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Genetical studies in M$_4$ generation of *Lathyrus*

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Abstract
The present study was conducted at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur. During *Rabi* 2020 in M$_4$ generation, 79 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. Intra class correlation (t) leads to the inference that differences between individuals within a family are large for all the characters except for days to first flower, but each family distinctly differentiated from others also at lower level in M$_4$ generation hence, equal weightage to σ^2f and σ^2w were suggested to be considered for selection in M$_4$ generation. Moderate genotypic and phenotypic coefficient of variation was recorded for plant height, number of pods plant^{-1} and seed yield plant^{-1} and low for other characters. High heritability was recorded for plant height and moderate heritability was observed for days to first flower, days to maturity, number of pod plant^{-1}, 100 seed weight, seed yield plant^{-1} and low heritability for number of branches plant^{-1}. Genetic advance as a percentage of mean were moderate for seed yield plant^{-1}, plant height, number of pods plant^{-1} and low for 100 seed weight, days to first flower, number of branches plant^{-1}, days to maturity. Three characters plant height, number of pods plant^{-1} and seed yield plant^{-1} exhibited moderate genotypic coefficient of variation, moderate heritability and moderate genetic advance as percentage of mean. Hence were suggested to be considered as a criteria for selection. But as only number of pods plant^{-1} was the only character which was less influenced by environment, hence considered for selection. As equal weightage to σ^2f and σ^2w was supposed to be given during selection, 73 individual plants from 38 mutant progenies exhibiting significant superiority over check for number of pods plant^{-1} were identified for their evaluation for one more generation in M$_5$ before forwarding to yield trials.

Keywords: *Lathyrus*, heritability, genetic advance percentage of mean, GCV, PCV, M$_4$ generation

Introduction

The *Lathyrus sativus* L. (2n = 14) is an annual herb and an important pulse crop, rich in protein content (28%) next to soybean locally called as grass pea, khesari dal, peavine or chanamatra. It belongs to family Leguminosae, sub family Papilionoideae and genus *Lathyrus* with 130 species occurring all over the 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, where 3600 years old remains have been discovered. The plant is considered as a great boon against drought, floods, hails and various pests. The plant is strongly drought resistant. It is mostly sown in standing crop of paddy as a 'Utera' or 'Paira' crop in *rabi* season. Secondly, the main pulse crop Tur (Pigeon pea) is grown only on bunds, hence the production of Tur is not sufficient for fulfilling 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) [19] and grows luxuriantly without any cultivation input and lastly, this pulse is consumed in various forms like chapatis, wadas and curries and fed to cattle as green fodder and stover (dried chaff) since ancient times. *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 form like chapatis, 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

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due to presence of neurotoxin, (β-N-oxalyl-L-α, β-diaminopropionic acid) β-ODAP in its seedlings and seeds. The traditional varieties of grass pea contain 0.5-2.5% β-ODAP (Kumar *et al.* 2011) [11]. Hence exploitation of genetic variability for neurotoxin has been observed for development of low β-ODAP and high yielding varieties. These are two prime objectives in grasspea breeding. However, there is considerable scope for improving yield potential and other agronomical characters in this crop.

The mutation breeding has been used worldwide for improvement of grain legumes through increased genetic variation and of novel alleles. Therefore, mutation breeding is more desirable to create variability in grasspea. Physical and chemical mutagens provide handy tools to enhance natural mutation rate, thereby enlarging the genetic variability and increasing the scope of obtaining desired mutants. In order to induce variability and utilize useful mutation for efficient plant breeding, the systematic and comparative study of induce mutagenic effectiveness and mutagenic efficiency in a variety of crop plant is essential. The present research work was, therefore, planned and undertaken.

Material 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* cultivar NLK-73 were made. Out of this, five lots of seeds were sent to Bhabha Atomic Research Centre, Trombay, for irradiation with five different doses of gamma rays i.e. 150Gy, 200Gy, 250Gy, 300Gy, 350Gy (Co^{60} at BARC) and used for raising M_1 and M_2 generations along with control during *rabi* 2017 and 2018 respectively and individual plants in each treatment were harvested separately. The harvested seeds were used to raise M_3 generation in *Rabi* 2019 for evaluation and 79 single plant mutants for desired characters were identified. The 79 mutants identified along with checks NLK-73 and Ratan were planted in RBD with three replications in *Rabi,* 2020. The mutants identified in M_3 like high pods, purple colour, tall plant, more branches etc. were also confirmed in M_4. In *rabi* 2020, harvested seed from each (79) mutants of M_3 generation along with 2 checks (NLK-73 and Ratan) were sown to raise M_4 generation in replicated trial using Randomized Block Design replicated thrice. Plot size was 0.9 m x 4 m. two rows were allotted for each mutant and check with 20 plant row^{-1}. The row to row distance was 45 cm and plant to plant distance was 20 cm. 10 plants in mutant and 5 plants in check were randomly selected in each replication and observations were recorded for 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} (g). The data recorded during M_4 generation were subjected to statistical analysis i.e. mean, range, genotypic variance, phenotypic variance, heritability (Hanson *et al.*, 1956) [7], genotypic coefficient of variation (%), phenotypic coefficient of variation (%) (Burton, 1953) [3]. Genetic advance (Robinson *et al.,* 1949) [15], genetic advance as percentage of mean (Johnson *et al.,* 1955) [8].

Results and Discussion
The data recorded on seven characters in 79 mutant progenies along with two checks were subjected to analysis of variance to know the genetic difference between families and within families. The results of this analysis are presented in Table 1 which showed highly significant mean squares 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 pod plant^{-1}, 100 seed weight and seed yield plant^{-1}. This indicated the presence of significant genetic variability between the families for all the characters studied which allowed the further estimation of genetic parameters. In accordance to this, results significant genetic variability between the families were also reported by Waghmare and Mehra (2000) [20] in *Lathyrus*, Tripathy *et al.* (2012) [18] in *Lathyrus*, Malek *et al*. (2014) [13] in soybean and Ahir *et al.* (2018) [1] in green gram.

The intra class correlation (t) which is the ratio of two variances i.e. between family variances ($\sigma^2 f$) and total phenotypic variance ($\sigma^2 p$) were estimated in M_4 generation in this study. This value was observed to range from 0.08 for number of branches plant^{-1} to 0.64 for days to first flower. Highest intra class correlation value was observed for days to first flower (0.64) followed by days to maturity (0.55), plant height (0.47), 100 seeds weight(g) (0.38), number of pods plant^{-1} (0.17) number of branches plant^{-1} (0.08) and seed yield plant^{-1}(g) (0.16). This revealed that 64%, 55%, 47%, 38%, 17%, 16% and 8% of variation for days to first flower, days to maturity, plant height (cm), 100 seeds weight, number of pods plant^{-1}, seed yield plant^{-1} and number of branches plant^{-1} respectively were due to differences between the families and 36%, 45%, 53%, 62%, 83%, 84% and 92% were due to within families. This indicated that differences between individuals within a family are large for all the characters except for days to first flower, but each family distinctly differentiated from other also at lower level. Therefore, equal weightage was suggested to be assigned to $\sigma^2 f$ and $\sigma^2 w$ in this generation also. This indicates that between family selection followed by within family selection will be more rewarding in M_4 generation.

The estimate of genetic parameters like mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were calculated for seven characters in M_4 generation and are presented in Table 2, 3, 4. The grand mean recorded for 79 mutants along with two checks were found to be 50.93 days for first flower, 110.11 days for maturity, 59.02 cm for plant height, 5.36 for number of branches plant^{-1}, 96.26 for number of pods plant^{-1}, 8.56g for 100 seed weight and 18.02g for seed yield plant^{-1} (Table 2). High range of 64.21 was exhibited for number of pod plant^{-1}, followed by plant height (30.20 cm) and seed yield plant^{-1} (13.28 g) which indicated that wide range of variation were functioning for these characters. Days to maturity (9.18), days to first flower (6.9), 100 seed weight (1.97g) and number of branches plant^{-1} (1.99) exhibited low range of variation. Even though a range of 13.28g was observed for seed yield plant^{-1} it was considerable as the maximum level of yield shown by check variety was only 15.79g. 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 Tripathy *et al.* (2012) [18] in *Lathyrus*, Gopinath and Pavadai (2015) [5] in Soybean and Ahir *et al*. (2018) [1] in green gram.

The coefficient of variation (CV) ranged from 1.64 to 12.42% for various characters (Table 2). The low coefficient of variation (≤ 10%) was observed for days to maturity (1.64%), days to first flower (2.42%), 100 seed weight (5.58%), plant height (7.40%) and number of branches plant^{-1} (9.63%) and

moderate coefficient of variation (10-20%) was observed for number of pods plant[-1] (10.37%) and seed yield plant[-1] (12.42%) which showed the best genetic potential and its genetic influence. Being the M_4 generation, the amount of variability should be low. However, seed yield plant[-1] and number of pods plant[-1] recorded moderate coefficient of variation indicating little influence of environmental fluctuations. Hence further selection and advancement of progenies is necessary for one more generation till attainment of homogeneity. In contrary to this result Shri Devi and Mullainathan (2012) [16] in black gram and Gaur *et al.* (2018) [6] in pigeon pea also observed high coefficient of variance and the influence of environment on yield and yield components.

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 3). Similar to this results Kumar and Dubey (2001) [9] and Tripathy *et al.* (2012) [18] in *Lathyrus*, Meshram *et al.* (2013) [12] in blackgram and Ahir *et al.* (2018) [1] in green gram 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 per 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 the moderate (10-20%) values for the characters such as number of pods plant[-1] (11.74%), seed yield plant[-1] (10.89%) and plant height (10.78%) and low (≤10%) values for days to first flower (2.80), days to maturity (1.35), number of branches plant[-1] (3.38) and 100 seed weight (5.19%). Similarly, phenotypic coefficient of variation was also observed to be moderate (10-20%) for characters seed yield plant[-1] (16.51%), number of pods plant[-1] (15.66%), plant height (13.08%) and number of branches plant[-1] (10.20%) and low phenotypic coefficient of variation was observed for days to maturity (2.13%), days to first flower (3.70%) and 100 seed weight (7.62%).

Heritability per cent ranged from 10.98% (number of branches plant[-1]) to 67.9% (plant height (cm) as observed from Table 4. High heritability was recorded for plant height (cm) (67.9%) and moderate heritability was observed for days to first flower (57.41%), number of pod plant[-1] (56.1%),100 seed weight (g) (46.38%), seed yield plant[-1] (g) (43.49%), days to maturity (40.52%) and low heritability for number of branches plant[-1] (10.98%). High to moderate estimate of heritability observed for most of the traits suggested less influence of environmental factor in the expression for these traits. In accordance to these results high heritability for yield and yield components were also reported by Kumar and Dubey (2001) [9] in *Lathyrus*, Basavaraja *et al.* (2008) [2], Pavadai *et al.* (2010) [14] in soybean. High to moderate heritability is an indication of presence of higher proportion of flexible additive variance in the population. Estimates of heritability revealed that the selection could be effectively made on phenotypic basis by considering the traits seed yield

plant[-1], number of pods plant[-1], 100 seed weight, days to first flower, days to maturity and plant height which exhibited moderate to high heritability. Genetic advance as a percentage of mean were moderate for seed yield plant[-1] (g) (12.64 %), Plant height (cm) (15.65%), Number of pod plant[-1] (15.49%) and low for 100 seed weight (6.22%), days to first flower (3.74%), number of branches plant[-1] (1.97%) and days to maturity (1.52%). Similar to these results high genetic advance as a percentage of mean was also reported by Malek *et al.* (2014) [13] and Pavadai *et al.* (2010) [14] in Soybean, Meshram *et al.* (2013) [12] in blackgram.

In this study high or moderate heritability estimate along with moderate genetic advance as per cent of mean was noticed in plant height, number of pods plant[-1] and seed yield plant[-1]. The high or moderate heritability coupled with moderate 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] can be improved by selection on the basis of phenotype for effective improvement in *Lathyrus*. All other characters exhibited low or moderate heritability but accompanied with low genetic advance which indicates the higher influence of environment. In accordance to this result Khan and Goyal (2009) [10] in mung bean, Wani *et al.* (2012) [21] in chickpea, Meshram *et al*. (2013) [12] in black gram and Dhaka *et al.* (2013) [4] in cowpea reported high heritability along with genetic advance as percent of mean for yield and yield contributing traits. When all the genetic parameters for seven characters were considered, it was found that the characters plant height, number of pods plant[-1] and seed yield plant[-1] exhibited moderate genotypic coefficient of variation, moderate heritability and moderate genetic advance as percentage of mean.

The main objective of this experiment was to identify superior segregant/mutants for yield and yield contributing characters. In M_4 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 days to first flower and days to maturity, but each family is also distinctly different from the other but at low level for plant height, 100 seed weight, seed yield plant[-1], number of pods plant[-1] and number of branches plant[-1]. Many of the progenies recorded low mean performance or at par when compared with check (Ratan) for all the above characters. This may be due to the high within family variance and also the influence of environment. Therefore, in M_4 generation equal weightage to $\sigma^2 f$ (between family variance) and $\sigma^2 w$ (within family variance) was suggested to be given during selection. Therefore, individual plant exhibiting significantly superiority over check for plant height, number of pods plant[-1], and seed yield plant[-1] from different progenies could be considered as the criteria of selection as these characters exhibited additive gene action in this study. As seed yield plant[-1] in this study is highly influenced by environment, number of pods plant[-1] was considered as the criteria of selection. Hence, individual plant exhibiting significantly over check for number of pods plant[-1] from different progenies were considered for selection. Based on this criteria 73 individual plants from 38 progenies out of 79 progenies studied, fulfilling the above criteria were identified for evaluation for one more generation.

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

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	80	400.23**	1602.83**	1365.14**	4.19**	4008.15**	12.62**	165.41**
Within families	1519	11.31	64.08	73.62	1.55	809.63	0.96	34.82
Intra class correlation (t)		0.64	0.55	0.47	0.08	0.17	0.38	0.16

** Significant at 1%

Table 2: Mean, minimum, maximum and range for different characters in M_4 generation

Sr. No.	Parameters	Mean	Min	Max	Range	CV (%)
1	Days to 1st flower	50.93	47.30	54.2	6.9	2.42
2	Days to maturity	110.11	104.39	3.57	9.18	1.64
3	Plant height (cm)	59.02	45.61	75.4	30.20	7.40
4	No. of branches plant^{-1}	5.36	4.5	6.57	1.99	9.63
5	No. of pod plant^{-1}	96.26	68.21	132.42	64.21	10.37
6	100 seed weight (g)	8.56	7.70	9.66	1.97	5.58
7	Seed yield plant^{-1} (g)	18.02	10.70	23.18	13.28	12.42

Table 3: Genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation estimates for different characters in M_4 generation

Sr. No.	Characters	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)
1	Days to 1st flower	2.04	3.57	2.80	3.70
2	Days to maturity	2.23	5.51	1.35	2.13
3	Plant height (cm)	40.52	59.61	10.78	13.08
4	No. of branches plant^{-1}	0.03	0.30	3.38	10.20
5	No. of pod plant^{-1}	127.79	227.44	11.74	15.66
6	100 seed weight (g)	0.19	0.43	5.19	7.62
7	Seed yield plant^{-1} (g)	3.82	8.86	10.89	16.51

Table 4: Heritability and genetic advance estimates for different characters in M_4 generation

Sr. No.	Characters	Heritability (%)	Genetic advance	Genetic advance (Percent of mean)
1	Days to 1st flower	57.41	1.90	3.74
2	Days to maturity	40.52	1.67	1.52
3	Plant height (cm)	67.90	9.23	15.65
4	No. of branches plant^{-1}	10.98	0.10	1.97
5	No. of pod plant^{-1}	56.10	14.91	15.49
6	100 seed weight (g)	46.38	0.53	6.22
7	Seed yield plant^{-1} (g)	43.49	2.27	12.64

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