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Genetic Variability, Correlation and Principal Component Analysis for Yield Related Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT

Background: Pigeon pea is an economical source of protein cultivated in arid and semi arid tropical areas of the world. Genetic improvement mainly depends upon the amount of genetic variability available in the population. It is necessary for a breeder to understand the extent of genotypic and phenotypic variation among the germplasm to design an effective breeding programme.

Methods: Eighty pigeon pea genotypes were evaluated for their variability with regard to yield and yield contributing traits. The experiment was carried out at Regional Research Station, Paiyur during 2021-2022 following randomized block design with two replications.

Result: The traits *viz*., plant height, number of primary branches per plant, number of pods per plant and single plant yield can be improved following simple selection method as they exhibited high variability in combination with high heritability and genetic advance. Principal Component Analysis (PCA) revealed three significant principal components (PCs), which accounted for 81.24% of phenotypic variation among the studied genotypes. The traits days to 50% flowering, days to maturity, number of primary branches per plant, number of pods per plant and hundred seed weight had significantly positive association and positive direct effect with yield. Hence, these traits can be used as good selection criteria for yield improvement.

Key words: Correlation, Path analysis, Pigeonpea, Variability.

INTRODUCTION

Pigeonpea is an important legume crop with extensive adaptablity to a range of soil types, temperature and rainfall. These hard woody shrubs are mainly cultivated for its edible seeds containing high dietary protein. It is also known as red gram, arhar, tur, congo pea, gungo pea and no-eye pea. In India, pigeon pea is the second most important pulse crop after chickpea with growing demand. It is predominantly cultivated under rainfed conditions providing 40-60 kg N/ha to the subsequent crop and improves the soil fertility (Sarkar *et al*., 2020). It is widely consumed in the form of dhal as an economical source of protein particularly in the vegetarian diet. The nutritional component of pigeon pea makes it crucial for human nutrition. Pigeon pea is a dense source of nutrients with protein, carbohydrate, minerals and vitamins such as thiamine, riboflavin, niacin and B-complex. It contains high amount of lysine, leucine, aspartic acid, glutamic acid, arginine and provides essential amino acids when consumed with cereals (Talari *et al*., 2018).

Correlation and path analysis helps in identifying the traits contributing to yield that are used to make significant genetic gain. Any crop improvement programme begins with identification of diversity among the plant genetic resources. (Patel *et al*., 2021). The selection of parents for varietal improvement programs depends on the knowledge of existing genetic variability in the crop. Hence, a research work was initiated with an objective to determine the genetic variability, heritability, genetic advance, principal components and association among the pigeonpea genotypes based on quantitative traits to select unique genotypes for different traits as it could be used in pigeonpea breeding programmes.

MATERIALS AND METHODS

The present study was conducted in the experimental farms of Regional Research Station, Paiyur during 2021-2022. The experimental material comprised of 80 pigeonpea genotypes that were sourced by ICRISAT, Department of Plant Genetic

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Resources and Department of Pulses, Tamil Nadu Agricultural University. The experiment was laid in a randomized block design (RBD) with two replications. Each genotype was raised in two rows of 2.5 m length with a spacing of 60 × 30 cm. The genotypes were evaluated for genetic variability based on ten quantitative traits *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), pod width (cm), number of seeds per pod, hundred seed weight (g) and single plant yield (g). All the recommended agronomic practices were followed for raising a healthy crop. Observations were recorded on five randomly selected competitive plants from each genotype.

Analysis of variance was performed for all traits as prescribed by (Panse and Sukhathme, 1967). Genotypic coefficient of variation and phenotypic coefficient of variation was calculated based on the procedures given by Burton (1952). Heritability and genetic advance were estimated utilizing the methodology by Lush (1940) and Johnson *et al*. (1955), respectively. Correlation coefficients were estimated by the procedure suggested by Pearson (1897) and path analysis was carried out as suggested by Dewey and Lu (1959). Principal component analysis was conducted and resulting PCs with eigen values greater than one were selected as proposed by Jeffers (1967).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating high genetic variability present in the population (Table 1).

Coefficients of variation

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) give a better picture of environmental influence on different traits. The estimates of various genetic parameters are presented in Table 2. The magnitude of PCV was slightly greater than GCV for all the traits, revealing little influence of environment in their expression. High estimates of PCV and GCV were recorded by the traits such as number of pods per plant (65.25, 64.35%), single plant yield (64.00, 62.75%), plant height (36.20, 35.25%) and number of primary branches per plant (28.44, 26.69%). This indicates the genetic control on these traits, so selection of these traits will be effective. Similar results were earlier reported in pigeon pea by Sharma *et al.* (2021) for single plant yield, Shruthi *et al.* (2019) for plant height and Parre *et al.* (2022) for number of primary branches per plant.

The traits days to 50% flowering (16.49, 16.09%), days to maturity (12.39, 11.99%), pod length (12.54, 11.79%), number of seeds per pod (11.92, 10.07%) and hundred seed weight (14.01, 13.85%) showed moderate PCV and GCV which implies that phenotypic selection based on these traits may cause improvement to certain extent. Lower value of PCV and GCV was exhibited by the trait pod width (9.51, 8.17%) which restricts its scope for selection. The above report was already made by Pandey *et al.* (2021) for days to 50% flowering, Vanniarajan *et al.* (2021) for days to maturity, Patel *et al.* (2021) for number of seeds per pod and Sahu *et al.* (2020) for hundred seed weight.

Table 1: Analysis of variance for ten quantitative traits in pigeonpea.

Source	DF	MSS									
		DFF	DM	PH	NBP	NPP	PL	PW	NSP	HSW	SPY
Genotype	79	394.02**	507.16**	3163.62**	9.45**	9458.47**	0.80**	0.01**	0.39**	3.24**	790.78**
Replication	1	85.56	187.06	696.01	12.50	2615.98	0.01	0.00	0.34	0.05	469.22
Error	79	507.16	16.98	84.33	0.60	132.08	0.05	0.00	0.06	0.04	15.63

**Significant at 1% level; DF- Degrees of freedom, MSS- Mean Sum of Square, DFF- Days to fifty per cent flowering, DM- Days to maturity, PH- Plant height, NBP- Number of primary branches per plant, NPP- Number of pods per plant, PL- Pod length, PW- Pod width, NSP- Number of seeds per pod, HSW- Hundred seed weight, SPY- Single plant yield.

Table 2: Variability parameters for ten quantitative traits in pigeon pea.

Characters	Mean	PCV (%)	GCV (%)	h^2 (%)	GAM
Days to fifty per cent flowering	86.16	16.49	16.09	95.27	32.36
Days to maturity	130.62	12.39	11.99	93.52	23.88
Plant height (cm)	111.32	36.20	35.25	94.81	70.70
Number of primary branches per plant	7.88	28.44	26.69	88.03	51.58
Number of pods per plant	106.12	65.25	64.35	97.25	130.72
Pod length (cm)	5.27	12.54	11.79	88.33	22.82
Pod width (cm)	0.62	9.51	8.17	73.78	14.45
Number of seeds per pod	3.98	11.92	10.07	71.37	17.52
Hundred seed weight (g)	9.14	14.01	13.85	97.68	28.19
Single plant yield (g)	31.38	64.00	62.75	96.12	126.73

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability in broad sense, GAM = Genetic advance as per cent of mean.

Heritability and genetic advance

The information on transmission of characters from parents to the progeny was provided by heritability estimates. Heritability was high for all the studied traits *viz*., days to fifty per cent flowering (95.27%), days to maturity (93.52%), plant height (94.81%), the number of primary branches per plant (88.03%), number of pods per plant (97.25%), pod length (88.33%), pod width (73.78%), number of seeds per pod (71.37%), hundred seed weight (97.68%) and single plant yield (96.12%). This implies low environmental effect and high capacity of the characters for transmission to subsequent generation.

High genetic advance as per cent of mean was exhibited by the traits *viz*., days to fifty per cent flowering (32.36%), days to maturity (23.88%), plant height (70.70%), the number of primary branches per plant (51.58%), number of pods per plant (130.72%), pod length (22.82%), hundred seed weight (28.19%) and single plant yield (126.73%). High heritability coupled with high genetic advance was showed by the traits *viz*., days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, hundred seed weight and single plant yield. It indicates the predominance of additive gene effects. Hence, these traits can be improved through direct selection. These results are in agreement with the findings of Sandeep *et al.* (2022); Pandey *et al.* (2021) and Parre *et al.* (2022).

Correlation and path analysis

The correlation coefficient was determined for all the quantitative traits with yield and among the traits themselves at both phenotypic and genotypic level (Table 3). Highly significant and positive correlation with yield was recorded by the traits *viz*., days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and hundred seed weight at both genotypic and phenotypic levels. These traits would be useful in selecting the high yielding genotypes in pigeon pea from the available genotypes. This is in accordance with the findings of Gaur *et al.* (2020) and Ranjani *et al.* (2018) for the traits days to fifty per cent flowering and days to maturity. The above report was already made by Sandeep *et al.* (2022) and Hussain *et al.* (2021) for the traits plant height, number of primary branches per plant and number of pods per plant. Rao *et al.* (2020) reported similar results for hundred seed weight. Highest positive significant correlation was observed between days to fifty percent flowering and days to maturity. Similar report was given by Vanniarajan *et al.* (2021). Thus, these traits can be used for selection either alone or in combination to improve the yield potential of the crop.

Correlation analysis provides only the relation between two variables, whereas, path coefficient analysis allows separation of the direct and their indirect effects through other traits by partitioning the correlation. Thus, correlation combined with path analysis gives better understanding of the relationship between different traits. The direct and indirect effects of various quantitative traits on yield were presented in Table 4. The path analysis of various yield contributing traits revealed that seven traits *viz*., days to 50% flowering, days to maturity, number of primary branches per plant, number of pods per plant, pod width, number of seeds per pod and hundred seed weight exhibited positive direct effect on yield. The presence of positive direct effect of traits on yield was earlier reported by Kandarkar *et al.* (2020) for days to 50% flowering, Ranjani *et al.* (2018) for days to maturity, Gaur *et al.* (2020) for number of pods per plant and Sharma *et al.* (2021) for number of seeds per pod. Hence, these traits can be utilized in selection programmes to improve the yield potential of pigeonpea.

Principal component analysis

Principal component analysis was performed based on ten quantitative traits and their results are given in Table 5. The first three principal components with eigen values greater than 1.0 together accounted for about 81.24% of the total variation. The first principal component (PC1) contributed maximum towards variability (43.56%) was correlated with days to 50% flowering, days to maturity, plant height, number of pods per plant and single plant yield. Thus, these traits had the largest participation in the divergence and responsible for the largest portion of its variability. Similar

Table 3: Genotypic and Phenotypic correlation coefficients among yield and yield component traits.

Traits	DFF	DM	PH	NBP	NPP	PL	PW	NSP	HSW	SPY
DFF	1.000	0.926**	0.642**	0.107	0.587**	-0.451**	-0.069	-0.250*	0.303**	0.625**
DM	0.916**	1.000	0.684**	0.219	0.633**	-0.361**	0.029	-0.147	0.402**	0.702**
PH	0.610**	0.645**	1.000	0.322**	0.719**	-0.404**	-0.136	-0.293**	0.139	0.685**
NB/P	0.093	0.183	0.318**	1.000	0.465**	0.064	0.009	-0.040	0.174	0.477**
NP/P	0.564**	0.599**	0.717**	0.452**	1.000	-0.382**	-0.179	-0.278*	0.139	0.948**
PL	-0.416**	-0.334**	-0.378**	0.044	-0.359**	1.000	0.764**	0.784**	0.326**	-0.217
PW	-0.042	0.054	-0.107	-0.002	-0.145	0.615**	1.000	0.792**	0.549**	0.054
NS/P	-0.197	-0.111	-0.273*	-0.037	-0.251*	0.724**	0.567**	1.000	0.339**	-0.077
HSW	0.295**	0.385**	0.130	0.155	0.133	0.299**	0.480**	0.277*	1.000	0.398**
SPY	0.599**	0.660**	0.673**	0.468**	0.938**	-0.195	0.054	-0.048	0.383**	1.000

*and** indicate significance at 5% and 1% levels, respectively. Upper diagonal correlations are genotypic correlations and lower diagonal correlations are phenotypic correlations.

findings were reported by Hemavathy *et al.* (2017) and Hussain *et al.* (2021). The second principal component (PC2) accounted for 26.28% of total variance contributed by the traits pod length, pod width, number of seeds per pod and hundred seed weight. The proportion of variance explained by the third principal component (PC3) was 11.38% and had noticeably high loading of number of primary branches per plant.

The principal component (PC) biplot of the quantitative traits among the studied pigeonpea genotypes is presented in Fig 1. The genotypes ICPL 87091, ICP 7035 and ICPL 99050 are peculiar as they were found far from the rest of genotypes in the biplot, which can be considered for further evaluation in the breeding programmes. Pod length and number of seeds per pod are far from single plant yield in biplot showing a negative correlation between these traits.

Table 4: Direct and indirect effects of yield components on yield at genotypic level.

Traits	DFF	DM	PH	NBP	NPP	PL	PW	NSP	HSW	SPY
DFF	**0.0183**	0.0243	-0.0151	0.0025	0.5382	0.0272	-0.0046	-0.0267	0.0607	0.625**
DM	0.0169	**0.0263**	-0.0161	0.0050	0.5809	0.0218	0.0019	-0.0158	0.0805	0.702**
PH	0.0117	0.0180	**-0.0235**	0.0074	0.6593	0.0244	-0.0090	-0.0314	0.0278	0.685**
NPB/P	0.0020	0.0057	-0.0076	**0.0230**	0.4263	-0.0039	0.0006	-0.0043	0.0348	0.477**
NP/P	0.0107	0.0166	-0.0169	0.0107	**0.9174**	0.0230	-0.0119	-0.0297	0.0279	0.948**
PL	-0.0083	-0.0095	0.0095	0.0015	-0.3500	**-0.0603**	0.0508	0.0840	0.0653	-0.217
PW	-0.0013	0.0008	0.0032	0.0002	-0.1643	-0.0461	**0.0665**	0.0848	0.1101	0.054
NS/P	-0.0046	-0.0039	0.0069	-0.0009	-0.2547	-0.0473	0.0526	**0.1071**	0.0680	-0.077
HSW	0.0055	0.0106	-0.0033	0.0040	0.1277	-0.0197	0.0365	0.0364	**0.2004**	0.398**

Residual effect = 0.1326; **Significant at 1% level of significance. Bold figure indicates direct effect.

Table 5: Principal Component (PC) analysis of ten quantitative traits.

Parameters	PC1	PC2	PC3
Eigen vector (loadings)			
Days to fifty per cent flowering	0.398	0.058	-0.411
Days to maturity	0.408	0.140	-0.334
Plant height	0.402	0.010	0.041
Number of primary branches per plant	0.194	0.139	0.723
Number of pods per plant	0.424	0.035	0.270
Pod length	-0.260	0.453	0.174
Pod width	-0.100	0.531	-0.121
Number of seeds per pod	-0.186	0.474	-0.009
Hundred seed weight	0.115	0.454	-0.196
Single plant yield	0.414	0.196	0.199
Eigenvalue	4.357	2.629	1.139
Proportion of variance	43.566	26.288	11.387
Cumulative variance	43.566	69.854	81.241

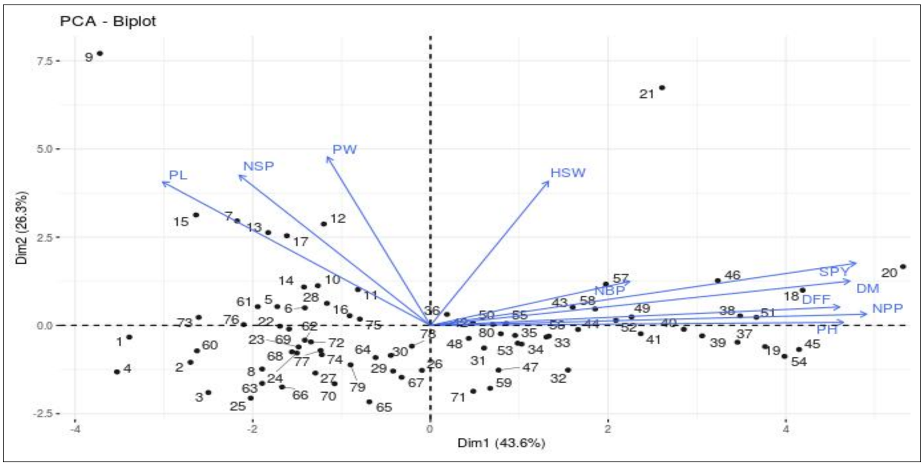

Fig 1: PCA biplot of ten quantitative traits in pigeon pea.

Based on principal component analysis, the traits accounting for most of the variation were days to 50% flowering, days to maturity, plant height, number of pods per plant and single plant yield. Selection of traits with high variability, heritability and genetic advance like plant height, number of primary branches per plant, number of pods per plant and single plant yield can be strictly considered for crop improvement.

CONCLUSION

All the studied traits expressed greater variability except the trait pod width.The estimates of heritability coupled with genetic advance was higher for the traits *viz*., days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, pod length, hundred seed weight and single plant yield. This implies that these traits are governed by additive genes to a great extent and can be improved effectively through phenotypic selection. As the traits days to fifty per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant and hundred seed weight exhibited significant positive association with yield, selection based on these traits would be rewarding for improvement of yield in pigeon pea.

Conflict of interest: None.

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