GENETIC STUDIES IN M$_3$ GENERATION OF LATHYRUS

Achal B. Kamble[1], Shanti R. Patil[2], Vandana S. Madke[3], Treio Dkhar[4], Vandana B. Kalamkar[5], Prema R. Manapure[6], Gopal Nawale[7] and Jadala Ravali[8]

ABSTRACT

The present study was conducted with the objectives to estimate variances due to between family and within family, to estimate genetic parameters and to identify superior mutants for utilization at research farm of Agricultural Botany Section, College of Agriculture, Nagpur. During *rabi* 2022 in M$_3$ generation 97 mutants along with check (NLK-73) were evaluated in three replications. Data were recorded on germination percentage, mortality percentage, 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 revealed the presence of significant genetic variability between the families. Intra class correlation (t) lead the inference that differences between individual within family is large and each family differentiated distinctly from the other at lower level in M$_3$ generation hence, equal weightage to ó^{2}f and ó^{2}w were suggested to be considered for selection in M$_3$ generation. Moderate genotypic coefficient of variation and high phenotypic coefficient of variation was recorded for all the characters. Heritability and genetic advance as a percentage of mean recorded low for all the characters. When all the genetic parameters for all the characters were considered, it was found that only the characters seed yield plant^{-1} and number of pods plant^{-1} recorded wide range, moderate GCV, high PCV, low heritability and genetic advance. Hence, these two characters were considered for selection in M$_3$ generation. 117 individual plants from 97 mutant progenies exhibiting significant superiority over check for seed yield plant^{-1} and number of pods plant^{-1} were identified for their evaluation for one more generation in M$_4$ before forwarding to yield trials.

(Key words: Lathyrus, mutation, GCV, PCV, heritability, genetic advance)

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. It 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 Leguminoceae (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 B$_1$, B$_2$, B$_6$, 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). 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.

1, 4, 7 & 8.   P.G. Students, Botany Section, College of Agriculture, Nagpur, Maharashtra, India
2.   Asstt. Professor, Botany Section, College of Agriculture, Gadchiroli, Maharashtra, India
3.   Asstt. Professor, Botany Section, College of Agriculture, Nagpur, Maharashtra, India
5.   Sr. Res.Asstt. Botany Section, College of Agriculture, Nagpur, Maharashtra, India
6.   Professor, Botany Section, College of Agriculture, Nagpur, Maharashtra, India

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 seeds of *Lathyrus sativus* cv. NLK-73 was obtained from Agricultural Botany Section, College of Agriculture, Nagpur. Four different lots of 500 seeds of Lathyrus cultivar NLK-73 were made. Out of these three lots of seeds were send to Bhabha Atomic Research Centre, Trombay, for irradiation with three different dosage of gamma rays *i.e* 250 Gy, 300 Gy and 350 Gy (Co60 at BARC) and used for raising M_1 generation along with control during *rabi*, 2020 and individual plant in each treatment was harvested separately. The harvested seeds were used to raise M_2 generation in *rabi* 2021 for evaluation from which 97 single plant mutants for desired characters were identified. The present work is the continuation of the above mentioned work. The 97 mutants identified along with checks NLK-73 were planted in RBD with three replications in *rabi* 2022 for their evaluation in M_3 generation. Plot size was 1.35 m × 4 m. Three rows were 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. 20 plants in mutant and 5 plants in check were randomly selected in each replication and observations were recorded for germination percentage on plot basis, mortality percentage on plot basis, 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_3 generation were subjected to statistical analysis i.e mean, range, coefficient of variation, genotypic variance, phenotypic variance, heritability (Hanson *et al.*, 1956), genotypic coefficient of variation (%) and phenotypic coefficient of variation (%) (Burton and Devane, 1953), genetic advance (Robinson *et al.,* 1949) and genetic advance as percentage of mean (Johnson *et al.,* 1955). Analysis of

variance was estimated as per the method given by Sharma (2006).

RESULTS AND DISCUSSION

Analysis of variance as observed from Table 1 resulted in highly significant mean squares for the germination percentage and mortality percentage. The results on analysis of variance as observed from Table 2 showed highly significant mean square due to between family for all the seven characters *viz.*, 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 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 Malek *et al.* (2014) in soybean, Nair and Mehta (2014) in cowpea, Wani *et al.* (2021) in lentil.

The intra class correlation (t) which is the ratio of two variances i.e. between family variances ($ó^2f$) and total phenotypic variance ($ó^2p$) were estimated in M_3 generation in this study. This value was observed to range from 0.046 for number of branches plant^{-1} to 0.080 for seed yield plant^{-1}. Highest intra class correlation value was observed for seed yield plant^{-1} (g) (0.080) followed by number of pods plant^{-1} (0.068), plant height (cm) (0.061), days to first flower (0.055), days to maturity (0.053), 100 seed weight (g) (0.051) and number of branches plant^{-1} (0.046). This revealed that 8.0%, 6.8%, 6.1%, 5.5%, 5.3%, 5.1% and 4.6% of variation for seed yield plant^{-1}(g), number of pods plant^{-1}, plant height (cm), days to first flower, days to maturity, 100 seeds weight and number of branches plant^{-1} respectively, were due to differences between the families and 92%, 93.2%, 93.9%, 94.5%, 94.7%, 94.9% and 95.4% were due to within families.

This indicated that differences between individuals within a family were large for all the characters but each family distinctly differentiated from other also at lower level. Therefore, equal weightage was suggested to be assigned to $ó^2f$ and $ó^2w$ in this generation. This indicates that between family selection followed by within family selection will be more rewarding in M_3 generation. In accordance to this study Jambulwar *et al.* (2021) and Ingle *et al.* (2021) also reported to assign equal weightage to $ó^2f$ and $ó^2w$ and also suggested between family selection followed by within family selection to be more rewarding in lathyrus.

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 M_3 generation and data are presented in Table 3. The grand mean recorded for 97 mutants along with check were found

to be 51.75 per cent for germination, 37.63 per cent for mortality percentage, 47.13 for days to first flower, 114.35 days to maturity, 46.68 cm for plant height, 3.52 for number of branches plant^{-1}, 46.40 for number of pods plant^{-1}, 6.80 g for 100 seed weight and 20.42 g for seed yield plant^{-1} (Table 3). High range of 224 was exhibited for number of pods plant^{-1}, followed by seed yield plant^{-1}(g) (70), plant height (cm) (64) and mortality percentage (45.11%) which indicated that wide range of variation were functioning for these characters. Germination percentage (39.20%), days to first flower (27), days to maturity (19), 100 seed weight (7g) and number of branches plant^{-1} (5) 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 component were also reported by Tripathy *et al.* (2012) in lathyrus and Jambulwar *et al.* (2021) in lathyrus.

Significant differences were observed between the progenies for all the seven characters studied. The coefficient of variation (CV) ranged from 4.95 to 29.26% for various characters. The low coefficient of variation (d"10%) was observed for days to maturity (4.95%), days to first flower (7.74%), plant height (7.86%) and number of pods plant^{-1} (8.57%) and moderate coefficient of variation (10-20%) was observed for seed yield plant^{-1} (12.71%) high coefficient of variation (e"20%) was observed for 100 seed weight (20.48%) and number of branches plant^{-1} (29.26%). Being the M$_3$ generation, the amount of variability should be moderate or low. The characters recorded from low to high coefficient of variation. Hence, further selection and advancement of progenies is necessary till attaining the homogeneity. In contrary to this result Sri Devi and Mullainathan (2012) in black gram, Girija *et al.* (2014) in cowpea and Ingle *et al.* (2021) in lathyrus 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 Tripathy *et al.* (2012) in lathyrus, Ingle *et al.* (2021) in lathyrus and Jambulwar *et al.* (2021) 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 all characters was of considerable amount indicating that these traits were highly influenced by environment. Genotypic coefficient of variation exhibited the values in moderate category (10-20%) for all the seven characters studied such as seed yield plant^{-1} (16.85%) followed by number of pods plant^{-1} (15.93%), plant height (12.72%), days to 1st flower (11.77%), days to maturity (11.56%), number of branches plant^{-1} (11.47%) and 100 seed weight (11.46%). Similarly phenotypic coefficient of variation was observed to be high for all the seven characters studied such as number

of pod plant^{-1} (61.25%) followed by seed yield plant^{-1} (59.62%), number of branches plant^{-1} (53.50%), plant height (51.64%), 100 seed weight (50.75%) and days to first flower (50.41%), and days to maturity (50.01%). Maximum GCV and PCV were recorded by seed yield plant^{-1} (16.85% and 59.62%) followed by number of pods plant^{-1} (15.93% and 61.25%). In accordance to this result, high GCV and PCV for seed yield plant^{-1} and number of pods plant^{-1} were also observed by Ajayi *et al.* (2017) in cowpea, Jambulwar *et al.* (2021) in lathyrus and Goyal *et al.* (2021) in urdbean.

Heritability per cent ranged from 4.60 % (number of branches plant^{-1}) to 7.99% (seed yield plant^{-1}). Low heritability was recorded for number of branches plant^{-1} (4.60%), 100 seed weight (g) (5.10%), days to maturity (5.33%), days to 1st flower (5.45%), plant height (cm) (6.07%), number of pods plant^{-1} (6.76%) and seed yield plant^{-1} (g) (7.99%). Low estimate of heritability for above traits suggested greater influence of environmental factor in the expression for these traits. In contrary to these results high heritability for yield and yield components were also reported by Kumar and Dubey (2001) in lathyrus, Girija *et al.* (2014) in cowpea, Ingle *et al.* (2021) in lathyrus and Jambulwar *et al.* (2021) in lathyrus.

Genetic advance is a measure of expected progress under selection scheme. It gives the magnitude of improvement per cycle in the base population by selection. Genetic advance as a percentage of mean were low for seed yield plant^{-1} (g) (8.38%), number of pods plant^{-1} (7.29), plant height (cm) (5.52%), days to 1st flower (4.84), days to maturity (4.69%), 100 seed weight (g) (4.55%), number of branches plant^{-1} (4.33%). In contrary to these results high genetic advance as a percentage of mean was also reported by Girija *et al.* (2014) in cowpea, Goyal *et al.* (2020) in black gram, Ingle *et al.* (2021) in lathyrus and Jambulwar *et al.* (2021) in lathyrus.

In this study all the seven characters exhibited low heritability accompanied with low genetic advance as percentage of mean. This reveals that the characters are highly influenced by environmental effects and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effect. This might be due to the high variance within family.

When all the genetic parameters for seven characters were considered, it was found that all the characters exhibited wide range, moderate genotypic coefficient of variation, low heritability and low genetic advance. Whatever may the category, seed yield plant^{-1} and number of pods plant^{-1} ranked first and second for range, GCV, heritability and genetic advance and hence may be considered for selection of plants for forwarding to next generation.

The main objective of this experiment was to identify superior segregants/mutants for yield and yield contributing characters. In M$_3$ generation, between family variance, within family variance and intra class correlation (t) revealed that difference between individuals within a family is larger but

Table 1. Analysis of variance for germination and mortality percentage in M₃ generation

Sources of variation	df	Mean sum of square	
		Germination (%)	Mortality (%)
Replications	2	357.92	197.60
Treatments	97	200.63**	195.69**
Error	194	128.91	67.37

**Significant at 1% level

Table 2. Analysis of variance for different characters in M₃ generation

Sources of variation	df	Mean sum of square						
		Days to 1st flower	Days to maturity	Plant ht. (cm)	No. of bran. plant⁻¹	No. of pods plant⁻¹	100 seeds wt.(g)	Seed yield plant⁻¹(g)
Between families	97	2383.28**	13561.10**	2663.88**	13.20**	4033.88**	47.81**	848.19**
Within families	5782	533.80	3097.30	545.92	3.39	753.39	11.31	136.51
Intra class correlation (t)		0.055	0.053	0.061	0.046	0.068	0.051	0.080

**Significant at 1% level

Table 3. Genetic parameter estimates for different characters in M₃ generation

Parameters	Germination (%)	Mortality (%)	Days to 1st flower	Days to maturity	Plant ht. (cm)	No. of bran. plant⁻¹	No. of pods plant⁻¹	100 seed wt. (g)	Seed yield plant⁻¹ (g)
Mean	51.75	37.63	47.13	114.35	46.68	3.52	46.40	6.80	20.42
Min	31.73	15.96	32.00	102.00	20.00	2.00	7.00	4.00	2.00
Max	70.57	61.07	59.00	121.00	84.00	7.00	231.00	11.00	72.00
Range	39.20	45.10	27.00	19.00	64.00	5.00	224.00	7.00	70.00
CV (%)	21.94	21.81	7.74	4.15	7.86	29.26	8.57	20.48	12.71
Genotypic variance	-	-	30.83	174.39	35.29	0.164	54.67	0.61	11.86
Phenotypic variance	-	-	564.62	3271.69	581.21	3.55	808.06	11.92	148.37
GCV (%)	-	-	11.77	11.54	12.72	11.47	15.93	11.46	16.85
PCV (%)	-	-	50.41	50.01	51.64	53.50	61.25	50.7	59.62
Heritability (%)	-	-	5.45	5.33	6.07	4.60	6.76	5.10	7.99
Genetic advance (GA)	-	-	2.28	5.36	2.57	0.15	3.38	0.31	1.71
GA (% of mean)	-	-	4.84	4.69	5.52	4.33	7.29	4.55	8.38

each family is also distinctly different from the other but at low level for all the seven characters studied. Many of the progenies recorded low mean performance or at par when compared with check (NLK-73) for all the above characters. This may be due to the high within family variance and also the influence of environment. Therefore, in M_3 generation equal weightage to $\acute{o}^2f$ (between family variance) and $\acute{o}^2w$ (within family variance) was suggested to be given during selection. Hence, selection of superior families followed by selection of individual plants in selected families were considered as the criteria of selection. Individual plant exhibiting significant superiority over check for seed yield plant^{-1}, number of pods plant^{-1}, bold seed etc. were selected from different treatment.

Thus, 117 M_3 mutant plants were selected from 97 mutants from different treatments of variety NLK-73 mainly on the basis of seed yield^{-1}, more pods and bold seed. In this study as additive gene action was found to be predominant for yield and yield components, it is suggested that the selected 117 mutant plants from M_3 generation should be raised in progeny rows for one more generation i.e. M_4 so that homozygosity will be attained and superior progenies can be then selected for forwarding to yield traits in the next generation.

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