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Genetic variability and association studies for yield and its attributes in Pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract

An investigation was carried out in the experimental field located at Regional Agricultural Research station, Warangal, Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana to study the Genetic variability, character association and path analysis between yield and its contributing traits in 24 Pigeonpea [*Cajanus cajan* (L.) Mill sp.] genotypes. Analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for number of pods per plant, number of branches per plant. High heritability was recorded for test weight, days to maturity, days to 50% flowering, and number of pods per plant. High heritability combined with high genetic advance was recorded for test weight and number of pods per plant, indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose. Grain yield was positively correlated with Plant height and number of pods per plant. Path coefficient analysis indicated that days to 50% flowering, Plant height and number of pods per plant were essential traits to be considered for realizing the improvement in yield.

Keywords: Genetic variability, correlation, path analysis and pigeonpea

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh], is one of the grain legume crop of rain-fed agriculture in the semi-arid tropics belongs to member of family *Fabaceae* and it is invariably cultivated as annual crop. Globally pigeonpea is cultivated in about 5.41 M ha with a production of 4.48 M tones and yielding an average of 724 kg/ha (FAOSTAT, 2016). India is the largest producer of pigeon pea followed by Myanmar, Malawi, United Republic and Kenya. Pigeon pea is the second largest pulse grown in India next to chickpea. It can fix up to 235 kg nitrogen per hectare and produce more nitrogen per unit area than any other legumes, thus being a source for sustainable agriculture (Peoples *et al.*, 1995) [9]. Pigeonpea is a perennial crop by its habitat and domesticated as annual crop due to its commercial demand. The success of recombination breeding depends on parental diversity to obtain progressive segregants. Crop yield is one of the complex characters controlled by several interacting genotypic and environmental factors. Therefore, selection for characters is not desirable if it is based on phenotypic expression. Hence it is necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Similarly it is necessary to workout genetic association between yield and yield components, which will help in selection. With this view in mind an attempt was made to analyze the nature of genetic variability and to find out correlations among yield and yield contributing characters in Pigeon pea.

Materials and Methods

The present experiment was conducted at Professor Jayashankar Telangana State Agricultural University, Regional Agricultural Research Station, Warangal (Longitude 79° 22' E and Latitude 18° 03' N) for Central Telangana agro- climatic zone of Telangana, South India during *Kharif*, 2016-17. The study was conducted by involving 24 genotypes, were sown in randomized complete block design (RBD) with three replications for exploring the genetic variability, cause and effect of yield and yield attributes. Row to row and plant to plant spacing were maintained at 120 and 20 cm, respectively. The quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, test weight and seed yield per hectare. The data were collected from five single competitive plants of each genotype over three replications.

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Phenotypic and genotypic coefficients of variation were computed based on the formulae suggested by Burton (1952)^[3]. Heritability in broad sense and genetic advance were calculated as per Johnson *et al.*, (1955)^[7]. The correlation coefficients and path analysis were carried out following the methods of Al-Jibouri *et al.*, (1958)^[1] and Dewey and Lu (1959)^[4] respectively.

Results and Discussion

The presence of variability among the individuals of a population is inevitable for crop improvement. Variability is an apparent index for choosing superior material in a plant breeding programme. Variability can be estimated by various methods. Measuring the components of variability is the primary step in reckoning variability. In the current study the analysis of variation shown highly significant differences among the genotypes for all the characters studied *viz.*, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, test weight and seed yield per hectare 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. Perusal the components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than Genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. Magnitude of PCV and GCV was moderate to high for number of pods per plant (19.6&16.8), number of branches per plant (18.8&15.2). These results were in conformity with that of Badru, (2011)^[2], P.J.M. Rao and V.T. Rao (2015)^[6], Thirumala Rao *et al.*, (2016)^[13] Ranjani *et al.*, (2018)^[10] Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain. Heritability in broad sense was high in most of the characters *viz.*, test weight (96.4), days to maturity (88), days to 50% flowering (87.2), and number of pods per plant (73.6). Similar results were reported by Sreelakshmi *et al.*, (2010)^[11]; Niranjan Kumar *et al.*, (2014)^[8], P.J.M. Rao and V.T. Rao (2015)^[6]. Thirumala Rao *et al.*, (2016)^[13]. Though high heritability indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication of the amount of genetic progress for selecting the best individuals. According to Johnson *et al.*, (1955)^[7], heritability estimates along with the genetic gain are usually more useful. High heritability coupled with high genetic advance as percent of mean was more for test weight and number of pods per plant indicating the role of additive gene

in expressing these traits, suggesting better scope for improvement of these traits through direct selection.

Association studies explain the relationship between different variables. It aids in the selection of traits having significant effect on yield and other desirable characters thereby offering a successful crop improvement scenario. In the present investigation the genotypic and phenotypic correlations are on par with each other suggesting the less influence of environment. Hence, in this paper the genotypic correlations only discussed (Table 2). Yield had significant and positive correlation with plant height and number of pods per plant, positive correlation with days to 50% flowering and days to maturity and significant negative correlation with test weight and negative correlation with number of branches per plant.

Days to 50% flowering significant and positive correlation with days to maturity, positive correlation with number of pods per plant and negative correlation with plant height, number of branches per plant and test weight. Days to maturity showing positive correlation with test weight and negative correlation with plant height, number of branches per plant and number of pods per plant. Plant height showing positive correlation with test weight and negative correlation with number of branches per plant and number of pods per plant. Number of branches per plant positive correlation with number of pods per plant and test weight. number of pods per plant positive correlation with test weight.

Correlation coefficients generally describe association between the characters in statistical terms and are inadequate in interpreting the cause and effect relationship. Hence, correlation coefficients between various characters are partitioned into direct and indirect relationship by the path analysis. Path coefficient analysis (Table 3) revealed that the highest direct positive effect of Days to 50% flowering, plant height and number of pods per plant, revealed on yield. These results are in agreement with the earlier findings of, Viridi *et al.*, (2004), Sreelakshmi *et al.*, (2011)^[12] Ranjani *et al.*, (2018)^[10]. Hence, a direct selection criterion should be followed for traits *viz.*, number of pods per plant, number of branches per plant to improve the seed yield.

The study of genetic parameters indicated the fact that characters *viz.* test weight and number of pods per plant exhibited high variability in combination with high heritability and genetic advance as per cent of mean. Hence the selection for above traits can be strictly considered while crop improvement pigeonpea for plant yield (g). The cause and effect analysis implied that the traits like Plant height, number of pods per plant, days to 50% flowering showed positive association and direct effect towards yield thus they can BE A Selection Index for Improving yield.

Table 1: Estimates of variability, heritability and genetic advance in Pigeon pea

Character	Mean	GCV (%)	PCV (%)	Heritability in Broadness (H ²)	Genetic advance	GA as percent of mean
Days to 50% flowering	130.58	2.470	2.645	87.2	7.954	6.09
Days to maturity	172.29	1.903	2.028	88.0	8.118	14.7
Plant height	165.66	5.924	9.290	40.7	16.524	9.975
Number of branches per plant	12.96	15.214	18.843	65.2	4.204	32.43
Number of pods per plant	194.03	16.877	19.666	73.6	74.195	38.23
Test weight	8.939	10.176	10.364	96.4	2.358	26.37
Seed yield per ha(q)	1860.254	11.001	16.615	43.8	357.732	19.23

Table 2: Genotypic correlation coefficients between different traits in Pigeonpea

Traits	DF	DM	PH	NBP	NPP	TW	Seed yield
Days to 50% flowering (DF)	1.0000	0.9803**	-0.0858	-0.0017	0.0508	-0.0139	0.2074
Days to maturity (DM)		1.0000	-0.0807	-0.0718	-0.0187	0.0523	0.1380
Plant height (PH)			1.0000	-0.1663	-0.0586	0.0389	0.6284**
Number of branches per plant (NBP)				1.0000	0.6284**	0.2907*	-0.0912
Number of pods per plant (NPP)					1.0000	0.1131	0.3603*
Test weight (TW)						1.0000	-0.3781**

*, ** Significant at P=0.05 and P = 0.01 level respectively

Table 3: Direct (diagnol) and indirect effects of yield contributing characters in Pigeonpea

Traits	DF	DM	PH	NBP	NPP	TW	Seed yield
Days to 50% flowering (DF)	0.9217	-0.9036	0.0791	-0.0016	0.0468	-0.0128	0.2074
Days to maturity (DM)	-0.6920	-0.7059	0.0569	0.0507	0.0132	-0.0369	0.1380
Plant height (PH)	0.0556	-0.0523	0.6488	-0.1079	-0.0380	0.0252	0.6284
Number of branches per plant (NBP)	0.0005	0.0204	0.0472	-0.2837	-0.1783	-0.0825	-0.0912
Number of pods per plant (NPP)	0.0281	-0.0103	-0.0325	0.3484	0.5545	0.0627	0.3603
Test weight (TW)	0.0046	0.0175	-0.0130	-0.0970	-0.0378	-0.3339	-0.3781

Residual effect(P) = 0.7610

Residual effect(G) = 0.3829

P=Phenotypic

G=Genotypic

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