TRENDS IN ANIMAL AND PLANT SCIENCES
https://doi.org/10.62324/TAPS/2024.021
www.trendsaps.com; editor@trendsaps.com

RESEARCH ARTICLE

Multivariate Analysis for Evaluation of Morphological Diversity in *Pisum sativum L.*

Muhammad Hamza[1], Umair Hamza[2], Nadia Shaheen[3], and Hafiza Mubeen Hayat[3]

[1]Ondokuz Mayıs Üniversitesi, Turkey
[2]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan
[3]Department of Horticulture, College of Agriculture, University of Sargodha-40100, Punjab, Pakistan
***Corresponding author: muhammadhamza293742@gmail.com**

Article History: 24-19 Received: 08-Dec-2023 Revised: 20-Jan-2024 Accepted: 23-Jan-2024

ABSTRACT

Pea (*Pisum sativum* L.) is the second most economically essential winter legume in Pakistan. Yield potential of this crop is low in Pakistan in contrary to other countries and little genetic diversity in the germplasm is the reason for it. This research was planned to determine the genetic diversity in pea genotypes. Twenty pea accessions collected from NARC and AARI were sown following the RCBD design in October, 2022 at the Department of Plant Breeding and Genetic. Data were collected for days to 50% flowering, pod length (cm), pod width (cm), yield per plant (g), plant height (cm), number of seeds per pod, hundred seeds weight (g), seed diameter (mm) and number of pods per plant. For estimating genetic diversity, LSD, and principal component analysis were employed. Significant variation was exhibited by all the studied genotypes. It was concluded by principal component analysis that first five PCs contributed 73.641 % in total variation and the leftover 26.359% was provided by other components. Through this study it is viewed that a great range of genetic diversity is present in assembled accessions which may be used in the breeding of high yielding pea cultivars.

Key words: Genetic variability, multivariate analysis, crop breeding.

INTRODUCTION

Pea *(Pisum sativum* L.) belongs to the family Leguminosae having the basic set of 2n=14 chromosomes. Pea is well-known green vegetable with significant importance in agriculture. It encloses amount of anti-oxidants and fibres. In pulses after common bean, pea is second important crop (Tran et al., 2023). It is an essential food and feed legume grown particularly from Asia to Europe and North America and across many temperate regions globally. Pea is extensively used as commercial protein because of its high availability, low price and sufficient production (Türkoğlu et al., 2023). It has different functional properties particular water and oil-holding capacities, foaming, solubility, gelling and emulsifying, and various health amenities viz antihypertensive, modulating intestinal bacteria activities and antioxidant are occupied by pea protein and its hydrolysates (Jiao, 2020). In some temperate and semi-tropical region, it is commonly grown for commercial purposes.

The main obstacles for pea breeders are to create high-yielding cultivars with other improved traits such as adequate photosynthesis, early maturing types, protein content, ratios of essential amino acids, assemblage of organic matter during the early growth phases and to develop resistance against diseases and resilient to changing climatic conditions (Zafar et al., 2020). For prolong selection gain, advanced understanding of genetic similarity and genetic diversity could help. The correlation between fitness and genetic variability should be assessed in order to develop predictions about the importance of genetic diversity for a certain population. Population history, mating system, level of environmental homogeneity and evolutionary history are the key points in determining the population's degree of genetic diversity (Zafar et al., 2021; Zafar et al., 2022; Zafar et al., 2023).

Examining the genetic variability of pea in various environmental conditions is favourable to identify pea genetic resources and that would be impactful to pea

Cite This Article as: Hamza M, Shaheen N, Hamza U and Hayat HM, 2024. Multivariate analysis for evaluation of morphological diversity in *Pisum sativum* L.. Trends in Animal and Plant Sciences 3: 1-9. https://doi.org/10.62324/TAPS/2024.021

breeding and productivity (Zhao et al., 2020). Pea has a great potential for hereditary performance but its average yield is unsatisfactory due to decrease in production, which can be restored through inter-crossing among genetically distinctive genotypes. As a result, it became necessary to identify genetically distinct lines of descent. (Lal et al., 2018).

Different methods are now available for analysing the genetic diversity of breeding lines, populations, and germplasm accessions. These methods depend on biochemical data, pedigree information, agronomic performance, morphology, and genetic data. The greatest contribution to genetic divergence was demonstrated by height of plant following days to maturity in peas through path analysis (Singh et al., 2017). Pea gene pools from the Near East, the United Kingdom, and Central Europe showed a significant range of genetic variation for seed size and protein content across native cultivars (Annicchiarico et al., 2017). Peas are adapted to a wide range of temperatures and elevations; therefore, their genetic makeup is extremely diverse. The objective of the current study is to access genetic variability based on morphological traits.

MATERIALS AND METHODS

Experimental Conditions

The current study was conducted during 2022-2023 in research area at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The city is located 186 meter above sea level and 73.08-degree on east and 31.42-degree north longitude and latitude respectively. It falls under arid climatic zone with higher rate of evapotranspiration. It also encompassed flat plains of east and northern Punjab. The experimental material comprised twenty peas (*Pisum sativum* L.) genotypes. Seeds of experimented accessions were sown in 2 replication following randomized complete block design (RCBD). Sowing was done with a plant-to-plant distance of 10 cm and a row-to-row distance of 30 cm. Proper agronomic practices were used for reasonable growth. Four germinated plant from each replication were tagged for data for the following morphological characters.

Data Collection

Data days to 50% flowering was collected by counting days from crop sown to a stage when 50% of the plants started to produced flower in both replications. At full pod development stage, average length of the fruiting pod from first reproductive node of four different plants was taken in centimetre (cm) from each replication. At full pod grown stage, average width of four different pods was recorded in centimetres for both replications. Numbers of seeds were counted from four largest pods and average was obtained. At maturity, with the help of a meter rod the height was measured from ground to tip of selected plant in centimetres. Reading was taken as average for every genotype. Numbers of pods were counted from four different plant in each replication and average was obtained. At full seed maturity stage, average diameter of four seed was recorded in millimetre from both replications. In grams the weight of hundred seeds were calculated when moisture in the seed reached to a level of 12% or less after sun drying and it was measured by employing electronic balance. The overall yield of the selected plant from each replication was measured by employing electronic balance. At maturity, with the help of a weighing balance the yield per plant was recorded of selected plant in grams. Reading was taken as average for every genotype.

Statistical Analysis

The LSD test proposed by Ronald Fisher was used to check out the level of significance with the help of Statistics 8.1. Data collected from the experiment was analysed through Principal Component Analysis (PCA). Principal Component Analysis (PCA) was used to find the interaction effect among the genotypes. It was performed by using R-software and a Bi-plot was obtained as a result.

RESULTS AND DISCUSSION

The significance variation among 20 pea genotypes were observed for all the character under study. The pairwise comparisons LSD test was employed to assess divergence among genotypes based on mean values. Sharma et al., (2003) determined that genetic diversity is necessary for crop improvement and the degree of variability available for a given character determines how far genetic improvement of that character may exhibit.

Plant Height (cm)

There were significant differences among genotype for plant height. Plants ranged in height from 24.45 cm to 64.87 cm, displaying a wide range of diversity. Maximum height of plant was obtained by genotype PGRI-32 that showed highest plant height 64.87 cm, followed by PGRI-37 and PGRI-31 having plant height 58.78 cm and 56.37 cm. On the other-hand lowest plant height 23.61 cm was showed by genotype F16 (Fig. 1) respectively. Genetic variations were observed in pea germplasm related to plant height ad reported by Hussain et al., (2015).

Days to 50% Flowering

The genotypes had non-significant variations for days to 50%. The genotype Chalan taken 85 days to produce maximum flower for days to 50% flowering, followed by genotypes Soffton and PGRI-06 showed 82.5 and 81.5 days to 50% blooming respectively (Fig. 2). The range for the number of days to 50% blooming varied from 70.5 to 83. These findings showed similarity with the results of Khan et al., (2013).

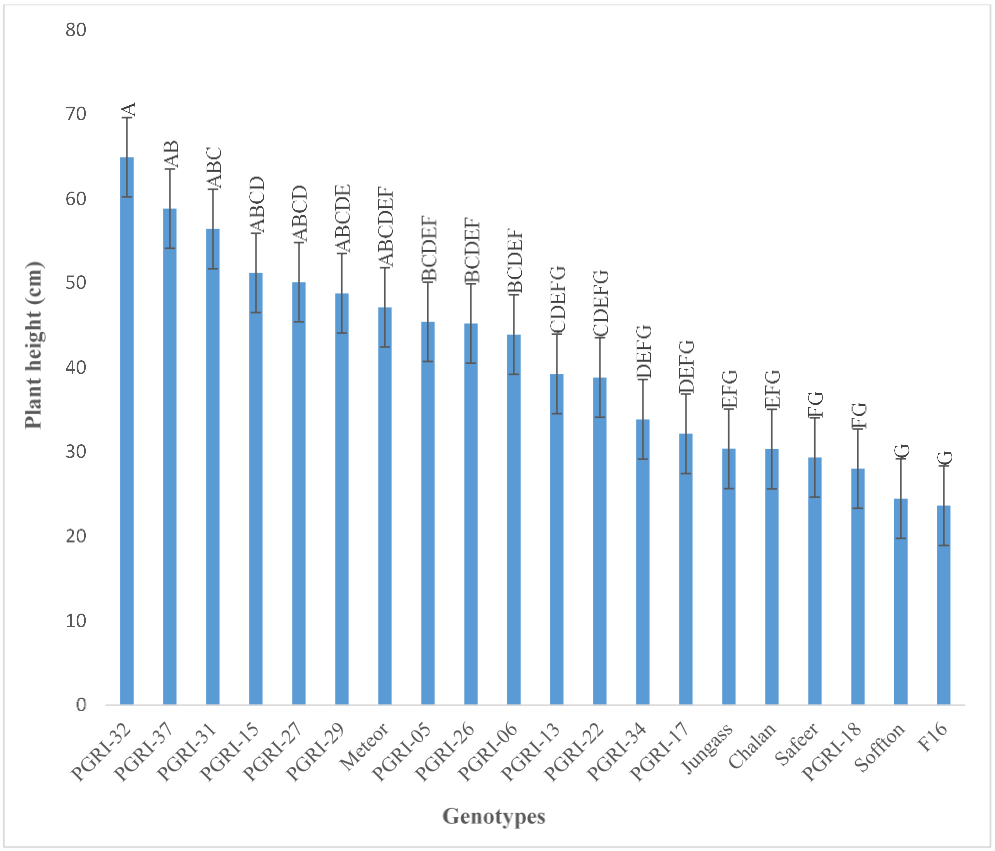

Fig. 1: Mean performance of Pea genotypes for plant height (cm)

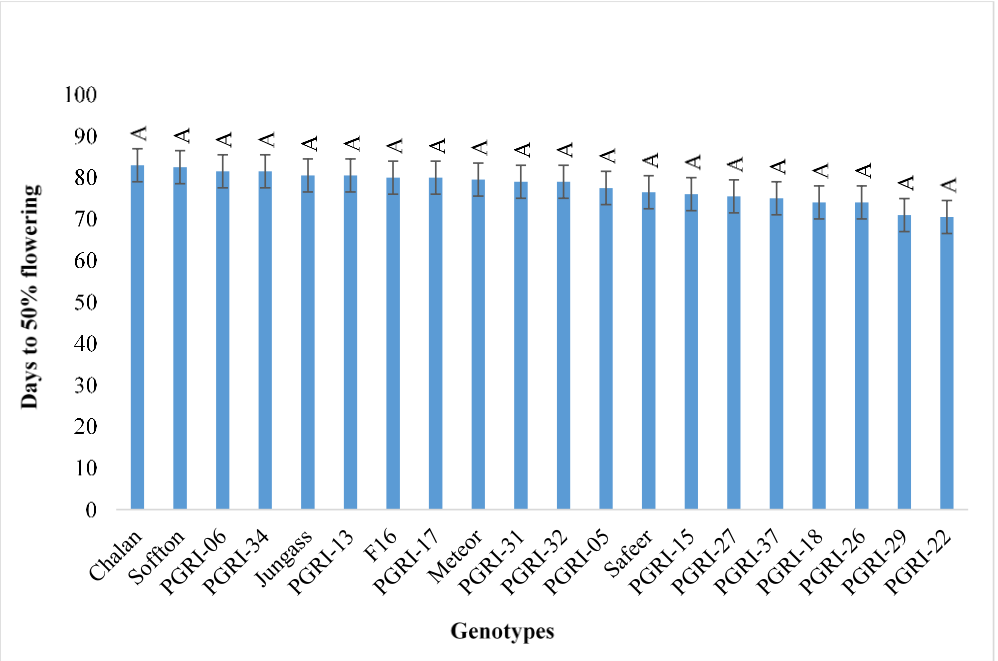

Fig. 2: Mean performance of Pea genotypes for days to 50% flowering

Pod Length (cm)

All the genotypes showed significant variations in pod length. Genotypes Chalan, Safeer and Soffton got highest pod length 8.15 cm, 7.22 cm and 6.52 cm respectively. Meanwhile genotype PGRI-06 showed lowest pod length 5 cm followed by PGRI-22 and Jungass with 5.18 cm and 5.47 cm respectively (Fig. 3). The range for pod length was extended form 5 cm to 8.15 cm. Genotypic differences for the pod length in pea germplasm have also been reported by Khan et al., (2013) and Saxesena et al., (2014).

Pod Width (mm)

Significant variability for pod width was present within the genotypes at 5% probability level. Genotype Safeer attained maximum pod width 1.11 mm followed by the genotypes PGRI-22 and PGRI-31 with 1.10 mm and 1.09 mm. While genotype Jungass attained minimum pod width 0.64 mm followed by Soffton and PGRI-29 with 0.68 mm and 0.793 mm pod width (Fig. 4). Pod width varied from 0.64 mm to 1.11 mm. The results of this study accorded with the research results of Ali et al., (2007) and Umar et al., (2014).

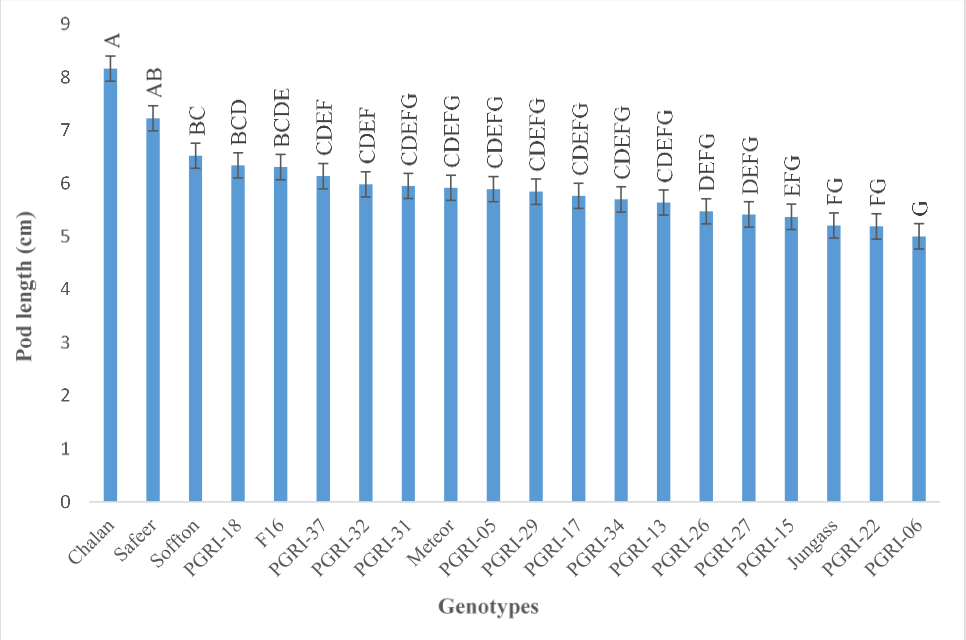

Fig. 3: Mean performance of Pea genotypes for pod length (cm)

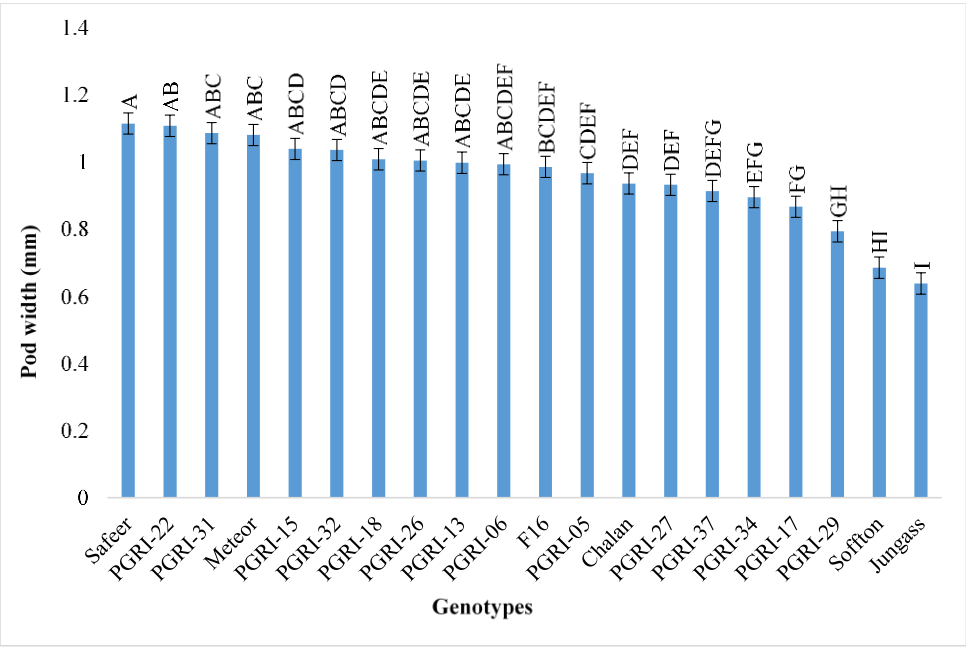

Fig. 4: Mean performance of Pea genotypes for pod width (mm)

Hundred Seeds Weight (g)

When assessed genotypes for hundred seed weight at 5% probability level, the significant differences were found. Maximum hundred seed weight was 38.37 grams attained by genotype PGRI-32 and next in order genotypes were PGRI-05 and PGRI-37 which showing 36.75 grams and 36.56 grams respectively. The lowest seed weight was obtained by genotypes PGRI-17, PGRI-34 and PGRI-06 which was 16.75 grams, 17.18 grams and 17.5 grams respectively. The range for this trait varied from 16.75 to 38.37 grams (Fig. 5). Genotypic differences for hundred seeds weight in pea germplasm were also obtained by Khan et al., (2013) and Ali et al., (2007).

Number of Seeds Per Pod

A significant variation in the number of seeds per pod among the pea genotypes. Maximum number of seeds per pod 6.08 was produced by genotype PGRI-29, whereas lowest magnitude of trait under study was exhibited by the genotypes PGRI-22, Jungass and PGRI-27 were produced 2.45, 2.83 and 3.16 with lowest number of seeds per pod respectively. Number of seeds per pod displayed range from 2.45 to 6.08 (Fig. 6). Environmental variation at the time of fertilization may be cause for low number of seeds. Genotypic differences for seeds per pod have been observed by Nawab et al., (2008) and Ali et al., (2007).

Seed Diameter (mm)

The highly significant difference is present among genotypes for seed diameter. The range of variability for by seed diameter was 0.65 mm to 0.85 mm. Maximum seed diameter was 0.85 mm obtained by genotype PGRI-32 followed by genotypes PGRI-37 and PGRI-05 which was 0.82 mm and 0.80 mm respectively.

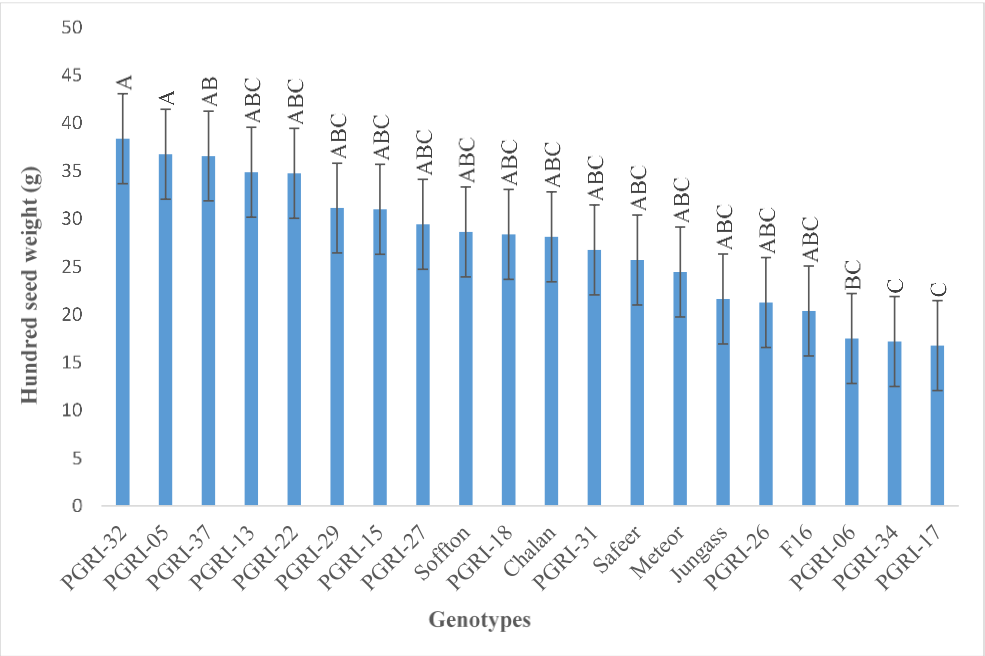

Fig. 5: Mean performance of Pea genotypes for hundred seed weight (g)

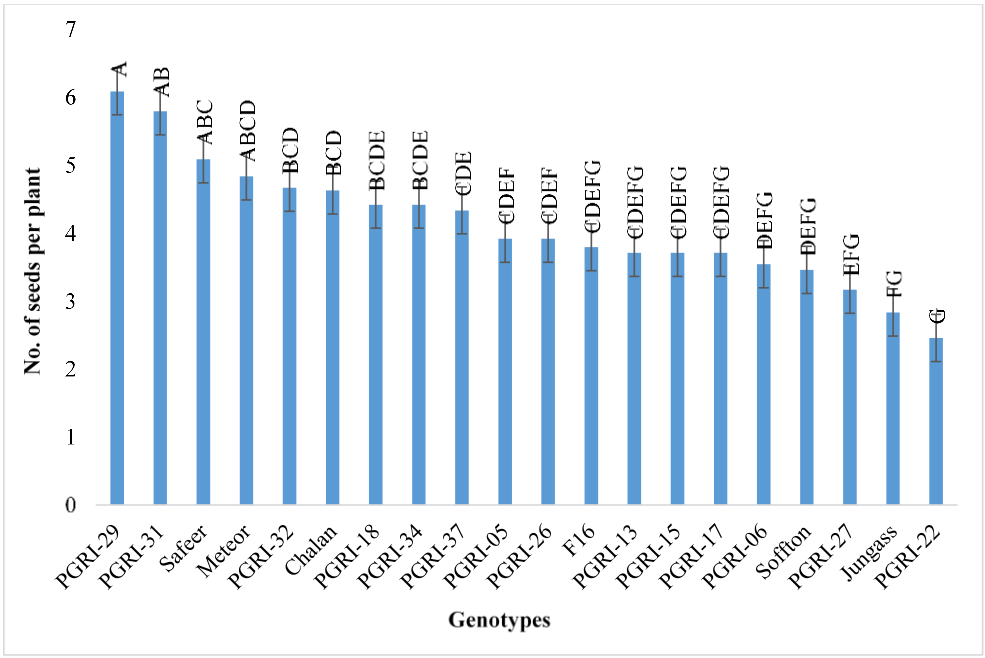

Fig. 6: Mean performance of Pea genotypes for number of seeds per pod

On the other-hand lowest seed diameter was 0.62 mm showed by genotype PGRI-17 (Fig. 7). Genotypic difference for seed diameter in pea germplasm were reported by Hussain et al., (2015).

Yield Per Plant (g)

Significant variations were observed between the genotypes for yield per plant. Maximum yield per plant were 31.75 gram showed by genotype Chalan, while minimum yield per plant 4.62 gram observed by genotype F-16 (Fig. 8). Genotypic difference for yield per plant in pea germplasm were reputed by Hussain et al., (2015).

Number of Pods Per Plant

The highly significant difference is present between genotypes for number of pods per plant. Wide range of variability was exhibited by number of pods per plant from 4.25 to 28.87 (Fig. 9). Maximum number of pods 28.87 were produced by genotype PGRI-29, followed by genotype PGRI-31that was 26.37. The lowest number of pods per plant 4.25 was showed by genotype F-16 (Fig. 9). Genotypic difference for number of pods in pea germplasm have been observed by Hussain et al., (2015).

Principle Component Analysis

With the help of XLSTAT software, principle component analysis was performed on mean data. From 9 principle components (PCs), more than 1 eigen value was exhibited by first five PCs. Between pea genotypes which were analysed for genetic diversity, first 4 PCs contributed 81.86% in total variation amongst the pea genotypes determined for different

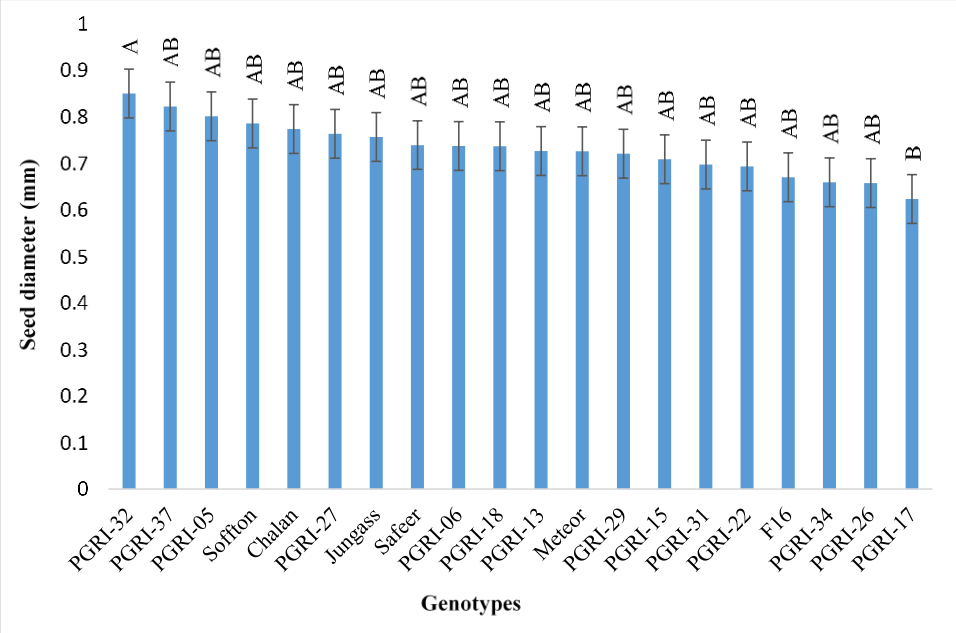

Fig. 7: Mean performance of Pea genotypes for seed diameter (mm)

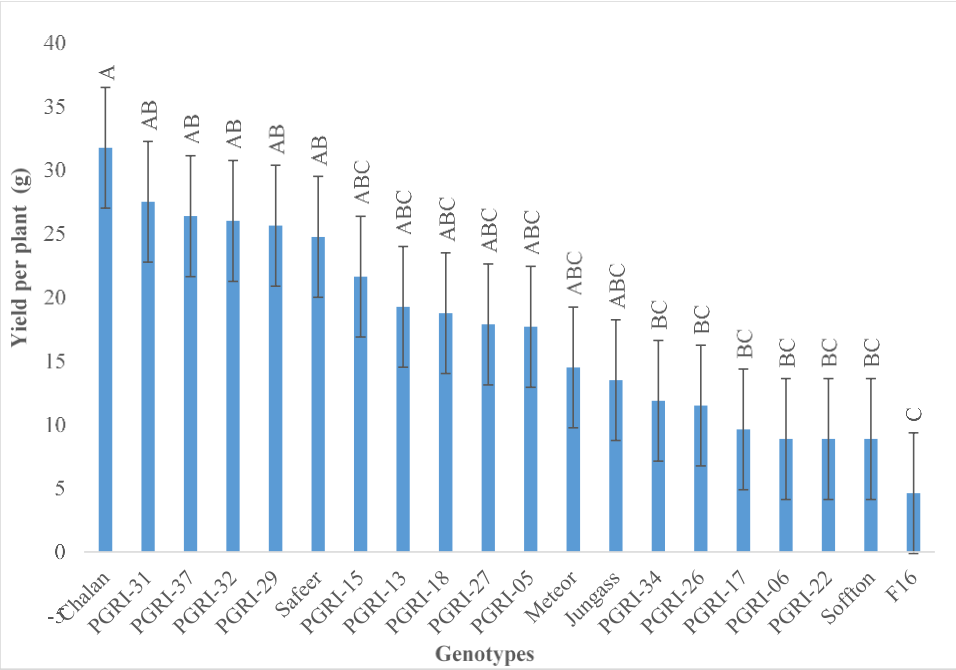

Fig. 8: Mean performance of Pea genotypes for yield per plant (g)

Table 1: Principal component analysis for 9 characters in 20 pea genotypes:

Principal Components	Eigen Value	% of Variance	Total Cumulative Variance %
PC 1	3.26	36.28	36.28
PC 2	1.56	17.38	53.66
PC 3	1.45	16.07	69.74
PC 4	1.09	12.12	81.86
PC 5	1.02	11.33	93.18

morphological traits (Table 1). Maximum variability contributed by PC 1 (36.28%) while followed by PC II (17.38), PC III (16.07) and PC IV (12.12) respectively. High participation of first 4 components in total variability relation to various plant characteristics has earlier been studied by Zafar et al., (2021).

Number of pods per plant, seed diameter, hundred seed weight, yield per plant and pod length were morphological traits contributing (36.28%) to variation in first principal component and all these traits were performed positively. Positive effects in first principal component were displayed by no. of seeds per pod, yield per plant, pod length, hundred seed weight and seed diameter (Table 2).

Table: 2: Total variances of principle components for 9 characters in 20 pea genotypes:

Variables	PC 1	PC 2	PC 3
PH	16.30	5.29	5.54
NPPP	15.34	5.81	3.98
SD	0.82	11.02	9.75
PW	0.0004	8.71	0.97
NSPP	13.91	3.27	0.001
HSW	5.88	0.04	8.77
YPP	4.63	1.18	2.06
PL	11.17	19.13	1.15
DFF	8.53	23.55	7.00

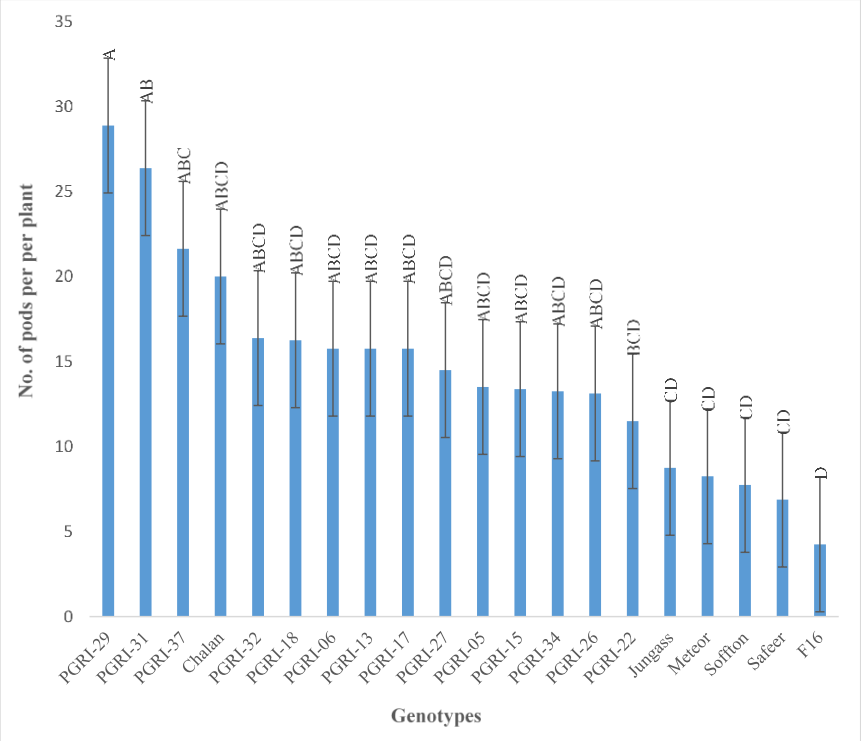

Fig. 9: Mean performance of Pea genotypes for number of pods per plant

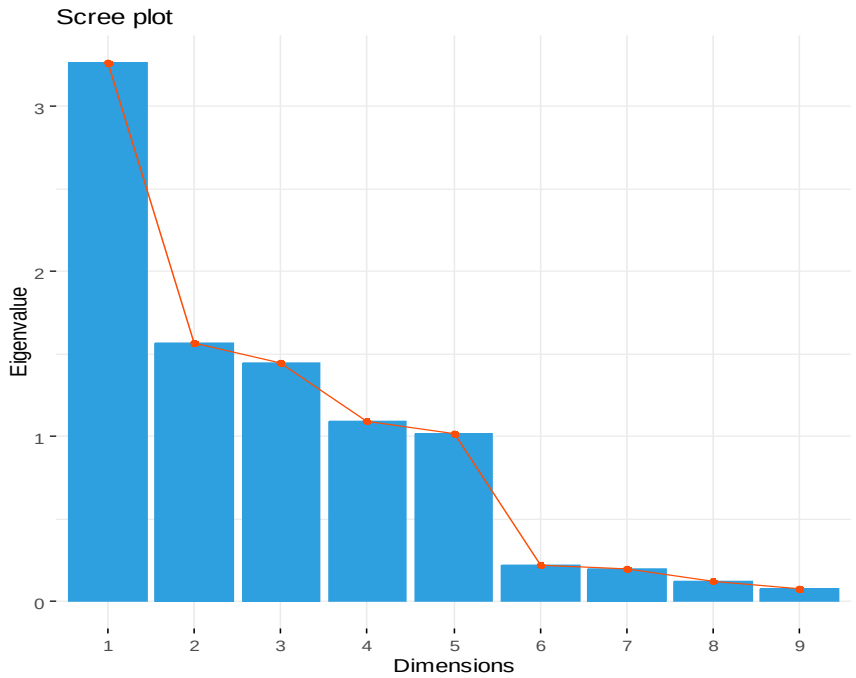

Fig. 10: Scree-plot between eigenvalue and principal components for various pea genotypes

In second principle component days to 50% blooming, no. of seeds per pod and height of plant supplied 17.38% variation among pea genotypes. Positive effects were noticed days to 50% blooming, no. of seeds per pod and height of plant in PC-II (Table 2). A total of 16.07% variation was contributed by pod width in third principle component. PC-III revealed positive effects for pod width (Table 2).

Scree Plot

By depicting a graph between principal component numbers along the x-axis and eigenvalue on the y-axis, percentage variance correlated with every principal component was explained by scree plot (Fig. 10). PC-I exhibited 36.28% variation having eigen value 3.26 in pea germplasm. It was noticeable from the scree plot that variation was diminished from PC-VI to PC-VIII and maximum variability was gained from PC-I to PC-V. By examining the graph, it was clear that PC-I acquired highest variation. So, accession selection from this principal component was significant for various traits (Fig. 11).

Variable plot of accession indicates arrows on the biplot which is known to be eigen vector (Fig. 11). The maximum eigen vector length showed by the yield variable and lesser by days to 50% flowering. The variable plot also exhibits the correlation between the variables.

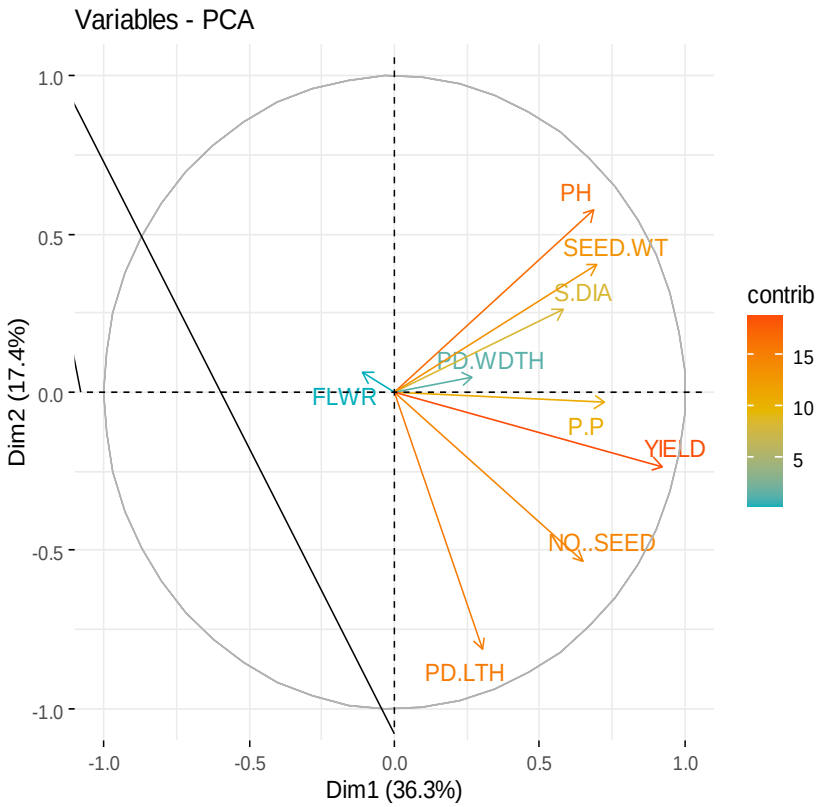

Fig. 11: Principal component variable vector graph for various pea genotype

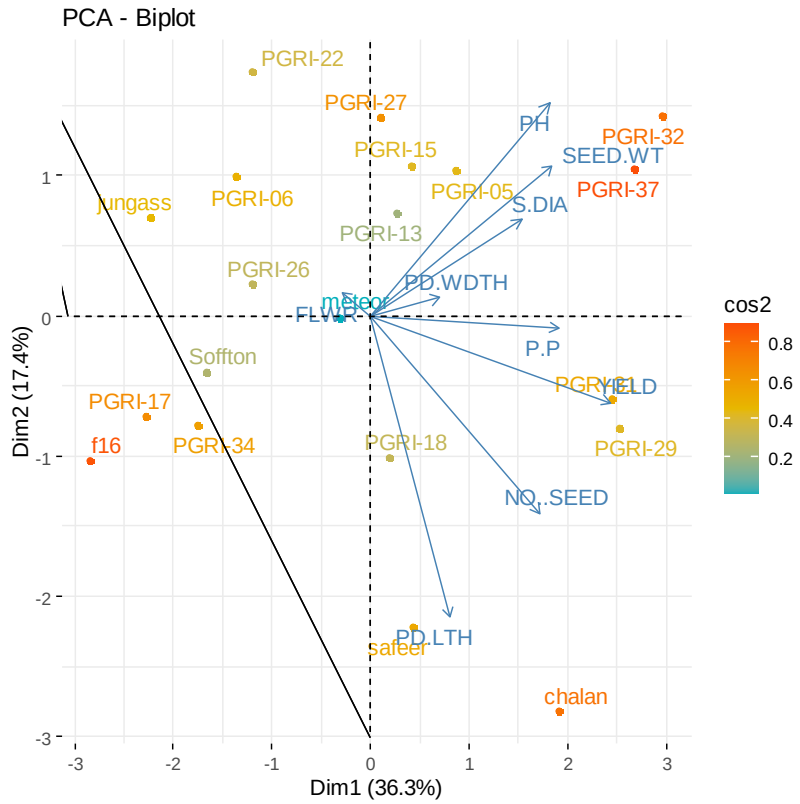

Fig. 12: Principal component biplot for various pea genotypes

Biplot

The closeness of the eigen vector depict that there is strong positive correlation among the variables. The maximum strong positive correlation was exhibited between the hundred seed weight and seed diameter variables. The strong negative correlation was seen between the height of plant and pod length. If the angle between the two variable is less than ninety degrees, there will be positive correlation between these variables and if less than ninety degrees then there will be negative correlation between the two variables. At the ninety-degree angle between the two variables it will indicate that there will be no correlation. All the variable for the pea genotypes contributed to the variability because all the variables had the angle below ninety degree (Fig. 12).

Scatter plot of accessions in the biplot indicates that those genotypes which are minute distant from each other are considered as alike or less variant and more scattered genotypes which are considerable apart from each other are recognized as diverse genotypes when analysed in relation with 9 variables. Five genotypes i.e., PGRI-22, Chalan, F16, Safeer and PGRI-29 as displayed by graph were very dissimilar and showed higher diversity as compared to all the remaining genotypes which were seen more alike with respect to PC-I and PC-II (Fig. 12).

The scatter plot in the biplot also reveals which pea genotypes contributed the maximum and minimum variability to principle component 1 (along the x-axis) and principle component 2 (along the y-axis), respectively. For principal component 1, the genotypes PGRI-32 and PGRI-37 were chosen because they had the highest positive values, whereas F16 and PGRI-17 had the highest negative values. For principal component 2, the genotypes PGRI-22 and PGRI-27 were chosen because they had the highest positive values, whereas Safeer and Chalan had the highest negative values.

Conclusion

Significant variation was exhibited by all the studied genotypes. It was concluded by principal component analysis that first five PCs contributed 73.641 % in total variation and the leftover 26.359% was provided by other components. Through this study it is viewed that a great range of genetic diversity is present in assembled accessions which may be used in the breeding of high yielding pea cultivars.

REFERENCES

Ali, Z., Qureshi, A.S., Ali, W., Gulzar, H., Nisar, M., and Ghafoor, A. (2007). Evaluation of genetic diversity present in pea (*Pisum sativum L.*) germplasm based on morphological traits, resistance to powdery mildew and molecular characteristics. *Pakistan Journal Botony*, 39(7): 2739-2747.

Annicchiarico, P., Nazzicari, N., Wei, Y., Pecetti, L., and Brummer, E.C. (2017). Genotyping-by-sequencing and its exploitation for forage and cool-season grain legume breeding. *Front. Plant Scince,* 8: 679.

Hussain, B., Khan, A.S., and Ali, Z. (2015). Genetic variation in wheat germplasm for salinity tolerance at seedling stage: improved statistical inference. *Turk Journal Agriculture For,* 39(2):182-192.

Jiao, A., Yang, Y., Li, Y., Chen, Y., Xu, X., and Jin, Z. (2020). Structural properties of rice flour as affected by the addition of pea starch and its effects on textural properties of extruded rice noodles. *International Journal Food Prop*, 23(1): 809-819.

Khan, T.N., Ramzan, A., Jillani, G., and Mehmood, T. (2013). Morphological performance of peas (*Pisum sativum*) genotypes under rainfed conditions of Potowar region. *Journal Agriculture Research,* 51(1): 51-60.

Lal, L., Kumar, R., Singh, V., Chaudhary, A.K., Yadav, H., and Kumar, A. (2018). Evaluation of genetic divergence for grain yield and its contributing traits in field pea (*Pisum sativum L. var. arvense*). *International Journal Current Microbiology Applied Science,* 7(6): 1821-1826.

Nawab, N.N., Subhani, G.M., Mahmood, K., Shakil, Q., and Saeed, A., (2008). Genetic variability, correlation and path analysis studies in garden pea (*Pisum sativum L.*). *Journal Agriculture Research,* 46(4): 333-340.

Saxesena, R.R., Vidyakar, V., Vishwakarma, M.K., Yadav, P.S., Meena, M.L., and Lal, G.M. (2014). Genetic variability and heritability analysis for some quantitative traits in field pea (*Pisum sativum L.*). *The Bioscan,* 9(2): 895-898.

Sharma, A.K., Singh, S.P., and Sharma, M.K. (2003). Genetic variability, heritability and character association in pea (*Pisum sativum L.*). *Crop Res. Hisar, India,* 26(1):35-139.

Singh, S.K., Mazeed, A., Singh, V.P., Srivastava, S., Dwivedi, A.K., Yadav, S.K., and Srivastava, R.K. (2017). Evaluation of Seed Yield and Genetic Divergence in the Germplasms of *Pisum sativum L. var. arvense*. *Journal Pharmacognosy and Phytochemistry*, 6(6S), 1016-1021.

Tran, C. T., Beissinger, T. M., Becker, H. C., and Horneburg, B. (2023). Genetic diversity of pea (Pisum sativum L.) genotypes differing in leaf type using SNP markers. *Genetic Resources and Crop Evolution*, *70*(4), 1085-1095.

Türkoğlu, A., Bolouri, P., Haliloğlu, K., Eren, B., Demirel, F., Işık, M. İ., and Niedbała, G. (2023). Modeling callus induction and regeneration in hypocotyl explant of fodder pea (Pisum sativum var. arvense L.) using machine learning algorithm method. *Agronomy*, *13*(11), 2835.

Umar, H.M.I., Ur-Rehman, S., Bilal, M., Atif, S., Naqvi, H., Manzoor, S.A., Ghafoor, A., Khalid, M., Iqbal, M.T., Qayyoum, A., and Ahmad, F., 2014. Evaluation of genetic diversity in pea (*Pisum sativum*) based on morpho-agronomic characteristics for yield and yield associated traits. *JBES*, 4(5):321-328.

Zafar, M. M., Razzaq, A., Farooq, M. A., Rehman, A., Firdous, H., Shakeel, A., and Ren, M. (2020). Insect resistance management in Bacillus thuringiensis cotton by MGPS (multiple genes pyramiding and silencing). *Journal of Cotton Research*, *3*(1), 1-13.

Zafar, M. M., Manan, A., Razzaq, A., Zulfqar, M., Saeed, A., Kashif, M., and Ren, M. (2021). Exploiting agronomic and biochemical traits to develop heat resilient cotton cultivars under climate change scenarios. *Agronomy*, *11*(9), 1885.

Zafar, M. M., Razzaq, A., Farooq, M. A., Rehman, A., Firdous, H., Shakeel, A., and Youlu, Y. (2022). Genetic variation studies of ionic and within boll yield components in cotton (Gossypium Hirsutum L.) Under salt stress. *Journal of Natural Fibers*, *19*(8), 3063-3082.

Zafar, M. M., Chattha, W. S., Khan, A. I., Zafar, S., Subhan, M., Saleem, H., and Xuefei, J. (2023). Drought and heat stress on cotton genotypes suggested agro-physiological and biochemical features for climate resilience. *Frontiers in Plant Science*, *14*.

Zhao, T., Su, W., Qin, Y., Wang, L., and Kang, Y., 2020. Phenotypic diversity of pea (*Pisum sativum* L.) varieties and the polyphenols, flavonoids, and antioxidant activity of their seeds. *Journal Ciencia Rural*, 50(5): 1678-4596.