Plant Archives Vol. 26, No. 1, 2026 pp. 979-784 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.1.134

ESTIMATION OF GENETIC VARIABILITY, DIVERSITY, ASSOCIATION OF CHARACTERS AND PRINCIPLE COMPONENT ANALYSIS OF SOME *LATHYRUS* GENOTYPES IN TERAI REGION OF NORTH BENGAL, INDIA

Puja Sarkar[1], Suvajit Karak[1], Soumendra Chakraborty[1]*, Rupsanatan Mandal[2], Suvendu Kumar Roy[1], Shubhrajyoti Sen[1], Lakhsmi Hijam[1] and Moumita Chakraborty[1]

[1]Department of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, West Bengal, India.
[2]Department of Plant Breeding, Genetics and Crop Physiology, Viswa Bharti University, West Bengal, India.
*Corresponding author E-mail : soumendra1@gmail.com; Orcid Id: 0000-0001-7200-8309

(Date of Receiving-12-01-2026; Date of Revision-27-02-2026; Date of Acceptance-22-03-2026)

ABSTRACT

The investigation was carried out in the university experimental farm involving 12 genotypes of lathyrus (*Lathyrus sativus* L) in the year 2021-2022 to find out the genetic potential under terai region of West Bengal. The characterization was done according to DUS descriptors developed by IPGRI, Rome, Italy (2000), of 16 morphological and yield attributing characters. Analysis of variance revealed that where days to 50% flowering, plant height, leaf length, pods per plant, seeds per plant, seed index, root length, biological yield per plant, yield per plant and ODAP were found to be significant at 1% and 5% level of significance which proved a wide range of variability in all the characters. In dendogram and cluster analysis four groups of clusters were found. Due to high GCV, PCV, moderate to high heritability and GAM, root length, ODAP content and biological yield can be considered for effective selection in this crop. In association of characters, genotypic correlation coefficient studies revealed leaf length, branches per plant, pods per plant, seeds per plant, 100 seed wt, yield per plant were having direct significant association with biological yield per plant. The eigen values of the first five PCA components were found to be greater than one, and the cumulative variance was found to be 85.02%. PCA analysis revealed high value of PCA loading in 100 seed weight, leaf length, pod width, pod length, biological yield per plant and yield per plant, where the contribution of these characters was found to be the greatest, as revealed by PCA biplot analysis.

Key words : DUS descriptors, ODAP, GCV, PCV, Heritability, PCA.

Introduction

Lathyrus sativus, also known as Grass pea (Chromosome number 2n=14), belongs to the family Fabaceae, subfamily Papilionaceae, is a strong legume crop that is considered one of the most resilient to climate changes and can survive during drought conditions. According to Smart (1984), grass pea is one of the oldest types of pulse crops. It is grown extensively throughout the world, particularly in Bangladesh, India, Nepal, and Ethiopia and to a limited extent in South America, northern Europe, Australia, some parts of Russia, Ukraine, China and also in south-west Asia. The name Lathyrus comes from the Greek word "lathyros", which means "exciting", and refers to the aphrodisiac properties attributed to grass pea (Loudon *et al.*, 1855). There is an epidemiological connection between Khesari dal consumption and a motor neural disease known as Lathyrism—the paralysis of the lower limbs in humans. The toxic principle identified as β-N-Oxalye-L-, β diaminopropionic acid (ODAP), also known as β-oxalyl amino alanine, is the primary causal agent (BOAA). This toxin can be found in all parts of the plant (Campbell *et al.*, 1994). Out of the 200 species and subspecies in this genus, only *Lathyrus sativus*, is widely farmed as a food crop (Razdan *et al.*, 1980; Jackson and Yunus, 1984). Less than 0.2% of ODAP concentration is considered safe for human ingestion (Moneim *et al.*, 1999). The investigation was carried out taking multivariate analysis of the quantitative and qualitative characters including ODAP biochemical value of the crop, which is an important parameter for releasing the varieties in India.

Materials and Methods

The experiment was carried out in the "Agricultural Research cum Instructional Farm", Uttar Banga Krishi Viswavidyalaya at Pundibari, Cooch-Behar, West Bengal, India. The genotypes taken for the investigation were Dhup-1, Dhup-2, Dhup-3, Dhup-4, Dhup-5, Pundibari-1, Pundibari-2, Pundibari-3, Pundibari-4, Pundibari-5, Coochbehar local and Prateek (Check variety). A standard method was employed to calculate the analysis of variance (Singh and Chaudhary, 1979). The analysis of variance method and the "F" test were used to determine the significance of the overall variation across genotypes for various features. The genotypic and phenotypic coefficients of variation were calculated as suggested by Burton (1952) method. The range of variance was categorized as proposed by Sivasubramanian and Menon (1973). In case of heritability estimations of heredity in the broadest sense were divided into four categories according to Johnson *et al.* (1955).

In case of cluster analysis for diversity analysis, all twelve grass pea genotypes were assembled into a hierarchy cluster using the Hierarchical cluster analysis in order to study their close and far links. Each observation was made from scratch using the agglomerative or "bottom-up" method. In this situation, average linkage clustering was used. Higher gaps between genotypes were found to produce clusters of distantly related individuals, whilst smaller gaps between genotypes were found to form closed groups or clusters. The Euclidean distance was used to calculate the separation between the dendogram's points. The distance was calculated using the Agglomerative technique utilizing the 'WARD' method, which used variances as a measurement for clustering. The PCA analysis (PCA) transforms a set of observations of potentially correlated variables into a set of values of linearly uncorrelated variables known as the principal component. ODAP value was calculated following Spectrophotometric assay for ODAP concentrations (Peter Martin Ferdinand Emmrich, 2017).

Results and Discussion

Analysis of variance was calculated for one season (2021-22) in all the characters in 12 genotypes, where plant height (185.92), leaf length (1.028), branches per plant (1.27), days to 50% flowering (73.97), pods per plant (78.25), root length (5.007), seeds per plant (1161.49), 100 seed weight (2.50), yield per plant (17.53), ODAP (0.002) and biological yield per plant (3.20) were found significant. All of the genotypes were found to be significantly different in both 5% and 1% level of significance.

Analysis of variance

Analysis of variance was calculated for one season (2021-22) for all the characters involving 12 genotypes where the genotypes were found to differ significantly for plant height (185.92), leaf length (1.028), branches per plant (1.27), days to 50% flowering(73.97), pods per plant(78.25), root length(5.007), seeds per plant (1161.49), 100 seed weight (2.50), yield per plant (17.53), ODAP (0.002) and biological yield per plant (3.20) Table 1). Parihar *et al.* (2015) also reported that in 368 diverse, indigenous, and exotic grass pea accessions, for the metric traits revealed that all accessions were significantly different from each other, indicating a high amount of variability for the majority of the traits studied. Abate *et al.* (2018) investigated 426 grass pea accessions for estimating variability and reported highly significant difference among grass pea accession for traits like plant height, number of primary branches, number of pods per plant, number of seeds per pod, days to flowering, days to maturity, 100 seed weight, seed yield/plant, biomass, and harvest index and reported similarly about the presence of variability in his experimental population.

Association of characters

In association of characters, leaf length was found to have strong positive genotypic correlation on biological yield per plant (0.679**) on both 5% and 1% level of significance. Similar results were found by Mishra (2020) who reported otherwise, where leaf length and yield had a negative but non-significant relationship in their investigation. Branches per plant was found to have strong positive correlation on biological yield per plant (0.734**) at both 5% and 1% level of significance. Similar results were found by Sharma *et al.* (1997) where the number of branches per plant had a strong positive genotypic association with plant height, days to maturity, and 100-seed weight which were both positively linked. Pods per plant was found to have strong positive correlation with biological yield per plant (0.877**) at both 5% and 1% level of significance. Das *et al.* (2002) found that pods per plant and seeds per pod had a continuous high positive association with seed yield per plant at both the phenotypic and genotypic levels. Seeds per plant was found to have strong positive correlation with biological yield per plant (0.808**) at both 5% and 1% level of significance. 100 seed wt. was found to have strong positive correlation with biological yield per plant (0.776**) at both 5% and 1% level of significance. Similar results were found by

Waghmare *et al*. (1996), who reported that the number of pods per plant and 100-seed weight had large positive and direct effects on seed yield while the remaining characters exhibited direct negative effects on seed yield. This character was found to have strong positive correlation on biological yield per plant (0.988**) at both 5% and 1% level of significance. All other characters were found to have non-significant effects on biological yield per plant. Characters like plant height, leaf length, branches per plant, days to 50% flowering, pods per plant, root length, seeds per pods, seed index and biological yield per plant were found to have very low GCV and PCV along with moderate to low heritability and low genetic advance against percentage of mean (Table 2) (Sivasubramanian and Menon, 1973; Johnson *et al*., 1955). Only in yield per plant and ODAP high GCV and PCV values along with moderate high heritability and high genetic advance against percentage of mean were found (Table 2). This indicated influence of additive gene action in these characters and they will be less influenced by environmental factors, henceforth they can be considered for future crop improvement programme.

PCA analysis

In Principle Component Analysis PCA analysis involving all the characters where eigen values were found, max. Value observed in PC1 (5.88) followed by PC2 (2.47), PC3 (2.25), PC4 (1.54) and PC5 (1.45) which were found values more than 1(Table 4). Highest contribution to variability/variance was found in 100 seed wt. (0.9304) followed by leaf length (0.8076), pod width (0.7637), pod length (0.7438), yield per plant (0.6688), biological yield per plant (0.7068) and other characters. From the PCA analysis, highest cumulative variance was found in 100 seed wt taking all the PC components (PC1 to PC5) followed by leaf length, pod width, pod length, yield pr plant in a positive influence towards the overall variability of the genotypes in this investigation (Table 4). Cluster analysis was done was evaluated by adapting agglomerative Hierarchical clustering using the Ward method (Fig. 1).

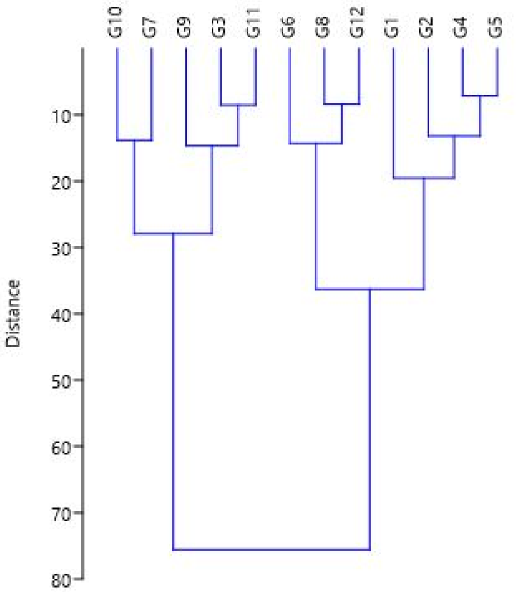

Fig. 1 : Dendogram graph with Euclidian distance taking all the 12 genotypes. G1=Dhup-1, G2= Dhup-2, G3= Dhup-3, G4= Dhup-4, G5= Dhup-5, G6= Pundibari-1, G7= Pundibari-2, G8= Pundibari-3, G9= Pundibari-4, G10= Pundibari-5, G11= Coochbehar local and G12= Prateek (Check variety).

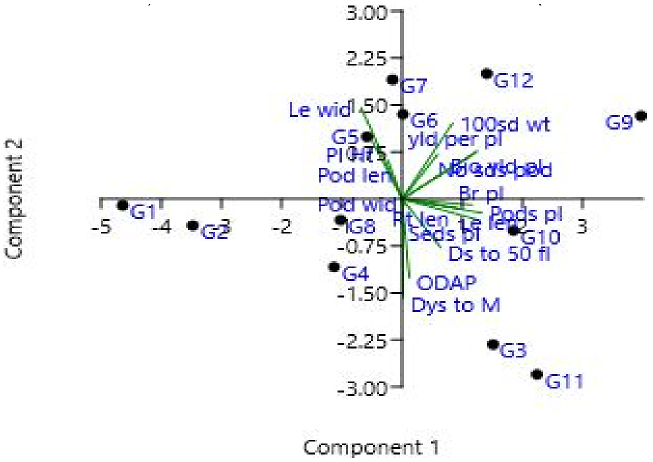

Fig. 2 : Bi plot analysis of 12 genotypes of *Lathyrus.*

In these clusters, four groups of clusters were found when Euclidian distance was taken as 20. The dendogram and cluster analysis showed four groups of clusters based on genotypic relatedness among 12 genotypes within the Euclidian distance of 20. Dhup- 1, Dhup- 2, Dhup- 4, and Dhup-5 formed a group in the first cluster. Pundibari-1, Pundibari- 3, and Prateek formed a group in the second cluster. Pundibari- 4, Dhup- 3, and Coochbehar local formed a group in the third cluster. Pundibari- 2 and Pundibari-5 formed a group in the fourth cluster. In the next group, first two groups were closely related with each other and third and fourth groups were also closely related with each other. In the next group, first two groups were closely related with each other and third and fourth groups were also closely related with each other. Dhupguri local 3, Pundibari local 2, Pundibari local 4, Pundibari local 5 and Coochbehar local were found to be genetically closely related than rest of the genotypes (Fig. 1). Closely linked genotypes should not be taken for crossing programs for the future breeding program but crossing programme between genotypes of different groups should be taken for future breeding programme. The principal component analysis (PCA) biplot revealed substantial multivariate variation among the twelve

Table 1 : Analysis of variance of 11 DUS descriptors of 12 *Lathyrus* genotypes.

Sources of variation	df	Mean sum of squares										
		PH	**LL**	**BPP**	**DFF**	**PPP**	**RL**	**SPPL**	**SI**	**YPP**	**ODAP**	**BYLD**
Replication	2	189.79	4.76	0.29	30.48	133.09	8.05	2053.52	3.51	50.96	0.001	42.11
Genotypes	11	185.92**	1.02**	1.27**	73.97**	78.257**	5.007**	1161.49**	2.50**	17.53**	0.002**	16.41**
Error	22	55.69	0.29	0.38	12.16	17.55	0.50	342.48	0.62	3.74	0.0003	3.20

5%* and 1 % ** level of Probability.

DFF- Days to 50% flowering, BPP - Branches per plant, PH - Plant Height, LL - Leaf length, PPP - Pods per plant, SPPL - Seeds per Plant, SI - Seed Index: 100 seed wt., RL - Root Length, BYLD - Biological yield per plant, df- Degrees of freedom and Rep- Replication

Table 2 : Relationship between GCV, PCV, Heritability and GAM.

Character	Mean	Range		GCV (%)	PCV(%)	H^2(%)	GAM (%)
		Lowest	Highest				
Plant height	81.44	68.73	96.09	8.09	12.22	43.80	11.03
Leaf length	7.14	6.30	7.95	6.93	10.26	45.59	9.63
Branches per plant	6.96	5.80	8.13	7.81	11.81	43.66	10.63
Days to 50% Flowering	76.48	69.33	82.66	5.93	7.48	62.87	9.69
Pods per plant	55.58	46.53	64.40	8.09	11.05	53.54	12.19
Root length	16.15	14.92	19.36	7.54	8.72	74.75	13.43
Seeds per pod	217.86	186.13	249.60	7.58	11.38	44.35	10.40
Seed Index	6.86	5.18	8.07	11.5	16.29	50.07	16.80
Yield per plant	14.56	10.32	19.07	14.72	19.83	55.10	22.51
ODAP	0.10	0.073	0.16	23.29	23.74	96.25	47.07
Biological yield per plant	25.34	21.23	29.51	8.27	10.88	57.90	12.97

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, GAM : Genetic Advance against percentage of Mean.

genotypes, clearly separating them based on yield-contributing traits, phenological parameters, and ODAP content. The dispersion of genotypes across the four quadrants indicates considerable genetic diversity among the Dhup, Pundibari, Coochbehar local and the check variety Prateek.

Bi plot analysis

Component 1 (PC1) appears to be primarily associated with yield-attributing traits, as evidenced by the strong positive loadings of biological yield, seed yield, number of pods per plant, number of branches per plant, seeds per plant, and 100-seed weight (Fig. 2). These vectors are closely aligned with one another, forming acute angles, which suggested strong positive correlations among these traits. This indicates that genotypes with higher pod number, branching, and seed number tend to exhibit superior biological and seed yield performance (Fig. 2). In contrast, pod width, pod length and plant height are oriented in the opposite direction along PC1, suggesting a negative association with the primary yield cluster.

Genotypes G9 (Pundibari-4), G10 (Pundibari-5), and G12 (Prateek, the check variety) are positioned on the positive side of PC1, indicating strong association with yield-related attributes (Fig. 2). Among these, G9 is located closest to the vectors representing seed yield and biological yield, suggesting its superior performance for these traits. The proximity of G12 to the yield cluster confirms the reliability of the check variety, while the comparable positioning of G9 and G10 suggests their potential as promising high-yielding genotypes.

Component 2 (PC2) appears to be influenced primarily by phenological traits and leaf characteristics. Traits such as leaf width and yield per plant show positive loadings along PC2, whereas days to maturity, days to 50% flowering, and ODAP content are negatively found. The downward orientation of ODAP along PC2 indicates that genotypes positioned in the lower quadrants may possess relatively higher ODAP content and later maturity, whereas those in the upper quadrants are associated with comparatively lower ODAP and favourable maturity duration.

Genotypes G3 (Dhup-3) and G11 (Coochbehar local) are distinctly separated in the lower right quadrant, closely aligned with ODAP and maturity traits. Their position suggests relatively higher ODAP content and longer maturity duration, which may be undesirable in breeding programs targeting low-toxin and early-maturing lines. Conversely, G7 (Pundibari-2) and G6 (Pundibari-1), located in the upper quadrant near leaf width and yield per plant, may possess advantageous combinations of vegetative vigor and yield potential.

Genotypes G1 (Dhup-1) and G2 (Dhup-2), positioned far on the negative side of PC1, are clearly separated from the high-yielding cluster, indicating comparatively lower association with yield-contributing traits. Similarly, G4 and G8 occupy intermediate positions near the origin, suggesting moderate or average performance across traits.

The angular relationships among trait vectors further highlight strong positive correlations among yield components, while ODAP and maturity traits appear negatively associated with yield. This suggests that selection for enhanced yield attributes may indirectly favor reduced ODAP content and improved maturity and it will be applicable for the future crop improvement programme also.

Overall, the PCA biplot effectively discriminated the genotypes into distinct groups based on yield performance, yield attributing characters and ODAP concentration. Genotypes G9 (Pundibari-4), G10 (Pundibari-5) and G12 (Prateek) were found to be as superior for yield-related traits, while G6 and G7 showed promising vegetative and yield characteristics. In contrast, G3 and G11 were associated with higher ODAP and later maturity. These findings provide G9 (Pundibari-4), G 10 (Pundibari -5) and G12(Prateek) can be chosen as important genotypes for parent selection in breeding programs aimed at improving yield while minimizing ODAP content.

Conclusion

From this investigation, maximum contribution of variability was found in 100 seed wt followed by leaf length, pod width, pod length per plant. In case of selection programme, leaf length, pod length, number of seeds per pod, 100 seed wt can taken into consideration for their influence on biological yield per plant. ODAP and yield per plant, root length can be taken as defining characters for selection due to their high heritability and medium genetic advance with mean for crop improvement programme. G9 (Pundibari-4), G 10 (Pundibari -5) and G12 (Prateek) can identified as important genotypes as parents for hybrid varieties in breeding programs with low ODAP content.

Conflict of interest

The authors declared that they do not have any conflict of interest in the research.

Acknowledgement

We are grateful to the Dean, Faculty of Agriculture, Dean, Post Graduate Studies, Director of Research and Director of Farms for providing us the facility of conducting the research trials in the University Research Farm and providing all the facilities for proper management of the crop and labour for successful completion of the experiment.

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