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GENETIC STUDIES IN GAMMA RAYS INDUCED M_3 GENERATION IN LATHYRUS

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ABSTRACT

The present study was conducted with the objectives to estimate between and within family variances, to estimate genetic parameters and to identify superior mutants for utilization at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur during *rabi* 2019. 123 mutants along with two checks (NLK-73 and Ratan) were evaluated in M_3 generation 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 families were highly significant for all traits, which revealed the presence of significant genetic variability between the families. Intra class correlation (t) lead to the inference that differences between individuals within family was large and each family differentiated distinctly from the other at lower level in M_3 generation hence, equal weightage to σ^2f and σ^2w were suggested to be considered for selection in M_3 generation. High genotypic and phenotypic coefficient of variation was recorded for seed yield plant^{-1} and 100 seed weight and moderate for other characters. High heritability was recorded for number of branches plant^{-1}, days to 1st flower, seed yield plant^{-1} and moderate for others. Genetic advance as a percentage of mean was high for seed yield plant^{-1}, 100 seed weight, number of branches plant^{-1} and plant height. Seed yield plant^{-1} was the only character which recorded high GCV, PCV, heritability and genetic advance, hence, this character was considered for selection in M_3 generation as influenced by additive gene action.As equal weightage to σ^2f and σ^2w was supposed to be given during selection, 174 individual plants from 123 mutants 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, M_3 generation, GCV, PCV, heritability, genetic advance)

INTRODUCTION

The *Lathyrus sativus* (L.) (2n = 14) is an annual herb and an important pulse crop rich in protein contain (28%) next to soybean locally called as grass pea, khesari dal, peavine or chanamatra. It belongs to family Leguminoceae, sub family Papilionoiceae and 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 center of domestication, were 3600 years old remains have been discovered.

Lathyrus *(Lathyrus sativus* L.*)* is one of the important pulse crops in India and other countries like Bangaladesh, 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. Globally, the area under grass pea cultivation is estimated at 1.50 million ha, with annual production of 1.20 million tonnes (Gupta *et al.,* 2018). In India area under lathyrus is about 0.58 million hactares 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 50,242 hectares area. (Anonymous, 2018).

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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 mutant. 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 isessential. The present research work was, therefore, planned and undertaken using the seeds of lathyrus cultivar NLK-73 subjected to treatment of different doses of gamma rays.

MATERIALS AND METHODS

Dry healthy and genetically pure seeds of *Lathyrus sativus* cv NLK-73 were 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* 150 Gy, 200 Gy, 250 Gy, 300 Gy, 350 Gy (Co 60 At BARC) and used for raising M_1 generation along with control during *rabi* 2017 and individual plant in each treatment were harvested separately. The harvested seeds were used to raise M_2 generation in *rabi* 2018 for evaluation and 123 single plant mutants for desired characters were identified. In *rabi* 2019, harvested seeds from each (123) mutants of M_2 generation along with 2 check (NLK-73 and Ratan) were sown to raise M_3 generation in replicated trial using Randomized Block Design replicated thrice. Plot size was 1.35 m x 4 m. Three rows were allotted 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. The sowing was undertaken on the fertile and well leveled piece of land at Shankar Nagar farm, Agril Botany section, College of Agriculture, Nagpur. 20 plants in mutant and 5 plants in check were randomly selected in each replication and observations 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, genotypic variance, phenotypic variance, heritability (Hanson *et al.*, 1956), genotypic coefficient of variation (%) and phenotypic coefficient of variation (%) (Burton and Deane,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

The data recorded on nine characters in 123 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 1a and 1b. Analysis of variance resulted in highly significant mean squares for the germination percentage and mortality percentage. The results on analysis of variance as observed 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 Waghmare and Mehra (2000) in lathyrus, Tripathy *et al.* (2012) in lathyrus, Malek *et al.* (2014) in soybean and Ahir *et al.* (2018) in green gram and Praksh Hosur *et al*., (2020) in mustard.

The intra class correlation (t) which is the ratio of two variances i.e. between family variances (σ^2f) and total phenotypic variance (σ^2p) were estimated in M_3 generation in this study. This value was observed to range from 0.531 for 100 seed weight to 0.782 for number of branches plant^{-1}. Highest value of intra class correlation observed for number of branches plant^{-1}(0.782)followed by days to first flower (0.698), seed yield plant^{-1}(g) (0.634), days to maturity (0.605), plant height (cm) (0.547), number of pods plant^{-1} (0.543)and 100 seeds weight (0.531). This revealed that 78%, 69%, 63%, 60%, 54%, 54% and 53% of variation for number of branches plant^{-1}, days to first flower, seed yield plant^{-1}(g), days to maturity, plant height (cm), number of pods plant^{-1} and 100 seeds weight respectively were due to differences between the families and 22%, 31%, 37%, 40%, 46%, 46% and 47% were due to within families.This indicated that differences between individuals within a family are large for all the characters except for all characters but each family distinctly differentiated from other also at lower level. Therefore, equal weightage was suggested to be assigned to ó^{2}f and ó^{2}w in this generation also. This indicates that between family selections followed by within family selection will be more rewarding in M_3 generation. In accordance to this result Bisane *et al*. (2019) also reported equal weightage of ó^{2}f and ó^{2}w in M_4 generation of soybean.

The grand mean recorded for 123 mutants along with two checks were found to be 63.40 per cent for germination, 15.63 per cent for mortality percentage, 62 for days to first flower, 117days to maturity, 80.48 cm for plant height, 4.15 for number of branches plant^{-1},109.58 for number of pods plant^{-1}, 8.67g for 100 seed weight and 11.58g for seed yield plant^{-1} (Table 2). High range of 479 was exhibited for number of pods plant^{-1}, followed by plant height (121.34 cm), seed yield plant^{-1} (58.30 g) and germination percentage (51%) which indicated that wide range of variation were functioning for these characters. Days to maturity (25), days to first flower (22), mortality percentage (19%), 100 seed weight (10.50g) and number of branches plant^{-1} (7) exhibited low range of variation. Even though a range of 58.30g was observed for seed yield plant^{-1} it was considerable as the maximum level of yield shown by check variety was only 20.18g. 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, Pavadai (2015) and Hoa and Giang (2012) in soybean and Ahir *et al.*(2018) in green gram.

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 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 2). Similar to this results Kumar and Dubey (2001) and Tripathy *et al.* (2012) in lathyrus, Meshram *et al.* (2013) in blackgram and Ahir *et al.* (2018) 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 all characters was small indicating that these traits were less influenced by environment. Genotypic coefficient of variation exhibited the values in high category **(> 20%)** for the characters such as seed yield plant^{-1}(39.94%) and 100 seed weight (20.31%) and moderate for plant height (16.24%), number of branches plant^{-1} (14.43%), days to 1st flower (13.84%), number of pods plant^{-1} (13.16%) and days to maturity (11.59%).Similarly phenotypic coefficient of variation was also observed to be high for the characters such as seed yield plant^{-1} (50.14%)followed by 100 seed weight (27.87%) and plant height (21.96%) and moderate phenotypic coefficient of variation observed in number of pods plant^{-1}(17.85), days to first flower (16.57), number of branches plant^{-1}(16.32) and days to maturity(14.89).

The heritability estimates provides information on transmission of traits from parents to offspring. Such estimate facilitates the evaluation of genetic and environmental effect aiding in selection. Estimation of heritability is often used to predict genetic advance under selection so that the plant breeder can anticipate improvement of different type and intensity of selection. The estimate of heritability and genetic advance estimated in material consisting 123 mutants along with two checks for 7 characters are reported in Table 2. Heritability per cent ranged from 53.09% (100 seed weight (g) to 78.21% (number of branches plant^{-1}). High heritability was recorded for number of branches plant^{-1} (78.21%), days to 1st flower (69.81%), seed yield plant^{-1} (g) (63.45%) and moderate heritability was observed for days to maturity (60.53%), plant height (cm) (54.68%), number of pods plant^{-1}(54.34%) and100 seed weight (g)(53.09). High to moderate estimate of heritability for above 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) in lathyrus, Basavaraja *et al.*(2008), Pavadai *et al.* (2010), Hoa and Giang (2012) in soybean.

Genetic advance as a percentage of mean were high for seed yield plant^{-1} (g) (55.99%), 100 seed weight (g) (26.04%), number of branches plant^{-1} (22.47%) and plant height (cm) (21.13%). Similar to these results high genetic advance as a percentage of mean was also reported by Malek *et al.*(2014), Meshram *et al.* (2013) and Pavadai *et al.* (2010) in soybean.

In the present study only one character seed yield plant^{-1} showed high GCV, high PCV, high heritability and high genetic advance as percentage of mean and hence, considered for selection in M_3 generation. This revealed that this character was influenced by additive gene action and selection would be effective in improving this trait, hence was considered as criteria for selection.

Between family variance, within family variance and intra class correlation (t) when considered, it was observed that difference between individuals within a family are large and each family is also different from the other but at higher level for the characters *viz.,*seed yield plant^{-1}, number of pods plant^{-1}, number of branches plant^{-1}, 100 seed weight, plant height, days to flowering and days to maturity. Therefore, it is suggested in this study to give equal weightage to ó^{2}f and ó^{2}w during selection in M_3 generation. Therefore, selections of superior families followed by selection of individual plants in selected families were considered as the criteria of selection.

Thus, 174 M_3 individual plants were selected from 123 mutants from different treatments of variety NLK-73 mainly on the basis of seed yield plant^{-1}, more pods, bold seed and early maturity.In this study as additive gene action was found to be predominant for yield and yield components, it is suggested that the selected 174 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.

Table 1a. Analysis of variance for different characters in M_3 generation

Source of variation	D f	Mean sum of square	
		Germination (%)	Mortality (%)
Replications	2	89.96	6.24
Treatments	122	209.05**	17.03**
Error	244	21.33	8.26

** Significant at 1% level

Table 1b. Analysis of variance for different characters in M_3 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	122	3394.95**	8673.88**	8058.67**	16.74**	9818.02**	146.52**	1004.12**
Within families	5581	31.37	120.29	141.52	0.10	174.7	2.74	12.32
Intra class correlation(t)		0.698	0.605	0.547	0.782	0.543	0.531	0.634

** Significant at 1% level

Table 2. Mean, range, genotypic variance, phenotypic variance, genotypic coefficient of variation and phenotypic coefficient of variation estimates for different characters in M_3 generation

Sr. No.	Characters	Mean	Minimum	Maximum	Range	Genotypic variance	Phenotypic variance
1	Germination (%) (plot basis)	63.40	37	88	51	-	-
2	Mortality (%)(plot basis)	15.63	8	27	19	-	-
3	Days to 1st flower	62	50	72	22	72.53	103.90
4	Days to maturity	117	102	127	25	184.45	304.74
5	Plant height (cm)	80.48	15.50	136.84	121.34	170.72	312.24
6	No. of branches plant^{-1}	4.15	2	9	7	0.36	0.46
7	No. of pods plant^{-1}	109.58	8	487	479	207.95	382.65
8	100 seed weight (g)	8.67	5.10	15.60	10.50	3.10	5.84
9	Seed yield plant^{-1} (g)	11.58	1.40	59.70	58.30	21.39	33.71

Sr. No	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic advance (per cent of mean)
1	Germination (%) (plot basis)	-	-	-	-	-
2	Mortality (%) (plot basis)	-	-	-	-	-
3	Days to 1st flower	13.84	16.57	69.81	12.52	20.36
4	Days to maturity	11.59	14.89	60.53	18.60	15.87
5	Plant height (cm)	16.24	21.96	54.68	17.00	21.13
6	No. of branches plant^{-1}	14.43	16.32	78.21	0.93	22.47
7	No. of pods plant^{-1}	13.16	17.85	54.34	18.71	17.07
8	100 seed weight (g)	20.31	27.87	53.09	2.26	26.04
9	Seed yield plant^{-1} (g)	39.94	50.14	63.45	6.48	55.99

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