L. interspecific hybrids. *J. Hered.,* **70(5)**, 185-193.

Ittah, M. A., Binang, W. B., Shiyam, J. O. and Idu, P. O. (2016). Genetic and correlation analyses of the variation in yield traits in x-ray irradiated groundnut mutants. *Sci. Agric.,* **1(1)**, 64-77.

Jerish, J. R., Saravanan, S., Geetha, K., Pillai, M. A., Sheela, J., Pushpam, A.K. and Mondal, S. (2024). Genetic Variability Analysis of Gamma Irradiated M_2 Populations for Higher Oleic Acid Content in TMV (Gn) 13 (*Arachis hypogaea* L.). *Legume Res.,* **48(3)**, 393-399.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Genotypic and phenotypic correlations in soybean and their implication in selection. *Agron. J.*, **47(2)**, 477-483.

Kavera. (2009). Oil quality improvement in groundnut (*Arachis hypogaea* L.) through induced mutagenesis. *Ph.D. Thesis*, University of Agricultural Sciences, Dharwad, India.

Kishore, N., Katna, G. and Sharma, N. (2023). Genetic variability and association among various traits in chickpea (*Cicer arietinum*) mutants. *HJAR.,* **49(1)**, 44-50.

Mensah, J. K. and Obadoni, B. (2007). Effect of sodium azide on yield parameters of groundnut (*Arachis hypogaea* L.). *African J. Biotechnol*., **6(6)**, 668-671.

Raina, A. and Khan, S. (2020). Mutagenic effectiveness and efficiency of gamma rays and sodium azide in M_2 generation of Cowpea (*Vigna unguiculata* (L.) Walp.). *bioRxiv*. **2(9)**, 20-23.

Shashikumara, P., Sanjeev, B. G. and Venkataravana, P. (2016). Assessment of genetic variability and identification of transgressive segregants for pod yield and its component traits in F_2 segregating generation of groundnut (*Arachis hypogea* L.). *Int. J. Farm Sci.*, **6(4)**, 53-60.

Sunderaraj, N., Nagaraju, S., Venkara R. M. N. and Jagannath, M. K. (1972). Designs and analysis of field experiments. *M.Sc. Thesis*, University of Agricultural Sciences, Bangalore, India.

Vasanthi, R. P., Suneetha, N. and Sudhakar, P. (2015). Genetic variability and correlation studies for morphological, yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Legume Res.*, **38(1)**, 9-15