Genetic variability estimation in forty pigeonpea germplasm for yield and yield attributing traits

Abstract

Aim: The present research aimed to estimate the genetic variability in forty pigeonpea germplasms for yield and yield-attributing traits such as initial plant stand, final plant stand, days to 50% flowering, primary branches, secondary branches, plant height, days to maturity, wilt incidence%, pod borer infestation %, 100 seed weight, number of pods per plant, yield (g/plot), yield (kg/ha).

Study design: study was conducted in randomised block desigh (RBD) design with two replications and spacing of 60cm X 30 cm.

Place and duration of study: The present investigation was carried out during *kharif* 2021-2022 and 2022-2023 at the research farm of Birsa Agricultural University farm located at Kanke, Ranchi.

Methodology: Forty pigeonpea genotypes were studied to determine genetic variability. Pooled data over two years were subjected to statistical analysis for estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2), and genetic advance as a percent of mean for fourteen quantitative traits such as initial plant stand, final plant stand, days to 50% flowering, primary branches, secondary branches, plant height, days to maturity, wilt incidence%, pod borer infestation%, 100 seed weight.

Results: The PCV varied from 2.45% (days to maturity) to 30.83% [yield (kg/ha), whereas the GCV ranged from 1.12% (days to maturity) to 17.67% [yield (g/plot)]. Days to 50% flowering (6.39%, 4.48%), days to maturity (2.45%, 1.12%), and 100 seed weight (8.53%, 5.65%) all had low GCV and PCV value. The broad sense of heritability (h^2) varied between plant height (16.9%) to days to 50% blooming (49.20%). Plant height (16.90%, 4.95%), number of pods per plant (21.10%, 9.95%), and days to maturity (20.90%, 1.05%) showed low heritability and genetic advance as a percentage of the mean, indicating ineffective selection.

Conclusion: genotypes showed high magnitude of variability for all the traits under study.

Keywords: Genetic Variability, GCV, PCV, Heritability, Genetic Advance as percent of mean

Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.] is the most important pulse crop after chickpea grown in India. It is commonly known as tur, red gram and arhar, congo pea, gungo pea and no-eye pea. It is predominantly a self-pollinated crop (cross pollination exceeds 40%) with 2n=2x=22 (diploid chromosome number) and its genome size is 833.07 Mb (Yadav *et al.* 2024). Globally, it ranks sixth after pea, broad bean, lentil, chickpea and common bean(Arega *et al*., 2023). India is the largest producer and consumer of pigeonpea. It is mostly used as dry split dal which is rich in proteins i.e., 21-25% (Jeevarathinam*et al*.,2020). It has a number of nutritive qualities, including protein, carbohydrates, vitamins B complex, carotenes, minerals (iron, magnesium, phosphorus), and thiamine, riboflavin, and niacin. When eaten with cereals, it provides essential amino acids and has high concentrations of lysine, leucine, glutamic acid, aspartic acid, and arginine (Akshaya *et al*., 2023). The pigeonpea plant, additionally known as the "biological plough," is considered to have several advantages for soil, including fixing nitrogen from the atmosphere (40-60 kg N/ha), contributing in addition of organic matter and micronutrients to soil, breaking up hard plough pans with its long tap roots. Pigeonpea is a multipurpose crop that grow well in a variety of soil types. They can provide reasonable yields of food that is rich in nutrients even on deteriorated soils with little help from outside resources. Despite being a crop rich in nutrients, the productivity of pigeonpea worldwide has been rather stagnant at 700–800 kg/ha (Saxena *et al*.,2020, Ranjani *et al*.,2021). Therefore, it is necessary to increase the production of pigeon pea to overcome the yield stagnation by developing high yielding varieties. To develop high yielding varieties, knowledge on the existing genetic variability in the crop needs to be studied.

Yield is a complex attribute that is highly swayed by environment and is controlled by number of individual traits. Therefore, for effective selection and improvement in any breeding program, estimates of genetic parameters i.e., genotypic coefficient of variation (GCV), phenotypic coefficient of variation will help in finding out the variability in the genotypes. However, GCV and PCV will only reveal the relative magnitude of genetic variability present in the genotypes. Estimates of heritability (h^2) along with genetic advance (GA) as percent of mean are expected to reveal more information related to variability. Therefore, present investigation was carried out to evaluate the significance of variability with respect to phenotypic and genotypic coefficient of variation, heritability in a broad sense h^2 (bs), and estimated genetic advancement in order to furnish additional information that might potentially enhance yield features.

Material and methods

The present investigation was carried out during *kharif* 2021-2022 and 2022-2023 at the research farm of Birsa Agricultural University farm located at Kanke, Ranchi. The study consisted of forty pigeonpea germplasms obtained from different sourcesgrown in randomized block design in two replications at a spacing of 60cm X 30 cm. observations were recorded from five randomly selected plants on initial plant stand, final plant stand, number of primary branches per plant, number of secondary branches per plant, plant height, wilt incidence (%), pod borer infestation (%), days to 50% flowering, number of pods per plant, days to maturity, 100 seed weight, yield (g/plot) and yield (kg/ha) from both the replication. The phenotypic and genotypic coefficients of variation were estimated according to the method suggested by Burton and Devane (1953), heritability in broad sense (h^2) (Lush, 1949) and genetic advance as per cent mean (GAM) (Johnson *et al.,* 1955) were estimated from the pooled data over two years.

Results and Discussions

The analysis of variance showed significant differences between the genotypes for all the thirteen traits (Table 1). Table 2 presents the range, mean, and genetic parameters like genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance as percent of mean. Wide range of phenotypic and genotypic coefficients of variation was found for almost all the traits under investigation. For all of the characters examined, the phenotypic coefficient of variation was rather high in comparison to the corresponding genotypic coefficient of variation, showing that the expression of these traits is influenced by the environment. PCV ranged from 2.45% (days to maturity) to 30.83% [yield (kg/ha)], whereas the range of GCV was from 1.12% (days to maturity) to 17.67% [yield (g/plot)]. The high values of PCV were detected for final plant stand (26.91%), primary branches (21.49%), secondary branches (20.35%), number of pods per plant (22.88%), yield (g/plot) (30.52%), yield (kg/ha) (30.83%). Similar results were reported by Patel *et al*., 2021, Akshya *et al*., 2023, Yadav *et al.*, 2024. Moderate estimate of PCV were recorded for initial plant stand (17.57%) and plant height (14.25%). The high values of GCV and PCV were found for wilt incidence (36.31%, 53.64%) and pod borer infestation (27.60%, 50.67%). These findings were similar to findings of Byatroy*et al*., 2022 for wilt infestation having higher estimates of GCV and PCV. Moderate estimate of GCV was observed for initial plant stand (11.75%), final plant stand (17.45%), primary branches (10.63%), secondary branches (12.05%), number of pods per plant (10.51%), yield (g/plot) (17.67%), and yield (kg/ha) (30.83%). Patel *et al*., 2021 also recorded moderate values of GCV for number of pods per plant, primary branches per plant, secondary branches per plant and plant height. Low magnitude of GCV was observed for plant height (5.85%). However, low estimates of GCV and PCV was recorded for days to 50% flowering (6.39%, 4.48%), days to maturity (2.45%, 1.12%), and 100 seed weight (8.53%, 5.65%). Low estimates of GCV and PCV shows less variability for the traits being studied. Hence, selection would be effective for these traits. Similar results were reported by Pushpavalli *et al*., 2017, Meena *et al*., 2017, Patel *et al*., 2021, Galian *et al*., 2015, Ajay *et al*., 2014, Patel *et al*., 2011. for plant height, days to 50% flowering, days to maturity, 100seed weight.

Although GCV could only show the presence of genetic variation but from breeding aspect, genetic variation is rewarding only if it is heritable. The extent of heritability in broad sense (h^2) varied from plant height (16.9%) to days to 50% flowering (49.20%). As heritability is also influenced by environment, therefore, heritability alone will not be helpful in selection of superior genotypes. Estimates of heritability along with genetic advance as per cent of mean (GAM) will be more rewarding for selecting best genotypes (Johnson *et al.*, 1955). Moderate estimate of broad sense heritability coupled with high genetic advance as per cent of mean was observed for final plant stand (42.00%, 23.30%), wilt incidence (45.80%, 50.64%), yield (g/plot) (33.50%, 21.07%) and yield (kg/ha) (32.20%, 20.43%) indicating that the characters are governed by additive genes. Low heritability and genetic advance as per cent of mean was recorded for plant height (16.90%, 4.95%), number of pods per plant (21.10%, 9.95%), and days to maturity (20.90%, 1.05%) indicating the preponderance of non-additive genes and thereby in-efficacy of selection. High genetic advance as per cent of mean was observed for final plant stand (23.30), wilt incidence (50.64), yield (g) (21.07), yield (kg/ha) (20.43). Low estimates of genetic advance as per cent of mean was found for plant height (4.95), days to 50% flowering (6.48), number of pods per plant (9.95), days to maturity (1.05) and 100 seed weight (7.71). Similar findings were reported by Tiwari et al., 2015, Mallesh *et al.*, 2017. Gautam *et al.*, 2021 also found moderate to low genetic advance as per cent of mean for number of pods per plant, days to maturity, plant height, 100 seed weight in chickpea.

Conclusions

In the present study, PCV values were significantly greater than GCV values, demonstrating that the characteristics were influenced by the environment. High GCV and PCV values have been found for wilt incidence and pod borer infestation, indicating that the environment has a more significant impact on these traits. Initial plant stand, final plant stand, primary and secondary branches, number of pods per plant, yield (g/plot), and yield (kg/ha) all exhibited moderate GCV estimates. Low estimates of GCV and PCV for days to 50% flowering, days to maturity, and 100 seed weight indicates that traits are less variable and that selection will be advantageous. Moderate estimate of broad sense heritability coupled with high genetic advance as per cent of mean was observed for final plant stand, wilt incidence, yield (g/plot) and yield (kg/ha) indicating that the characters are governed by additive genes and these traits can be selected for improvement in further breeding programme.

	sources of variation					
	Replication	**Environments**	**Interactions**	**Overall Sum**	**Genotypes**	**Error**
(df)	1	1	1	3	39	117
Initial Plant Stand	3.34	469.40 **	3.91	158.88 **	52.95 **	12.50
Final Plant Stand	8.45	1795.80 **	0.21	601.49 **	63.82 **	16.37
Wilt (%)	0.03	415.35 **	2.97	139.45 **	106.16 **	24.21
Plant height (cm)	1723.51	336198.80 **	5.60	112642.64 **	1162.47 *	641.35
Primary Branches	6.28	76.25 **	0.00	27.51 **	6.84 **	2.98
Secondary Branches	17.44	84.10 **	0.00	33.85 **	18.13 **	5.73
Days to percent flowering	74.98	81.18 **	0.00	52.05 *	79.38 **	16.28
Number of pods per plant	4266.60	166667.50 **	31.59	56988.55 **	4360.09 **	2105.23
Pod Borer (%)	4.26	15.14 **	0.00	6.47 **	23.80 **	8.86
Days to maturity	53.93	191.43 **	0.50	81.95 *	34.71 *	16.88
100 Seed weight (g)	0.01	2.08	1.83	1.31 *	1.73 **	0.42
Yield (g)	25516.64	427511.50 **	133.13	151053.75 **	43480.32 **	14415.24
Yield (Kg/ ha)	72406.47	1187523.00 **	168.20	420032.44 **	120778.00 **	41679.24

Table 1. Analysis of variance (ANOVA) for pooled RBD for thirteen characters in pigeon pea genotypes

***significant at 5%, **significant at 1% probability level**

Table 2. Genetic Variability Parameters of thirteen quantitative characters of forty Pigeonpea germplasm

Traits	Range		GCV	PCV	h^2 (Broad Sense)	GA 5%	GA as % of Mean (5%)
	min	max					
IPS	20.75	35.00	11.757	17.578	44.700	4.381	16.197
FPS	13.75	29.00	17.451	26.919	42.000	4.600	23.306
Wilt (%)	6.48	28.24	36.311	53.634	45.800	6.313	50.642
PH (cm)	162.40	229.75	5.857	14.253	16.900	9.661	4.957
PB	7.00	12.25	10.634	21.493	24.500	1.002	10.839
SB	10.00	20.75	12.058	20.350	35.100	2.149	14.718
DFF	80.25	96.00	4.488	6.397	49.200	5.739	6.485
NPP	168.50	300.00	10.516	22.882	21.100	22.478	9.956
PoB (%)	2.69	13.27	27.601	50.678	29.700	2.168	30.967
DM	181.00	195.50	1.123	2.456	20.900	1.988	1.057
100 SW (g)	8.96	12.04	5.657	8.539	43.900	0.782	7.719
Yield (g)	294.25	673.13	17.670	30.523	33.500	101.656	21.073
Yield (Kg/ ha)	490.42	1121.88	17.490	30.833	32.200	164.324	20.438

IPS=initial plant stand**; FPS**= final plant stand**; PH**= plant stand**; PB**= primary branches**; SB**= secondary branches**; DFF**= days to 50% flowering**; NPP**= number of pods per plant**; PoB%=** pod borer infestation (%)**; DM**= days to maturity**; 100 SW**= 100 seed weight

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