**"Experimental Analysis of Genetic Divergence in Garden Pea (*Pisum sativum* L. var. hortense)”**

**ABSTRACT**

Research work on genetic divergence, analysis was estimated in 25 genotypes of Garden Pea (*Pisum sativum* L. var. hortense). During rabi season of the year 2023-2024 at Horticulture Research Farm No.1, Babasaheb Bhimrao Ambedkar University, Lucknow. The main objective of this study was to characterize morphological differences and yield related traits among 25 pea accessions. The estimation of genetic diversity among tested genotypes was highly significant, which got grouped into 5 clusters with cluster V comprising maximum genotypes. Maximum intra-cluster distance (3.401) was observed in cluster II followed by cluster I (3.249), cluster V (3.170), cluster III (2.988) and cluster IV (1.538). Similarly maximum inter cluster distance was recorded between the cluster IV and I (7.897) followed by cluster V and IV (5.844) followed by cluster IV and III (5.686), cluster IV and II (5.656) respectively. Although maximum cluster means for seed yield traits was recorded for cluster IV and II respectively, suggesting a wider range of diversity for most of the economic traits that would enable breeder to identify the genotypes with suitable traits to be used in direct selection and also in improvement programmed for broadening the genetic base. 25 accession showed distinguished variation in the dendrogram for all the studied parameters.

**Keywords:** *Randomized Block Design, divergence analysis, genotypes, pea.*

**INTRODUCTION**

Matar, or (*Pisum sativum L*. var. hortense), is a common name for garden peas. With diploid chromosome number 2n=14, it is a self-pollinating crop that is a member of the Fabaceae family. Grown all throughout the world during the cool season, it is a significant legume vegetable (Taran *et al.*, 2005). One of the earliest domestic crops in the globe is the pea (Ambrose, 1995). The Near East and Ethiopia are the secondary centers of diversity, with the Mediterranean region serving as the principal center (Blixt, 1974). It is limited to lower elevations in the tropics and the subtropics throughout the winter, with the most cultivation occurring in temperate zones.

One wild species that is thought to have been the ancestor of *Pisum sativum* is *Pisum elatium*. There are two subspecies: *Pisum sativum*, the white-flowered horticultural or garden pea often known as sweet pea, and *Pisum arvense*, the colourful-flowering field pea. The garden pea is an annual herbaceous plant that grows in bushy or ascending ways. It has hollow, angular or roundish stems that are covered in waxy blooms. The leaves are made up of many pairs of opposite leaflets that are borne on petioles along with multiple pairs of tendrils; the inflorescence is a raceme-type structure. The blooms are both hermaphrodite and zygomorphic. The fruit is a pod with multiple seeds within that is flat when young but subsequently becomes round or almost circular and splits along the sides. The seeds could have wrinkles, dents, or be round. According to Gautam *et al.* (2019), seeds can have mottling and range in hue from creamy white to brown. Pea cultivars are categorized as bush, medium, and tall varieties based on plant height; as well as early, mid, and late season types based on pod maturity and seed morphology (smooth and wrinkled). The early group genotypes are dwarf/bush kinds that can typically be harvested twice or three times during a 60–70 day growing season Archi *et al.* (2017). The genotypes in the mid group are medium varieties that take 90 days to mature, and three harvests are typically possible. Tall genotypes in the late group can be harvested four or five times throughout a 120-day period and tall with 4 to 5 feet height need staking (Mohan *et al.,* 2013).

Even though pea is believed to be an essential component of major crops, the genetic resources of these indigenous underutilized species are in danger of being rapidly destroyed due to the degradation of traditional agricultural practices, changes in traditional eating patterns, and the introduction and adaptation of high yielding crops. In actuality, there is pea germplasm available in gene banks. One of the main reasons for concern is that pea accessions, or land races, are affected by climate change or dwindling arable land. Therefore, it is essential to describe, document, and develop strategies to prevent the extinction of the unique resources of local pea species (Yadav *et al.* 2021).

The process by which two or more populations of an inherited species accumulate unique genetic alterations (mutations) over time, usually after the population has been temporarily isolated from one another in terms of reproduction, is known as genetic divergence. Programmed assessment of genetic divergence in pea germplasm is crucial for long-term crop improvement. It goes without saying that determining genetic diversity is crucial for both parent selection in breeding and germplasm conservation. An organism's biological variations result from a combination of environmental, phenotypic, and genotypic factors. Among which, the genotypic variation which includes both non-heritable (dominance and epistatic components) and heritable (additive) components is crucial from the perspective of crop improvement. The current study, has been designed with the aim of estimating the genetic divergence (D2) among the genotypes for different features, taking into consideration all of the aforementioned data (Mahalanobis,1928).

**MATERIAL AND METHODS**

The field experiment was carried out at the Horticulture Research Farm-1, Department of Horticulture, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya-Vihar Rae Bareli Road, Lucknow-226025 (U.P), during Ravi season of 2023-24 from the November to march. Geographically it is situated 26º50 North latitude and 80º52 East longitude and an altitude of 111 meters above the mean sea level (MSL). The topography of the experimental field is plain. This region lies under 5th Agro climate zone of Uttar Pradesh.

**Experimental Details**

The experimental material for the present investigation comprised 25 genotypes of garden pea collected from ICAR-Indian Institute of Vegetable Research Varanasi, Uttar Pradesh and experiment was carried out and maintained at the Horticulture Research Farm-1, Department of Horticulture, School of Agricultural Sciences and Technology, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya-Vihar, Rae Bareli Road, Lucknow (U.P.). The 25 genotypes of garden pea used in the experiment

The experiment was conducted in Randomized Block Design with three replications during Rabi season in 2023-24 to assess the performance of 25 genotypes. Each treatment replicated thrice. The seeds of garden pea were sown on 04th November 2023. Each entries were grown in the gross plot size of 1.70 m x 1.20 m. The line sowing was done with the spacing of 30 cm × 10 cm. All the recommended agronomic package of practices and plant protection measures were followed to raise a good crop.

Five plants randomly selected and tagged before flowering from each plant to investigate on different characters were considered. The statistical analysis was done by using the techniques of analysis of “Randomized Block Design”. These designs were developed by. Through non-hierarchical Euclidean cluster analysis, the genetic divergence among 25 genotypes. The detailed description among different cluster is given under K- mean clustering of standardized data was used to identify the more significant level of discrimination between the cluster for each of variable (Mahalanobis,1928).

**Table 1. Genotypes passport data in table**

|  |  |  |
| --- | --- | --- |
| **S. No.** | **Genotypes** | **Sources** |
| 1 | **Kashi Samridhi** | IIVR, Varanasi |
| 2 | **Pusa Pragati** | IARI, New Delhi |
| 3 | **NDVP-2** | NDUAT, Faizabad |
| 4 | **PB-89** | PAU, Ludhiana |
| 5 | **Kashi Udai** | IIVR, Varanasi |
| 6 | **Kashi Nandini** | IIVR, Varanasi |
| 7 | **K.S.-210** | IIVR, Varanasi |
| 8 | **DVP-8** | IIVR, Varanasi |
| 9 | **Azad Pea-1** | CSAUA&T, Kanpur |
| 10 | **Arka Priya** | IIHR, Bengaluru |
| 11 | **Azad Pea-4** | CSAUA&T, Kanpur |
| 12 | **HUDP-15** | IIVR, Varanasi |
| 13 | **Solan Nirog** | UHF, Solan |
| 14 | **Azad Pea-2** | CSAUA&T, Kanpur |
| 15 | **Snow Pea** | IIVR, Varanasi |
| 16 | **Arkel** | IARI, New Delhi |
| 17 | **Arka Uttam** | IIHR, Bengaluru |
| 18 | **NDVP-5** | NDUAT, Faizabad |
| 19 | **Shihara Local** | IIVR, Varanasi |
| 20 | **Kashi Mukti** | IIVR, Varanasi |
| 21 | **VRPD-1** | IIVR, Varanasi |
| 22 | **VL-3** | VPKAS, Almora |
| 23 | **NDVP-104** | NDUAT, Faizabad |
| 24 | **Kashi Ageti** | IIVR, Varanasi |
| 25 | **Azad Pea-3** | CSAUA&T, Kanpur |

**RESULT AND DISCUSSION**

Following is a summary of the findings from the current study as well as relevant discussions. Selection of suitable parent plays an important role in a successful genetic divergence analysis. Various methods are available for estimating genetic diversity. Twenty-five genotypes of pea taken for Euclidian analysis were differed significantly with regard to the characters under study and showed marked divergence, when taking all 20 characters together. Average inter and intra cluster distance were calculated and exhibited in the Table 2. Intra cluster distance showed divergence among the genotype within a cluster while inter cluster distance showed relative divergence among the cluster. The cluster mean for 20 characters among the five clusters are also presented in Table 3.

**3.1 Clustering of Genotypes**

The 25 genotypes of pea were grouped into 5 distinct non-overlapping clusters. Highest number of genotypes (8) were found in Cluster V pursued by cluster I (7), cluster II (4), cluster III (4) and cluster IV (2). The pattern of genotypes distribution among various clusters also resulted that there is none geographical parallism in the genotypes grouping, denoting that genotypes of various geographical origin may be grouped along or vice-versa. Similar findings have been also reported by Tiwari *et al.* (2004), Yadav *et al.* (2009), Asha *et al.* (2023).

**3.2 Intra and Inter Cluster Distance Average**

Estimation of intra and inter-cluster distance for ten clusters have been given in Table 3. Cluster V (31.23) were observed as a maximum intra cluster distance pursued by cluster IV (15.51), cluster II (14.32), cluster VII (11.86), cluster VI (11.04), cluster III (9.67), cluster I (5.45) while cluster VIII (0.00) have consisted lowest intra cluster distance.

Inter-cluster distance maximum value was found between cluster V with cluster VIII (111.88), pursued by cluster III with cluster VIII (111.81), cluster II and cluster VIII (93.80), cluster I and cluster VIII (93.04), cluster IV and cluster VIII (91.53), cluster VII and cluster VIII (86.12), cluster VI and cluster VIII (82.97), cluster V and cluster VII (40.83), cluster II and cluster V (35.76) cluster IV and cluster V (32.71), cluster V and cluster VI (32.05) cluster III and cluster V(31.89), cluster V and V (31.23).

The minimum inter cluster distance found between I and II cluster (14.88) pursued by I and VI cluster (15.45). Lower inter-cluster values between the clusters meant that the genotypes of the clusters were not significantly genetically different from one another, but higher inter cluster distances indicated greater genetic divergence between the genotypes of those clusters. Same findings were also founded by Taran *et al.* (2005), Sureja and Sharma (2001), Kumar *et al.* (2022).

**3.3 Cluster Mean**

The cluster means for various traits denoted that there were considerable differences between the clusters as shown in Table 4. Cluster I showed maximum mean value for green pod yield per plant (107.52) followed by days to first pod harvest (68.99), plant height at the time of harvesting (59.93) and days to 50 % flowering (49.45). Cluster II showed maximum mean value for green pod yield per plant (138.14), days to first pod harvest (86.29) and plant height at the time of harvesting (82.27). Cluster III showed maximum mean value for green pod yield per plant (155.05), plant height at the time of harvesting (83.97) and days to first pod harvest (79.68). Cluster IV showed maximum mean value for green pod yield per plant (243.58), seed yield per plant (110.03), plant height at the time of harvesting (105.95) and days to first pod harvest (83.20). Cluster V showed maximum mean value for plant height at the time of harvesting (133.82), green pod yield per plant (83.13) and days to first pod harvest (82.08). Cluster I showed minimum mean value for number of pods per cluster (1.26) followed by pod width (1.43), number of primary branches per plant (1.67) and reducing sugar percent (2.83). Cluster II showed minimum mean value for pod width (1.19), number of primary branches per plant (1.67) and number of pods per cluster (1.73). Cluster III showed minimum mean value for pod width (1.37), number of pods per cluster (1.48) and number of primary branches per plant (1.94). Cluster IV showed minimum mean value for pod width (1.38) followed by number of pods per cluster (2.00), number of primary branches per plant (2.25) and reducing sugar percent (2.70). Cluster V showed minimum mean value for pod width (1.28) and number of pods per cluster (1.65). Singh (1999), Singh *et al.* (2007), Saxesena *et al.* (2013).

**Table 2. Clustering Pattern of 25 genotypes of pea**

|  |  |  |
| --- | --- | --- |
| **Cluster** | **No. of Genotypes** | **Genotypes** |
| **I** | 7 | Kashi Uday, Kashi Nandini, Solan Nirog, Snow pea, Arkel, Kashi Mukti, Azad Pea-3 |
| **II** | 4 | PB-89, DVP-8, Arka Priya, NDVP-5 |
| **III** | 4 | NDVP-2, Azad Pea-1, VL-3, Kashi Ageti |
| **IV** | 2 | Kashi Samridhi, HUDP-15 |
| **V** | 8 | Pusa Pragati, K.S.-210, Azad Pea-4, Azad Pea-2, Arka Uttam, Shihara Local, VRPD-1, NDVP-104 |

**Table 3. Intra and Inter cluster D2 value for 5 cluster in pea**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Cluster** | **I** | **II** | **III** | **IV** | **V** |
| **I** | **3.249** |  |  |  |  |
| **II** | 5.572 | **3.401** |  |  |  |
| **III** | 3.772 | 3.482 | **2.988** |  |  |
| **IV** | 7.897 | 5.656 | 5.686 | **1.538** |  |
| **V** | 5.051 | 4.264 | 4.212 | 5.844 | **3.170** |

**Table 4. Intra cluster group means for 20 characters in pea**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster** | Days to 50 % flowering | **Node to first flower appearance** | **Plant height at the time of harvesting** | **Number of primary branches per plant** | **Number of pods per cluster** | **Number of pods per plant** | **Days to first pod harvest** | **Pod length (cm)** | **Pod width (cm)** | **Number of seeds per pod** |
| **I** | 49.45 | 6.72 | 59.93 | 1.67 | 1.26 | 14.32 | 68.99 | 9.27 | 1.43 | 6.32 |
| **II** | 63.96 | 7.62 | 82.27 | 1.67 | 1.73 | 31.62 | 86.29 | 8.27 | 1.19 | 8.35 |
| **III** | 57.16 | 10.07 | 83.97 | 1.94 | 1.48 | 26.27 | 79.68 | 9.10 | 1.37 | 7.67 |
| **IV** | 66.68 | 8.68 | 105.95 | 2.25 | 2.00 | 61.97 | 83.20 | 6.42 | 1.38 | 6.68 |
| **V** | 62.00 | 7.32 | 133.82 | 2.63 | 1.65 | 22.47 | 82.08 | 6.76 | 1.28 | 6.24 |

Continue

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Cluster** | **Seed diameter (mm)** | **100 green seed weight (g)** | **Weight of per pod (g)** | **Shelling %** | **T.S.S. (0Brix)** | **Total sugar percent** | **Reducing sugar percent** | **Non-reducing sugar percent** | **Green pod yield per plant (g)** | **Seed yield per plant (g)** |
| **I** | 9.64 | 49.38 | 7.95 | 39.40 | 13.43 | 7.96 | 2.83 | 4.86 | 107.52 | 41.19 |
| **II** | 8.64 | 34.17 | 4.76 | 49.23 | 13.14 | 9.27 | 3.12 | 5.84 | 138.14 | 64.49 |
| **III** | 8.83 | 44.50 | 6.21 | 44.16 | 13.80 | 8.36 | 3.33 | 4.78 | 155.05 | 58.72 |
| **IV** | 7.65 | 29.00 | 3.85 | 46.78 | 15.77 | 7.60 | 2.70 | 4.64 | 243.58 | 110.03 |
| **V** | 9.05 | 33.46 | 3.86 | 46.48 | 13.95 | 7.92 | 2.73 | 4.93 | 83.13 | 36.10 |

**CONCLUSION**

The current investigation's findings support the notion that there is a great deal of variation in the pea germplasm. Cluster IV and I were found to have the greatest inter-cluster distance. In the future, crossing between the genotypes of clusters V and IV could result in the production of desired F1/segregates.

**FUTURE SCOPE**

Future generations and academics who are interested in working on the varied breeding program will benefit from the foundational work laid by the current experiment. The acquired elite variants might serve as donor parents for qualities related to the economy. In order to accomplish a thorough improvement in pea genotype, they stress the significance of multidisciplinary techniques that integrate conventional breeding with contemporary biotechnological tools.

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