***Original Research Article***

**Genetic Variability Studies for Yield and Quality Traits in Short Duration Pigeon pea genotypes in Kerala.**

**ABSTRACT**

Red gram (*Cajanus cajan* L. Millsp.), commonly known as pigeon pea, is a widely cultivated legume valued for its nutritional and agronomic importance. This study aimed to assess genetic variability, heritability, and genetic advance for yield and quality traits in 30 short-duration pigeon pea genotypes grown in Kerala. Analysis of variance revealed highly significant differences among genotypes for all 16 traits studied, indicating considerable genetic variability. The genotypic and phenotypic coefficients of variation (GCV and PCV) exhibited high values for traits like the number of primary branches per plant, number of pods per plant, seed yield per plant, biological yield, and the content of total phenol, tannin, and methionine, indicating a strong potential for enhancement through selection. High heritability coupled with high genetic advance as a percentage of the mean was observed for most traits, indicating the predominance of additive gene action, making direct selection effective. Traits with moderate and low PCV and GCV, including days to 50% flowering and total protein content, exhibited moderate genetic gain, suggesting limited potential for improvement. The findings provide valuable insights into the selection of promising genotypes for developing high yielding red gram varieties suitable for Kerala’s agro-climatic conditions.

*Keywords:**GCV, PCV, Heritability, Genetic Advance.*

**1. INTRODUCTION**

Red gram [*Cajanus cajan* (L.) Millsp.] is a widely cultivated legume in tropical and subtropical regions, primarily grown for its edible seeds. It is known by various local names across the world (Saxena, 2008), with "pigeon pea" being the most commonly recognized name globally. In India, it is commonly known as red gram, tur, or arhar and has been cultivated in the country since ancient times.

Red gram is a fast-growing, hardy, and drought-resistant crop with high adaptability. It is a diploid species (2n = 2x = 22) with a genome size of 1C = 858 Mbp and is classified under the sub-tribe Cajaninae, which falls within the agriculturally important tribe Phaseoleae of the sub-family Papilionoideae in the Fabaceae family. The Phaseoleae tribe includes several edible bean species such as *Phaseolus*, *Vigna*, *Cajanus*, and *Lablab*. However, *C. cajan* is the only domesticated species within the Cajaninae sub-tribe.

Red gram is consumed both as a green vegetable and in the form of decorticated split peas, commonly known as ‘dhal.’ It is a valuable source of protein, iron, iodine, carbohydrates, vitamins, lipids, essential minerals, and key amino acids such as lysine, methionine, and tryptophan. Dry pigeon pea seeds contain 20-22% protein, 67% carbohydrates, 1.9% fat, and 6.6% crude fiber, along with essential minerals, including calcium (120.8 mg 100g-1), magnesium (122 mg 100-1), copper (1.3 mg 100g-1), iron (3.9 mg 100g-1) and zinc (2.3 mg 100g-1) (Saxena *et al.,* 2010).

When consumed with cereals, red gram offers a nutritionally balanced diet for humans. It has the potential to combat hunger and malnutrition while promoting sustainable productivity in smallholder farming systems. Its drought tolerance makes it vital for food security in areas with inconsistent rainfall. The green leaves and plant tops serve as nutritious fodder and are also used as green manure. Additionally, the dried stalks are utilized for fuel, basket weaving, and thatching. The roots of pigeon pea establish a symbiotic relationship with *Bradyrhizobium* spp., enabling biological nitrogen fixation and improving soil fertility.

India is the largest producer of pulses, with red gram being the second most widely cultivated legume after chickpea, covering an area of 4.9 million hectares, yielding 4.22 million tonnes, and having a productivity of 861.2 kg/ha (FAOSTAT, 2022). In Kerala, although red gram is an integral component of the diet, its commercial cultivation remains minimal.

The success of a plant breeding program primarily relies on the genetic variability present within a crop species. The efficiency of selection is closely tied to the extent of genetic diversity available in the plant population. Consequently, the potential for improving any trait depends on the level of variability present in the gene pool for that trait. Assessing the magnitude of genetic variability within a species is essential for breeders to develop an effective and well-structured breeding program (Asseng *et al.*, 2015).

The reliability of genetic parameters, including genotypic and phenotypic coefficients of variation, heritability, and genetic advance, is crucial for enabling effective selection in breeding materials. This investigation aimed to assess the variability, heritability, and genetic advance for different traits in short-duration pigeon pea grown in Kerala. This assessment will help identify promising genotypes that can be utilized in breeding programs to develop pigeon pea varieties suitable for Kerala’s agro-climatic conditions.

**2. MATERIALS AND METHODS**

**2.1 Experimental Site and Experimental Design**

The present study was carried out at the College of Agriculture, Vellayani, Thiruvananthapuram, Kerala, from June to September 2023. The material used in the study comprised of thirty pigeon pea genotypes *viz*; ICPL 11249, ICPL 11256, ICPL 11259, ICPL 11263, ICPL 11273, ICPL 20338, ICPL 20340, ICPL 20341, ICPL 11242, ICPL 11279, ICPL 11296, ICPL 11298, ICPL 11300, ICPL 11318, ICPL 11326, ICPL 20326, ICPL 20327, ICPL 20328, ICPL 20329, ICPL 20333, ICPL 11255, ICPL 11301, MN5, ICPL 22045, ICPL 22077, ICPL 22084, ICPL 22110, ICPL 22081, APK 1 and Pusa Arhar 16. All genotypes originated from ICRISAT, Hyderabad, except APK 1 and Pusa Arhar 16, which originated from TNAU, Coimbatore, and IARI, New Delhi, respectively. All genotypes were grown in 2 rows of 3m length in randomized complete block design (RCBD) with three replications. Row to row and plant to plant spacing were maintained at 40 and 20 cm, respectively. All recommended agronomic practices were implemented to raise a healthy crop.

**2.2 Characters Studied**

Observations were recorded for sixteen traits, including days to flower bud initiation, days to flower initiation, days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant (g), 100-seed weight (g), biological yield (g), harvest index (%), total protein content (%), total phenol content (mg/g), total tannin content (mg/g), total methionine content (mg/g), and days to physiological maturity. Data were collected from five randomly selected plants of each genotype in each replication. However, days to flower bud initiation, days to flower initiation, days to 50% flowering, and days to physiological maturity were recorded on a plot basis.

**2.3 Statistical Analysis**

The overall mean values of various traits were analysed statistically. Analysis of variance was performed using the randomized block design (RBD) method as outlined by Panse and Sukhatme (1978). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following the method proposed by Burton and de Vane (1953).

Heritability in the broad sense was estimated using the method proposed by Hanson *et al*. (1956). The genetic advance as per cent of mean (GAM) was estimated by adopting the method suggested by Johnson *et al.* (1955).

**3. RESULTS AND DISCUSSION**

**3.1 Analysis of Variance**

The extent of genetic variability in base population determines the success of any breeding programme, therefore it is essential to subject a population for selection to achieve enhancement in a particular character. In the present study the analysis of variation shown highly significant differences among the genotypes for all the characters studied, indicating the existence of considerable genetic variation in the experimental material. This variability can be utilized effectively to develop high yielding cultivars through hybridization followed by selection. These findings were in conformity with Shruthi *et al.* (2019) and Bhatt *et al.* (2024).

**3. 2 Genotypic and Phenotypic Coefficient Variation**

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the various traits examined are shown in Table 1. An examination of the variance components revealed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied, highlighting the influence of environmental variance on total variation. However, the small differences between them suggest that environmental influence on character expression was minimal.

High PCV and GCV values were observed for number of primary branches/plant (27.35) and (26.37), number of pods/plant (31.15) and (30.27), seed yield/plant (34.05) and (32.71), biological yield/plant (24.66) and (22.96), phenol content (43) and (42.77), tannin content (39.30) and (39.06) and methionine content (40.93) and (40.75) indicating a higher potential for improving these traits through selection. Mallesh *et al*. (2017), Bhatt *et al.* (2024)*,* Rangare *et al.* (2013),and Kumar *et al.* (2023) previously reported high PCV and GCV estimates for some traits in pigeon pea.

However, moderate PCV and GCV was observed for days to flower bud initiation (19.76) and (18.89), days to flower initiation (11.80) and (10.25), plant height (18.02) and (16.12), number of seeds per pod (14.43) and (13.02) and harvest index (16.89) and (14.98). Pal *et al.* (2018), Kumar *et al* (2023)*.*, Bhatt *et al.* (2024)*,* Rangare *et al.* (2013)and Gaur *et al.* (2020), previously reported moderate PCV and GCV estimates for some traits in pigeon pea.

Low PCV and GCV values were observed for days to fifty percent flowering (9.02) and (7.30) and protein content (8.75) and (7.38). Gaur *et al.* (2020) and Pal *et al.* (2018), previously reported low PCV and GCV estimates for some traits in pigeon pea.

Low GCV and moderate PCV was observed for 100 seed weight (9.56) and (12.61). These findings are in conformity with the earlier finding for this trait in pigeon pea by Bhatt *et al.* (2024).

The magnitude of PCV ranged from 8.75 for protein content to 40.93 for methionine content while GCV ranged from 7.30 for days to flower bud initiation to 42.77 for total phenol content. Traits with a high phenotypic coefficient of variation indicated greater influence of environmental factors.

Total phenol content, total tannin content and total methionine content exhibited slightly higher phenotypic coefficient of variation compared to genotypic coefficient of variation, suggesting that these traits were minimally influenced by environmental factors. Days to flower bud initiation, days to fifty percent flowering, plant height, number of seeds per plant, seed yield per plant, biological yield, harvest index, 100 seed weight, total protein content and days to physiological maturity exhibited a higher phenotypic coefficient of variation than genotypic coefficient of variation, suggesting that these traits were more affected by environmental factors. The level of PCV and GCV for all traits are illustrated in Fig. 1.

**3.3 Heritability and Genetic Advance**

The estimates of heritability and genetic advance for the various traits studied are presented in Table 1. Although GCV indicates a high degree of genetic variation, the heritable portion can be accurately determined only through estimates of heritability and genetic gain. In the current study, broad-sense heritability was high for most traits, including days to flower bud initiation (91.40%), days to flower initiation (75.48%), days to 50 % flowering (65.40%), plant height (79.96%), number of primary branches per plant (92.99%), number of pods per plant (94.44%), number of seeds per pod (81.47%), seed yield per plant (92.32%), biological yield (86.68%), harvest index (78.67%), total protein content (71.29%), total phenol content (98.95%), total tannin content (98.79%), total methionine content (99.14%), days to physiological maturity (66.37%). Pranati *et al.*, Galian *et al.*, Nagaraja *et al.*, previously reported high heritability for some traits in pigeon pea. Medium heritability was recorded for 100 seed weight (57.50).

High genetic advance (per cent of mean) was observed for traits such as days to flower bud initiation (37.20), plant height (29.68), number of primary branches per plant (52.38), number of pods per plant (60.60), number of seeds per pod (24.21), seed yield per plant (64.74), biological yield (44.03), harvest index (27.37), total phenol content (87.65), total tannin content (79.97), total methionine content (83.58). Similar results were reported by Sncvl *et al.* (2018) for number of primary branches per plant and number of pods per plant; Yadav *et al.* (2024) for plant height and seed yield per plant.

Medium genetic advance (per cent of mean) was recorded for days to flower initiation (18.35), days to 50 % flowering (12.16), 100 seed weight (14.93), total protein content (12.84) and days to physiological maturity (13.27). Similar results were reported by Pranati *et al.* (2024) for 100 seed weight.

According to Johnson *et al.* (1955), heritability estimates combined with genetic gain are generally more valuable. High heritability combined with high genetic advance as a percentage of the mean was observed for days to flower bud initiation, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant, biological yield, harvest index, total phenol content, total tannin content, total methionine content. This suggests the influence of additive gene action in the expression of these traits, indicating a greater potential for improvement through direct selection. The levels of heritability and genetic advance for all traits are illustrated in Fig. 1.

**Table 1. Estimates of genetic parameters for yield and quality in Pigeon pea**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sl.****No.** | **Genetic Parameters** | **GCV** | **PCV** | **h2** **(Broad** **Sense) (%)** | **GA** | **GAM** |
| **1** | Days to flower bud initiation | 18.89 | 19.76 | 91.40 | 14.19 | 37.20 |
| **2** | Days to flower initiation | 10.25 | 11.80 | 75.48 | 8.47 | 18.35 |
| **3** | Days to 50% flowering | 7.30 | 9.02 | 65.40 | 6.34 | 12.16 |
| **4** | Plant height (cm | 16.12 | 18.02 | 79.96 | 22.22 | 29.68 |
| **5** | Number of primary branches per plant | 26.37 | 27.35 | 92.99 | 1.95 | 52.38 |
| **6** | Number of pods per plant | 30.27 | 31.15 | 94.44 | 23.07 | 60.60 |
| **7** | Number of seeds per pod | 13.02 | 14.43 | 81.47 | 0.86 | 24.21 |
| **8** | Seed yield per plant (g) | 32.71 | 34.05 | 92.32 | 11.02 | 64.74 |
| **9** | Biological yield | 22.96 | 24.66 | 86.68 | 30.48 | 44.03 |
| **10** | Harvest index (%) | 14.98 | 16.89 | 78.67 | 6.58 | 27.37 |
| **11** | 100-seed weight (g) | 9.56 | 12.61 | 57.50 | 1.33 | 14.93 |
| **12** | Total protein content (%) | 7.38 | 8.75 | 71.29 | 2.43 | 12.84 |
| **13** | Total phenol content (mg/g) | 42.77 | 43.00 | 98.95 | 1.82 | 87.65 |
| **14** | Total tannin content (mg/g) | 39.06 | 39.30 | 98.79 | 8.08 | 79.97 |
| **15** | Total methionine content (mg/g) | 40.75 | 40.93 | 99.14 | 0.97 | 83.58 |
| **16** | Days to physiological maturity | 7.91 | 9.71 | 66.37 | 12.00 | 13.27 |

**Fig. 1. PCV, GCV, Heritability and Genetic Advance for yield and quality traits in Pigeon pea**

DFBI- Days to flower bud initiation, DFI- Days to flower initiation, DFF- Days to 50 % flowering, PH- Plant height (cm), NPB- Number of primary branches per plant, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, SYPP- Seed yield per plant (g), BY- Biological yield (g), HI- Harvest index (%), TW- 100 seed weight (g), Protein- Total protein content (%), Phenol- Total phenol content (mg/g), Tannin- Total tannin content (mg/g), Methionine- Total methionine content (mg/g) and DM- Days to physiological maturity.

**4. CONCLUSION**

The present study highlights the significant genetic variability among 30 short duration pigeon pea genotypes grown in Kerala, which can be effectively utilized in breeding programs. High heritability and genetic advance for traits such as days to flower bud initiation, plant height, number of primary branches, number of pods, seed yield per plant, and phenol, tannin, and methionine content suggest the predominance of additive gene action, making these traits ideal candidates for direct selection. Moderate heritability and genetic gain observed for traits like days to flower initiation, 50% flowering, and 100-seed weight indicate a moderate scope for genetic improvement. The findings emphasize that traits exhibiting high genetic variability and heritability can be exploited to develop high-yielding, early-maturing, and nutritionally rich pigeon pea varieties suited for the agro-climatic conditions of Kerala.

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