

International Journal of Statistics and Applied Mathematics

ISSN: 2456-1452
Maths 2024; SP-9(1): 334-337
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<https://www.mathsjournal.com>
Received: 21-12-2023
Accepted: 27-01-2024

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Genetic divergence studies in pigeon pea [*Cajanus cajan* (L.) Millsp.]

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Abstract

A set of 20 genotypes of pigeon pea [*Cajanus cajan* (L.) Millsp.] grown in a randomized block design with three replications during *kharif*, 2021-22 at College of Agriculture, Navsari Agricultural University, Bharuch Campus to assess their variability and genetic divergence. The genotypes were grouped into eight different clusters based on Mahalanobis D^2 statistics. Plant height followed by secondary branches per plant, primary branches per plant, pod length and seed yield per plant contributed maximum towards divergence.

Keywords: Pigeon pea, randomized block design, variability, genetic divergence

Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.], a versatile food legume that was once overlooked but is now a staple crop in the agricultural industry, is a staple crop for resource-constrained farmers in tropical and subtropical parts of Asia, Africa, and Latin America. It is a member of the Fabaceae family and is also known as "Arhar" or "Tur." It is typically used to make "Dal", a dish that is consumed by the majority of vegetarians in India and is high in protein (24-25%) and minerals. The pigeon pea has $2n=22$ chromosomes and is diploid with 833 Mb genome size (Varshney *et al.*, 2012) [8]. The pigeon pea is well-known as a forage/cover crop as well as a food crop (dry peas, flour, or green vegetable peas). Pigeon peas, along with grains, create a wholesome human meal.

As a frequently cross-pollinated crop, pigeon pea can be genetically improved using breeding techniques for both self and cross-pollinated crops. It is a strong, woody shrub that can thrive in a variety of soil conditions. Rhizobium spp. and pigeon pea roots collaborate to achieve biological nitrogen fixing. Based on the flowering pattern, the stem's branching pattern might be of the determinate, semi-determinate, or non-determinate type and can range from bush type to compact upright type. The plant can grow as tall as 2-4 m, with an average height of 1-2 m. The size of pods varies greatly. Vegetable varieties have lengthy pods that contain 4-7 seeds each. The colour of the pods ranges from green to deep purple with varied amounts of streaks that are brownish or purplish. Pods typically has simple or glandular hairs in varied degrees of density. Because it is a feature that is undesired for grain harvest, mature pod shattering is infrequent in cultivated cultivars.

Pigeon pea may be produced in locations with less than 650 mm of annual rainfall since it is particularly drought resistant. For every 100 grammes of pigeon pea, it has 22.3% protein, 1.7% fat, 3.5% minerals, 1.5% fibre, 57.6 grammes of carbohydrates, 73 mg of calcium, and 0.5 mg of iron, respectively (Subramani *et al.*, 2020) [7]. It contains phosphorus, potassium, zinc, and sodium as well as vitamins and minerals such thiamine, riboflavin, niacin, vitamin B-6, and vitamin A. If we regularly eat pigeon pea, it can also preserve the liver. Its foliage is utilised as fodder, and the leftovers from its milling process are fed to pets. Plants' tips and green leaves provide for excellent feed. The dried stalks are utilised for thatching, producing baskets, and as fuel. Human breast cancer cells undergo apoptosis when exposed to cajanol, a new anticancer compound derived from pigeon pea roots.

The approach advocated by Wright (1921)^[9] of dividing the correlation into direct and indirect effects by path-coefficient analysis offers helpful insight into the relative value of the features in the selection criterion. A useful technique for calculating the degree of population divergence between two populations is the Mahalanobis (1936)^[3] D² statistics. Numerous studies using this method also revealed that genetic diversity and geographic isolation are not always associated. It consequently provides a more accurate understanding of the degree of divergence, is independent of sample size, and serves as the foundation for choosing parental lines for further breeding programme.

Materials and Methods

Twenty genotypes made up the experimental material, which was set up in Kharif 2021-22 using a randomised block design (RBD) with three replications. A single-row plot of fifteen plants, positioned 90 x 20 cm apart, was used to display each entry. All suggested agronomic procedures and plant protection techniques were implemented consistently and on schedule. Information gathered from 11 yield-related variables, including the days to 50% flowering, days to maturity, plant height (cm), primary and secondary branches per plant, pods per plant, pod

length (cm), seeds per pod, 100 seed weight (g), seed yield per plant (g), and protein content (%). The path analysis was adopted from Wright (1921)^[9], Dewey and Lu (1959)^[11]. Using Mahalanobis' D² analysis from 1936, genetic diversity between genotypes was calculated. Rao's Ward's minimum variance approach was used to group the genotypes into various clusters (1952)^[5].

Results and Discussion

Genetic diversity analysis

Composition of Cluster: All twenty genotypes classified in eight Clusters and the composition of the Clusters is given in Table 2. The Cluster I was largest having 10 genotypes. Cluster II was the second largest which contained 4 genotypes. Cluster III, IV, V, VI, VII and VIII had 1 genotype. Thus, the present results indicated that geographical distribution and genetic divergence did not follow the same pattern. Similar findings have been reported by Reddy *et al.* (2015)^[11], Patel *et al.* (2018)^[3], Kandarkar *et al.* (2020)^[12]. Therefore, it can be concluded that the selection of parents for hybridization should not be based on geographical diversity only, but it should have a base of both geographical origin as well as genetic divergence.

Table 1: Distribution of 20 genotypes of pigeon pea in different Cluster as per the Tochers method

| Cluster | No. of genotypes | Genotypes include |
|---------|------------------|--|
| I | 10 | IPAE-15-05, IPAE-18-06, IPAE-18-04, VLA-1, PA-509, CRG-16-12, AL-2207, PA-650, PUSA-2020-2, UPAS-120 |
| II | 4 | GNP-2, BP-16-261, GT-104, IPAE-15-06 |
| III | 1 | IPAE-15-08 |
| IV | 1 | RVKT-333 |
| V | 1 | AL-2184 |
| VI | 1 | GT-105 |
| VII | 1 | CORG-9701 |
| VIII | 1 | AH-17-13 |

Table 2: Independent character contribution towards total divergence in 11 character of pigeon pea

| S.N. | Character | Times ranked first | Per cent of contribution (%) |
|------|------------------------------|--------------------|------------------------------|
| 1 | Days to 50% flowering | 0 | 0.00 |
| 2 | Days to maturity | 0 | 0.00 |
| 3 | Plant height (cm) | 124 | 65.26 |
| 4 | Primary branches per plant | 12 | 6.32 |
| 5 | Secondary branches per plant | 36 | 18.95 |
| 6 | Pods per plant | 2 | 1.05 |
| 7 | Pod length (cm) | 7 | 3.68 |
| 8 | Seeds per pod | 2 | 1.05 |
| 9 | 100 seed weight (g) | 2 | 1.05 |
| 10 | Seed yield per plant | 2 | 1.05 |
| 11 | Protein content (%) | 3 | 1.58 |

Contribution of various characters towards divergence:

The analysis on contribution of various characters towards the expression of genetic divergence indicated that the characters *viz.*, plant height (65.26%), secondary branches per plant (18.95%), primary branches per plant (6.32%), pod length

(3.68%), protein content (1.58%), seed yield per plant (1.05%), 100 seed weight (1.05%), seeds per pod (1.05%) and pods per plant (1.05%) contributed very much towards genetic divergence in the present material (Table 3). Those accounted for 100 per cent of total divergence in the material.

Table 3: Intra and inter-Cluster distances amongst genotypes of pigeon pea

| Cluster | I | II | III | IV | V | VI | VII | VIII |
|---------|------|-------|-------|-------|-------|-------|-------|-------|
| I | 9.31 | 27.73 | 13.45 | 14.64 | 14.10 | 13.81 | 14.01 | 15.70 |
| II | | 7.95 | 38.11 | 38.98 | 38.64 | 25.10 | 34.57 | 38.10 |
| III | | | 0.00 | 6.23 | 6.32 | 19.44 | 12.72 | 11.14 |
| IV | | | | 0.00 | 7.80 | 20.68 | 10.81 | 14.13 |
| V | | | | | 0.00 | 19.88 | 11.31 | 10.26 |
| VI | | | | | | 0.00 | 21.83 | 15.97 |
| VII | | | | | | | 0.00 | 18.89 |
| VIII | | | | | | | | 0.00 |

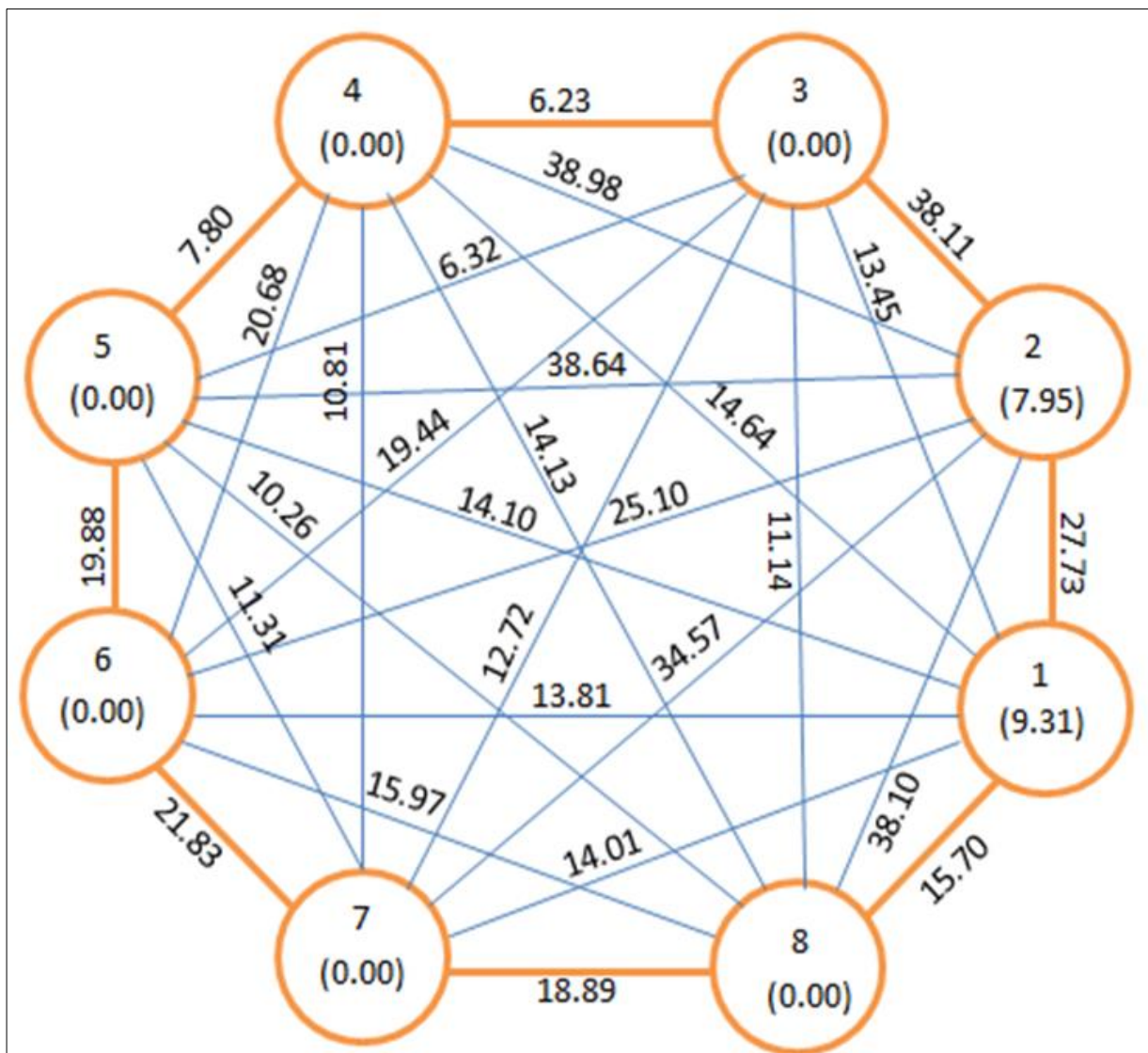
Intra and inter cluster distance: Inter and intra Cluster distance values are given in Table 4. The maximum inter-Cluster distance ($D=38.98$) was found between Clusters II and IV carrying 4 and 1 genotypes followed by II and V ($D=38.64$) and II and III ($D=38.11$) indicating that genotypes included in these Clusters are genetically diverse and may give rise to high heterotic response. The minimum inter-Cluster distance was ($D=6.23$) found between Clusters III and IV indicating a close relationship among the genotypes included in these Clusters.

The lowest intra-Cluster distance were in Clusters III, IV, V, VI, VII and VIII ($D=0.00$) indicating that genotypes within this Clusters were similar. Whereas, the highest intra-Cluster distance was in Cluster I ($D=9.31$). diagrammatic presentation of intra and inter cluster presented in Fig. 1. In general, intra-Cluster distance values were lower than the inter-Cluster distances which indicated substantial diversity present among the genotypes studied.

Table 4: Mean of Cluster by Tocher for 11 morphological characters among the genotypes in pigeon pea

| Sr. No. | Characters | Mean of Cluster | | | | | | | |
|---------|------------------------------|-----------------|--------|--------|--------|--------|--------|--------|--------|
| | | I | II | III | IV | V | VI | VII | VIII |
| 1 | Days to 50% flowering | 100.77 | 101.67 | 98.33 | 97.00 | 100.00 | 97.67 | 102.33 | 93.67 |
| 2 | Days to maturity | 155.23 | 154.00 | 142.33 | 155.00 | 148.00 | 153.00 | 160.67 | 144.33 |
| 3 | Plant height | 168.17 | 233.48 | 140.00 | 137.00 | 140.60 | 169.87 | 157.87 | 138.80 |
| 4 | Primary branches per plant | 14.33 | 15.45 | 13.67 | 12.07 | 13.67 | 14.00 | 11.73 | 13.60 |
| 5 | Secondary branches per plant | 23.50 | 28.93 | 20.53 | 20.40 | 22.67 | 32.27 | 18.87 | 28.93 |
| 6 | Pods per plant | 169.15 | 208.78 | 157.53 | 173.67 | 169.40 | 217.67 | 203.47 | 161.07 |
| 7 | Pod length | 5.45 | 5.86 | 5.60 | 5.18 | 4.58 | 6.05 | 4.12 | 5.24 |
| 8 | Seeds per pod | 3.76 | 3.89 | 4.27 | 4.00 | 3.93 | 4.00 | 3.93 | 3.87 |
| 9 | 100 seed weight | 8.93 | 9.72 | 9.03 | 7.34 | 8.55 | 9.01 | 9.77 | 9.75 |
| 10 | Seed yield per plant | 53.50 | 65.79 | 59.20 | 64.77 | 62.53 | 68.39 | 63.75 | 52.28 |
| 11 | Protein content | 24.59 | 24.53 | 24.10 | 25.07 | 25.73 | 24.80 | 26.10 | 24.13 |

Tocher’s method



Mahalanobis Euclidean Distance (Not to the scale)

Fig 1: Intra and inter Cluster distance (D^2) among eight Clusters in pigeon pea genotypes by Tocher’s method

Cluster means for different characters: Cluster means for all the eleven characters are presented in Table 4. The results clearly indicated appreciable difference among Cluster means for most of the characters. As far as Cluster means are concerned, a greater range of mean values among the Clusters was recorded for different traits. The Cluster II revealed maximum mean values for plant height (233.48) and primary branches per plant (15.45). The Cluster III revealed maximum values for seeds per pod (4.27). The Cluster VI had high mean values for pods per plant (217.67), seed yield per plant (68.39), secondary branches per plant (32.27) and pod length (6.05). The Cluster VII had high mean values for days to 50% maturity (102.33), days to maturity (160.67) and 100 seed weight (9.77). Cluster I had a minimum mean value for seeds per pod (3.76). Cluster III had a minimum mean value for days to maturity (142.33), pods per plant (157.53) and protein content (24.10). Cluster IV had a minimum mean value for plant height (137.00) and 100 seed weight (7.34). Cluster VII had a minimum mean value for primary branches per plant (11.73), secondary branches per plant (18.87) and pod length (4.12). Cluster VIII had minimum mean value for days to 50% flowering (93.67) and seed yield per plant (52.28).

It could be concluded that high yielding genotypes coupled with other desirable physiological traits like days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, pods per plant, pod length, seeds per pod, 100 seed weight and protein content could be selected as parents for hybridization programme from Clusters II, III, VI and VII. Intercrossing genotypes from these Clusters might result in a wide array of variability for exercising effective selection. genotypes from these Clusters might results in hybrids having high vigour and may further results in a wide array of genetic variability for exercising effective selection.

Conclusion

Based on the maximum genetic distance, it is advisable to attempt a crossing of the genotypes from Clusters II (BP-16-261, GT-104 and GNP-2) with Cluster IV (RVKT-333), Cluster V (AL-2184) and Cluster III (IPAE-15-08) for developing a broad spectrum of favourable genetic variability for yield improvement in pigeon pea.

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