

GENETIC STUDIES IN F₃ POPULATION OF LATHRUS

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ABSTRACT

The present study was conducted with the objectives to estimate between family and within family variances, to estimate genetic parameters and to identify superior progenies for forwarding to next generation on the basis of yield and yield contributing characters at experimental farm of Agricultural Botany Section, College of Agriculture, Nagpur during *rabi* 2018 in F₃ generation. 240 progenies along with checks and the parents involved in the crosses (Ratan, Prateek, NLK-06, NLK-12, NLK-40, NLK-48, NLK-73, LL-14-2 and LL-14-5) were evaluated in two replications in progeny rows and the observations on seven traits *i.e.* days to flowering, days to maturity, plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹ were recorded. Analysis of variance indicated that the mean square due to between family were highly significant for all traits, which revealed the presence of significance genetic variability between the families. Intra class correlation (*t*) lead to the conclusion that differences between individual within family is large and each family differentiated distinctly from the other one at lower level in F₃ generation hence, equal weightage to σ^2_f and σ^2_w were suggested to be considered for selection in F₃ generation. When all the genetic parameters for seven characters were considered, it was found that plant height, number of branches plant⁻¹ and 100 seed weight exhibited high genotypic coefficient of variation, high heritability along with high genetic advance as percentage of mean. Similarly other characters days to flowering, days to maturity, plant height and number of pods plant⁻¹ exhibited high GCV, moderate heritability and high genetic advance as percentage of mean. This indicated that all these seven characters were influenced by additive gene action operating in the expression of these traits in F₃ generation and hence, helps as a criteria for making selection. 639 individual plants from 180 families out of 240 families from 10 crosses studied were identified for raising in progeny rows for one more generation so that homozygosity will be attained and superior progenies can be then selected for forwarding to yield traits in the next generation.

(Key words: Genetic variability, F₃ segregating generations, lathyrus, yield components, heritability and genetic advance)

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 Papilionaceae 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.

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 (Pigeonpea) is grown only on bunds, hence the production of tur is not sufficient for the requirements of these regions. 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.

Crop improvement achieved through any breeding method depends on the variability available for selection and methodology of selection. The magnitude of genetic variability and extent to which the desired characters are

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heritable and has considerable role in any breeding programme. This has in turn attracted the attention of biometrician to study the genetic aspects of economically important characters, such as yield and its components. Segregating populations are more important for improving plant types by operating further selection. Successful selection of genetically superior plants is directly associated with the occurrence of genetic variability from segregating generations for further selection. Like F_2 , F_3 generation is equally important in the process of selection in which segregation and recombination are maximum for imposing selection.

In crop like lathyrus, production of hybrid is out of question and hybridization followed by selection is the main procedure for improvement. Being highly self-pollinated crop, natural variability for yield and yield related traits is very narrow in lathyrus making selection ineffective. However, proper evaluation of the extent of genetic variation available for yield components, their heritability values and genetic advance could be of great significance for the breeders in order to choose best genotypes for improvement. Estimates of genetic parameters provides an indication of the relative importance of the various types of gene effects affecting the total variation of a plant character. Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance among F_3 progenies of ten different crosses.

MATERIALS AND METHODS

The experimental material comprised of 240 IPS of ten F_3 crosses selected on the basis of yield performance of F_2 and nine parents involved in the development of the ten crosses. These material were sown to raise F_3 generation during *rabi* 2018 in randomized block design replicated twice with spacing of 45 x 20 cm² and plot size of 0.9 x 4 m². All the cultural practices were followed to raise a good crop. The sowing was undertaken on the fertile and well levelled piece of land at research farm of Agril. Botany section, College of Agriculture, Nagpur. Total 20 plants were chosen randomly from each F_3 progeny and 5 from each parent during *rabi* 2018 for recording observations. Observations were recorded on days to first flower, days to maturity, plant height (cm), number of primary branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g) and seed yield plant⁻¹(g). The analysis of variance was done as suggested by Sharma (2006). The genotypic and phenotypic coefficients of variation were worked out according to the method given by Burton and Devane (1953). Heritability in broad sense and expected genetic advance on the basis of per cent of mean were worked out according to the method given by Hanson *et al.* (1956) and Robinson *et al.* (1949) respectively.

RESULTS AND DISCUSSION

The data on the analysis of variance resulted in highly significant mean squares due to between family for

all seven characters studied *i.e.* days to flowering, 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). This indicated the presence of significant genetic variability between the families for all seven characters which allowed the estimation of genetic parameters. In accordance to this results significant variability between the families were also reported by Costa *et al.* (2008) in soybean and Byadagi *et al.* (2018) in groundnut.

The intra class correlation (t) estimated in F_3 generation ranged from 0.31 = 31% for seed yield plant⁻¹ to 0.90 = 90% for number of branches plant⁻¹. Highest intra class correlation value was observed for number of branches plant⁻¹ 0.90 = 90% followed by plant height (0.68 = 68%), days to 1st flower (0.49 = 49%), days to maturity (0.48 = 48%), number of pods plant⁻¹ (0.38 = 38%), 100 seed weight (0.37 = 37%) and seed yield plant⁻¹ (0.31 = 31%). This revealed that 90%, 68%, 49%, 48%, 38%, 37% and 31% of variation for number of branches plant⁻¹, plant height, days to 1st flower, days to maturity, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹ respectively were due to differences between the families and 10%, 32%, 51%, 52%, 62%, 63% and 69% were due to within families. This indicated that differences between individuals within a family are large for all the characters except for number of branches plant⁻¹ and plant height but each family distinctly differentiated from other also at lower 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 F_3 generation for seed yield plant⁻¹ and its important component like number of pods plant⁻¹, 100 seed weight, days to maturity and days to first flower.

The characters under investigation were analyzed for mean, range, coefficient of variance (CV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as per cent of mean and presented in Table 2.

The grand mean recorded for 240 progenies along with nine parents were found to be 55.43 days for flowering, 115.41 days for maturity, 78.64 cm for plant height, 3.07 for number of branches plant⁻¹, 50.83 for number of pods plant⁻¹, 9.07 g for 100 seed weight and 9.98 g for seed yield plant⁻¹ (Table 2). High range of 193 was exhibited for number of pods plant⁻¹, followed by plant height (103 cm) and seed yield plant⁻¹ (34 g) which indicated that wide range of variation were functioning for these characters. Days to flowering (19), days to maturity (16), 100 seed weight (8.1 g) and number of branches plant⁻¹ (5) exhibited low range of variation. Even though a range of 34 g was observed for seed yield plant⁻¹, it was considerable as the maximum level of yield shown by check variety was only 13.39 g. The estimates of range provides new clue about the occurrence of genotypes with extreme expression which varied with the trait. In accordance to this result Rajeev Ranjan *et al.* (2007) reported maximum range of 17.33 days for days to maturity followed by 7.90 g for seed yield plant⁻¹ and 2.23 for number of branches plant⁻¹ among 400 F_3 progenies in lathyrus.

The coefficient of variation (CV) ranged from 17.60% to 43.54% for various characters (Table 2). The moderate coefficient of variation (10–20%) was observed for the characters plant height (17.60%) and 100 seed weight (18.26%) which showed the best genetic potential and its genetic influence. The high coefficient of variation (> 20%) was observed for seed yield plant⁻¹ (43.54%) followed by number of pods plant⁻¹ (38.09%), number of branches plant⁻¹ (30.52%), days to maturity (27.68%) and days to flowering (27.44%) which indicates more influence of environmental fluctuation. Being the F₃ generation, the amount of variability should be moderate or low. However, all the characters recorded high or moderate coefficient of variation for all the characters. Hence, further selection and advancement of progenies is necessary till attainment of homogeneity. Similar to this result high variability estimated for yield plant⁻¹ and yield components have been reported earlier by Shoba *et al.* (2012) in groundnut F₃ population.

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 Rajeev Ranjan *et al.* (2007) in lathyrus and also reported that phenotypic coefficient of variation was greater than their corresponding genotypic coefficient variation for all the characters studied.

Genotypic coefficient of variation exhibited the values in high category (> 20%) for all the characters studies. Highest genotypic coefficient of variation was recorded for number of branches plant⁻¹ (30.52%) followed by number of pods plant⁻¹ (30.07%), seed yield plant⁻¹ (28.91%), days to 1st flower (26.69%), days to maturity (26.40%), plant height (25.86%) and 100 seed weight (25.77%). Similarly phenotypic coefficient of variation was also observed to be high for different characters. Maximum phenotypic coefficient of variation was observed for seed yield plant⁻¹ (52.27%) followed by number of pods plant⁻¹ (48.53%), days to flowering (38.28%), days to maturity (38.25%), number of branches plant⁻¹ (32.17%), 100 seed weight (31.58%) and plant height (31.28%).

High genotypic coefficient of variation and phenotypic coefficient of variation observed for all the seven traits under study indicates greater scope for selection to improve upon these characters in the F₃ progenies of 10 crosses studied, which indicated the chances for obtaining desirable high yielding segregants after virtual homozygosity is attained. In accordance to this result Rajeev Ranjan *et al.* (2007) obtained high phenotypic coefficient of variation for seed yield plant⁻¹ (22.6%) and moderate genotypic coefficient of variation (18.37%) in F₃ generation of lathyrus. The magnitude of GCV and PCV was reported by them to be highest for seed yield plant⁻¹ followed by number of branches plant⁻¹ and days to maturity.

Heritability per cent ranged from 30.61% (seed yield plant⁻¹) to 89.95% (number of branches plant⁻¹). High heritability (> 60%) was recorded for number of branches

plant⁻¹ (89.95%), plant height (68.35) and 100 seed weight (66.57%). Moderate heritability (30–60%) was observed for days to maturity (47.63%), days to 1st flower (46.61), number of pods plant⁻¹ (38.40%) and seed yield plant⁻¹ (30.61%). High to moderate estimate of heritability for above traits suggested less influence of environmental factor in the expression for these traits. Estimate of heritability revealed that the selection could be effectively made on phenotypic basis by considering the above mentioned traits. In accordance to this result Rajeev Ranjan *et al.* (2007) also reported high estimate of heritability for days to flower, number of branches plant⁻¹ and seed yield plant⁻¹ in F₃ population of lathyrus. Moderate to high heritability estimate were also reported for all the 11 characters in majority of the segregating F₃ population of mungbean was also reported by Shiv *et al.* (2017).

Genetic advance as a percentage of mean were high (> 20%) for number of branches plant⁻¹ (50.94%), plant height (37.63%), 100 seed weight (37.00%), number of pods plant⁻¹ (32.80%), days to 1st flower (32.75), days to maturity (32.07%) and seed yield plant⁻¹ (28.15%). Similar to these results high genetic advance as a percentage of mean was also reported by Rajeev Ranjan *et al.* (2007) in lathyrus for seed yield plant⁻¹. In this study high heritability estimates along with high genetic advance as per cent of mean was noticed in plant height, number of branches plant⁻¹ and 100 seed weight and moderate heritability estimates along with high genetic advance was observed days to first flower, days to maturity, number of pods plant⁻¹, seed yield plant⁻¹. The high or moderate heritability coupled with high genetic advance reveals the presence of lesser environmental influence and performance of additive gene action in their expression. Hence, these characters can be improved by selection on the basis of phenotype for effective improvement in lathyrus. In accordance to this result Rajeev Ranjan *et al.* (2007) observed high genetic advance and high heritability for seed yield in F₃ generation of lathyrus. Similarly Sabale *et al.* (2018) also noticed high heritability estimates along with high genetic advance as per cent in seed yield plant⁻¹, number of pods plant⁻¹, plant height, number of primary branches plant⁻¹, 100 seed weight and harvest index.

The main objective of this experiment was to identify superior segregants for yield and yield contributing characters. As discussed above, in F₃ generation, between family variance, within family variance and intra class correlation (t) rewarded that differences between individuals within a family is large and each family is also different from the other but at low level for seed yield plant⁻¹, number of pods plant⁻¹, 100 seed weight, days to maturity and days to first flower. Out of these characters for days to maturity and days to first flower maximum progeny out of 240 progenies showed early flower and maturity as compared to check (Ratan). But for seed yield plant⁻¹, number of pods plant⁻¹ and 100 seed weight many of the progenies recorded low mean performance when compared with check. Therefore, in F₃ generation equal weightage to σ^2_f (between family variance) and σ^2_w (within family variance) was suggested

Table 1. Analysis of variance for different characters in F₃ generation

Source of variation	df	Mean sum of squares						
		Days to 1 st 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)
Between families	239	4394.95**	18673.88**	8058.67**	16.74**	4818.02**	106.52**	177.15**
Within families	4325	231.37	1020.29	191.52	0.10	374.70	2.74	18.87
Intra class correlation (t)		0.49	0.48	0.68	0.90	0.38	0.37	0.31

Table 2. Coefficient of variation, genotypic variance, phenotypic variance, genotypic coefficient of variation phenotypic coefficient of variation, heritability estimates for different characters in F₃ generation

Parameters	Mean	Range	CV	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability (%)	(Genetic advance per cent of mean)
Days to 1 st flower	55.43	47-66	27.44	218.90	450.27	26.69	38.28	46.61	32.75
Days to maturity	115.41	106-122	27.68	928.12	1948.41	26.40	38.25	47.63	32.07
Plant height (cm)	78.64	25-128	17.60	413.61	605.13	25.86	31.28	68.35	37.63
No. of branches plant ⁻¹	3.07	1-6	30.52	0.87	0.97	30.52	32.17	89.95	50.94
No. of pods plant ⁻¹	50.83	5-198	38.09	233.60	608.30	30.07	48.53	38.40	32.80
100 seed weight (g)	9.07	6-14.1	18.26	5.46	8.20	25.77	31.58	66.57	37.00
Seed yield plant ⁻¹ (g)	9.98	3-37	43.54	8.32	27.19	28.91	52.27	30.61	28.15

to be given during selection. Therefore, individual plant exhibiting significant superiority over check for seed yield plant⁻¹ (g), number of pods plant⁻¹ and 100 seed weight (g) from different progenies were considered as the criteria of selection. Based on these criteria 639 individual plants from 180 progenies out of 240 progenies from 10 crosses studied fulfilling the above criteria were identified for evaluation for one more generation.

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