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Genetic Divergence Analysis of Garden Pea (*Pisum sativum* L.) Genotypes based on Yield and its Contributing Traits under Protected Conditions

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Abstract

The present study aimed to assess genetic divergence among 156 garden peas under polyhouse conditions during the winter seasons 2023-24 and 2024-25 following an alpha lattice design, replicated twice. Based on Mahalanobis D^2 statistics, the genotypes were grouped into eight clusters over the years, indicating considerable genetic variability among genotypes. The highest inter-cluster distances were observed between Clusters V and VIII (9.40), suggesting wide genetic divergence among clusters. Cluster mean analysis revealed Cluster VIII as superior performing for pod length, pod width, seeds per pod, shelling percentage and average pod weight, whereas Cluster I had the same for pod yield during pooled environments. Further, average pod weight contributed the most towards total genetic divergence, followed by pod width and pod length. These results revealed the presence of substantial genetic variability among the studied genotypes, and hybridisation between genetically divergent genotypes from different clusters may be effectively utilised to develop improved garden pea cultivars.

Keywords: Clusters, Hybridisation, Mahalanobis D^2, Means, Pod Traits, Variability

Legume vegetables, comprising domesticated, wild and orphan crops belonging to the large plant family Fabaceae, represent an important source of protein, essential amino acids and mineral nutrients and play a significant role in ensuring food and nutritional security under changing climatic conditions[1,2]. Among the legume vegetables, garden pea (*P. sativum* L.) is an important cool-season crop cultivated worldwide for its tender green pods and seeds. It possesses a diploid chromosome number of 2n = 14 and a relatively large genome size of approximately 4.45 Gb[3]. Pea is consumed in both fresh and processed forms and is valued for its high nutritional quality, being a rich source of protein, dietary fibre, vitamins and minerals, particularly ascorbic acid, folic acid and vitamin K[4]. In addition to its dietary importance, pea contributes significantly to sustainable agriculture through biological nitrogen fixation, which enhances soil fertility and reduces dependence on synthetic fertilisers[5]. These attributes make garden pea an important component of diversified and sustainable farming systems.

Globally, pea is cultivated on a large scale and ranks among the most important grain legumes. India is one of the leading producers of pea and contributes nearly 21 per cent of the world's production[6]. In India, pea cultivation is concentrated in several northern

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states including Himachal Pradesh, Uttarakhand and Jammu and Kashmir, where favourable agro-climatic conditions support its cultivation[7,8]. In the north-western Himalayan region, pea is grown as a winter crop in the plains and as a summer crop in the hills, and also serves as an important off-season vegetable supplying fresh green pods to markets in the plains[4]. This provides a distinct market advantage to hill farmers by enabling supply during the lean period in the plains. In recent years, the adoption of protected cultivation technologies such as polyhouses and net houses has gained considerable importance for vegetable production, particularly in hilly regions where climatic variability often restricts open-field cultivation. Protected cultivation creates a controlled microclimate by regulating temperature, humidity and other environmental factors, thereby promoting improved plant growth, enhanced productivity and extended harvesting periods[9]. Such controlled environments also improve resource-use efficiency and reduce the risk of crop failure due to erratic weather conditions. Under such conditions, cultivation of garden pea has shown promising potential for early and off-season production with higher yield and better pod quality, making it an alluring option for farmers seeking higher economic returns. Despite its economic importance, increasing temperature and the incidence of various biotic and abiotic stresses often reduce the yield and quality of garden pea, thereby limiting crop profitability for farmers[10-12]. Under such circumstances, protected cultivation can partially mitigate environmental stresses by providing a favourable growing environment. However, the success of such production systems largely depends on the availability of genetically superior and adaptable varieties. Genetic diversity plays a fundamental role in the adaptation and improvement of crop species. It facilitates the identification of genetically divergent parents for hybridisation, enabling the exploitation of heterosis and the development of superior recombinants. Garden pea germplasm exhibits considerable morphological and genetic variability, which can be effectively utilised to broaden the genetic base and accelerate breeding programmes aimed at developing climate-resilient and high-yielding cultivars[16].

Most studies on garden pea have been conducted under open field conditions with emphasis on region-specific genotype evaluation. Evaluation of genotype performance under protected cultivation provides an opportunity to better understand the influence of microclimate on trait expression, yield and selection efficiency. Therefore, a comprehensive assessment of genetic diversity in garden pea germplasm is essential for identifying promising genotypes and designing efficient breeding strategies. Considering the economic importance of garden pea and the growing relevance of protected cultivation for off-season vegetable production, the present study was undertaken to assess the extent of genetic diversity among 156 garden pea genotypes based on important pod and yield-related traits under polyhouse conditions. The findings of this study are expected to provide a scientific basis for identifying superior genotypes and formulating effective selection strategies for future garden pea breeding programmes.

MATERIALS AND METHODS

The experiment comprising 156 garden pea genotypes from different premier institutes was conducted during the winter seasons of 2023-24 and 2024-25 under naturally ventilated polyhouse conditions at the Vegetable Research Farm, College of Agriculture, CSK Himachal Pradesh Agricultural University, Palampur. The genotypes were evaluated following an alpha lattice design with two replications across the environments. Each genotype was sown in a single row of 1.5 m length over the replications with inter and intra-row spacing of 45 cm and 10 cm, respectively. Standard agronomic practices under protected cultivation were followed to ensure healthy plant growth throughout the experiment. The observations were recorded on five randomly taken plants of each genotype over the replications for 7 quantitative pod traits *viz.*, pod length (cm), pod width (mm), seeds per pod, shelling

percentage (%), number of pods per plant, average pod weight (g) and pod yield.

Statistical Analysis

Genetic divergence among the genotypes based on 7 quantitative pod traits was assessed using the software INDOSTAT following the method proposed by Mahalanobis[13]. The genotypes were grouped into different clusters using Tocher's method as described by Rao[14]. The average intra and inter-cluster distances were calculated to determine the extent of genetic diversity among the clusters. The relative contribution of each trait towards total genetic divergence was also estimated to identify the most important characters responsible for genetic variability among the genotypes. The clustering pattern obtained from the analysis was further used to identify genetically diverse parents for potential use in hybridisation programmes aimed at crop improvement.

RESULTS AND DISCUSSION

Genetic diversity plays a crucial role in crop improvement programmes as it provides the basis for effective selection and hybridisation[2,15]. The assessment of genetic divergence among genotypes helps breeders identify genetically diverse parents that can be utilised to develop superior recombinants with improved yield and other desirable traits[17]. Among the different statistical approaches, the multivariate analysis based on Mahalanobis D^2 statistics and clustering through Tocher's method is widely used to evaluate genetic divergence among genotypes for multiple quantitative traits simultaneously.

Clustering Pattern of Genotypes Based on Mahalanobis D^2 Analysis

The multivariate analysis (D^2) for genetic divergence grouped the garden pea genotypes into eight clusters in pooled analysis over the years (Table 1). The multivariate analysis using Tocher's method revealed considerable genetic diversity among the garden pea genotypes. Cluster II contained the maximum number of genotypes (101), followed by Cluster I (35), Cluster VI (9), Cluster V (7) and one genotype each (mono-genotypic) in Clusters IV, VII and VIII. The presence of a large number of genotypes in a single cluster indicates relatively lower genetic divergence among them, while clusters containing only one genotype (mono-genotypic clusters) suggest that those genotypes are highly divergent from the rest of the population, which may serve as valuable parents in hybridisation programmes for broadening the genetic base of garden pea. Similar clustering patterns and the occurrence of mono-genotypic clusters have been reported earlier in garden pea by Sharma *et al.*[18], who emphasised that genetically distant clusters are useful for selecting parents to obtain higher heterosis and wider variability. Sharma *et al.*[19] grouped 56 garden pea genotypes into six clusters, with Cluster I being the largest (30 genotypes) followed by Cluster III (20 genotypes), while Cluster IV contained three genotypes and Clusters II, V and VI were mono-genotypic.

INTRA AND INTER-CLUSTER DISTANCES AMONG CLUSTERS

Assessment of genetic divergence through intra and inter-cluster distances provides valuable insight into the extent of variability present among genotypes. Intra-cluster distance reflects the magnitude of genetic variability within a cluster, whereas inter-cluster distance indicates the degree of genetic divergence between clusters[20]. Greater inter-cluster distance suggests wider genetic diversity among the genotypes, which can be effectively exploited in hybridisation programmes for the development of superior recombinants and desirable transgressive segregants[21]. The intra-cluster distance varied from 0 to 5.00, with the highest in Cluster VI (5.00), followed by Cluster I (4.52), Cluster V (4.51) and Cluster II (4.48), while the remaining mono-genotypic clusters, *i.e.,* Clusters III, IV, VII and VIII, had zero intra-cluster distance in pooled over years (Table 2). Maximum intra-cluster variation among genotypes was also observed by *Sharma et al.*[21] and Chauhan and Sharma[22]

Table 1. Distribution of 156 garden pea genotypes during pooled over years (2023-25), showing genetic relationship based on quantitative traits as per Mahalanobis D^2 analysis

Cluster Group	Number of Genotypes	List of Genotypes
Cluster-I	35	HPMP-1, SP-10, SP-3, Him-Palam-Matar-1, DPP-SN-2, DPP-SN-5, DPP-SN-6, SP-6, DPP-SN-22, Pb-89, DPP-89-101-9, SP-18, HPMP-2, DPEPP-15-1-1, DPPM-65, PS-72 (IC-278261), DPP-SN-10, DPP-89-101-1, DPP-SN-8-2, Him-Palam-Matar-2, PAUM-18-8, Azad P-1, PS-68 (IC-208366), PAUM-16-4, C-26-Pot-4-P4, DPPMR-09-1, Pb-87, SP-12, MA-8, L-0.4-8, DPP-89-101-8, ST-1, DPP-89-101-5, PS-77 (EC-598704), Kashi Mukti
Cluster-II	101	Kashi Nandini, DPEPP-1, MA-7, PAUM-17-7, AP-50-1, L-0.4-5, L-0.4-3, L-0.4-11, Pusa Pragati, VRP-358, VL-3, KS-205, Solan Nirog, L-40-1014, C-1-Pot-P7, Pusa Shree, Kashi Samridhi, C-7-Pot-1-P5, CHP-2, HUDP-15, B-L1-Pot-7-P2, DPPMFWR-30-2, DPPMP-WR-27, VRPM-10, Arkel, PAUM-16-6, PS-69 (IC-208378), PAUM-8-5, Matar Ageta, Lincoln, JI-2302, L-0.3-139, VRP-104, Swarna Mukti, L-0.4-1, PAUM-17-4, Palam Triloki, C-8-Pot-2-P2, Kashi Udai, Tiger, Swarna Amar, Pant Matar-2, PS-35 (IC-381453), PS-75 (EC-598538), DAVP-10, DPPM-74, Azad P-3, DPPMP-WR-20, Kashi Samrath, Arka Kartik, C-11-Pot-4-P2, PS-73 (EC-381866), PS-29 (IC-342029), PS-9 (IC-218993), Winner, VRP-382, AP-0.3-1, IC-296678, L-0.4-7, C-1-Pot-2, Easy Peasy, VRPM-19, VRP-304, Kashi Ageti, Arka Priya, VRPD-1, VRPM-11, Arka Sampoorna, NDVP-104, L-0.4-4, AP-0.3-2, PAUM-17-3, Arka Ajeet, Palam Priya, L-60-2, Cascalia, L-0.4-9, L-0.4-6, PAUED-16-1, AP-0.3-129, Pusa Prabal, PS-21 (IC-329410), C-3-Pot-10-P3, VRP-355, PS-79 (EC-598757), PS-70 (IC-218988), Arka Uttam, AP-0.3-33, C-11-Pot-4-P1, PS-24 (IC-342022), L-50-1, AP-50-2, PAUM-10-3, Sabre, DPPMFWR-30, Nepal, PAUM-9-6, PAUM-18-6, L-0.4-10, L-60-1, PS-11 (IC-219002)
Cluster-III	1	PAUM-15-7
Cluster-IV	1	DVP-8
Cluster-V	7	VRP-112, L-0.4-2, PS-12 (IC-219008), PS-5 (IC-218984), PS-8 (IC-218991), Shihara Local, PS-3 (IC-209125)
Cluster-VI	9	DPPEPP-2AP, EPP-2, DPPMR-09-6, Kashi Shakti, PS-26 (IC-342026), PAUM-17-1, PAUM-16-8, PAUM-16-7, Meethi Phali
Cluster-VII	1	Shighra
Cluster-VIII	1	Palam Sumool

The inter-cluster distance ranged from 4.36-9.40 during pooling over years, respectively (Table 2). The highest inter-cluster genetic divergence was found in Clusters V and VIII (9.40), followed by Clusters III

Table 2. Average intra and inter-cluster values of D^2 and $\sqrt{D^2}$ among clusters for pooled over years (2023-25)

Clusters	I	II	III	IV	V	VI	VII	VIII
I	20.43	38.44	56.07	41.05	60.16	37.52	46.69	47.35
	4.52	6.20	7.49	6.41	7.76	6.13	6.83	6.88
II		20.10	27.39	27.36	31.45	41.39	27.94	68.64
		4.48	5.23	5.23	5.61	6.43	5.29	8.28
III			0.00	36.12	19.01	50.18	33.95	81.93
			0.00	6.01	4.36	7.08	5.83	9.05
IV				0.00	41.51	55.31	43.74	76.75
				0.00	6.44	7.44	6.61	8.76
V					20.36	55.65	30.35	88.29
					4.51	7.46	5.51	9.40
VI						24.97	43.64	41.82
						5.00	6.61	6.47
VII							0.00	73.37
							0.00	8.57
VIII								0.00
								0.00

and VIII (9.05), and Clusters IV and VIII (8.76) which further indicated that the genotypes included in the clusters with high inter-cluster distance showed wide genetic diversity, and selection of parents from these diverse clusters would be beneficial in hybridisation programme for improving yield and other desired pod traits. Based on inter-cluster distance, Rana *et al.*[23] have also suggested the selection of parents from genetically diverse clusters to obtain desirable transgressive segregants.

CLUSTER MEAN PERFORMANCE FOR QUANTITATIVE POD TRAITS

Cluster mean analysis provides useful information regarding the relative performance of different clusters for various yield and yield-contributing traits. It helps in identifying clusters possessing desirable trait combinations, which can be effectively utilised in selecting suitable parents for hybridisation programmes[24,25]. The comparison of cluster means also facilitates the identification of genetically superior and diverse clusters that may contribute to the development of high-yielding genotypes in garden pea improvement programmes (Srishti et al.[2]). Cluster means indicated considerable variation among clusters for different traits across the years. Cluster VIII exhibited superior performance for pod length (12.47 cm), pod width (19.63 mm), seeds per pod (8.75), shelling percentage (50.32 %) and average pod weight (7.86 g). Cluster I recorded the highest pod yield per plant (176.31 g), while Cluster IV showed the maximum number of pods per plant (31.03) (Table 3).

Table 3. Cluster means for different traits of garden pea genotypes distributed in 8 clusters for pooled over years (2023-25)

Traits	I	II	III	IV	V	VI	VII	VIII	Mean	Max	Min
Pod length (cm)	10.39	8.21	7.63	10.19	5.98	9.17	5.70	12.47	8.72	12.47	5.70
Pod width (mm)	14.40	13.39	13.70	11.01	13.09	17.75	13.82	19.63	14.60	19.63	11.01
Seeds per pod	8.56	6.40	5.28	7.03	4.90	7.09	4.38	8.75	6.55	8.75	4.38
Shelling percentage (%)	48.34	47.11	50.04	46.14	47.60	45.78	50.23	50.32	48.20	50.32	45.78
Number of pods per plant	28.33	27.86	21.98	31.03	25.60	25.62	22.90	20.23	25.44	31.03	20.23
Average pod weight (g)	6.26	4.37	3.02	3.62	3.35	5.60	6.28	7.86	5.05	7.86	3.02
Pod yield per plant (g)	176.31	120.04	66.04	112.69	85.45	143.62	143.54	159.03	125.84	176.31	66.04

RELATIVE CONTRIBUTION OF TRAITS TO TOTAL GENETIC DIVERGENCE

The relative percent contribution of studied characters for genetic divergence (Table 4) showed that average pod weight (46.64 %) contributed maximum towards total genetic divergence followed by followed by pod width (26.79 %), pod length (17.85 %), seeds per pod (6.06 %) and number of pods per plant (1.99 %) during pooled over years also showed notable contributions towards genetic diversity. These results indicate that traits such as average pod weight, pod width and pod length played a major role in the expression of genetic divergence among the genotypes and could therefore be considered as important selection parameters while choosing genetically diverse parents for hybridisation to create greater variability in the breeding population. Similar findings, where average pod weight contributed the maximum towards genetic divergence in garden pea, were also reported by Sekhon *et al.*[26].

Table 4. Relative contribution (%) of individual traits to the genetic divergence among vegetable pea genotypes for pooled over years (2023-25)

Source	Contribution (%)
Pod length (cm)	17.85
Pod width (mm)	26.79
Seeds per pod	6.06
Shelling percentage (%)	0.16
Number of pods per plant	1.99
Average pod weight (g)	46.64
Pod yield per plant (g)	0.51

CONCLUSION

The Mahalanobis D^2 analysis grouped the genotypes into eight clusters, indicating considerable variability for important pod and yield-related traits. Large inter-

cluster distances observed among certain clusters suggested the presence of genetically divergent genotypes that can be effectively utilised in breeding programmes. Cluster mean analysis identified clusters possessing superior performance for key yield traits, particularly Cluster VIII for pod length, pod width, seeds per pod, shelling percentage and average pod weight, while Cluster I recorded the highest pod yield per plant in the pooled analysis. The relative contribution analysis indicated that average pod weight, pod width and pod length were the major contributors to total genetic divergence, highlighting their importance in parent selection. Therefore, pea genotypes belonging to clusters with high inter-cluster distances and superior trait performance can be used as potential parents in hybridisation programmes to exploit heterosis and develop high-yielding garden pea varieties suitable for protected cultivation systems.

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CONFLICT OF INTEREST

The authors declare no conflict of interest in relation to this research article.

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AUTHORS CONTRIBUTION

AP: Performed the experiments, data analysis and prepared the original draft of the manuscript. AS: conceived and designed the research programme, developed the methodology, provided resources, supervision and critically edited the manuscript. PS: data curation, validation and management of experimental datasets. S: data curation, preparation of tables and figures. VS: data curation, data interpretation and validation of experimental findings. PS: data curation, compilation of research records and manuscript review.