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Research Article

Exploring Genetic Diversity for Yield Improvement in Pea (*Pisum sativum* L.) Genotypes using Multivariate Analysis

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ABSTRACT

Genetic variability can play an essential role in the pea breeding strategies to develop new varieties of peas with enhanced yield. This study evaluates 12 traits in 25 diverse genotypes of peas which include NARC and UAF genotypes. All the studied characters showed high to moderate values for both genotypic and phenotypic coefficients of variance along with significant heritability and genetic advance except for number of secondary branches and plant height at first flower. For all the characters studied, values for PCV were generally greater than the GCV values. While principal component analysis studies clarified that a total of 81.41% of variation was exhibited by first four components among the genotypes having the eigenvalues higher than 1. Further, K-means cluster analysis, based on cluster biplot between PC1 and PC2, classifies the 25 cultivars into three separate clusters. Overall genotypes present in Cluster I acquired higher mean values compared to Clusters II and III. Cluster I was grouped by seven accessions and other two clusters were grouped with 9 genotypes each. Highest mean values were exhibited by yield per plant (47.74), number of pods (155.94), plant height at maturity (246.43), number of nodes (83.33) and number of effective pods (135.36) for genotypes in Cluster I. For genotypes in Cluster II, plant height at first flower (54.53), number of primary branches (11.17), and 100 seed weight (19.35) revealed maximum means. While high mean values were shown by number of secondary branches (21.23), pod length (6.88) and seed per pods (5.93) in Cluster III. Genotypes from the cluster I performed better which may contribute to the future breeding programs.

Keywords: Cluster analysis, Genetic diversity, Multivariate analysis, *Pisum sativum*, Principal component analysis, Yield

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INTRODUCTION

The pea (*Pisum sativum* L.) having 2n=2x=14 chromosomes, among the major self-pollinated legume crop, an annual herbaceous in nature, belongs to the Fabaceae family. It is suitable for a cold humid environment with temperate conditions. The pea is a leguminous grain cultivated in the lowlands during winter and in the highlands during summer season in Pakistan (Ali *et al.*, 2021). Four distinct pea origin centers were identified by Vavilov (1926) based on genetic diversity. According to genetic diversity, the pea originated in the region that includes Central Asia, the Near East, Abyssinia, and the Mediterranean region. Archaeological data also backs up this claim, demonstrating that peas have been in Near East and Central Asia from 10,000 B.C. It is also believed that the Mediterranean region serves as its major center of origin, with Ethiopia and the Near East as secondary center of origin (Devi *et al.*, 2021).

The pea is well-suited for large-scale farming due to its shorter growing season and ability to grow under water deficit conditions. Regardless of its high economic value, productivity of pea remained low. Being a part of the legume family, it can engage in a symbiotic relationship with particular soil-borne bacteria known as Rhizobia, enabling them to fix atmospheric nitrogen, so enhancing soil quality (Yumkhaibam *et al.*, 2019). Pea are important sources of micro as well as macronutrients, which contain major portions of protein having essential amino acids along with readily metabolized carbohydrates. It also contains vitamin B, minerals and dietary fibers both in soluble and insoluble form (Rawal *et al.*, 2019; Rasskazova and Kirse-Ozolina, 2020). The dry matter (DM) composition of a whole pea seed ranges from 21.2% to 32.9% protein, 36.9% starch, 20.7% amylose, 14 to 26% dietary fiber which includes 2-9% fibers in soluble form while other portion contain 10-15% insoluble fibers, 5.3%-8.7% soluble sugars, 1.2%-2.4% total lipids, and 2.3%-3.4% ash (Dahl *et al.*, 2012).

Improving pea performance in different environments is a main objective for pea breeders. This is because the development and production of crops are greatly affected by both the environment and the impacts of G × E interactions (Bocianowski *et al.*, 2019). Improvement and development of high yielding verities of peas are challenging due to lack of variation. In crop improvement Genetic diversity is seen as a crucial component and an important need for agricultural enhancement and research programs aimed at achieving high-yielding genotypes (Georgieva *et al.*, 2016). Heritability, genetic advancement, genotypic and phenotypic coefficient of variation are factors that influence the effective utilisation of genetic variety via selection (Latha *et al.*, 2024). Better selection can be achieved by pea breeders when they have an excellent understanding of the relative importance of yield related characteristics. When it comes to classify genotypes and finding good parents for crossbreeding, multivariate methods like principal component analysis along with cluster analysis are crucial (Koij and Saba, 2015; Yadav *et al.*, 2025).

The objective of the current research was to identify the extent of genetic variability among 25 diverse pea genotypes for agronomic traits. This evaluation of genotypes involves the study of the pea production related traits through variability analysis. This investigation assesses the phenotypic and genotypic coefficients, genetic advancement, heritability, and the characteristics relating to pea production in order to ascertain their function in the process of selection and improvement. Principal component analysis and cluster analysis helps in the identification of groups of verities having better characteristics. The findings will contribute to identify better performing verities and key agronomic traits enhancing breeding programs to improve and develop pea germplasm.

MATERIALS AND METHODS

The current study of diverse genotypes was held at the research field of University of Agriculture Faisalabad during 2024-2025. 25 edible Pea accessions were cultivated using a randomized complete block method with two repetitions. Each replication contained ten plants that were sown on 2 ridges side by side, keeping the plant-to-plant distance 6 inches and row to row 2.5 feet respectively. The observations on different parameters were recorded. The crop was raised to maturity with standard production practices. The recommended agronomic techniques were employed to cultivate the genotypes, and five plants that exhibited competitive growth were randomly chosen from each replication to record their morphological observations.

Following are the traits which were assessed including, days to first flower. Plant height at first flower(cm), number of pods/plants, number of primary branches/plants, number of secondary branches/plants, plant height at maturity(cm), number of nodes/plants, number of effective pods/plants, pod length(cm), seeds/pods, 100-seed weight(cm), Yield/plant.

For statistical analysis, R software (R Studio version 4.5.0) was used to perform all the statistical analysis in this study (Team, 2016). A number of genetic parameters were computed which included genotypic, phenotypic and environmental variance along with their coefficient of variations, heritability, and genetic advance/mean percentage were analyzed with the help of variability package which were developed by Popat *et al.* (2020) based on the methods used by Singh and Chaudhary (1981). Principal component analysis was conducted through the FactoMineR (Lê *et al.*, 2008) and FactoExtra (Kassambara and Mundt, 2016) package in R studio. After PCA, cluster analysis was performed using cluster package and visualize it by using ggplot2 package.

RESULTS

Table 1 displays the values of the phenotypic and genotypic coefficients of variance. Phenotype and genotype coefficient of variation values below 10% considered as low, intermediate values ranged from 10 to 20%, and the values above 20% were regarded as high (Alemu *et al.*, 2020).

Table 1. Genetic variability parameters of 12 quantitative traits parameters of 25 Pea (*Pisum sativum*) genotypes.

	DFF	PHFF	NP	NPB	NSB	PHM	NN	NEP	PL	SP	HSW	PY
Maximum	101.4	65.080	255.20	14.69	25.49	280.60	91.13	200.80	7.840	7.640	24.34	106.8
Minimum	44.20	43.69	32.00	5.85	15.58	50.60	17.13	27.20	5.26	3.43	9.98	12.80
Grand Mean	77.91	53.50	100.02	9.67	20.77	169.40	57.44	82.06	6.16	5.23	17.20	40.82
SEm	1.114	1.331	1.807	0.662	0.718	15.182	3.103	1.992	0.105	0.438	0.417	0.461
CD1	3.251	3.886	5.274	1.932	2.096	44.313	9.057	5.815	0.306	1.279	1.217	1.346
CD2	4.405	5.266	7.148	2.619	2.840	60.051	12.27	7.880	0.415	1.733	1.650	1.824
Ve	2.481	3.545	6.531	0.877	1.031	460.98	19.26	7.937	0.022	0.384	0.348	0.425
Vg	399.5	17.047	2489.7	5.571	2.280	5527.4	681.7	1943.5	0.490	0.761	9.847	545.7
Vp	402.0	20.592	2496.2	6.448	3.312	5988.4	701.0	1951.4	0.512	1.145	10.2	546.2
CVe	2.022	3.520	2.555	9.686	4.890	12.674	7.640	3.433	2.411	11.84	3.429	1.597
CVg	25.65	7.718	49.889	24.41	7.271	43.887	45.46	53.721	11.36	16.67	18.24	57.24
CVp	25.73	8.482	49.954	26.27	8.762	45.681	46.09	53.830	11.61	20.44	18.56	57.26
Hbs	99.4	82.8	99.7	86.4	68.9	92.3	97.3	99.6	95.7	66.5	96.6	99.9
GA	41.05	7.739	102.65	4.520	2.581	147.14	53.05	90.631	1.410	1.465	6.353	48.11
GA%	52.69	14.465	102.64	46.76	12.43	86.858	92.34	110.43	22.90	28.00	36.93	117.8

Heritability % (Broad Sense) high if >80%, moderate if 50% to 80%, low if <50%, GAPM high if >20%, moderate if 10% to 20%, low if <10% DFF=Days to first flower, PHFF=Plant height at first flower(cm), NP=Number of pods/plants, NPB=Number of primary branches/plants, NSB=Number of secondary branches/plants, PHM=Plant height at maturity(cm), NN=Number of nodes/plants, NEP=Number of effective pods/plants, PL=Pod length(cm), SP= seeds/pods, HSW=100-Seed weight(g), PY=Yield/plant, Standard Error of Mean (SEm), Critical Difference at P<0.05 (CD1), Critical Difference at P<0.01 (CD), Environmental Variance (Ve), Genotypic Variance (Vg), Phenotypic Variance (Vp), Environmental Coefficient of Variance (CVe), Genotypic Coefficient of Variance (CVg), Phenotypic Coefficient of Variance (CVp), Heritability % in Broad Sense (Hbs), Genetic Advance (GA), Genetic Advance as percentage of mean (GA%).

Low values for PCV and GCV were observed in plant height at first flower (8.48, 7.72) and number of secondary branches (8.76, 7.27). Intermediate values were observed for the pod length (11.61,11.36) and 100 seed weight (18.56,18.24) and high values were recorded for days to first flower (25.74,25.66), number of pods (49.95, 49.89), number of primary branches (26.27, 24.41), plant height at maturity (45.68,43.89), number of nodes (46.09,45.46) number of effective pods (53.83,53.72) and yield per plant (57.26,57.24). seed per pod showed intermediate value for GCV (16.67) but high value for phenotypic coefficients (20.44). There were low to slightly intermediate values for environmental coefficient of variance (Table 1). Broad sense heritability(h2) values under 50% considered as low, between 50% to 80% values were intermediate and values above 80% are regarded as high (Bello *et al.*, 2012). High values for heritability were observed in days to first flower (99.4%), plant height at first flower (82.8%), number of pods (99.7%), number of primary branches (86.4%), plant height at maturity (92.3%), number of nodes (97.3), number of effective pods (99.6%), pod length (95.7%), 100-seed weight (96.6%), yield per plant (99.9). While intermediate values were observed in number of secondary branches (68.9%) and seed per pod (66.5%) (Table 1). Heritability values ranged from 66.5% to 99.9%, which indicates there were no traits with low heritability.

Genetic advance as percentage of mean considered high at >20%, intermediate ranges from 10 to20% and below 10% it indicates low value (Alemu *et al.*, 2020). GAPM values were ranged from 117.85% to 12.43, which means there were no traits having low genetic advance. Highest genetic advance as percentage of mean was observed in yield per plant(117.85%) followed by number of effective pods (110.44), number of pods (102.64), number of nodes (92.34), plant height at maturity (86.86%), days to first flower (52.69%), number of primary branches (46.76%), 100 seed weight (36.93%), seed per pod (28%) and pod length (22.90%). And intermediate values for genetic advance as percentage of mean were recorded for plant height at first flower (14.47%) and number of secondary branches (12.43%).

Principal Component Analysis

Principal component analysis for 12-character parameters of 25 pea genotypes was calculated and visualized in biplot (Figure 1). Initial 4 components among the 12 principal components (PCs) studied showed the eigenvalue higher than 1 as shown in Table 2 and Figure 2A. PC1 contribution was highest, which were 38.74% The primary factors contributing to this variation include the number of nodes, the height of the mature plant, the length of the pod, and the duration until the first flower appears (Figure 2B). 19.23% of the total variation was explained by PC2. This variation was mainly influenced by attributes like number of effective pods, total pods, yield per plant, and seeds per pod. PC3 represents 14.63% of the variation, mostly influenced by the number of secondary branches, plant height at first flowering, and 100-seed weight. PC4 contributed 8.81% of variation mainly by the factors like primary branches number, 100 seed weight.

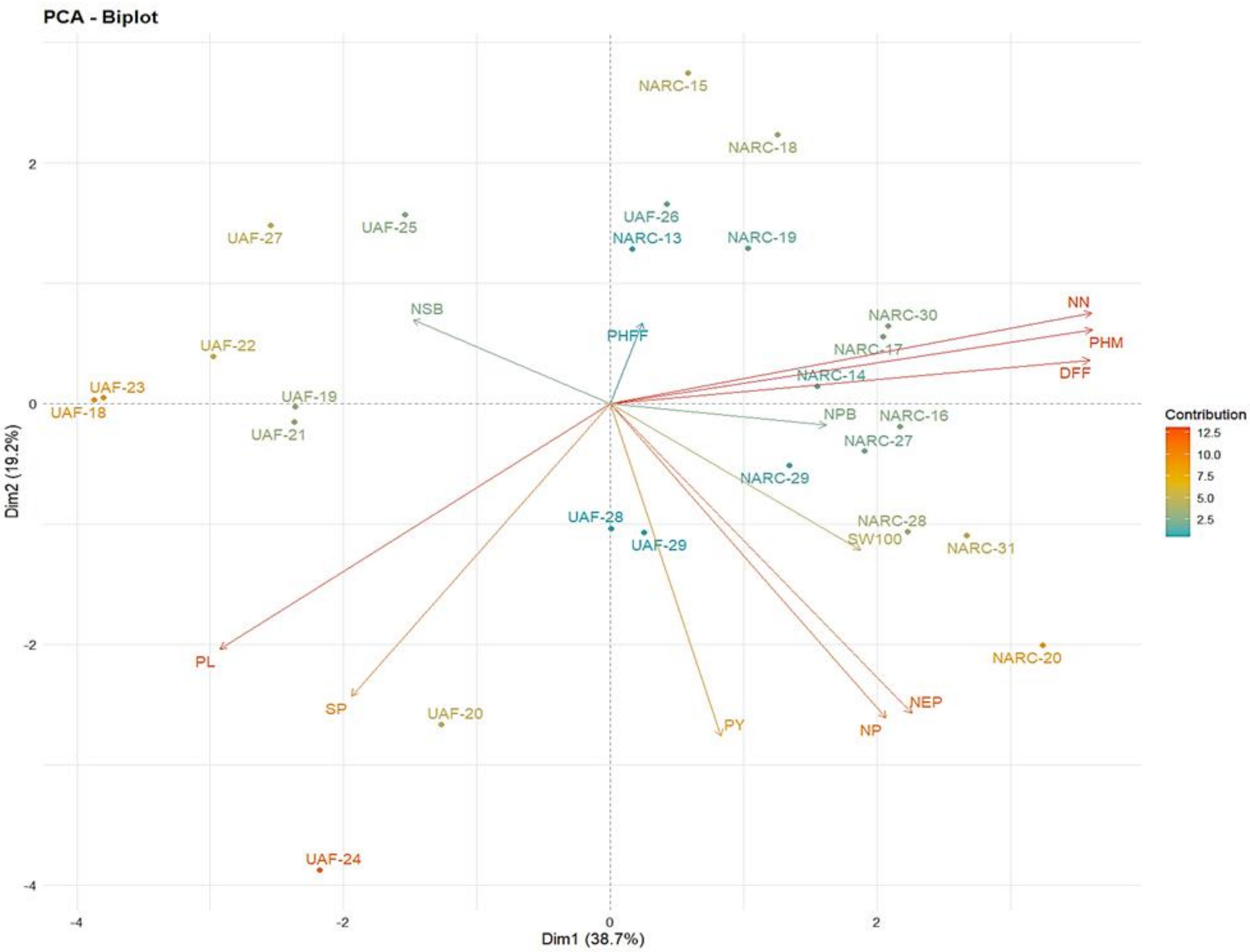

Figure 1. Biplot for the 25 pea (*Pisum sativum*) genotypes and 12 traits along the first 2 principal components. Dim1=PC1, Dim2=PC2, DFF=Days to first flower, PHFF=Plant height at first flower(cm), NP=Number of pods/plants, NPB=Number of primary branches/plants, NSB=Number of secondary branches/plants, PHM=Plant height at maturity(cm), NN=Number of nodes/plants, NEP=Number of effective pods/plants, PL=Pod length(cm), SP= seeds/pods, SW100=100-Seed weight(g), PY=Yield/plant.

Table 2. First 4 principal components for 12 traits in 25 pea genotypes.

	PC1	PC2	PC3	PC4
Eigenvalue	4.649	2.307	1.755	1.057
Variance (%)	38.74	19.23	14.63	8.81
Cumulative variance (%)	38.74	57.97	72.59	81.40

Cluster analysis

K-mean cluster analysis categorized 25 distinct genotypes into three separates groups on the basis of similarities between these genotypes towards the studied traits contributed in PC1 And PC2 (Figure 4). Cluster I comprises seven accessions, Cluster II grouped with nine genotypes and cluster III also contained 9 genotypes. The comparisons of mean values of all the three clusters are presented in Table 3. Cluster 1 had the greatest average for yield per plant (47.74), followed by Cluster II (39.20). Yield per plant (37.06) showed minimum average value for genotypes presented in Cluster III. Number of pods (155.94), plant height at maturity (246.43), number of nodes (83.33) and number of effective pods (135.36) showed greatest averages for Cluster I. In cluster II, the greatest means for plant height at first flower (54.53), number of primary branches (11.17), and weight of 100 grains (19.35) were observed. Cluster 3 had highest values for secondary branches' number (21.23), pod length (6.88) and seed per pod (5.93).

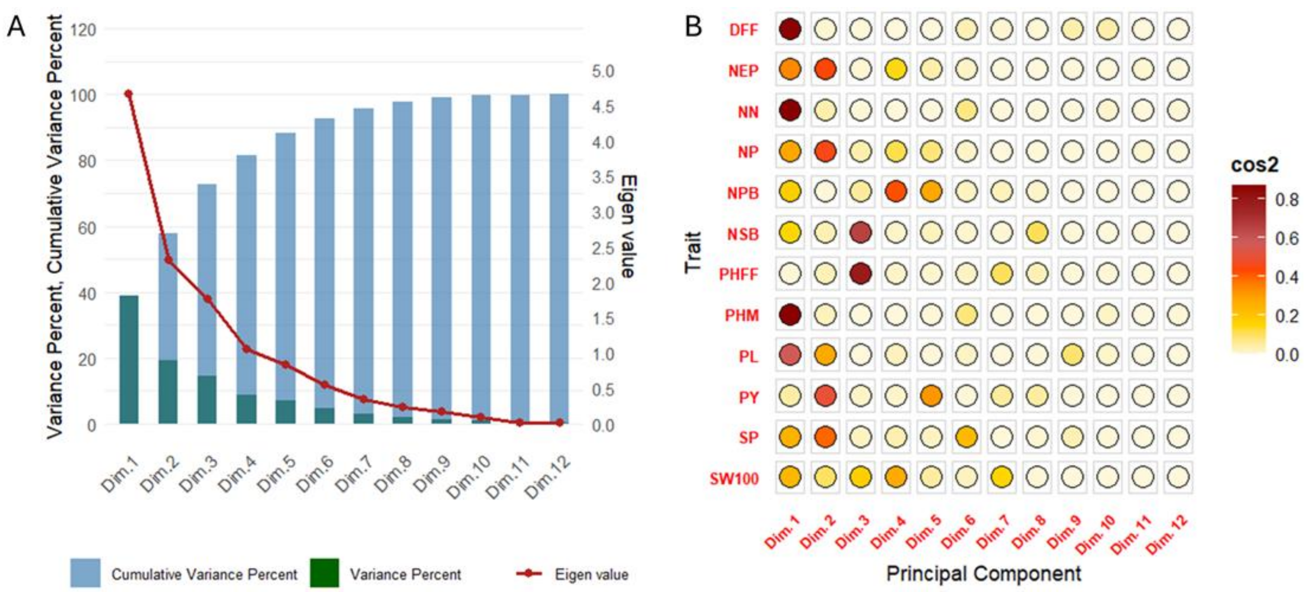

Figure 2. PC analysis of pea genotypes. A) Eigenvectors and total percentage variation among the 12 traits within 25 pea (*Pisum sativum*) genotypes. Dim.1=PC1, Dim.2= PC2, Dim.3=PC3, Dim.4= PC4, Dim.5=PC5, Dim.6=PC6, Dim.7= PC7, Dim.8=PC8, Dim.9= PC9, Dim.10=PC10, Dim.11=PC11, Dim.12=PC12. B) Most contributing traits for each principal component. DFF=Days to first flower, PHFF=Plant height at first flower(cm), NP=Number of pods/plants, NPB=Number of primary branches/plants, NSB=Number of secondary branches/plants, PHM=Plant height at maturity(cm), NN=Number of nodes/plants, NEP=Number of effective pods/plants, PL=Pod length(cm), SP= seeds/pods, SW100=100-Seed weight(g), PY=Yield/plant, Dim.1=PC1, Dim.2= PC2, Dim.3=PC3, Dim.4= PC4, Dim.5=PC5, Dim.6=PC6, Dim.7= PC7, Dim.8=PC8, Dim.9= PC9, Dim.10=PC10, Dim.11=PC11, Dim.12=PC12.

Table 3. Cluster means values for various characters in garden pea genotype.

Cluster	No. of genotypes	DFF	PHFF	NP	NPB	NSB	PHM	NN	NEP	PL	SP	SW100	PY
1	7	96.71	53.36	155.94	9.34	20.39	246.43	83.33	135.36	5.67	4.97	17.69	47.74
2	9	85.18	54.53	76.28	11.17	20.61	195.86	67.79	59.42	5.82	4.75	19.35	39.20
3	9	56.01	52.56	80.26	8.43	21.23	83.04	26.96	63.26	6.88	5.93	14.68	37.06

DFF=Days to first flower, PHFF=Plant height at first flower(cm), NP=Number of pods/plants, NPB=Number of primary branches/plants, NSB=Number of secondary branches/plants, PHM=Plant height at maturity(cm), NN=Number of nodes/plants, NEP=Number of effective pods/plants, PL=Pod length(cm), SP= seeds/pods, SW100=100-Seed weight(g), PY=Yield/plant

DISCUSSION

Estimating the genotypic along with phenotypic components of variance is necessary to determine the relative magnitude of heritable and non-heritable variation. In current study variability analysis demonstrated increased values for characteristics in PCV and GCV like yield, pods number, number of effective pods and other yield related traits, which indicates significant variation (Table 1).

These variations also showed that there were considerable and significant influences of genetics. This highlights the possibility for substantial genetic improvement through selection (Yadav *et al.*, 2025). Conversely, those characteristics which expressed low PCV and GCV, indicating restricted phenotypic and genotypic diversity, which could lead to limited potential for genetic enhancement (Jeberson *et al.*, 2016). The extent of phenotypic coefficients was greater compared to genotypic coefficients for yield attributes studied, indicates how these agronomic traits were expressed in response to environmental factors. Similar patterns of GCV and PCV values were noted by Katoch *et al.* (2016), Thakur *et al.* (2022) and Kumar *et al.* (2023). On the other hand, traits which exhibit lower values for PCV instead of GCV indicate there were strong genetic influence (Bello *et al.*, 2012). In contrast even if it is negligible but, PCV value was observed slightly higher than GCV as shown in Table 1 which demonstrates that there were minimal environmental influences present. Maximum PCV and GCV values were identified for the yield per plant along with the effective pods count, pods count, number of nodes and plant height at maturity which emphasize the capacity for substantial genetic enhancement via selection. Similar observations have been made by Tolessa (2017) and Singh *et al.* (2019).

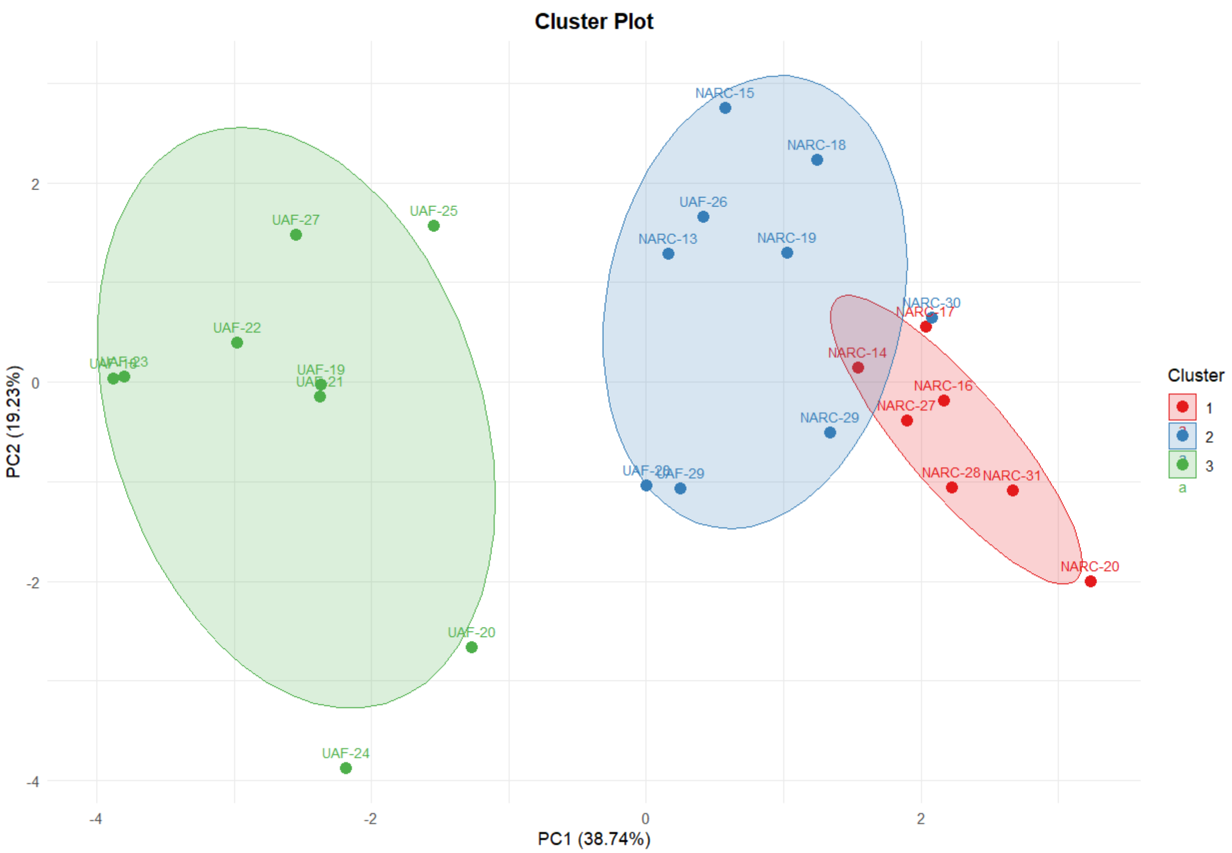

Figure 4. K-means cluster for 25 pea (*Pisum sativum*) genotypes.

But environmental factors cannot be neglected although they are minimal in major yield related traits in current study which have potential to influence the yield related traits in current climate changing scenario. These results highlight how important. It is essential to evaluate both genetic as well as environmental aspects when choosing traits most importantly yield that are affected by the environment (Yadav *et al.*, 2025). Although GCV provides the explanation of variation in polygenic traits, it does not exclusively ascertain the inheritable changes (Magomere *et al.*, 2024).

In the present investigation, most characters expressed high heritability estimates. Yield per plant showed greater heritability next to average pods count, number of effective pods, days to first flower, nodes count, 100 seed weight, pod length, plant height at maturity, number of primary branches and plant height at first flower. Yadav *et al.* (2025) also observed high heritability for pod length, pods count per plant and plant height. The higher heritability for these characters indicates a reduced interaction between genotype and environment, reflecting a stronger genetic contribution to variation and lowered environmental influence (Hamidou *et al.*, 2012; Persaud *et al.*, 2022). This suggests possible stability across diverse pea cultivation regions and highlights several options to select optimal genotypes based on all assessed criteria. The characteristics exhibited a significant level of heredity. This study supports prior findings about garden peas by Bhardwaj *et al.* (2020). The heritability of studied traits suggests not major, but considerable impact on some traits from environmental factors which highlights the necessity of employing genomic methods, such as marker-assisted selection and QTL mapping, to enhance phenotypic selection (Mahadevaiah *et al.*, 2021).

Genetic advance estimation makes it easier to anticipate possible gains that could be made by improving particular traits. Highest GAPM was documented in yield per plant, number of effective pods, number of nodes, plant height at maturity, days to first flower, number of primary branches, 100 seed weight, seed per pod and pod length. These outcomes were also additionally acknowledged by Luthra *et al.* (2020), Bishnoi *et al.* (2021) and Bhatt *et al.* (2024). This suggests that using phenotypic selection techniques to identify favorable traits can easily result in a beneficial increase in pea seed production. Previous studies showed that the extent of genetic gain, heritability, and the genotypic coefficient of variation are all related in the effective enhancement of crop (Vagadiya *et al.*, 2013). It is essential to recognize that, without significant genetic advancements, High heritability does not ensure effective selection in subsequent generations until significant genetic advances does not ensure. For every character studied, it showed a valuable interaction among- elevated heritability and genetic advance, indicating that the population of edible-podded peas are expected to experience remarkable improvements through selective breeding guided by genetic data. This suggests that selection relying on phenotypic aspects is valid since phenotypes consistently represent their genotypes for these qualities. Additionally, qualities demonstrate favorable additive gene activity, rendering them appropriate for breeding programs (Yadav *et al.*, 2024).

PCA is an effective technique for identifying significant features that exert a greater impact on the overall variations. The coefficient of each vector represents the corresponding share of each variable linked with every principal component (Azam *et al.*, 2024). Principal component analysis revealed 12 principal components. Out of these 12 principal components, the initial four Principal conditioned 81.41% of the entire variation present within the studied pea genotypes. PC1 contributed most to the diversity as reported by previous studies in different crops (Ali *et al.*, 2009; Ali *et al.*, 2015; Jabran *et al.*, 2021; Sabar *et al.*, 2021). PC1 captures twice as much variation from traits and genotypes than PC2 as shown in Figure 2. Principal component analysis between PC1 and PC2 were demonstrated the dataset using a two-dimensional biplot. The biplot of PC1 and PC2 exhibited a significant amount of variability coupled with a distribution pattern of genotypes with traits. Days to first flower, plant height at maturity and nodes count showed close and positive association among them. Genotypes close to these traits showed high values for these traits like most of the genotypes from National Agriculture Research Center showed late flowering and exhibited longer heights as compared to genotypes from university of agriculture. These characters also showed positive correlation between pod length and seeds per pod since they are in same quadrant and pointed in same direction (Figure 1). Number of primary branches, 100 seed weight, effective pods count, number of pods, and yield per plant showed close relation to each other. Genotypes present closer to this yield associated attributes can be effective for selection in yield enhancement. Among 12 studied traits, specifically yield and other primarily traits contribute major role in the total variation observed among the examined pea genotypes. In pea varietal development projects, the genotypes present in different quadrants of biplot, might be used for hybridization, especially with regard to yield and yield-related factors. Eigenvectors showed a considerable correlation between factors with similar patterns, highlighting how they work together to enhance the traits under investigation. Nearly all of the variables showed distinguishing and markedly influence to the total variability across the examined garden pea accessions, according to an analysis of the first and second dimensions (PC1, PC2). This demonstrates how these specific characteristics play a critical role in nutrient enrichment and greatly contribute to the variations seen in garden peas. Screening initiatives must thus target these high seed output potential traits in order to improve the genetic quality of edible-podded peas (Yadav *et al.*, 2024). Previous studies on garden peas by Fikreselassie (2012), Ouafi *et al.* (2016) and Parveen *et al.* (2025) also confirmed that yield related attributes including plant height at maturity, number of pods and seed per pods play significant role in variability present in initial principal components.

Based on the cluster plot between first two principal components, 25 genotypes of pea were classified into three distinct clusters. The average value of Cluster I, which contains 7 genotypes, surpassed the overall mean of Cluster II and Cluster III in the total studied population. These results demonstrate that genotypes present in Cluster I exhibit significant performance for yield per plant, number of pods, plant height at maturity number of nodes, and number of effective pods. Higher overall mean values for 7 genotypes and their closeness to each other in Cluster I as compared to 9 genotypes present in each Cluster II and III revealed close resemblance to each other for these important yield related traits. As a result, it can be suggested that the verities present in Cluster I exhibited the highest yield capacity and were more suitable for selection than those in the other clusters as shown in Table 3. The potential of these genotypes can be harnessed for hybridization in programs aimed at varietal enhancement. While genotypes in Cluster II showed only better results for plant height at first flower, primary branches count, and weight of 100 grain. Cluster III showed better performance for number of secondary branches, average length of pods and seed per pods. This study also revealed that many of these genotypes are valuable for multiple traits and can be utilized in this way to shorten the duration of varietal development (Azmat *et al.*, 2011). It was also observed that some clusters gave better results for certain traits parameters (Azam *et al.*, 2024). Cluster analysis is a useful method to categorize pea verities in relation to how well they performed on the observed characteristics, as shown in the continuing study. It is recommended that the most significantly divergence characteristic be given priority after choosing the cluster type to continue with selection and the hybridization pattern (Singh and Tewari, 2015).

CONCLUSION

In current study, significant genetic variation was found between diverse genotypes of pea. This helpful information can lead to initiating the successful breeding program. This variation in pea genotypes can also be used to enhance certain yield and yield related characteristics. This research concluded that the traits like yield per plant, plant height at maturity, number of effective pods and weight of 100 seeds had a high degree contribution towards the genetic diversity which makes them suitable marker for enhance the yield by considering them in future breeding programs. This study employed phenotypic identification of field pea genotypes for commercial productivity. Identification and selection of good performing pea verities can assist in the to develop numerous valuable pure lines for future verities development. In the present study although, most of the genotypes from NARC mature late but performed better like NARC-20, NARC-31, NARC-16. Among UAF genotypes only UAF-29 and UAF-27 showed better results. Overall, these well performed genotypes can facilitate the selection of garden pea germplasm for the purpose of creating genetic markers, population mapping for the purpose of molecular breeding, and quantitative trait locus discovery for the purpose of improving growth and yield.

AUTHOR CONTRIBUTIONS

Muhammad Shoaib: Writing – original draft, Writing – review & data analysis, formal analysis. Mudassar Iqbal and Muhammad Rizwan Shafiq: Validation, Writing – review & editing. Amir Shakeel: Conceptualization, Supervision, Resources, Validation.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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