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Genetic variability studies in M₅ generation of *lathyrus*

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Abstract

The present study was conducted with the objectives to estimate variances due to between family and within family, to estimate genetic parameters and identify superior mutants for utilization at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. During *rabi* 2021 in M₅ generation, 50 mutants along with two checks (NLK-73 and Ratan) were evaluated in three replications. Data were recorded on days to first flower, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹. Analysis of variance indicated that the mean square due to between family were highly significant for all traits, which reveals that the mutant progenies had significant amount of genetic variability among themselves for seed yield plant⁻¹ and other yield components. Intra class correlation (t) lead to the inference that equal weightage to σ^2_f (variance between families) and σ^2_w (variance within families) should be considered for selection in M₅ generation. High genotypic and phenotypic coefficient of variation for number of pods plant⁻¹ and seed yield plant⁻¹, moderate for plant height, and low for 100 seed weight, number of branches plant⁻¹, days to first flower, and days to maturity. Moderate heritability was observed for plant height, seed yield plant⁻¹, number of pod plant⁻¹, and low heritability for days to first flower, days to maturity, 100 seed weight and number of branches plant⁻¹. Genetic advance as a percentage of mean were high for seed yield plant⁻¹, number of pod plant⁻¹, moderate for plant height, and low for days to first flower, days to maturity, number of branches plant⁻¹ and 100 seed weight. When all the genetic parameters for all the characters were considered, it was found that the characters number of pods plant⁻¹ and seed yield plant⁻¹ exhibited high genotypic coefficient of variation, moderate heritability and high genetic advance as percentage of mean, hence were considered as a criteria for selection. The range exhibited by individual plant within the progenies also were high for these characters. 149 individual plants from 36 selected mutant progenies exhibiting significant superiority over check for number of pods plant⁻¹ and seed yield plant⁻¹ were identified for further evaluation for one more generation in M₅ before forwarding to yield trials.

Keywords: *Lathyrus*, heritability, genetic advance percentage of mean, GCV, PCV, M₅ generation

Introduction

The *Lathyrus sativus* L. (2n=14) is an annual herb and important pulse crop rich in protein (28%) next to the soybean and locally known as kesari dal, grass pea, blue sweet pea, chickling vetch, Indian pea, white pea, and white vetch, is a legume commonly grown for human consumption and livestock feed in Asia and East Africa. Grass pea is a food, feed and fodder crop belonging to the family Leguminosae (Fabaceae), subfamily papilionoideae. Genus *Lathyrus* with 130 species occurring all over temperate region of Northern hemisphere and the higher altitude of tropical Africa. In India, besides the ornamental *Lathyrus odoratus*, the only other species cultivated is *Lathyrus sativus* which yield the khesari dal. The edible *Lathyrus sativus* originated in the West Central Asia Mediterranean region and North India was its centre of domestication, were 3600 years old remains have been discovered. Chhattisgarh, Bihar, Madhya Pradesh and West Bengal are some of the lathyrus producing states in India. Grass pea has high nutritional value and is a good source of minerals. Its protein and carbohydrate content values are up to 28% and 53.9%, fat - 0.9% and Ash - 3.2% respectively. Legumes have an important place in human and animal nutrition. Legumes and their seeds contain many vitamins such as vitamin K, vitamin B1, B2, B6, vitamin C, vitamin E and niacin. Determining the vitamin content and amount of food it is important to standardize the quantity of food that must be taken daily for human and animal nutrition (Arsan, 2017) [2]. Grass pea, providing an economic yield under environmental conditions and with a great potential for use in marginal low-rainfall areas is a popular crop in subsistence farming in certain developing countries. *Lathyrus* leaves about 36 - 48 kg ha⁻¹ nitrogen which is economical for the succeeding crops.

It is mostly sown in standing crop of paddy as a Utera or Paira crop in rabi season. Secondly, the main pulse crop tur (Pigeonpea) 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) and grows luxuriantly without any cultivation input. This research work has wide scope to create additional genetic variability that may be utilized in the development of cultivars for specific purposes or with specific adaptations. This study helps for the improvement of this crop by developing cultivars with high protein content, high yield and low neurotoxin. Lathyrus being a potential legume crop of India has immense scope for genetic improvement for various qualitative and quantitative characters. Improvement in any crop is based on the extent of genetic variation and degree of improvement depends upon the magnitude of useful genetic variability. By using this technique we can develop high yielding, dwarf and early maturing varieties.

Materials and Methods

Dry, healthy and genetically pure seed of *Lathyrus sativus* cv. NLK-73 was obtained from Agricultural Botany Section, College of Agriculture, Nagpur. Six different lots of 500 seeds of lathyrus seed cv. NLK-73 were made. Out of this five lots of seeds were sent to Bhabha Atomic Research Centre, Trombay for irradiation with five different dosage of gamma rays 150 Gy, 200 Gy, 250 Gy, 300 Gy and 350 Gy (CO⁶⁰ at BARC) and used for raising M₁ generation along with control during *rabi*, 2017 and individual plant in each treatment were harvested separately. The harvested seed were raised as M₂ generation in *rabi* 2018 and evaluated from which 123 single plant mutant were identified for desired characters. In *rabi*, 2019 these 123 single plant mutants along with check and parent were raised as M₃ generation and evaluated. In M₃ generation 152 individual mutant plants for desired characters were identified. These 152 individual mutant plants along with check and parent were raised as M₄ generation and evaluated during *rabi* 2020. In M₄ generation 174 individual plant from 85 mutant families were selected for desired characters. The present work is the continuation of above-mentioned work. The top performing 50 mutants out of 174 identified along with check Ratan and parent NLK-73 were planted in RBD with three replications in *rabi*, 2021 for their evaluation in M₅ generation. Plot Size 0.9 m x 4 m. Two rows allocated for each mutant and check with 20 plants rows⁻¹. The row to row distance 45 cm and plant to plant distance was 20 cm. Five plants from each mutant and five from check were randomly selected in each replication and observations were recorded for days to first flower, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g) and seed yield plant⁻¹(g). The data recorded during M₅ generation were subjected to the statistical analysis i.e., mean, range, genotypic variance, phenotypic variance, heritability (broad sense) (Hanson *et al.* 1956)^[4], genotypic coefficient of variation (%), phenotypic coefficient of variation (%) (Burton and Devane, 1953)^[3], genetic advance (GA) (Robinson *et al.*, 1949)^[8], genetic advance as percentage of mean (Johnson *et al.*, 1955)^[5].

Results and Discussion

The analysis of variance of 50 mutants families and two

checks genotypes with respect to seven quantitative characters are presented in table 2. The data on the analysis of variance revealed that the mean sum of squares due to the mutants were highly significant for all the seven characters studied *i.e.* days to first flower, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹. This indicated the presence of significant genetic variability between the mutants for all seven characters. This allowed further estimation of genetic parameters. In accordance with this result significant variability between the mutants were also reported by Waghmare and Mehra (2000)^[9], Kumar and Dubey (2001)^[6], Tripathy *et al.* (2012)^[11], Ramezani *et al.* (2017)^[12] and Srikanth *et al.* (2021)^[13] in lathyrus.

The result on the analysis between family and within family variance in M₅ generation is presented in table 3. The mean squares due to between families were observed to be highly significant for all the seven characters studied which indicated the presence of significant variation between the mutant families for all the characters.

The intra class correlation (t) which is the ratio of two variances i.e. between family variances (σ^2_f) and total phenotypic variance (σ^2_p) were estimated in M₅ generation in this study. This value was observed to range from 0.08 for number of branches plant⁻¹ to 0.57 for plant height. Highest intra class correlation value was observed for plant height (0.57) followed by number of pods plant⁻¹ (0.55), seed yield plant⁻¹ (0.30), 100 seeds weight (0.24), days to maturity (0.22), days to first flower (0.14) and number of branches plant⁻¹ (0.08). This revealed that 57%, 55%, 30%, 24%, 22%, 14% and 8% of variation for plant height (cm), number of pods plant⁻¹, seed yield plant⁻¹(g), 100 seeds weight, days to maturity, days to first flower and number of branches plant⁻¹ respectively were due to differences between the families and 43%, 45%, 70%, 76%, 78%, 86% and 92% were due to within families.

This indicated that differences between individuals within a family are large for all the characters except for plant height and number of pods plant⁻¹. But each family distinctly differentiated from other also at considerable level. Therefore, equal weightage was suggested to be assigned to σ^2_f and σ^2_w in this generation also. This indicates that between family selection followed by within family selection will be more rewarding in M₅ generation.

Creation of variability is a prerequisite either for development of variety or inbred lines. Considerable amount of variability can be generated by induced mutation. The estimate of genetic parameters like mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance which are indicators of variation were calculated for seven characters in M₅ generation and are presented in table 3 and 4.

One of the way to assess the extent of variability is to examine the mean and range, which directs the extent of phenotypic variability in respect of the trait under consideration indicating genotypic, phenotypic, environmental and interaction components. The grand mean recorded for 50 mutants along with two checks were found to be 48.97 for days to first flower, 110.11 for days to maturity, 72.77 cm for plant height, 5.30 for number of branches plant⁻¹, 72.21 for number of pods plant⁻¹, 7.41 g for 100 seed weight and 15.49 g for seed yield plant⁻¹ (Table 4). The mean value of the mutant families as observed from table 4 reveals that 36

mutant families for seed yield plant⁻¹, 15 for 100 seed weight, 38 for number of pods plant⁻¹, 38 for number of branches plant⁻¹, 6 for plant height and 12 for days to maturity were found to be significantly superior over Ratan in the desirable direction. In accordance to these results mutant families showing significant superiority over check were also reported by Waghmare and Mehra (2000)^[9], Kumar and Dubey (2001)^[6] and Srikanth *et al.* (2021)^[13] in lathyrus.

Significant differences were observed between the progenies for all the seven characters studied. The coefficient of variation (CV) ranged from 5.95 per cent to 32.46 per cent for various characters (Table 4). The lowest coefficient of variation ($\leq 10\%$) was observed for days to maturity (2.24%), days to first flower (5.95%), 100 seed weight (9.77%) which showed best genetic potential and its genetic influence. Moderate coefficient of variation (10-20%) was observed for plant height (11.09%) and highest coefficient of variation ($>20\%$) was observed for number of branches plant⁻¹ (21.43%), number of pods plant⁻¹ (21.74%) and seed yield plant⁻¹ (32.46%) which indicates influence of environmental fluctuation. Being the M₅ generation, the amount of variability expected should be low to moderate for all the characters. But in this study coefficient of variation ranged from low to high. Hence, further selection and advancement of progenies is necessary for one more generation till attainment of homogeneity. In accordance to this result, Tripathy *et al.* (2012)^[11], Ramezani *et al.* (2017)^[12] and Srikanth *et al.* (2021)^[13] in lathyrus, also observed high coefficient of variance and the influence of environment on yield and yield components.

The minimum, maximum and range estimated for all the seven characters in M₅ generation are presented in table 5. High range of 128 was exhibited for number of pod plant⁻¹, followed by plant height (68 cm) and seed yield plant⁻¹ (37.80 g) which indicated that wide range of variation were functioning for these characters. Days to maturity (17), days to first flower (17), 100 seed weight (5.90 g) and number of branches plant⁻¹ (6) exhibited low range of variation. The estimates of range provides new clue about the occurrence of genotypes with extreme expression which varied with the trait. In accordance to these results wide range of variation for yield and yield components were also reported by Waghmare and Mehra (2000)^[9], Kumar and Dubey (2001)^[6], Tripathy *et al.* (2012)^[11], Ramezani *et al.* (2017)^[12] and Srikanth *et al.* (2021)^[13] in lathyrus.

Knowledge on relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to breed improved cultivars. The estimates of genotypic coefficient of variation and phenotypic coefficient variation, which reflects average inter genotype differences, are more useful tools to understand variability among the genotypes. The differences between the GCV and PCV values indicates the level of environmental variations that contribute a major part in the expression of traits. The phenotypic variance and phenotypic coefficient of variation was observed to be greater than genotypic variance and genotypic coefficient of variation for all seven characters studied (Table 5) indicating the environmental influence over the character studied. Similar to this Waghmare and Mehra (2000)^[9], Kumar and Dubey (2001)^[6], Tripathy *et al.* (2012)^[11], Ramezani *et al.* (2017)^[12] and Srikanth *et al.* (2021)^[13] in lathyrus, also reported that phenotypic coefficient of variation was greater than their

corresponding genotypic coefficient variation for all the characters studied. The difference between genotypic and phenotypic coefficient of variation for the characters days to first flower, days to maturity, number of branches plant⁻¹ and 100 seed weight were small indicating that these traits were less influenced by environment. On the contrary the difference was observed to be high for characters number of pods plant⁻¹, seed yield plant⁻¹ and plant height indicating that these traits were highly influenced by the environment.

Genotypic coefficient of variation exhibited high ($>20\%$) values for the characters such as number of pods plant⁻¹ (23.87%) seed yield plant⁻¹ (21.48%) and the moderate (10-20%) value for the character plant height (12.67%) and low ($\leq 10\%$) values for days to first flower (2.37%), days to maturity (1.19%), number of branches plant⁻¹ (6.34) and 100 seed weight (5.51%). Similarly, phenotypic coefficient of variation also recorded high ($>20\%$) values for the characters seed yield plant⁻¹ (38.93%), number of pods plant⁻¹ (32.29%), number of branches plant⁻¹ (22.35%) and the moderate (10-20%) value for the character plant height (16.83%) and 100 seed weight (11.22%) and low phenotypic coefficient of variation was observed for days to first flower (6.40%) and days to maturity (2.54%).

The coefficient of variation indicates only the extent of variability existing for various characters, but does not give any information regarding heritable proportion of it. Hence, amount of heritability permits greater effectiveness of selection by separating out the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified phenotypically. In the present study, broad sense heritability, which includes both additive and non-additive gene effects (Hanson *et al.*, 1956)^[4] were estimated.

The heritability estimates provides information on transmission of traits from parent to offspring. Such estimates facilitates the evaluation of genetic and environmental effect aiding in selection. Estimation of heritability is often used to predict the genetic advance under selection so that the plant breeder can anticipate improvement of different types and intensity of selection. The estimate of heritability and genetic advance estimated in material consisting of 50 mutants along with two checks for seven characters are reported in table 5 and fig. 2. Heritability per cent ranged from 8 per cent (number of branches plant⁻¹) to 57 per cent (plant height). Moderate heritability was recorded for plant height (57 per cent), number of pods plant⁻¹ (55 per cent) and seed yield plant⁻¹ (30 per cent). Low heritability was exhibited for 100 seed weight (24 per cent), days to maturity (22 per cent), days to first flower (14 per cent) and number of branches (8 per cent). Moderate to low estimate of heritability for above traits suggested influence of environmental factor in the expression for these traits. In accordance to these results moderate to low heritability for yield and yield components were also reported by Waghmare and Mehra (2000)^[9], Kumar and Dubey (2001)^[6], Tripathy *et al.* (2012)^[11], Ramezani *et al.* (2017)^[12] and Srikanth *et al.* (2021)^[13] in lathyrus.

Genetic advance as percentage of mean were low, moderate and high for all the characters under the present study. Genetic advance as a percentage of mean were high for number of pods plant⁻¹ (31.05%) and seed yield plant⁻¹ (20.87%), moderate for plant height (16.77%) and low for 100 seed weight (4.76%), number of branches plant⁻¹ (3.17%), days to first flower (1.55%), days to maturity (0.99%).

Similar to these results high genetic advance as a percentage of mean was also reported by Waghmare and Mehra (2000) [9], Kumar and Dubey (2001) [6], Tripathy *et al.* (2012) [11], Ramezani *et al.* (2017) [12] and Srikanth *et al.* (2021) [13] in lathyrus.

Heritability alone promotes no information on amount of genetic progress that would result from the selection. The broad sense heritability reported in the present study provide only a broad idea about the extent to which the traits are fixable. Heritability estimates along with genetic advance would be valuable in predicting the success in selecting the best individual. Therefore, it is vital to consider the predictable genetic advance along with heritability estimates as a tool in the selection. In this study high or moderate heritability estimates along with moderate genetic advance as a per cent of mean was noticed in plant height, number pods plant⁻¹ and seed yield plant⁻¹. The moderate heritability accompanied with the high genetic advance reveals the presence of lesser environmental influence and performance of additive gene action in their expression. Hence, plant height, number of pods plant⁻¹ and seed yield plant⁻¹ which exhibited moderate heritability and high genetic advance can be improved by the selection of phenotype for effective improvement in lathyrus. All the other characters exhibited low or moderate heritability but accompanied with low or moderate genetic advance which indicates the higher influences of environment. In accordance to this result Waghmare and Mehra (2000) [9], Kumar and Dubey (2001) [6], Tripathy *et al.* (2012) [11], Ramezani *et al.* (2017) [12] and Srikanth *et al.* (2021) [13] in lathyrus reported high heritability along with genetic advance as a per cent of mean for yield and yield contributing traits. When all the genetic parameters for seven characters were considered, it was found that two characters, seed yield plant⁻¹ and number of pods plant⁻¹ exhibited high genotypic coefficient of variation, moderate heritability and high genetic advance as the percentage of mean. This indicates that there is lesser influence of environment and that these characters were governed by additive gene action and selection for such traits in M₅ may be rewarding. Any appraisal of the breeding material permitting elimination of material of low potential is clearly advantageous because all important programme have limitations and elimination of poor material enhances the probability of finding superior segregants in remaining material (Allard, 1960) [1]. One of the main objectives of this experiment was to identify superior mutants for forwarding to

yield trial. Individual mutants were selected from M₄ on the basis of high seed yield plant⁻¹, pods plant⁻¹, more branches, height, early flowering. The selected mutants from M₄ generation were raised in M₅ generation to test the performance and homozygosity.

Selection of superior progenies in lathyrus on the basis of single character *i.e.* seed yield plant⁻¹ may not be effective and hence plant breeder has to involve large number of component characters simultaneously in the selection programme. But handling of large number of component characters simultaneously becomes cumbersome and hence selections of plants on the basis of characters having high GCV, high heritability and high genetic advance as percentage of mean was considered.

In the present study only two characters number of pods plant⁻¹ and seed yield plant⁻¹ showed high GCV, high PCV, moderate heritability and high genetic advance as percentage of mean and hence were considered as criteria for selection in M₅ generation. This revealed that these characters were influenced by additive gene action and selection would be effective in improving these traits, hence were considered as criteria for selection.

Between family variance, within family variance and intra class correlation (t) when considered, revealed that σ^2_f and σ^2_w should be given equal weightage for all characters. Therefore selection of superior families followed by selection of individual plants in selected families for seed yield plant⁻¹ and number of pods plant⁻¹ were considered as the criteria of selection. Based on these criteria out of 50 mutant families 149 individual plants were selected from 36 families. The performance of these selected individual plants are presented in table 6, figure 3 and plate 2 to 4 It was observed from table 6 that the seed yield plant⁻¹ of selected individual ranged from 20 to 42 g, number of pods plant⁻¹ from 80 to 149 Similarly 100 seed weight ranged from 6.7 to 8.9 g, number of branches plant⁻¹ from 4.00 to 6, plant height from 52 to 100 cm and days to maturity from 104 to 109 days.

In this study as additive gene action was found to be predominant for yield and yield components, it is suggested that the selected 149 individuals plants from M₅ should be raised in progeny rows for one more generation so that homozygosity will be attained and superior progenies can be then selected for forwarding to yield trials in the next generation.

Table 2: Analysis of variance for experimental design in M₅ generation

Source of variation	df	Mean sum of square						
		Days 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 (g)
Replication	2	14.08	7.95	19.50	0.32	2846.51	0.50	309.22
Treatments	51	5.77**	6.04**	263.24**	0.58*	878.20**	0.60**	36.20**
Error	102	2.54	2.57	25.92	0.37	177.13	0.25	13.87

* Significant at 5% level

**Significant at 1% level

Table 3: Analysis of variance between family and within family variance in M₅ generation

Source of variation	df	Mean sum of square						
		Days 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 (g)
Between families	51	28.71**	30.24**	1334.78**	2.99**	4757.62**	3.02**	192.69**
Within families	728	8.47	5.76	64.89	1.29	249.41	0.52	25.46
Intra class correlation(t)		0.14	0.22	0.57	0.08	0.55	0.24	0.30

** Significant at 1% level

Table 4: Mean performance of 50 mutant progenies along with parents for various characters

Sr. No.	Mutant Progeny/ Parents	Days to 1 st flower	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pod plant ⁻¹	100 seed weight(g)	Seed yield plant ⁻¹ (g)
1	T4-90-123-10	48.80	108.53	88.27	5.27	56.20	7.48	12.61
2	T4-90-123-1	47.33	110.80	87.33	5.60	58.13	6.45	14.22
3	T2-204-81-13	49.27	108.53	89.73	5.07	55.67	7.14	15.29
4	T3/232-75-5	48.67	109.07	71.87	6.00	58.13	7.65	12.37
5	T3/131-115-18	48.80	107.60	84.87	4.53	59.20	7.49	15.75
6	T3/250-74-9	49.07	109.33	77.53	4.87	42.13	7.94	12.00
7	T3/131-115-9	49.80	109.67	78.47	4.53	42.93	7.49	11.33
8	T2/222-36-9	48.93	105.93	83.20	5.80	36.40	7.25	8.52
9	T3/216-39-3	50.00	107.73	80.47	4.53	73.80	7.82	19.03
10	T2/54-19-17	48.40	105.80	52.73	5.53	48.93	6.17	12.83
11	T2/209-70-11	49.20	105.00	79.73	5.33	43.27	7.59	10.07
12	T2/204-70-14	48.67	105.80	61.40	5.60	51.20	7.44	11.32
13	T2/65-145-1	48.60	106.60	69.87	4.27	63.07	7.17	18.69
14	T2/54-19-7	49.20	104.73	73.40	5.40	55.20	7.02	14.77
15	T2/54-74-12	48.07	107.13	67.80	5.40	50.07	7.82	10.40
16	T3/244-57-6	46.67	107.20	83.60	5.73	80.87	7.45	18.70
17	T4/9-152-8	48.80	106.93	70.20	5.80	71.80	7.75	15.17
18	T2/204-7-16	49.73	108.00	77.73	5.33	83.60	7.98	20.83
19	T2/6-77-3	48.67	107.00	81.67	5.07	88.27	8.07	18.33
20	T2/204-27-15	48.47	105.80	67.13	5.27	87.67	8.25	16.77
21	T2/222-36-19	50.40	107.47	69.00	4.93	76.47	7.69	14.00
22	T4/90-142-5	47.27	107.60	74.20	5.13	88.80	7.93	15.05
23	T3/100-14-7	50.80	108.47	74.53	5.00	105.60	7.78	18.54
24	T3/131-115-6	51.40	109.47	58.73	6.20	81.40	6.45	17.04
25	T3/224-13-2	50.27	107.40	62.47	6.47	73.53	7.27	12.96
26	T2/7-170-8	46.80	106.27	67.40	4.80	71.13	7.81	18.77
27	T4/90-100-10	47.67	107.00	70.60	5.53	93.60	7.72	18.33
28	T2/6-123-10	48.27	106.13	87.27	5.00	88.47	7.73	15.56
29	T2/7-114-10	47.33	106.40	68.13	5.40	73.07	7.59	11.31
30	T4/90-131-9	49.87	106.87	92.27	4.93	80.47	7.07	14.69
31	T2/6-126-9	46.20	106.20	63.20	5.20	90.87	6.90	17.52
32	T2/54-04-1	51.13	106.53	78.00	5.27	105.60	7.77	26.89
33	T2/54-107-3	48.00	104.73	56.80	5.47	107.00	7.42	21.11
34	T2/204-7-15	49.60	106.47	71.47	5.60	89.40	7.57	21.98
35	T2/215-21-5	49.87	104.87	69.13	5.20	88.13	7.29	15.18
36	T4/112-46-10	48.20	106.53	76.93	5.67	80.13	7.58	13.75
37	T2/204-27-9	47.47	105.13	64.33	4.73	73.33	7.03	14.63
38	T2/222-36-1	49.87	106.53	76.13	5.27	83.47	7.17	16.46
39	T3/244-57-1	47.67	108.07	75.93	5.27	76.40	6.91	14.90
40	T3/131-115-20	50.07	108.80	65.27	5.73	75.60	7.22	12.47
41	T1/239-27-3	46.80	106.40	66.27	5.40	75.87	7.51	12.13
42	T2/54-79-17	49.47	105.47	72.93	5.40	73.00	7.00	15.81
43	T2/65-145-11	49.60	109.00	76.67	4.93	84.53	7.05	16.05
44	T3/131-115-15	52.33	109.00	79.07	5.93	73.40	7.28	13.59
45	T4/90-100-2	48.80	105.80	68.27	5.27	86.87	6.57	19.08
46	T2/7-114-20	49.33	106.80	55.93	5.80	78.20	7.03	15.67
47	T2/54-88-6	50.07	105.27	75.33	4.93	60.20	7.75	13.57
49	T2/201-90-3	50.07	107.00	79.27	5.00	73.73	7.35	20.43
50	T3/116-152-5	52.67	107.40	75.67	5.67	52.80	8.08	16.37
51	RATAN	47.53	106.33	63.93	4.87	56.27	7.63	12.97
52	NLK-73	49.40	107.07	52.13	4.93	51.60	7.86	11.55
	Mean	48.97	110.11	72.77	5.30	72.21	7.41	15.49
	S.E _m ±	0.10	0.09	0.29	0.04	0.57	0.03	0.18
	C.D. (5%)	0.29	0.24	0.80	0.11	1.57	0.07	0.50
	C.V. (%)	5.95	2.24	11.09	21.43	21.74	9.77	32.46

Table 5: Genetic parameter estimates for different characters in M₅ generation

Parameters	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)
Mean	48.96	107.09	72.64	5.30	72.64	7.41	15.54
Min	42.00	102.00	37.00	2.00	20.00	3.60	4.20
Max	59.00	115.00	105.00	8.00	148.00	9.50	42.00
Range	17.00	17.00	68.00	6.00	128.00	5.90	37.80
Genotypic variance	1.35	1.63	84.66	0.11	300.55	0.17	11.15
Phenotypic variance	9.82	7.39	149.55	1.41	549.96	0.69	36.61
GCV (%)	2.37	1.19	12.67	6.34	23.87	5.51	21.48
PCV (%)	6.40	2.54	16.83	22.35	32.29	11.22	38.93
Heritability (%)	14.00	22.00	57.00	8.00	55.00	24.00	30.00
GA	0.76	1.06	12.18	0.17	22.56	0.35	3.24
GA (% of mean)	1.55	0.99	16.77	3.17	31.05	4.76	20.87

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