The Pharma Innovation Journal 2023; 12(11): 2384-2386

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(11): 2384-2386

www.thepharmajournal.com
Received: 07-08-2023
Accepted: 09-09-2023

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Investigation of genetic variability in pigeon pea for yield and its attributing traits. (*Cajanus cajan* L. Millsp.)

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Abstract
The study titled “Investigation of genetic variability in pigeon pea for yield and its attributing traits (*Cajanus cajan* L. Millsp.)" took place at the Research and Education farm, Botany Department, College of Agriculture, Dapoli, during the Kharif season of 2022. Across all 14 traits examined, the PCV(phenotypic coefficient of variation) surpassed the GCV (genotypic coefficient of variation) in magnitude. Notably, per plot seed yield, % pod borer damage, plant height exhibited high PCV. Conversely, per plot seed yield, % pod borer damage, pods / plant displayed high GCV.
Appreciable heritability estimates were noted across all evaluated traits, with the highest heritability observed for harvest index, test weight, and days to fifty% flowering. Genetic advance was most pronounced in per plot seed yield, followed by % pod borer damage. Moreover, % pod borer damage, per plot seed yield (g), seed yield / plant (g) showcased comparatively higher estimates of genetic advance as a percentage of mean.
In terms of performance, the genotypes LOCAL-7, IPAWD-36, and IPAWD-25 emerged as top performers, demonstrating the highest seed yield / plant and maximum yield-related characteristics. These genotypes hold promise as valuable genetic resources for future breeding programs.

Keywords: Genotype, variability, heritability, genetic advance etc.

Introduction
Pulse crops have a significant impact on Indian economy, often dubbed as the "Poor man’s meat" due to their affordability and high-quality protein content. Grain legumes or pulses hold a crucial position in meeting human dietary and nutritional needs. They serve as key components in the diets of many, particularly in developing nations, augmenting cereal-based diets and enhancing their nutritional value by providing valuable protein source. Throughout history, combination of cereals and pulses has consistently offered enhanced nutrition to people worldwide. Furthermore, pulses play vital role in bolstering soil health through biological N_2 fixation, fostering sustainable cropping systems, diversifying crops, and managing natural resources.
The pigeon pea, a crucial legume crop in rainfed agriculture within semiarid tropics, demonstrates high drought resistance and thrives in areas with less than 650 mm annual rainfall. It exists in both perennial and annual varieties, with the former lasting 3 to 5 years and the latter more suitable for seed production. Typically cultivated in tropical or subtropical regions across various soils (ranging from sandy to heavy, with pH levels from 5.0 to 8.0), pigeon peas cannot withstand even light frost during growth stages. However, compared to other pulse crops, they display superior adaptability to marginal climates. Genetic diversity epicenters for pigeon pea are found in Africa and India, with India regarded as the primary origin and West Africa as a secondary center. Pigeon pea are rich in protein and contains essentially amino acids such as methionine, lysine, and tryptophan.
Globally, pigeon pea cultivation spans 5.40 million hectares, yielding an annual production of 4.48 million metric tons, averaging a productivity of 827 kilograms per hectare (FAOSTAT, 2021). Specifically in India, pigeon pea is grown across 3.88 million hectares, resulting in a production of 2.84 million metric tons and a productivity of 733 kilograms per hectare (FAOSTAT, 2021). Notably, in Maharashtra alone, pigeon pea is cultivated over an average area of 20.98 lakh hectares in 2021, yielding total production of 12.66 lakh tons (Source - Kharif prospects, Bhopal).

Pigeon pea, a robust and adaptable crop, exhibits notable drought tolerance. Its varied maturity range facilitates adaptation to various environments and cropping systems. Farmers cultivate it both as a sole crop and in intercropping systems with urd bean, mung bean, castor, sorghum, soybean, cotton, maize, and groundnut. Its resilience to drought and hardy nature enables thriving in marginal, less fertile soils, even under poor management and rainfed conditions.

Materials and Methods

During the *kharif* season of 2022, the study was carried out at Educational and Research Farm within the Botany Department, College of Agriculture, located in Dapoli, Dist. Ratnagiri, Maharashtra. Throughout the experimentation phase, meteorological data was collected from meteorological observatory situated at the Department of Agronomy, College of Agriculture, Dapoli. The experiment employed a randomized block design with two replications, where each plot covered an area of approximately 10.80 meters × 1.20 meters, containing 2 rows per genotype. Within each row, there was 18 plants, summing up to total of 36 plants/plot. For field observations, five plants were chosen randomly from each genotype. A comprehensive record of 14 characteristics was collected, encompassing observations such as Days to flower initiation, Days to fifty% flowering, Days to maturity, No. of branches /plant, No. of seeds / plant, Pods / plant, % pod borer damage, Test weight, Pod length, Plant height, Seed yield / plant, Per plot seed yield, Harvest index, Protein content.

The data for individual characteristics underwent analysis of variance using the commonly applied method in the RBD, as outlined in (Panse and Sukhatme 1985) [6].

Results and Discussion

Components of Variation

The total variance among the genotypes was divided into genotypic, phenotypic, and environmental components. Across all studied characteristics, the magnitude of phenotypic variance exceeded that of genotypic variance. Phenotypic variance ranged from 0.08 (pod length) to 731.59 (per plot seed yield) for different traits. The highest phenotypic variance was observed for per plot seed yield, followed by % pod borer damage, plant height, pods / plant, days to maturity, days to flower initiation, days to fifty % flowering, seed yield / plant. The variance was moderate for harvest index, while it was lowest for pod length, followed by No. of seeds / pod, No. of branches / plant, protein content, test weight.

In all traits, except for No. of seeds / pod, pod length, and protein content, genotypic variance exhibited greater magnitude than environmental variance. The most substantial genotypic variance was observed in per plot seed yield, followed by pod borer damage, pods / plant, plant height, days to maturity, days to fifty % flowering, days to flower initiation, and seed yield / plant. Moderate genotypic variance was noted for harvest index. Pod length, No. of seeds / pod, protein content, followed by No. of branches / plant, displayed the lowest magnitude of genotypic variances. Pashwan et al. (2021) [7] similarly reported findings with the highest genotypic variance for plant height and moderate variance for pod length,No. of branches / plant.

Environmental variance showed greater magnitude for per plot seed yield, followed by % pod borer damage and plant height. It was moderate for No. of pods / plant, days to flower initiation, and days to maturity, while being lowest for No. of seeds / pod, pod length, test weight, No. of branches / plant, harvest index, protein content, days to fifty % flowering, seed yield / plant. Patro et al. (2019) [9] and Ekka and Sahu (2019) [12] similarly confirmed these results, particularly concerning plant height and pod length.

Table 1: Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for 14 quantitative characters of pigeon pea.

Sr. No.	Characters	σ^2_p	σ^2_g	σ^2_e
1	Days to initiation of flowering	53.65	41.59	12.06
2	Days to fifty% flowering	49.93	43.57	6.36
3	Days to maturity	56.23	45.62	10.61
4	Plant height at harvest (cm)	88.08	50.69	37.39
5	No. of branches / plant	0.93	0.70	0.24
6	Pods / plant	81.34	66.30	15.04
7	No. of seeds / pod	0.04	0.02	0.03
8	Pod length (cm)	0.08	0.01	0.09
9	Test weight (g)	1.55	1.36	0.19
10	% pod borer damage	300.41	224.15	76.27
11	Seed yield / plant	38.29	30.46	7.82
12	Per plot seed yield	731.59	622.59	109
13	Harvest index (%)	12.66	11.74	0.92
14	Protein content (%)	1.12	0.07	1.04

Coefficient of variation

The findings indicated that the PCV surpassed the respective GCV in magnitude. % pod borer damage, seed yield / plant, and per plot seed yield exhibited the highest PCV. Moderate PCV was observed for the pods / plant, test weight, No. of branches / plant, harvest index. Kumar et al. (2014) [5] and Fousiya et al. (2021) [3] observed similar patterns, noting the highest PCV for seed yield / plant and per plot seed yield.

The lowest magnitude of PCV was recorded for days to maturity, followed by protein content, pod length, days to fifty% flowering, plant height, No. of seeds / pod, and days to initiation of flowering. Priyanka et al. (2016) [10] reported comparable results.

The genetic variation among the 41 genotypes was assessed in terms of GCV. The highest GCV was found in % pod borer damage, followed by seed yield / plant and per plot seed yield. Moderate GCV was observed in traits such as pods / plant, test weight,No. of branches / plant. The lowest GCV was seen in harvest index, days to initiation of flowering, days to fifty% flowering, plant height, No. of seeds / pod, days to maturity, pod length, and protein content. This categorization based on GCV and PCV utilized the standard scale provided by Sivasubramanian and Menon (1973) [14].

Heritability and genetic advance

The broad-sense heritability ranged from 6.70% (protein content) to 92.80% (Harvest index). It was recorded high for harvest index, followed by test weight, days to fifty% flowering, per plot seed yield, pods / plant, days to maturity, seed yield / plant, days to flower initiation, % pod borer damage, No. of branches / plant, plant height, No. of seeds / pod. Pod length and protein content exhibited the lowest heritability. Similar results indicating high heritability in harvest index and test weight were also reported by Rao and Rao (2020) [11] and Patel and Patel (2020) [8].

The genetic advance spanned from 0.08 (pod length) to 47.42 (per plot seed yield). Per plot seed yield exhibited a moderate level of genetic advance. Conversely, the lowest magnitude of genetic advance was observed in % pod borer damage, pods / plant, days to fifty% flowering, days to maturity, days to flower initiation, plant height, seed yield / plant, harvest index, test weight, No. of branches / plant, No. of seeds / pod, and protein content. Singh et al. (2013) [13] documented similar findings, particularly noting low magnitude of genetic advance for seed yield / plant, harvest index, test weight.

The genetic advance as a percentage of mean (GAM) ranged from 0.68% (protein content) to 49.50% (% pod borer damage). The highest GAM was seen in % pod borer damage, followed by seed yield / plant, per plot seed yield, pods / plant, test weight, and No. of branches / plant. Harvest index, days to flower initiation, days to fifty % flowering displayed a moderate estimate of GAM. The lowest magnitude of GAM was recorded for plant height, days to maturity, No. of seeds / pod, and pod length.

This categorization of Heritability, Genetic advance, and Genetic advance as a percentage of mean was determined following the standard scale outlined by Johnson et al. (1955) [4].

Table 2: Estimates of genetic parameters for 14 quantitative characters in pigeon pea

Sr. No.	Characters	PCV (%)	GCV (%)	ECV (%)	h^2b (%)	GA	GAM (%)
1	Days to initiation of flowering	7.79	6.86	3.70	77.50	11.70	12.45
2	Days to fifty% flowering	6.29	5.88	2.25	87.30	12.70	11.31
3	Days to maturity	4.26	3.84	1.85	81.10	12.53	7.12
4	Plant height at harvest	6.90	5.23	4.50	57.50	11.13	8.18
5	No. of branches / plant	13.35	11.53	6.73	74.60	1.48	20.52
6	Pods / plant	19.12	17.26	8.22	81.50	15.14	32.10
7	No. of seeds / pod	6.74	4.38	5.13	42.10	0.18	5.85
8	Pod length (cm)	6.19	2.35	6.62	14.40	0.08	1.84
9	Test weight (g)	13.36	12.51	4.69	87.70	2.25	24.14
10	% pod borer damage	32.20	27.82	16.23	74.60	26.64	49.50
11	Seed yield / plant	28.33	25.27	12.80	79.60	10.14	46.43
12	Per plot seed yield	23.77	21.93	9.18	85.10	47.42	41.67
13	Harvest index (%)	10.11	9.74	2.72	92.80	6.80	19.32
14	Protein content (%)	4.92	1.27	4.75	6.70	0.15	0.68

Conclusion

The study concluded that a broad range of variability existed among the genotypes across various quantitative traits. Traits like % pod borer damage, per plot seed yield (g), and seed yield / plant (g) exhibited high heritability coupled with a high genetic advance as a percentage of mean. This combination suggests an additive gene action and signifies their suitability for direct selection, indicating the need to prioritize this traits in selection programs.

Among genotypes studied, LOCAL-7, followed by IPAWD-36 and IPAWD-25, emerged as top performers, displaying the highest seed yield / plant and attributing maximum yield-related characteristics. LOCAL-5 exhibited the highest test weight, while LOCAL-7 excelled in the pods / plant, protein content, pod length, harvest index. IPAWD-36 displayed the highest per plot seed yield, IPAWD-26 had the maximum pod length, and IPAWD-27 showed the least % pod borer damage.

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