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GENETIC DIVERGENCE ANALYSIS OF YIELD POTENTIAL AND β-ODAP CONTENT IN GRASSPEA (*Lathyrus sativus* L.)

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ABSTRACT

A field experiment was carried out to evaluate the magnitude of genetic variability and genetic divergence among twenty-five grasspea (*Lathyrus sativus* L.) genotypes, including three standard checks, across three sowing environmentsduring *Rabi* 2024–25. The study aimed to identify genetically diverse and superior genotypes in terms of high yield with low ODAP content across the environment for their potential utilization in grasspea improvement programmes. Analysis of variance exhibited highly significant differences among genotypes for all the studied characters, confirming the existence of substantial variability in the experimental material. The phenotypic coefficient of variation exceeded the corresponding genotypic coefficient of variation for all traits, reflecting the influence of environmental factors on trait expression. High heritability associated with moderate to high genetic advance was recorded for ODAP content, seed yield per plant and effective pods per plant, indicating the predominance of additive gene action and suggesting the effectiveness of direct selection for these traits. Genetic divergence analysis grouped the genotypes into four distinct clusters. Higher inter-cluster distances than intra-cluster distances indicated wider genetic divergence, with the maximum inter-cluster distance recorded between Cluster I and Cluster II (20.515). Such genetically divergent clusters may serve as valuable sources for parent selection in hybridization programmes to get superior recombinants. The findings of the study emphasized the availability of substantial genetic diversity in grasspea and highlighted the potential of selected genotypes for utilization in future breeding programmes targeting yield improvement and wider adaptability.

***Key words*:** Genetic variability, Heritability, Genetic divergence, Cluster analysis, ODAP content.

Introduction

Grasspea is an important pulse crop widely cultivated in South Asia, the Mediterranean region and several parts of Africa (Campbell, 1997). In India, Grasspea is commonly grown as a relay or utera crop after the harvest of rice, especially in states such as Chhattisgarh, Bihar, West Bengal, and Madhya Pradesh. (Sahu *et al*., 2022) This crop is well known for its ability to withstand harsh environmental conditions, such as drought, temporary waterlogging and poor soil fertility (Lambein *et al*., 2019). When ploughed in, grass pea is a good green manure that returns nutrients to the soil and provides organic matter (Lazanyi 2000). Moreover, its nitrogen-fixing capability significantly enhances soil fertility, creating a symbiotic cycle that benefits both the ecosystem and the farming communities that rely on it.

Pulsesare cheap and wonderful sources of protein in vegetarian diet. The nutritional composition of legumes

comprises a high proportion of proteins, carbohydrates, dietary fibers, also including small quantities of fats, B-grouped vitamins (thiamin, riboflavin, niacin) and different types of minerals (Prodanov *et al.,* 2004). Grass pea seeds contain 25–28% protein, 1.84–2.47% lysine, 0.1–0.15% methionine, 0.6–1.9% fats, 4–15% fibre carbohydrates and 3% ash (Petterson *et al*., 1997). Although rich in protein, the utilization of grass pea grain is considerably constrained due to the presence of a water soluble non-protein amino acid β-N-oxalyldiaminopropionic acid (β-ODAP) [synonym: β-oxalylaminoalanine (BOAA)], which acts as a neurotoxin causing crippling of the lower limbs.

For crop improvement programmes, identifying genotypes that can produce consistent yields under different environmental conditions is of great importance (Bose *et al.*, 2014). A genotype that performs well in one environment may not necessarily maintain the same level of performance in another due to variations in climatic and environmental factors (Finlay & Wilkinson, 1963). Therefore, understanding genotype × environment interaction (Tadesse *et al*., 2018; Sarker *et al*., 2019) is essential for identifying stable and widely adaptable genotypes.

Materials and Methods

The present study was carried out during *rabi* season of 2024-25 with twenty-five different genotypes of grass pea including three check varieties which were selected on the basis of yield attributing traits and previously reported information regarding low ODAP content and grown at the Research-cum-Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi KrishiVishwavidyalaya, Raipur. (21°16′N, 81°31′E & 289.56 m) in Randomized Complete Block Design (RCBD) with two replications. Three distinct environments were created based on different sowing dates: E_1 (20 November 2024, normal sowing), E_2 (01 December 2024, late sowing), and E_3 (10 December 2024, extra-late sowing). The experimental plot consisted of 3 m long row and spacing between rows and plants were 30 cm and 15 cm respectively. The standard package of practices was followed to raise the crops. Data were recorded considering five randomly selected plants from each plot to measure plant height (cm), days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, number of seeds per pod, Number of effective pods per plant, 100-seed weight (g), harvest index %, Biological yield per plant (g) seed yield per plant (g), seed crude protein content% and ODAP.

Table 1: Experimental materials and their sources.

S. No.	Genotype	Source
1.	BANG-249-S11	Bangladesh
2.	IGC-2012-74/10-7-S9	IGKV, Raipur
3.	IFLA2026-S8	ICARDA
4.	BANG-309-S4	Bangladesh
5.	BANG-310-S7	Bangladesh
6.	IFLA118-S4	ICARDA
7.	IFLA2441-S14	ICARDA
8.	IFLA1913-S11	ICARDA
9.	IFLA2990-S1	ICARDA
10.	Bio520-S2	ICARDA
11.	IFLA479-S11	ICARDA
12.	IFLA220-S1	ICARDA
13.	IFLA2750-S4	ICARDA
14.	IFLA276-S10	ICARDA
15.	IGC-2012-70/1-9-S2	IGKV, Raipur
16.	AKL-19	Akola, M.H.
17.	RLS-21931	IGKV, Raipur
18.	SEL-S04	NBPGR, New Delhi
19.	JRL-41-1992	J JNKV, Jabalpur
20.	SEL-522-1956	NBPGR, New Delhi
21.	BIOR-231	BCKV, Kolkata
22.	JRYL-9	JNKV, Jabalpur
23.	Ratan	IRAI, New Delhi
24.	Mahateora	IGKV, Raipur
25.	Prateek	IGKV, Raipur

Results and Discussion

Analysis of variance (ANOVA) (Table 1) revealed highly significant differences among genotypes for most of the traits, namely plant height, number of primary branches per plant, pod-bearing length, number of pods per plant, number of seeds per pod, number of effective pods per plant, 100-seed weight, harvest index, seed yield per plant, biological yield per plant, protein content and ODAP content, indicating the presence of substantial genetic variability. However, days to 50% flowering and days to maturity showed non-significant variation, suggesting limited variability for these phenological traits. The observed genetic variability for yield and quality traits offers considerable scope for selection and genetic improvement in grasspea. Similar findings have also been reported in earlier studies on grasspea by Singh *et al*.,

Table 1: Analysis of variance for seed yield and its relative traits in grass pea germplasm.

S. No.	Source of Variation / Degree of freedom (df)	R 1	T 24	E 24
	Mean sum of square			
1	Days to 50% flowering	0.98	3.9824**	0.4319
2	Days to maturity	0.08	15.977**	1.7066
3	Plant height (cm)	17.05	12.7547**	1.3424
4	Primary branches per plant	0.01	0.0964**	0.0504
5	No. of pods perplant	2.83	7.0171**	2.1343
6	Pod bearing length (cm)	16.93	3.5647 **	1.4804
7	Number of effective pods per plant	0.84	4.7600 **	0.7687
8	No. of seeds per pod	0.19	0.101**	0.0939
9	100 seed weight(g)	0.02	1.1291**	0.1910
10	Harvest index (%)	0.46	1.4306**	0.1846
11	Seed yield per plant(g)	0.05	1.5041**	0.4495
12	Biological yield per plant (g)	1.28	129.7**	22.525
13	Protein content(%)	0.025	9.2485**	0.1614
14	ODAP content(%)	0.0002	0.0170**	0

R: Replication; T: Treatment; E: Error;
(Note:**significant 1% level.)

(2012), Parihar *et al*., (2015), Ullah *et al.,* (2019) and Mishra *et al.,* (2025).

Mean performance of twenty-five grasspea genotypes for fourteen quantitative and quality traits is presented in Table 2. Based on the mean performance of important yield-contributing traits, particularly seed yield per plant genotypes AKL-19, BANG-249-S11, JRYL-9, Prateek and JRL-41-1992 were identified as promising genotypes. The superior performances genotypes could be considered promising breeding materials owing to their favourable expression of important yield-contributing traits and overall agronomic performance.

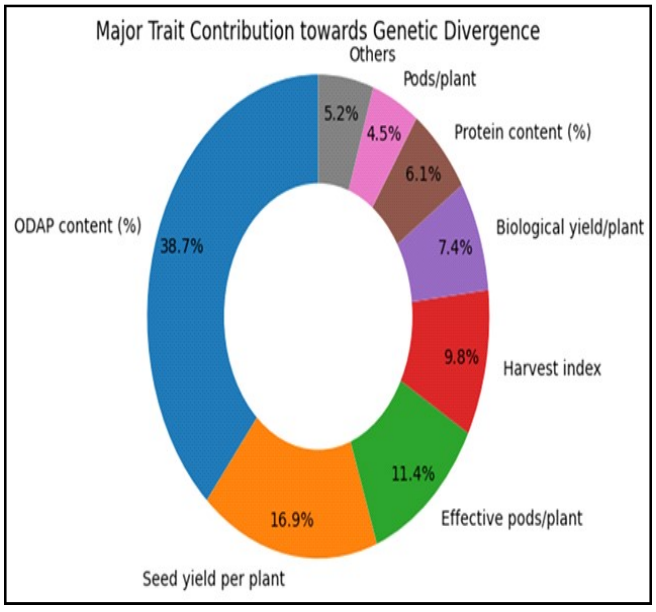


Fig. 1: Contribution of different characters towards total genetic divergence.

The assessment of genetic variability revealed that PCV values were slightly higher than the corresponding GCV values for all the traits, indicating the influence of environmental factors on trait expression. High PCV and GCV were observed for ODAP content, followed by seed yield per plant and harvest index, suggesting the presence of substantial variability for these traits. Moderate estimates were recorded for number of pods per plant, number of effective pods per plant, biological yield per plant, protein content and 100-seed weight, whereas low values were observed for days to 50% flowering, days to maturity, plant height and number of seeds per pod. The narrow differences between PCV and GCV for most traits indicated relatively low environmental influence on their expression.

Heritability estimates ranged from 3.76% to 99.00%. High heritability was observed for ODAP contentpercent, protein content, plant height, days to maturity, days to

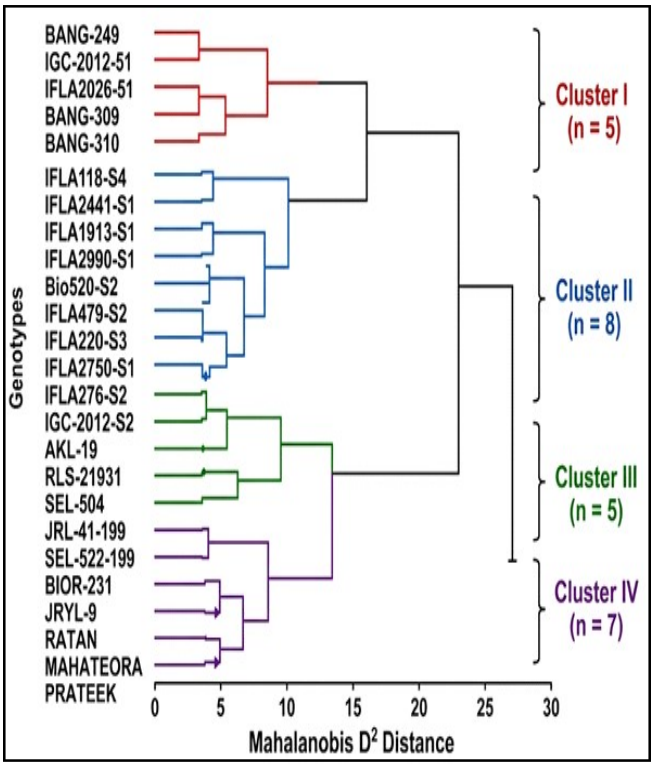


Fig. 2: UPGMA denogram showing genetic relationship among twenty five grasspea genotypes based on Mahalanobis D^2 statistics.

Table 2: Estimates of genetic variability parameters for fourteen different characters of grasspea genotypes.

S. No.	Characters	Mean	Range		GCV	PCV	h^2 (bs)	GA as % mean
			Min.	Max.				
1	Days to 50% flowering	50.28	47.5	52.8	2.64	2.95	80.43	4.89
2	Days to maturity	100.36	95	105.7	2.65	2.96	80.7	4.91
3	Plant height (cm)	47.25	41.4	52.9	5.05	5.61	80.96	9.36
4	Primary branches per plant	4.15	3.4	4.6	3.64	6.51	31.31	4.20
5	Number of pods per plant	21.41	17.3	26.3	7.29	9.99	53.36	10.98
6	Pod bearing length (cm)	22.83	19	26.9	4.47	6.95	41.31	5.91
7	Number of effective pods per plant	18.88	15.8	23.3	7.48	8.80	72.19	13.09
8	Number of seeds per pod	3.88	3.0	4.6	1.55	8.04	3.76	0.62
9	100 seed weight (g)	10.05	8.6	11.5	6.81	8.08	7.1	11.8
10	Harvest index (%)	63.69	41.3	85.2	11.49	13.69	7.04	19.8
11	Seed yield per plant (g)	6.744	4.8	8.4	11.70	13.32	77.1	21.17
12	Biological yield per plant (g)	10.89	8.3	12.9	6.77	9.15	54.82	10.33
13	Protein content (%)	26.73	23.31	33.41	7.97	8.11	96.57	16.13
14	ODAP content (%)	0.237	0.01	0.41	38.66	38.85	99.0	79.27

50% flowering and seed yield per plant, while moderate heritability was recorded for number of effective pods per plant, biological yield per plant and number of pods per plant. Genetic advance as percent of mean was highest for ODAP content, followed by seed yield per plant, harvest index and protein content. High heritability coupled with high genetic advance for ODAP content, seed yield per plant and protein content indicated the predominance of additive gene action and suggested that direct selection would be effective for the improvement of these traits. Similar findings have been reported by Pandey *et al*., (2000), Ranjan *et al*., (2007) and Das *et al*., (2015).

Genetic Divergence Analysis

The genetic divergence analysis based on Mahalanobis D^2 statistics grouped the twenty-five grasspea genotypes into four distinct clusters (Table 3), indicating the presence of considerable genetic diversity among the genotypes. Cluster II was the largest, comprising eight genotypes, followed by Cluster IV with seven genotypes, while Clusters I and III contained five genotypes each. The distribution of check varieties into different clusters reflected their genetic distinctiveness and diverse genetic backgrounds.

The intra-cluster distances ranged from 4.772 to 7.116, indicating varying degrees of homogeneity within clusters (Table 4). Cluster III recorded the lowest intra-cluster distance (4.772), suggesting close genetic similarity among its constituent genotypes. In contrast, Cluster I exhibited the highest intra-cluster distance (7.116), indicating relatively greater genetic variability among the genotypes within this cluster.

The maximum inter-cluster distance was observed between cluster I and cluster II (20.515), followed by cluster II and cluster III (19.858), indicating that genotypes belonging to these clusters were genetically most divergent. The minimum inter-cluster distance was recorded between cluster III and cluster IV (9.298), suggesting a closer genetic relationship between these two clusters.Higher inter-cluster distances indicate greater genetic divergence, and crosses between genotypes from such clusters are expected to produce higher heterosis

Table 3: Clustering pattern of 25 grasspea genotypes. (Mahalanobis D^2 statistics).

Cluster	No. of Genotypes	Genotype Names
Cluster I	5	BANG-249-S11, IFLA2026-S8, AKL-19, JRL-41-1992, SEL-522-1956.
Cluster II	8	IGC-2012-74/10-7-S9, IFLA2441-S14, IFLA1913-S11, IFLA2990-S10, Bio520-S2, RLS-21931, SEL-S04, JRYL-9.
Cluster III	5	IFLA118-S4, IFLA220-S1, BIOR-231, Mahateora, Prateek.
Cluster IV	7	BANG-309-S4, BANG-310-S7, IFLA479-S11, IFLA2750-S4, IFLA276-S10, IGC-2012-70/1-9-S2, Ratan.

Table 4: Intra and inter-cluster distances.

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	**7.116**	20.515	9.759	9.507
Cluster II	-	**6.603**	19.858	11.836
Cluster III	-	-	**4.772**	9.298
Cluster IV	-	-	-	**6.310**

and wider variability in segregating generations. These findings are in agreement with earlier reports emphasizing the importance of inter-cluster distances in parental selection (Rao, 1952; Sharma *et al*., 2020; Yadav *et al*., 2022).

The results of genetic divergence analysis indicated that genotypes from cluster I and cluster II, as well as cluster II and cluster III, could be effectively utilized in hybridization programmes to exploit maximum heterosis and generate superior recombinants. Clusters II and IV, which exhibited higher mean seed yield per plant, can be considered as potential donor clusters for yield improvement, while cluster III may serve as a valuable source for earliness and yield-contributing traits. The wide genetic divergence observed among clusters provides ample scope for the development of improved grasspea varieties through systematic breeding strategies.

Table 5: Contribution of different characters towards total genetic divergence.

S. No.	Character	Contribution (%)
1	ODAP content (%)	38.72
2	Seed yield per plant (g)	16.85
3	Number of effective pods per plant	11.42
4	Harvest index (%)	9.76
5	Biological yield per plant (g)	7.38
6	Protein content (%)	6.14
7	Number of pods per plant	4.52
8	Pod bearing length (cm)	2.41
9	Plant height (cm)	1.82
10	100-seed weight (g)	0.98
11	Number of primary branches per plant	0.92
12	Number of seeds per pod	0.64
13	Days to maturity	0.29
14	Days to 50% flowering	0.15
	Total	**100.00**

The percent (%) contribution of characters to total divergence is presented in Table 5. Among the fourteen characters studied, ODAP content contributed the highest proportion (38.72%) towards total genetic divergence, followed by seed yield per plant (16.85%), number of effective pods per plant (11.42%) and harvest index (9.76%). The higher contribution of these traits indicated their major role in differentiating the genotypes. Conversely, days to 50% flowering and days to maturity contributed the least towards genetic divergence, suggesting limited variability for these traits. The results indicate that ODAP content, seed yield and related yield components should be given greater emphasis in future grasspea breeding programmes.

The dendrogram generated through hierarchical cluster analysis (presented in Fig. 2) revealed the existence of substantial genetic diversity among the twenty-five grasspea genotypes. Based on genetic distances, the genotypes were grouped into four distinct clusters, indicating the presence of considerable variability within the experimental material. The clustering pattern corresponded closely with the Mahalanobis D^2 analysis, suggesting that the genotypes included in the study possessed diverse genetic backgrounds.

Cluster I comprised five genotypes and represented a distinct group characterized by comparatively higher

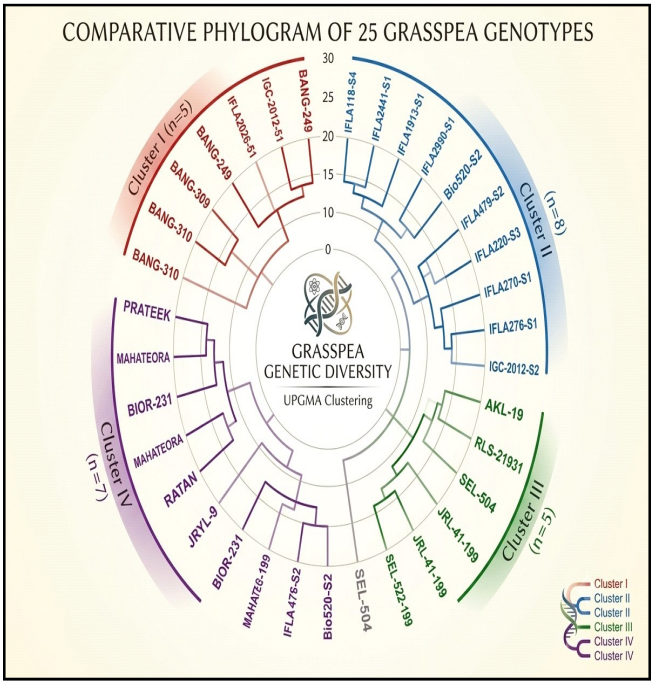


Fig. 3: Comparative phylogram of Grasspea genotypes.

genetic divergence from the remaining clusters. Cluster II was the largest cluster containing eight genotypes, indicating greater genetic similarity among its members. Cluster III consisted of five genotypes, while cluster IV contained seven genotypes. The distribution of genotypes across different clusters irrespective of their geographical origin suggested that genetic diversity was not necessarily associated with geographic distribution but rather with the accumulation of favourable allelic combinations during the course of evolution and selection.

The dendrogram further demonstrated that cluster III and cluster IV were genetically closer to each other, as evidenced by their early fusion in the hierarchical tree. In contrast, cluster II exhibited greater divergence from the remaining clusters, confirming the results obtained from Mahalanobis D^2 statistics. The wide separation among clusters indicated the existence of ample scope for exploiting heterosis and generating broad-spectrum variability through hybridization.

Overall, the dendrogram analyses confirmed the presence of substantial genetic diversity among the evaluated grasspea genotypes and highlighted the potential of genetically divergent parents for the development of high-yielding, nutritionally superior and low-ODAP cultivars with wider adaptability.

Conclusion

The present investigation demonstrated the existence of substantial genetic variability among the twenty-five grasspea genotypes for most of the agronomic and quality traits studied, thereby providing a strong foundation for genetic improvement through selection and hybridization.

Collectively, the findings of the present study indicate that simultaneous improvement of seed yield, nutritional quality, and reduction of ODAP content is achievable through the judicious exploitation of the available genetic variability. The identified superior and genetically divergent genotypes constitute valuable breeding materials and may be effectively utilized in future breeding programmes aimed at developing high-yielding, nutritionally superior, and low-ODAP grasspea cultivars suited to diverse agro-ecological conditions.

References

Bose, L.K., Jambhulkar N.N., Pande K. and Singh O.N. (2014). Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. *Chilean Journal of Agricultural Research*, **74(1)**, 3–9.

Campbell, C.G. (1997). *Grass pea (Lathyrussativus L.): Promoting the conservation and use of underutilized and neglected crops 18*. Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben/International Plant Genetic Resources Institute (IPGRI), Rome.

Das, A., Barpete S., Khare D. and Gupta P. (2015). Genetic variability and character association studies in grasspea (*Lathyrussativus* L.). *Legume Research*, **38(4)**, 471–476.

Finlay, K.W. and Wilkinson G.N. (1963). The analysis of adaptation in a plant-breeding programme.*Australian Journal of Agricultural Research*, **14(6)**, 742–754.

Lambein, F., Travella S., Kuo Y.H., Van Montagu M. and Heijde M. (2019). Grass pea (*Lathyrussativus* L.): Orphan crop, nutraceutical or just plain food? *Planta*, **250**, 821–838.

Lazányi, J. (2000). The role of grass pea (*Lathyrussativus* L.) in sustainable agriculture. *Acta Agronomica Hungarica*, **48(4)**, 321–330.

Mahalanobis, P.C. (1936). On the generalized distance in statistics.*Proceedings of the National Institute of Sciences of India*, **2**, 49–55.

Mishra, A., Sahu M. and Pandey H.K. (2025). Assessment of variability and association among green forage yield and contributing traits in indigenous genotypes of grass pea [*Lathyrus sativus* (L.)]. *Journal of Advances in Biology and Biotechnology*, **28(1)**, 503–512.

Pandey, R.L., Singh N.B. and Gupta S. (2000). Variability and heritability studies in grasspea. *Indian Journal of Pulses Research*, **13(2)**, 121–124.

Parihar, A.K., Dixit G.P. and Singh N.P. (2015). Genetic variability and character association in grasspea (*Lathyrussativus* L.). *Legume Research*, **38(2)**, 160–164.

Petterson, D.S., Sipsas S. and Mackintosh J.B. (1997). The chemical composition and nutritive value of Australian pulses.*Grain Research and Development Corporation*, Canberra.

Prodanov, M., Sierra I. and Vidal-Valverde C. (2004). Influence of germination on the nutritive value of legumes. *European Food Research and Technology*, **219**, 44–48.

Ranjan, R., Singh A.K. and Kumar R. (2007). Genetic variability and heritability estimates in grasspea. *Indian Journal of Pulses Research*, **20(1)**, 52–55.

Rao, C.R. (1952). *Advanced statistical methods in biometric research*. John Wiley & Sons.

Sahu, M., Mishra A. and Pandey H. (2022). Characterization and assessment of genetic diversity in local and improved accessions of grass pea (*Lathyrus sativus* L.) for green forage yield traits. *Range Management and Agroforestry*, **43(2)**, 237–246.

Sarker, A., Erskine W. and Singh M. (2019). Genotype × environment interaction and stability analysis in food legumes.*Legume Perspectives*, **15**, 24–29.

Sharma, R.N., Chitale M.W. and Agrawal K.C. (2000). Neurolathyrism and β-ODAP toxicity in grasspea. *Indian Journal of Agricultural Sciences*, **70(4)**, 217–220.

Tadesse, T., Bekele A. and Mekbib F. (2018). Genotype by environment interaction and stability analysis of grasspea genotypes.*Euphytica*, **214**, 1–12.

Ullah, M.Z., Hasan M.J., Rahman A.H.M.A. and Saki A.I. (2019). Genetic variability and trait association in grasspea (*Lathyrussativus* L.). *Bangladesh Journal of Agricultural Research*, **44(2)**, 231–243.

Yadav V.K., Radhakrishna A., Das M.M., Singh T., Yadav V., Mishra S.A. and Sarker A. (2022). Deciphering Genetic Diversity in Grass Pea (*Lathyrussativus* L.)Collections Using Agronomic and Forage Quality Traits and SSR Markers. *Journal of Agricultural Science and Technology*, **11(2)**, 1-9.