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Genetic studies in germplasm lines of lathyrus

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Abstract

The investigation was undertaken during *rabi* 2022 at the Research farm of Agricultural Botany Section, College of Agriculture, Nagpur to estimate the genetic parameters among 55 genotypes of lathyrus. These 55 genotypes were grown in RBD. The ANOVA shows the presence of considerable genetic variation among 55 genotypes for eight characters studied. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters which shows the effect of environment on the characters. The GCV was recorded high for number of pods plant⁻¹ (25.34%), yield plant⁻¹ (22.44%). The PCV was high for number of pods plant⁻¹ (26.27%), yield plant⁻¹ (22.67%), High heritability values coupled with high genetic advance as percent of mean showing high to high heritability estimates were observed for the characters *viz.*, yield plant⁻¹ (98.00%, 45.75%) number of pods plant⁻¹ (93.00%, 50.34%), 100 seed weight (83%, 22.59%), number of seeds pod⁻¹ (78%, 22.26%). Thus, the high heritability with high genetic advance confirmed the presence of additive gene effect for all the studied characters and hence can be enhanced through selection.

Keywords: Genetic variability, germplasm, heritability, lathyrus

Introduction

Grass pea is mainly used as a food in the form of seeds, hay, green food, and also as a green fertilizer. Compared to other leguminous crops, grass pea plants are more resistant to diseases and pests and are practically not damaged by bruchus (Vishnyakova *et al* 2006) [11] and (Zaytseva *et al* 2014) [12]. Grass pea can tolerate adverse climatic variation and nutrient deficiency in soil. It withstands unfavorable conditions including excessive moisture at sowing, which is often followed by moisture stress at advanced growth stages (Dixit *et al* 2016) [4]. This nature of the plant provides a good opportunity to introduce the plant to arid and semi-arid areas for food and nutrition security.

The study was carried out to record the variability among the genotypes. Genotypic and phenotypic coefficient of variations were studied to record the influence of environmental interactions on characters chosen for investigation. Heritability was measured to observe how much the character would be transferred to the next generation and how much it will be influence from the environment. Genetic advance was measured to investigate how much the chosen character will have advantage over the past performance. These investigations were very important to figure out the influence of characters over yield, influence of environment over the chosen characters for reaching out the conclusion (Barai *et al* 2022) [2].

Materials and Methods

The present investigation was undertaken during *rabi* 2022 at the Research farm of Agricultural Botany Section, College of Agriculture, Nagpur to estimate the genetic parameters among 55 genotypes of lathyrus. These 55 genotypes were grown in randomized block design. Data was recorded on five competitive plants for eight characters *i.e.*, days to 50% flowering (on a plot basis), days to maturity (on a plot basis), plant height (cm), number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, 100 seed weight (g) and yield plant⁻¹ (g). Data was subjected to statistical analysis. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) computed by the formula suggested by (Burton *et al* 1952). The PCV and GCV values were ranked as low (0-10%), medium (10-20%) and high (>20%). The heritability in per cent in broad sense was calculated by the procedure suggested by [10]. Heritability values are categorized on the basis of range of percentage as low (<50%), moderate (50- 70%) and high (>70%).

Genetic advance was expressed as percentage of mean by using the formula suggested by (Johnson *et al* 1955) ^[7]. Genetic advance as per cent of mean was classified as low (0-10%), moderate (10- 20%) and high (>20%).

Results and Discussion

The ANOVA shows the presence of considerable genetic variation among the genotypes for character studied. This allows the further estimation in the experimental material. Data from Table 1. shows that the analysis of variance was highly significant for all eight characters studied i.e., days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹ (g), 100 seed weight (g), and yield plant⁻¹ indicating the presence of significant genetic variation among all the genotypes for eight characters. These results are in conformity with. The general mean, range and S.E. for variance is given in Table 2. This considerable variability gives a good chance of improvement in Lathyrus. One of the important considerations in any crop improvement is the detailed study of genetic variability. Variability is a measure by estimation of mean Genotypic and Phenotypic variation, Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h²) in the broad sense, genetic advance and genetic advance as percent of the mean. This would be of great help to the breeder in evolving a selection programme for genetic improvement of crop plant. The estimates of mean Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h²) in broad sense, Genetic advance and Genetic advance as percent of mean for all the eight characters studied are presented in Table 3.

To evaluate the genetic variability statistics has offered various analytical techniques. A genotypic and phenotypic coefficient of variation is one of them which offer to estimate the extent of variability in material under investigation. The estimation of genotypic and phenotypic components of variation gives us an idea of relative extent of heritable and non-heritable variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated. The phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters. The genotypic coefficient of variation and phenotypic coefficient of variation were categorized as low (<10%), moderate (10-20%) and high (>20%). The GCV was recorded high for number of pods plant⁻¹ (25.34%), yield plant⁻¹ (22.44%). The GCV was moderate for number of seeds pod⁻¹ (12.23%) and 100 seed weight (12.00%) and the GCV was low for rest of the characters like days to 50% flowering (3.12%), days to maturity (1.55%), plant height (6.94%) and number of primary branches plant⁻¹ (6.75%). The PCV was high for number of pods plant⁻¹ (26.27%), yield plant⁻¹ (22.67%), moderate for number of seeds pod⁻¹ (13.86%) and 100 seed weight (13.13%) and it was low for rest of the characters like days to 50% flowering (8.90%), days to maturity (2.37%), plant height (9.03%) and number of primary

branches plant⁻¹ (8.18%). In present study genotypic coefficient of variation (GCV) for number of pods plant⁻¹ and yield plant⁻¹, was noted high which suggest good scope for yield improvement through direct selection. However, number of seeds pod⁻¹ and 100 seed weight has considerable genetic variability which can be further exploited for yield improvement. Magnitude of phenotypic coefficient of variation (PCV) for number of pods plant⁻¹ and yield plant⁻¹ was noted high indicating the influence of environmental factors on seed yield and its component traits hence, estimation of GCV will be more reliable. These results were collaborated with the findings of (Kumar *et al* 2017) ^[8], (Banik *et al* 2018) ^[11] and (Gautam *et al* 2021) ^[5] Heritability and genetic advance separates out environmental influence from total variability hence they are important genetic parameters and forms a good scope for selection of genotype. Heritability estimates along with genetic advance are more useful in predicting the gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al* 1955) ^[7]. An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson 1966. In present investigation high heritability recorded for yield plant⁻¹ (98.00%) followed by number of pods plant⁻¹ (93%), 100 seed weight (83%) and number of seeds pod⁻¹ (78%) and moderate heritability recorded for number of primary branches plant⁻¹ (68%), days to 50% flowering (64%) and plant height (59%) and low heritability was estimated for days to maturity (42%). The genetic advance as percentage of mean was observed high for number of pods plant⁻¹ (50.34%) followed by yield plant⁻¹ (45.75%), 100 seed weight (22.59%), number of seeds pod⁻¹ (22.26%) it was moderate for number of primary branches plant⁻¹ (11.48%) and plant height (10.98%) and low for days to 50% flowering (5.14%) and days to maturity (2.09%). Similar findings were obtained by (Barai *et al* 2022) ^[2], (Gautam *et al* 2021) ^[5] and (Jeberson *et al* 2018) ^[6] It may be concluded that, if the value of genetic advance is high, then the character is governed by additive genes and selection will be rewarding for improvement of such traits. Low magnitude of genetic advance reveals the presence of dominance or epistatic variances in the control of aforesaid characters. The low value of genetic advance suggests influence of environment and hence selection for these traits would be worthwhile in later generations because the character is governed by non-additive genes and heterosis breeding may be useful. High heritability values coupled with high genetic advance as percent of mean showing high to high heritability estimates were observed for the characters viz., yield plant⁻¹ (98.00%, 45.75%) number of pods plant⁻¹ (93.00%, 50.34%), 100 seed weight (83%, 22.59%), number of seeds pod⁻¹ (78%, 22.26%) Characters showing high to low heritability estimates coupled with medium to low genetic advance as percentage of mean indicating greater contribution of dominance and epistatic variance in the expression of the characters.

Table 1: Analysis of variance for various characters

Source of variance	d.f.	Mean sum of squares							
		Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	No. of primary branches plant ⁻¹	No. of pods plant ⁻¹	No of seeds pod ⁻¹	100 seed weight (g)	Yield plant ⁻¹ (g)
Replication	2	2.21	22.71	190.26	0.02	110.31	0.15	0.59	3.08
Genotype	54	17.87**	24.66**	151.70**	0.36**	1067.02**	0.43**	4.38**	38.95**
Error	108	6.44	14.13	62.23	0.11	74.79	0.10	0.72	4.49

Table 2: Range, Grand mean and S.E for various characters in Lathyrus

Sr. No	Characters	Range		Grand mean	S.E. difference
		Min	Max		
1	Days to 50% flowering	56.00	67.33	62.52	1.47
2	Days to maturity	115.33	129.00	120.57	2.17
3	Plant height	57.66	95.33	79.52	4.55
4	No. of primary branches plant ⁻¹	3.50	4.90	4.23	0.20
5	No. of pods plant ⁻¹	32.33	109.34	72.09	4.99
6	No. of seeds pod ⁻¹	1.93	3.83	2.73	0.18
7	100 seed weight	6.26	11.93	9.35	0.49
8	Yield plant ⁻¹	8.26	24.00	17.61	1.22

Table 3: Genetic parameters estimate

Sr. No.	Characters	Coefficient of variability		Heritability (%)	Genetic advancement (5%)		Genetic advance in percent of mean	
		GCV	PCV		5%	1%	5%	1%
2	Days to maturity	1.55	2.37	42	2.52	3.23	2.09	2.68
3	Plant height	6.94	9.03	59	8.64	11.07	10.98	14.07
4	No. of primary branches plant ⁻¹	6.75	8.18	68	0.48	0.62	11.48	14.71
5	No. of pods plant ⁻¹	25.34	26.27	93	36.12	46.29	50.34	64.51
6	No. of seeds pod ⁻¹	12.23	13.86	78	0.60	0.78	22.26	28.52
7	100 seed weight	12.00	13.13	83	2.07	2.66	22.59	28.95
8	Yield plant ⁻¹	22.44	22.67	98	7.90	10.13	45.75	58.64

Conclusion

In conclusion, the analysis of variance (ANOVA) conducted on the genetic variation among the genotypes for various traits in Lathyrus reveals significant variability across all eight characters studied. These findings, supported by previous research, underscore the potential for further improvement in Lathyrus through breeding programs. The estimation of genetic variability parameters such as genotypic and phenotypic coefficients of variation, heritability, and genetic advance provides valuable insights into the heritable and non-heritable components influencing trait expression. The high heritability and genetic advance observed for yield-related traits like number of pods plant⁻¹ and yield plant⁻¹ indicate the potential for direct selection to enhance yield. Conversely, traits with lower genetic advance suggest the influence of environmental factors and the potential utility of heterosis breeding. The delineation of genetic parameters aids breeders in formulating effective selection strategies for crop improvement. These findings contribute to our understanding of the genetic architecture of Lathyrus and offer valuable guidance for future breeding efforts.

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