International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating: 5.29
IJABR 2025; 9(6): 1132-1136
www.biochemjournal.com
Received: 27-04-2025
Accepted: 30-05-2025

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Genetic studies in M_4 progenies of lathyrus CV. NLK-73

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i6m.4680

Abstract
The present investigation entitled, "Genetic studies in M_4 progenies of Lathyrus CV. NLK-73" aimed to estimate variances due to within family and between family, to estimate genetic parameters and to identify superior mutants for yield and yield contributing characters with low ODAP content. The experiment was conducted in *Rabi* 2024 season at Research farm of Agricultural Botany Section, College of Agriculture, Nagpur. Material under study 29 M_4 mutants along with the checks NLK-73 and Ratan, were evaluated in a Randomized Complete Block design with three replications. Seven traits days to first flowering, days to maturity, plant height, number of branches plant^{-1}, pods per plant, 100-seed weight and seed yield per plant were recorded and subjected to analysis of variance. Highly significant family mean squares for all traits confirmed substantial genetic variability among the M_4 progenies. Intraclass correlation coefficients indicated considerable within-family variation and clear differentiation among families, suggesting that both among-family ($\sigma^2 f$) and within-family ($\sigma^2 w$) variance components should be weighted equally during selection. The genotypic and phenotypic coefficients of variation ranged from high to low across characters, as did broad-sense heritability and genetic advance expressed as a percentage of the mean. When all genetic parameters were considered jointly, only seed yield per plant, pods per plant and branches per plant combined moderate to high GCV, moderate to high heritability and high genetic advance, marking them as the most promising traits for selection. Considering the above three characters, NLM-12, NLM-13, NLM-17, NLM-20, NLM-21, NLM-22, NLM-23, NLM-26, NLM-27 and NLM-28 were isolated as superior mutant lines for forwarding to the yield trial.

Keywords: Lathyrus, M_4, mutation, GCV, PCV, heritability, genetic advance

Introduction
The *Lathyrus sativus* L. is a leguminous and self pollinated crop belong to family 'leguminous' (Fabaceae) having chromosomes number 2n=14 also known as grass pea, chickling vetch, indian pea, white pea, white vetch and kesari dal is an annual herb and an important pulse crop rich in protein content (28%) next to soybean, Genus Lathyrus with 130 Lathyrus species are distributed across the temperate regions of the Northern Hemisphere and at higher elevations in tropical Africa. In India, aside from the ornamental *Lathyrus odoratus*, L. sativus is the only cultivated species, yielding the pulse commonly known as khesari dal. The edible *L. sativus* in North India part of its West Central Asian Mediterranean origin where seed remains dating to approximately 3600 years ago have been recovered.
Economically, Lathyrus spp. play a vital role in India, Bangladesh, Pakistan, Nepal and Ethiopia. Beyond South Asia, the genus has become extensively naturalized across Central, Southern and Eastern Europe from Germany through the Iberian Peninsula and eastward into the Balkans and southern Russia—as well as on Mediterranean islands (Crete, Rhodes, Cyprus) and throughout West Asia and North Africa (Syria, Lebanon, Palestine, Egypt, Iraq, Afghanistan, Morocco, Algeria).
Sharma reported that the protein quality of lathyrus is better than any other pulses. Chemical composition of *Lathyrus sativus* grain shows also the presence of minerals like Ca, Fe, P and vitamins like B_1, B_2 and niacin. It is also rich in carbohydrates (58.2%). On a global scale, grass pea is grown on roughly 1.50 million hectares, yielding about 1.20 million tonnes

annually. (Gupta. *et al.*, 2018) [6]. In India area under lathyrus is about 0.58 million hectares and the major area under lathyrus is in Uttar Pradesh, Bihar, West Bengal, Madhya Pradesh and Maharashtra contributing about 4.5% total pulse production of the country. In Maharashtra it is cultivated in Bhandara, Chandrapur, Gadchiroli, Gondia and Nagpur districts of eastern Vidarbha, accounting to 33125 hectares.

Area, Production and Productivity of Lathyrus crop during year 2024-25

Region	Area	Production	Productivity
World	1.50 mha	1.2 mt	5.33 qha^{-1}
India	0.58 mha	0.45 mt	7.42 qha^{-1}
Maharashtra	33125 ha	-	3.00 qha^{-1}

(Anonymous, 2025)

Grass pea is regarded as an invaluable crop under abiotic stresses drought, flooding and hail as well as biotic challenges from pests, owing to its strong drought tolerance. As a legume, it forms root nodules that fix atmospheric nitrogen, part of which enriches the soil for subsequent crops. It is commonly sown as an Utera or Paira intercrop in standing paddy during the Rabi season. Additionally, the main pulse crop, Tur (Pigeon pea) is grown only on bunds, hence the production of tur is not sufficient for the requirements of these region. This gives the chance to lathyrus to serve as alternative pulse. Thirdly, the lathyrus plant type is considered to be strongly drought resistant (Tripathy *et al.*, 2011) [20] and Grass pea (*Lathyrus sativus*) flourishes with minimal agronomic intervention and has long served as a multipurpose pulse processed into flatbreads, fritters and stews for human diets and utilized as green forage and stover for livestock. Despite satisfying a substantial portion of national pulse demand, its cultivation has been curtailed in many regions due to neurolathyrism, an irreversible neuro degenerative disorder linked to β-N-oxalyl-L-α,β-diaminopropionic acid (β-ODAP) present in seeds and seedlings. Traditional grass pea cultivars accumulate 0.5-2.5% β-ODAP (Kumar *et al.*, 2011), highlighting the need to harness genetic variation both for lowering β-ODAP content and for enhancing yield two principal breeding objectives. Additionally, considerable untapped potential exists for improving yield and other agronomic traits in this species.

Mutation breeding, which has globally enriched the genetic base and introduced novel alleles in grain legumes, offers a particularly attractive approach for grass pea improvement. Physical and chemical mutagens can amplify the natural mutation rate, thereby broadening genetic variability and increasing the probability of recovering desirable mutants. To efficiently induce and deplay such variation, it is essential to conduct systematic, comparative evaluations of mutagenic effectiveness and efficiency across target genotypes. In light of these considerations, the present study was conceived and undertaken.

Materials and Methods

Dry, healthy, genetically pure seeds of Lathyrus sativus cv. NLK-73 were procured from the Agricultural Botany Section, College of Agriculture, Nagpur. Four seed lots of 500 seeds each were prepared; three lots were sent to the Bhabha Atomic Research Centre (BARC), Trombay, for (CO60) γ-irradiation at doses of 250, 300 and 350 Gy, while the fourth served as an untreated control. All seed lots were sown to establish the M_1 generation in the 2020 Rabi season, and each M_1 plant was harvested individually. The progeny seed from these plants were used to raise the M_2 generation in Rabi 2021, during which 97 single-plant mutants exhibiting desirable traits were identified. In the subsequent 2022 Rabi season, these 97 mutants, together with the parent NLK-73 and the check variety Ratan, were advanced as the M_3 generation and 29 single plant mutants were identified for desired characters. The present work is the continuation of the above mentioned work. The 29 mutants identified along with check Ratan and parent NLK-73 were planted in RBD with three replication in *Rabi* 2023-2024. The mutants identified in M_3 generation like high pods, High seed yield and low ODAP content were also confirmed in M_4 progenies. Plot size was 0.9 m x 4 m. Each M_4 mutant line and the two checks were grown in two rows of twenty plants each, with 45 cm between rows and 20 cm between plants. In each replication, five plants per entry were randomly selected for phenotypic evaluation of days to first flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, 100-seed weight (g) and seed yield per plant (g). These observations were analysed to compute descriptive statistics (mean, range, coefficient of variation), variance components (genotypic and phenotypic variances), broad-sense heritability (Hanson *et al.*, 1956) [9], genotypic and phenotypic coefficients of variation (Burton & Devane, 1953) [16], expected genetic advance (Robinson *et al.*, 1949) [16] and genetic advance expressed as a percentage of the mean (Johnson *et al.*, 1955). Analysis of variance was estimated as per the method given by Sharma (1969) [17].

Results and Discussion

Analysis of variance was performed on seven traits measured in 29 mutant progenies along with two checks to partition genetic variation into between and within-family components. As summarized in Table 1, family mean squares were highly significant for all traits, days to first flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plant indicating substantial genetic variability among families and justifying subsequent estimation of genetic parameters. Comparable levels of between-family variability have been documented in cowpea by Dhaka *et al.* (2013) [5] and in soybean by Malek *et al.* (2014) [15], Bisane *et al.* (2019) [4] and Kamdi *et al.* (2020) [12].

In the M_4 generation, the intraclass correlation coefficient (t) calculated as the ratio of between-family variance ($\sigma^2 f$) to total phenotypic variance ($\sigma^2 p$) was estimated for all traits. This value was observed to range from 0.87 for number of branches plant^{-1} to 0.41 for seed yield plant^{-1}. Highest intra class correlation value was observed for number of branches plant^{-1} (0.87) followed by days to first flower (0.74), 100 seed weight (g) (0.60), plant height (cm) (0.58), day to maturity (0.55), number of pods plant^{-1} (0.48) and seed yield plant^{-1} (g) (0.41). This revealed that 87%, 74%, 60%, 58%, 55%, 48% and 41% of variation for number of branches plant^{-1}, days to first flower, 100 seed weight (g), plant height (cm), day to maturity, number of pods plant and seed yield plant^{-1} (g) respectively were due to differences between the families and 13%, 26%, 40%, 42%, 45%, 52% and 59% were due to within families.

These findings reveal that, although individual variability within each family remains pronounced for all evaluated traits, families themselves are clearly differentiated even at lower hierarchical levels. Accordingly, it is prudent to assign equal emphasis to between family (σ^2f) and within family (σ^2w) variance components when selecting in the M_4 progenies. A two-stage breeding approach first selecting among families, then within families should therefore maximize genetic gain. Jambulwar *et al.* (2021) [10] and Srikanth *et al.* (2021) [19] like wise recommended equal weighting of σ^2f and σ^2w and sequential family then within family selection as an optimal strategy.

Generating adequate genetic variation is fundamental to cultivar or inbred-line development, and induced mutation offers an effective means of expanding the variability pool. To quantify this variation in our M_4 progenies, we calculated key genetic parameters mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2) and genetic advance (GA) for seven traits. The summary of these estimates is provided in Table 3.

Mean and Range

Table 3, summarizes the grand means for 29 M_4 mutants along with parent and check, (46.48) days to first flowering, (106.18) days to maturity,(61.26) cm plant height, (3.70) branches plant^{-1}, (46.10) pods plant^{-1}, (7.56 g) 100-seed weight and (19.53 g) seed yield plant^{-1}. The widest phenotypic range was recorded for pods per plant (19.27) and plant height (16.53), indicating substantial variability for these traits. Intermediate ranges were observed for seed yield plant^{-1} (8.66 g), days to first flowering (6.47 days) and days to maturity (6.20 days), whereas branches plant^{-1} (1.06) and 100-seed weight (0.87 g) exhibited relatively narrow variation. Range estimates highlight the presence of genotypes expressing extreme phenotypes and thus identify traits with high selection potential. Comparable wide variation in yield and its components has also been reported in mung bean (Khan and Goyal, 2009) [13]. Barshile and Apparao (2012) [2] in chickpea, Sridevi and Mullainathan (2012) [18] in blackgram, Wani *et al.* (2010) [22] in chickpea.

Genotypic variance, phenotypic variance and their respective coefficient of variation

Genotypic coefficient of variation exhibited the values in High category (>20%) for the character number of branches plant^{-1} (42.06%) and number of pod plant^{-1} (20.86%) and moderate category (10-20%) for the character seed yield plant^{-1} (16.83%) and low (<10%) for the characters plant height (9.27%),100 seed weight (8.99%), day to first flower (4.41%), and day to maturity (1.75%).

Similarly PCV were observed as high (> 20%) for the characters such as number of branches plant^{-1} (44.97%) followed by number of number of pod plant^{-1} (29.84%) and seed yield per plant and moderate (10-20%) for characters plant height (12.12%) and 100 seed weight (11.53%) and low phenotypic coefficient of variation were observed for day to 1st flower (5.12%) and days to maturity (2.36%). The estimates of genotypic coefficient of variation and phenotypic coefficient of variation values for all the characters showed less difference which indicates less influence of environment. Similar to this result Tripathy *et al.* (2012) [21] in lathyrus, Ahir *et al.* (2018) [1] in green gram, jambulwar *et al.* (2021) [10] in lathyrus and Srikanth *et al.* (2021) [19] in lathyrus.

Heritability and genetic advance

Table 3, presents the broad-sense heritability estimates and corresponding genetic advance values for seven traits across 29 families and two check genotypes. Heritability percent ranged from 41.40% (seed yield plant^{-1}) to 87.46% (number of branches plant^{-1}). High heritability was recorded for number of branches^{-1} (87.46%), day to first flower (74.18%) and 100 seed weight (60.85%). Moderate heritability was observed for plant height (58.43%), day to maturity (55.12%), number of pods plant (48.79%) and seed yield plant^{-1} (41.40%). All characters show moderate to high estimate of heritability for above traits suggested less influence of environmental factors in the expression of these traits.

Genetic advance as a percentage of mean were high for number of branches plant^{-1} (81.03%), number of pod plant^{-1} (29.98%) and seed yield plant^{-1} (22.30%), moderate for plant height (14.59%), 100 seed weight (14.45%), and low for days to first flower (7.83%) and day to maturity (2.68%). A comprehensive appraisal of the genetic parameters showed that seed yield per plant, pods per plant and branches per plant each exhibited moderate to high genotypic coefficients of variation, moderate to high broad-sense heritability, and high genetic advance expressed as a percentage of the mean. This indicated that less influence of environment in M_4 progenies and on the basis of above criteria selected mutants forwarding yield trial. Similar findings were also reported by Giriji *et al.* (2013) [7] in cowpea, Goyal *et al.* (2020) [8] in black gram jambulwar *et al.* (2021) [10] in lathyrus and Srikanth *et al.* (2021) [19] in lathyrus.

Selection of superior mutants

In the M_4 progenies, seed yield per plant, pods per plant and branches per plant each demonstrated moderate to high genotypic coefficients of variation, moderate to high broad-sense heritability and high genetic advance as a percentage of the mean. Such parameter profiles point to a strong additive genetic component, suggesting that selection for these traits in M_4 progenies will be particularly effective. Accordingly, these three characters were chosen as primary selection criteria. Superior mutants from M_4 progenies which was selected from 29 mutants on the basis of seed yield plant^{-1} and yield contributing characters. Ten mutants were selected from 29 mutants to be forwarded to yield trial. viz., NLM-12, NLM-13, NLM-17, NLM-20, NLM-21, NLM-22, NLM-23, NLM-26, NLM-27 and NLM-28 for yield and yield contributing characters which observed to be significantly high as compared to highest check NLK-73 for seed yield plant^{-1}, number of pod plant^{-1} and number of branches plant^{-1}.

Table 1: Analysis of variance to estimate within family and between family variance in M_4 progenies

Mean sum of squares								
Source of variation	**df**	**Day to first flower**	**Days to maturity**	**Plant height (cm)**	**Number of branches plant^{-1}**	**Number of pods plant^{-1}**	**100 seeds weight (g)**	**Seed yield plant^{-1}**
Between families	30	64.66**	55.01**	506.84**	2.45**	1485.2**	0.48**	177.49**
Within families	434	1.47	2.83	22.95	0.35	96.80	0.31	15.30
Intra class correlation (t)		0.74	0.55	0.58	0.87	0.48	0.60	0.41

** Significant at 1% level.

Table 2: Mean performance of 29 mutants along with two checks

Sr. No	Progeny	Day to 1st flower	Day to maturity	Plant height	No. of branches plant^{-1}	No. of pod plant^{-1}	100 seed weight (g)	Seed yield plant^{-1}	ODAP Content (%)
1	NLM-1	44.00	106.2	55.86	3.46	49.53	7.53	20.66	0.226
2	NLM-2	45.93	105.2	60.13	3.26	53.20	7.33	22.13	0.231
3	NLM-3	47.80	103.6	67.40	3.26	44.53	7.46	18.60	0.233
4	NLM-4	43.66	107.7	54.60	3.53	43.26	7.53	18.06	0.228
5	NLM-5	48.86	103.8	58.80	3.33	51.73	7.33	16.00	0.225
6	NLM-6	45.46	104.3	63.80	3.20	52.33	7.46	23.06	0.208
7	NLM-7	44.20	108.2	55.60	4.06	43.20	7.46	15.80	0.210
8	NLM-8	47.46	104.4	57.66	3.26	52.73	7.53	16.20	0.221
9	NLM-9	46.00	107.2	64.13	3.26	45.20	7.46	17.93	0.208
10	NLM-10	44.00	108.2	56.40	3.80	53.06	7.53	19.70	0.185
11	NLM-11	48.06	104.9	59.60	3.33	47.13	7.66	17.80	0.219
12	NLM-12	44.13	107.9	64.13	4.03	50.80	7.46	20.66	0.169
13	NLM-13	46.26	109.2	57.06	4.26	53.10	7.66	21.46	0.185
14	NLM-14	44.06	106.0	65.86	4.00	50.20	7.53	18.33	0.204
15	NLM-15	48.26	104.2	69.26	4.06	51.00	7.60	19.66	0.219
16	NLM-16	44.13	104.7	55.53	3.40	38.86	7.46	16.26	0.227
17	NLM-17	46.86	108.3	64.80	4.13	51.60	7.60	23.40	0.219
18	NLM-18	50.00	105.3	70.93	3.40	43.26	7.46	16.60	0.226
19	NLM-19	47.00	107.9	54.40	3.33	46.86	7.60	21.20	0.205
20	NLM-20	43.93	103.3	65.46	4.20	49.73	7.60	23.86	0.196
21	NLM-21	47.06	106.2	70.66	4.00	52.33	7.66	23.60	0.184
22	NLM-22	45.13	103.0	55.86	4.06	49.73	7.46	23.20	0.182
23	NLM-23	47.86	107.2	65.40	4.20	49.93	7.60	24.46	0.213
24	NLM-24	50.13	109.0	70.46	4.13	33.93	7.46	16.40	0.209
25	NLM-25	46.46	105.0	63.40	3.73	51.53	7.66	20.06	0.213
26	NLM-26	49.80	106.7	55.53	4.20	49.40	7.66	23.13	0.177
27	NLM-27	44.80	103.8	70.93	4.26	48.53	8.20	23.06	0.190
28	NLM-28	44.06	106.8	56.60	4.20	50.53	7.80	21.20	0.203
29	NLM-29	47.40	104.9	61.46	3.26	45.40	8.00	16.46	0.220
30	NLK-73 (ch)	49.26	109.2	52.40	3.06	31.00	7.30	13.93	0.240
31	Ratan (ch)	49.00	108.4	53.06	3.00	30.93	7.46	13.66	0.260
	Mean	46.48	106.18	61.26	3.70	46.12	7.56	19.53	0.21
	S.E m±	0.70	0.97	2.77	0.34	5.69	0.32	2.26	0.01
	C.D. (5%)	1.93	2.69	7.66	0.94	15.76	0.87	6.26	0.04

Table 3: Genetic parameters estimate for different characters in M_4 progenies.

Parameters	Days to first flower	Days to maturity	Plant height (cm)	Number of branches Plant^{-1}	Number of pods plant^{-1}	100 seed weight (g)	Seed yield plant^{-1}
Mean	46.48	106.18	61.26	3.70	46.10	7.56	19.53
Min	43.66	103.0	64.40	3.20	33.93	7.33	15.80
Max	50.13	109.2	70.93	4.26	53.20	8.20	24.46
Range	6.47	6.20	16.53	1.06	19.27	0.87	8.66
Genotypic variance	4.21	3.47	32.26	2.42	92.56	0.464	10.81
Phenotypic variance	5.67	6.31	55.2	2.77	189.3	0.762	26.11
GCV (%)	4.41	1.75	9.27	42.06	20.86	8.99	16.83
PCV (%)	5.12	2.36	12.12	44.97	29.84	11.53	26.15
Heritability (%)	74.18	55.12	58.43	87.46	48.79	60.85	41.40
GA	3.64	2.85	8.94	3.00	13.83	1.09	4.35
GA (% of mean)	7.83	2.68	14.59	81.03	29.98	14.45	22.30

Conclusion

The present investigation entitled “"Genetic studies in M_4 progenies of Lathyrus CV. NLK-73"” was carried out to estimate the significant difference among 29 mutants and 2 checks. The results obtained from this work are concluded here. The ANOVA results indicated significant differences among all seven characters, as evidenced by analysis of variance. Mean performance showed that several mutant

lines surpassed the checks in different trait. seed yield per plant, pods per plant and branches per plant all exhibited moderate to high genotypic coefficients of variation and broad-sense heritability and high genetic advance (as a percentage of the mean), indicating strong additive gene action and validating their use as primary selection criteria. Moreover, the relative magnitudes of between family and within family variance components, coupled with the intraclass correlation (t), justify equal weighting of both variance sources during selection. Hence, ten mutants from 29 mutants exhibiting superiority over check for seed yield plant^{-1} with yield contributing characters with low ODAP content were identified for forwarding to yield trials.

Acknowledgement
I gratefully acknowledge the invaluable contributions of everyone who made this research possible. My deepest thanks go to my research guide for their expert guidance and insightful feedback throughout the study. I also extend sincere appreciation to the Research Farm of the Agricultural Botany Section, College of Agriculture, Nagpur, for generously providing the facilities and resources essential to this work.

References

1. Ahir DK, Kumar R, Chetariya CP, Jalu PK. Estimation of variability parameter in M3 generation of green gram (*Vigna radiata* (L.) R. Wilczek). The Pharma Innovation Journal. 2018;7(7):559-563.
2. Barshile J, Apparao B. Genetic improvement of chickpea (*Cicer arietinum* L.) cultivar 'Vijay' (Phule G 81-1-1) through induced mutagenesis. Bioremediation, Biodiversity and Bioavailability. 2012;6(1):103-106.
3. Burton GW, De Vane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
4. Bisane RD, Kamdi SR, Deotale RD, Meshram MP, Patil SR, Pawar VS, Bambodkar PP. Genetic studies in M4 population of soybean cultivar TAMS-38. Journal of Soils and Crops. 2019;29(2):354-359.
5. Dhaka S, Singh VV, Krishna KR. Studies on evaluation of M4 progenies and effectiveness of selection on M3 progenies in cowpea (*Vigna unguiculata* L.). Legume Research-An International Journal. 2013;36(5):392-395.
6. Gupta P, Udupa SM, Gupta DS, Kumar J, Kumar S. Population structure analysis and determination of neurotoxin content in a set of grass pea (*Lathyrus sativus* L.) accessions of Bangladesh origin. The Crop Journal. 2018;6(4):435-442.
7. Girija M, Dhanavel D, Gnanamurthy S. Gamma rays and EMS induced flower color and seed mutants in cowpea (*Vigna unguiculata* L. Walp). Electronic Journal of Plant Breeding. 2013;4(2):1201-1205.
8. Goyal S, Wani MR, Laskar RA, Raina A, Khan S. Performance evaluation of induced mutant lines of black gram (*Vigna mungo* (L.) Hepper). Acta Fytotechnica et Zootechnica. 2020;23(2):70-77.
9. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy Journal. 1956;48(6):268-272.
10. Jambulwar AP, Patil SR, Kalmakar V, Dada ND, Sapkal AD, Ghige A. Genetic studies in gamma rays induced M3 generation in *Lathyrus*. The Pharma Innovation Journal. 2021;10(6):857-861.
11. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47(7):314-318.
12. Kamdi S, Bhure S, Gupta SK, Kankal G, Dadas N. Genetic improvement of soybean cultivar for yield and its related traits by induced mutation. Souvenir & Abstracts, Indian Society of Genetics and Plant Breeding. 2020;:142-144.
13. Khan S, Goyal S. Mutation genetic studies in mungbean IV. Selection of early maturing mutants. Thai Journal of Agricultural Science. 2009;42(2):109-113.
14. Kumar S, Bejiga G, Ahmed S, Nakkoul H, Sarker A. Genetic improvement of grass pea for low neurotoxin (β-ODAP) content. Food and Chemical Toxicology. 2011;49(3):589-600.
15. Malek MA, Rafii MY, Afroz MSS, Nath UK, Mondal MA. Morphological characterization and assessment of genetic variability, character association, and divergence in soybean mutants. The Scientific World Journal. 2014;2014:968796.
16. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. 1949;41(8):353-359.
17. Sharma D, Padmanabham S. In: Liener IE, editor. Food Science and Technology. New York: Academic Press; 1969. p. 209-233.
18. Devi AS, Mullainathan L. Effect of gamma rays and ethyl methane sulphonate (EMS) in M3 generation of blackgram (*Vigna mungo* L. Hepper). African Journal of Biotechnology. 2012;11(15):3548-3552.
19. Srikanth PA, Patil SR, Ingle AD, Madke VS, Sapana B, Baviskar TD. Genetical studies in M4 generation of *Lathyrus*. The Pharma Innovation Journal. 2021;10(7):898-902.
20. Tripathy SK, Lenka D, Ranjan R. Maximization of mutation frequency in grasspea (*Lathyrus sativus* L.). Legume Research-An International Journal. 2011;34(4):296-299.
21. Tripathy SK, Ranjan R, Lenka D. Effectiveness and efficiency of single and combined treatments of physical and chemical mutagens in grasspea (*Lathyrus sativus* L.). World Applied Sciences Journal. 2012;20(5):738-741.
22. Wani MR, Kozgar MI, Khan S, Dar NA. Induction of genetic variability through artificial mutagenesis in chickpea (*Cicer arietinum* L.). Notulae Scientia Biologicae. 2010;2(2):98-103.