

GENETIC VARIABILITY STUDIES IN M₄ GENERATION OF LATHYRUSAnita D. Ingle¹, Shanti R. Patil², P. Srikanth³, Vandana S. Madke⁴ and Sapana B. Baviskar⁴**ABSTRACT**

The present study was conducted at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. During *rabi* 2020 in M₄ generation, 73 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 squares due to between family were highly significant for all traits, which reveals that the mutant progenies had significant amount of genetic variability among themselves. Intra class correlation (t) lead the inference that differences between individuals within a family are large for all the characters except for 100 seed weight and days to first flower, but each family distinctly differentiated from other also at lower level in M₄ generation hence, equal weightage to σ^2_f (variance between families) and σ^2_w (variance within families) were suggested to be considered for selection in M₄ generation. Moderate genotypic and high phenotypic coefficient of variation was recorded for number of pods plant⁻¹ and low GCV and moderate PCV for seed yield plant⁻¹ and moderate to low for other characters. High heritability was recorded for days to first flower and moderate heritability was observed for days to maturity, plant height (cm), number of pod plant⁻¹, 100 seed weight, seed yield plant⁻¹ and number of branches plant⁻¹. Genetic advance as a percentage of mean were moderate for number of pods plant⁻¹ and low for plant height, seed yield plant⁻¹, days to first flower, number of branches plant⁻¹, 100 seed weight and days to maturity. When all the genetic parameters for different characters were considered, the characters number of pods plant⁻¹ exhibited moderate genotypic coefficient of variation, moderate heritability and moderate genetic advance as percentage of mean, hence considered as a criteria for selection. During selection, 101 individual plants from 47 mutant progenies exhibiting significant superiority over check for number of pods plant⁻¹ were identified for further evaluation for one more generation in M₅ before forwarding to yield trials.

(Key words: Lathyrus, heritability, genetic advance percentage of mean, GCV, PCV, M₄ generation)

INTRODUCTION

The *Lathyrus sativus* (L.) (2n=14) also known as kesari dal, grass pea, cicerchia, 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. 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 31.9% and 53.9%, fat - 0.9% and Ash - 3.2%. Legumes and their seeds contain many vitamins such as vitamin K, vitamin B1, B2, B6, vitamin C, vitamin E and niacin (Arjan, 2017). Lathyrus (*Lathyrus sativus* L.) is one of the important pulse crop in India and other countries like Bangladesh, Australia, South America

and North Africa. This pulse is consumed in various forms like chapaties, wadas and curries and feeds to cattle as green fodder and stover since ancient times. It fulfils major pulse need in our country. But ban is imposed due to association with Neurolathyrism a non-reversible neurological disorder in human and animals due to presence of neurotoxin, ($\hat{\alpha}$ -N-oxalyl-L- $\hat{\alpha}$, $\hat{\alpha}$ -diaminopropionic acid) $\hat{\alpha}$ -ODAP in its seedlings and seeds. The traditional varieties of grass pea contain 0.5 – 2.5% $\hat{\alpha}$ -ODAP (Kumar *et al.*, 2011). These are two prime objectives in grasspea breeding. However, there is considerable scope for improving yield potential and other agronomical characters in this crop. Mutation breeding has become increasingly popular in recent times as an effective tool for crop improvement and an efficient means supplementing existing germplasm for cultivar improvement in breeding programs. Mutation breeding is one of the efficient method for the improvement of this crop which is towards developing cultivar with high protein content, high yield and low neurotoxin.

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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 seeds 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 73 individual mutant plants for desired characters were identified. The 73 individual mutant plants identified along with check Ratan and parent NLK-73 were sown to raise M₄ generation in replicated trial using Randomized Block Design replicated thrice. Plot Size was 0.9 m x 4 m. Two rows allocated for each mutant and check with 20 plants row⁻¹. The row to row distance was 45 cm and plant to plant distance was 20 cm. Ten 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 M₄ generation were subjected to the statistical analysis i.e., mean, range, genotypic variance, phenotypic variance, heritability (broad sense) (Hanson *et al.* 1956), genotypic coefficient of variation (%), phenotypic coefficient of variation (%)(Burton and Devane, 1953), genetic advance (GA) (Robinson *et al.*, 1949), genetic advance as percentage of mean (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The data recorded on seven characters in 73 mutant progenies along with two checks were subjected to analysis of variance resulted in highly significant mean square due to between family 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(Table 1). The intra class correlation (t) which is the ratio of two variances *i.e.* between family variances (δ^2f) and total phenotypic variance (δ^2p) were estimated in M₄ generation in this study. This value was observed to range from 0.11 for seed yield plant⁻¹ to 0.66 for 100 seed weight. Highest intra class correlation value was observed for 100 seeds weight (0.66) followed by days to first flower (0.55), days to maturity (0.49), plant height (cm) (0.47), number of branches plant⁻¹(0.38), number of pods plant⁻¹ (0.22) and seed yield plant⁻¹(g) (0.11). This revealed that 66%, 55%, 49%, 47%, 38%, 22% and 11% of variation

for 100 seeds weight, days to first flower, days to maturity, plant height (cm), number of branches plant⁻¹, number of pods plant⁻¹ and seed yield plant⁻¹(g) respectively were due to differences between the families and 44%, 45%, 51%, 53%, 62%, 78% and 89% were due to within families. This indicated that differences between individuals within a family are large for all the characters except for 100 seed weight and days to first flower, but each family distinctly differentiated from other also at lower level. Therefore, equal weightage was suggested to be assigned to δ^2f (variance between families) and δ^2w (variance within families) in this generation also. This indicates that between family selection followed by within family selection will be more rewarding in M₄ generation.

The coefficient of variation (CV) ranged from 1.64 to 26.62% for various characters (Table 2). The low coefficient of variation (<10%) was observed for days to maturity (1.64%), days to 1st flower (2.46%) and 100 seed weight (3.73%) and moderate coefficient of variation (10 - 20%) was observed for plant height (10.15%), number of branches plant⁻¹ (10.68%) and number of pods plant⁻¹ (17.96%) which showed the best genetic potential and its genetic influence. The high coefficient of variation (>20%) was observed for seed yield plant⁻¹ (26.62), which indicates more influence of environmental fluctuation. Being the M₄ generation, the amount of variability should be low, however, most of the characters recorded moderate or high coefficient of variation. In accordance to this result Shri Devi and Mullainathan (2012) in black gram, Gaur *et al.* (2018) in pigeon pea also observed high coefficient of variation and the influence of environment on yield and yield component.

Phenotypic variance and phenotypic coefficient of variation was observed to be greater than genotypic variance and genotypic coefficient of variation for all the seven characters studied (Table 3). Similar to this result Wani *et al.* (2012) in chickpea, Kavera and Nadaf (2017) in groundnut, Gaur *et al.* (2018) in pigeonpea and Bisane *et al.* (2019) in soybean also reported that phenotypic coefficient of variation was greater than their corresponding genotypic coefficient of variation for all the characters studied. The difference between genotypic and phenotypic coefficient of variation for all the characters except seed yield plant⁻¹ was small indicating that these traits were less influenced by environment.

Genotypic coefficient of variation exhibited the values in moderate category (10 - 20%) for the character number of pods plant⁻¹ (11.28%) and low (< 10%) for the characters seed yield plant⁻¹(9.65%), plant height (6.85%), number of branches plant⁻¹ (3.85%), and days to 1st flower (3.19%), 100 seed weight (2.34%) and days to maturity (1.50%). Similarly phenotypic coefficient of variation was observed to be high (> 20%) for the characters such as seed yield plant⁻¹ (28.31%) followed by number of pods plant⁻¹ (21.21%) and moderate (10-20%) for characters plant height (12.24%) followed by number of branches plant⁻¹ (11.35%) and low phenotypic coefficient of variation was observed

Table 1. Analysis of variance to estimate between and within family variances

Source of variation	df	Mean squares						
		Days to first flower	Days to maturity	Plant height (cm) plant ⁻¹	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)
Between families	74	673.29**	3164.27**	1690.69**	10.79**	7487.29**	15.79**	212.57**
Within families	1385	26.91	159.09	90.97	0.84	1130.40	0.41	60.61
Intra class correlation (t)	-	0.55	0.49	0.47	0.38	0.22	0.66	0.11

** Significant at 1 % level

Table 2. Mean, minimum, maximum, range and co-efficient of variation different Characters in M₄ generation

Sr. No.	Parameters	Mean	Min	Max	Range	CV (%)
1	Days to 1 st flower	49.33	45.86	53.94	8.08	2.46
2	Days to maturity	107.71	104.10	113.17	9.06	1.64
3	Plant height (cm)	61.26	47.52	70.79	23.27	10.15
4	No. of branches plant ⁻¹	5.38	4.55	6.21	1.66	10.68
5	No. of pods plant ⁻¹	111.32	73.94	151.33	77.40	17.96
6	100 seed weight (g)	7.65	7.16	8.27	1.11	3.73
7	Seed yield plant ⁻¹ (g)	16.62	10.88	25.82	14.93	26.62

Table 3 . Genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation estimates for different characters in M₄ generation

Sr. No.	Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)
1	Days to 1 st flower	2.48	3.95	3.19	4.02
2	Days to maturity	2.61	5.74	1.50	2.22
3	Plant height (cm)	17.61	56.31	6.85	12.24
4	No. of branches plant ⁻¹	0.04	0.37	3.85	11.35
5	No. of pods plant ⁻¹	157.80	557.64	11.28	21.21
6	100 seed weight (g)	0.03	0.11	2.34	4.40
7	Seed yield plant ⁻¹ (g)	2.57	22.14	9.65	28.31

Table 4. Heritability and genetic advance estimates for different characters in M₄ generation

Sr. No.	Characters	Heritability (%)	Genetic Advance	Genetic advance (per cent of mean)
1	Days to 1 st flower	62.79	2.19	4.45
2	Days to maturity	45.62	1.92	1.78
3	Plant height (cm)	31.28	4.13	6.74
4	No. of branches plant ⁻¹	11.53	0.12	2.30
5	No. of pods plant ⁻¹	33.29	11.76	10.56
6	100 seed weight (g)	28.41	0.16	2.20
7	Seed yield plant ⁻¹ (g)	11.61	0.96	5.78

for 100 seed weight (4.40%), days to first flower (4.02%), and days to maturity (2.22%).

The estimates of heritability and genetic advance estimated in material consisting 73 mutants along with check (Ratan) and parent (NLK-73) for seven characters are reported in Table 4. Heritability per cent ranged from 11.53% (number of branches plant⁻¹) to 62.79% (days to first flower). High heritability was recorded for days to first flower (62.79%). Moderate heritability was observed for days to maturity (45.62%), plant height (31.28%) and number of pods plant⁻¹ (33.29%) and low heritability was observed for 100 seed weight (28.41%), seed yield plant⁻¹ (11.61%), and number of branches plant⁻¹ (11.53%). High to low estimate of heritability observed for the above characters revealed that there was less influence of environmental factors in the expression of traits exhibiting moderate and high heritability and there was high influence of environmental factors in the expression of traits exhibiting low heritability. In accordance to these results high heritability for yield and yield components were reported by Khan and Goyal (2009) in mungbean, Barshile and Apparao (2012) in chickpea, Wani *et al.* (2012) in chickpea and More and Borkar (2016) in French bean.

Genetic advance as a percentage of mean were moderate for number of pods plant⁻¹ (10.56%) and low for characters plant height (6.74%), seed yield plant⁻¹ (5.78%), days to first flower (4.45%), number of branches plant⁻¹ (2.30%), 100 seed weight (2.20%) and days to maturity (1.78%). Similar to these results moderate genetic advance as percentage of mean was also reported in mungbean by Khan and Goyal (2009), Wani *et al.* (2012) for number of branches in chickpea, Nagarajan *et al.* (2017) in soybean for number of pods plant⁻¹ and Gaur *et al.* (2018) in pigeon pea for number of pods plant⁻¹ and seed yield plant⁻¹.

The main objective of this experiment was to identify superior segregants/mutants for yield and yield contributing characters. As discussed in M₄ generation, between family variance, within family variance and intra class correlation (t) revealed that difference between individuals within a family is large for all the characters except for 100 seed weight and days to first flower but each family is also distinctly different from the other but at low level for days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹ and seed yield plant⁻¹. In M₄ generation equal weightage to σ^2_f (between family variance) and σ^2_w (within family variance) was suggested to be given during selection. Therefore, individual plant exhibiting significant superiority over check for number of pods plant⁻¹ from different progenies were considered as the criteria of selection as this was the only character exhibiting

additive gene action in this study. Based on this criteria 101 individual plants from 47 progenies out of 73 progenies studied, fulfilling the above criteria were identified for evaluation for one more generation.

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Rec. on 25.06.2021 & Acc. on 03.07.2021