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RESEARCH ARTICLE

Phenotypic Characterization of Pigeonpea (*Cajanus cajan*) Germplasm Collected from Jharkhand, India

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The present investigation was carried out with an aim to study genetic diversity, trait correlation and path analysis among one hundred pigeonpea accessions collected from geographically diverse locations of Jharkhand state of India. These accessions were evaluated in an augmented block design for two years for nine yield attributing traits and analysis of variance, path analysis, correlation and hierarchical cluster analysis was performed on the recorded data to estimate the extent of variability among genotypes and to measure the direct and indirect contribution of different yield attributing traits on yield. Significant genetic variability was observed among the accessions for all the studied traits with high estimates of heritability and genetic advance. Highly significant and positive correlation was found between different traits and yield per plant. The hierarchical cluster analysis grouped the genotypes into 11 distinct non-overlapping clusters. It was concluded that the genotypes possess significant variability enabling them as candidate genotypes to be utilized as parents for breeding of pigeonpea varieties with desired attributes.

Key Words: Cluster analysis, Genetic divergence, Germplasm, Phenotypic characterization, Pigeonpea.

Introduction

Pigeonpea (*Cajanus cajan* L. Millspaugh) is a highly adaptable, stress-tolerant and high in protein grain legume, which possesses valuable traits for enhancing the sustainability of dry sub-tropical and tropical agricultural systems (Khoury *et al.,* 2015; Kaoneka *et al.,* 2016). It stands next only to chickpea in terms of importance as a mainstream pulse crop in India. However, the yield potential of pigeonpea remains unrealized due to various biotic and abiotic stresses (Khalekar *et al.,* 2013). India is the principal pigeonpea growing country and contributes nearly 90% of world's acreage and production, followed by Myanmar, Kenya, and Malawi (FAOSTAT, 2014). The total area under pigeonpea cultivation is reported to be 3.88 mha in India with a total production of 3.17 mt and an average productivity of 849 kg per ha (Indiastat, 2015). India has now been conclusively recognized as the centre of origin as proposed by Vavilov (1951) and primary centre of diversity for pigeonpea (Saxena *et al.,* 2014; Kaoneka *et al.,* 2016). In India, the North-Eastern part of the Deccan Plateau along with the adjoining Chhotanagpur plateau, forming the parts of the present day Odisha, Chhattisgarh and Jharkhand states, boast tremendous genetic diversity in pigeonpea germplasm. Therefore, there is a high probability of finding elite germplasm in the form of locally adapted land races with desirable agro-morphological traits which may culminate into breeding of pigeonpea varieties with higher productivity. The role of genetic diversity in conducting successful plant breeding programmes involving productivity, quality parameters and stress tolerance is very important (Walunjkar *et al*., 2015). The market demand of pigeonpea is bound to increase in demographically expanding India, where *per capita* pulse availability has declined from 69 grams in 1961 to 32 grams in 2005 (Swaminathan and Bhavani, 2013). The importance of pigeonpea in India is manifold as protein malnutrition is a major problem due to widespread poverty and vegetarian food habit of a significant proportion of the population. Further, as the Eastern India is being viewed as a potential ground for second green revolution in order to realize the national dream of permanent and complete food self-sufficiency, the genetic erosion of precious germplasm is highly likely as was the case with the first green revolution in the Northern India. Moreover, the introduction of

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**Author for Correspondence: Email- santoshkumar.8@icar.gov.in* pigeonpea hybrids in the area targeted for exploration and germplasm collection is also a potent threat to the locally adapted precious land races. Therefore, collection and characterization of the pigeonpea germplasm from this part of the country assumes great significance. The characterization data provides valuable information about genetic diversity in the germplasm collections and this information is helpful in understanding the pattern of genetic variation in a crop species (Rao and Hodgkin 2002) and its further utilization. The pattern of variation enables the breeders to select effective and efficient parent for a crossing programme. In view of these facts the present study was conducted with the objectives to phenotypically characterize, classify and to study divergence and relationship among the collected pigeonpea germplasm accessions in order to estimate the genetic worth of the material for subsequent inclusion in the breeding programmes.

Material and Methods

The experimental material consisted of 100 accessions of pigeonpea germplasm collected from northern Jharkhand during the year 2012 as per the standard germplasm collection guidelines of the National Bureau of Plant Genetic Resources, New Delhi. These germplasm accessions were characterized in an augmented block design (ABD) along with two checks viz. Bahar (local check) and NDA-1 (National check) for two years under sub-tropical, sub-humid climate of Ranchi. The observations were recorded on nine quantitative traits viz. days to 50% flowering, days to maturity, primary branches per plant, 100 seed weight (g), plant height (cm), number of pods per cluster, pod length (cm), number of grains per pod and seed yield per plant (g) on the 100 accessions collected from Jharkhand. The mean values of the recorded observations were used for statistical analysis to assess the genetic diversity among listed accessions. The data was analysed by using the software Windostat Version 9.2 from Indostat services, Hyderabad. The genetic parameters i.e. genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance at 5% selection intensity and correlation coefficients were estimated as per Singh and Chaudhary (1979). The correlation coefficients were partitioned into direct and indirect effects using the path coefficient analysis according to Dewey and Lu (1959). Euclidean distances can theoretically estimate the genetic distances between parents to maximize the transgressive segregation upon crossing and cluster analysis is an appropriate method for determining family relationships. Among various methods used for genetic diversity analysis the Tocher's method is one of the most popular ones. Mahalanobis (1936) generalized distance (D^2) was used to determine the degree of divergence and cluster analysis was performed following Tocher's method (Rao, 1952).

Results and Discussion

The descriptive statistics of the studied traits revealed that the trait seed yield per plant (CV=35.06%) exhibited maximum variation while minimum variation was observed for days to 80% maturity (CV=5.65%) (Table 1). Among all the traits investigated, seed yield per plant had highest standard error, standard deviation as well as highest coefficient of variation. It indicated that the characterized accessions differ considerably on the basis of yield per plant. The descriptive statistics clearly indicated the presence of significant genetic variability among genotypes for other traits also. The traits seed yield per plant and primary branches per plant exhibited maximum variability among all the traits. Both of these two traits are important yield component traits and thus they are determinative of the genetic worth of the germplasm. Similar findings with significant

Table 1. Descriptive statistics of nine traits in pigeon pea

Trait	Mean	Standard Error (±)	Minimum	Maximum	Standard Deviation	CV (%)
Days to 50% flowering	175.90	1.36	139.65	197.65	13.75	7.82
Days to 80% maturity	227.88	1.28	194.80	252.30	12.88	5.65
Primary branches per plant	22.75	0.52	12.22	36.36	5.29	23.25
100 Seed weight (gm)	11.16	0.15	7.80	14.21	1.52	13.63
Plant height (cm)	270.54	2.90	197.05	347.55	29.27	10.82
Pods per cluster	3.58	0.06	2.42	5.49	0.59	16.51
Pod length (cm)	4.94	0.07	2.98	7.00	0.67	13.48
Seeds per pod	4.57	0.04	3.85	5.83	0.44	9.70
Seed yield per plant (g)	98.40	3.42	46.69	190.17	34.50	35.06

variation in seed yield and primary branches per plant were reported by Saroj *et al.* (2013) and Kumara *et al.* (2014). The analysis of variance showed that genotype mean squares for all studied traits were highly significant except for primary branches per plant and hundred seed weight. Among test entries versus control all the traits except primary branches per plant, plant height and seeds per pod showed significant differences for the genotypes under study. It was inferred that the diversity in pigeonpea genotypes is mainly due to the variability in yield per plant, plant height, days to 50% flowering, days to maturity and primary branches per plant which is in agreement with the earlier reports of De *et al.* (1992); Katiyar *et al.,* 2004 and Nag *et al.* (2012). The environmental variance was lower than the corresponding genotypic variance for all the studied traits. The lower environmental variance implied that the studied traits were under genetic control and selection should be effective in their improvement. Similar results were reported by Vange and Egbe (2009), Mahiboobsa *et al.* (2012) and Saroj *et al.* (2013).

The GCV was highest for yield per plant followed by the traits primary branches per plant and pods per cluster (Table 2). Linge *et al.* (2010) Saroj *et al.* (2013) reported similar results regarding GCV in pigeonpea. High GCV and minimum difference with the corresponding PCV indicates a lesser role of environment in the expression of these traits and their amenability for improvement through selection. High broad sense heritability estimates were found for yield per plant (0.97), seeds per pod (0.94), pod length (0.93), pods per cluster (0.88), plant height (0.88), days to 80% maturity (0.88) and days to 50% flowering (0.87). The heritability estimates were moderate for primary branches per plant (0.52) and low for 100 seed weight (0.14). The estimates of heritability indicated the possibility of trait improvement through selection and generally, similar pattern of heritability estimates for different traits were reported by Dahiya and Brar (1977) and Manyasa *et al.* (2008). However, Saroj *et al.* (2013) have reported low broad sense heritability for number of seeds per pod and high heritability for 100 seed. The traits with high heritability can be used as descriptor for classification of studied germplasm (Abu-Alrub, 2004). Genetic advance is an indicator of the genetic progress in a trait under selection. In the present study high genetic advance was estimated for the traits yield per plant (66.97), pods per cluster (27.40), pod length (24.55) and primary branches per plant (21.28). When both genetic advance and heritability are high for a trait, it indicates the predominance of additive gene effects and as per Panse, (1957) selection should be effective in the improvement of these traits. To assist and accelerate the process of selection, positive and significant phenotypic association between yield and its component traits is highly desirable. In the present investigation, positive correlation with yield per plant was exhibited by all the traits under study (Table 3). Pods per cluster exhibited significant positive correlation with yield per plant and highly significant positive correlation was exhibited by the traits days to 50% flowering and days to 80% maturity, days to 50% flowering and plant height, days to 50% flowering and pods per cluster, days to 80% maturity and plant height and pods per cluster, primary branches per plant and plant height and pod clusters per plant, 100 seed weight with pod length and seeds per pod, plant height with pods per cluster, pod length with seeds per pod. The traits 100 seed weight and pods per cluster were found to be negatively correlated and the correlation was significant. The positive correlation among traits indicated that selection based on these traits

Table 2. Genetic parameters of the studied genotypes

Trait	Mean	Variance			Heritability	GCV	PCV	GA
		Environmental	Genetic	Phenotypic				
Days to 50% flowering	175.76	23.17	152.03	175.20	0.87	7.02	7.53	13.46
Days to 80% maturity	228.03	19.08	138.43	157.51	0.88	5.16	5.50	9.96
Primary branches per plant	22.80	9.90	10.68	20.59	0.52	14.34	19.90	21.28
100 seed weight	11.13	1.38	0.22	1.60	0.14	4.22	11.36	3.22
Plant height	270.43	98.14	740.03	838.17	0.88	10.06	10.71	19.47
Pods per cluster	3.57	0.03	0.26	0.29	0.88	14.15	15.05	27.40
Pod length	4.92	0.03	0.37	0.39	0.93	12.33	12.76	24.55
Seeds per pod	4.57	0.01	0.16	0.17	0.94	2.11	8.66	17.32
Yield per plant	97.78	35.56	1044.74	1080.30	0.97	33.06	33.61	66.97

Table 3. Phenotypic correlation coefficients

Trait	Number of days to 50% flowering	Number of days to 80% maturity	Number of primary branches per plant	100 Seed weight (gm)	Plant height (cm)	Number of pods per cluster	Pods length (cm)	Number of grains per pod	Seed yield per plant (g)
Days to 50% flowering	**1.000**	0.773***	-0.090	-0.048	0.428***	0.216*	-0.108	-0.179	0.101
Days to 80% maturity		**1.000**	0.039	0.015	0.334***	0.264**	-0.058	-0.035	0.127
Primary branches per plant			**1.000**	0.144	0.196*	0.201*	0.028	0.184	0.154
100 Seed weight (gm)				**1.000**	0.004	-0.006*	0.211*	0.375***	0.154
Plant height (cm)					**1.000**	0.413***	-0.075	0.050	0.158
Pods per cluster						**1.000**	0.006	0.030	0.263**
Pods length (cm)							**1.000**	0.607***	0.129
Seeds per pod								**1.000**	0.150
Seed yield per plant (g)									1.000

* Significant at 5% ** Significant at 1% *** Significant at 0.1%

should positively contribute towards improvement of the seed yield. These results are supported by the earlier findings of Salunke *et al*. (1995) and Sodavadiya *et al*. (2009). Padi (2003) have reported significantly positive correlation between pods per plant and yield per plant. However, Vange and Moses (2009) reported negative correlation between days to 50% flowering and days to maturity which was not observed in the present study. The path coefficient analysis for seed yield per plant through estimated genotypic correlation coefficients between yield per plant and its component traits is presented in the Fig. 1. It revealed that number of pods per cluster gave the maximum direct effect (0.217) on the yield followed by 100 seed weight (0.111). The maximum direct effect of pods per cluster followed by 100 seed weight, primary branches per plant, days to 50% flowering, seeds per pod, plant height and number of days to 80% maturity as revealed by path analysis are in general agreement with the results reported by Brar *et al.* (1991) and Nag and Sharma (2012). However, Udensi and Ikpeme (2012) reported that 100 seed weight was having highest direct effect on yield per plant. The trait, pods per plant, manifested through number of pods per cluster was having the highest direct effect on seed yield and was found to be the main yield component trait in the present study. Similar findings have been reported by Padi (2003). The collected genotypes were subjected to genetic diversity and relationship analysis

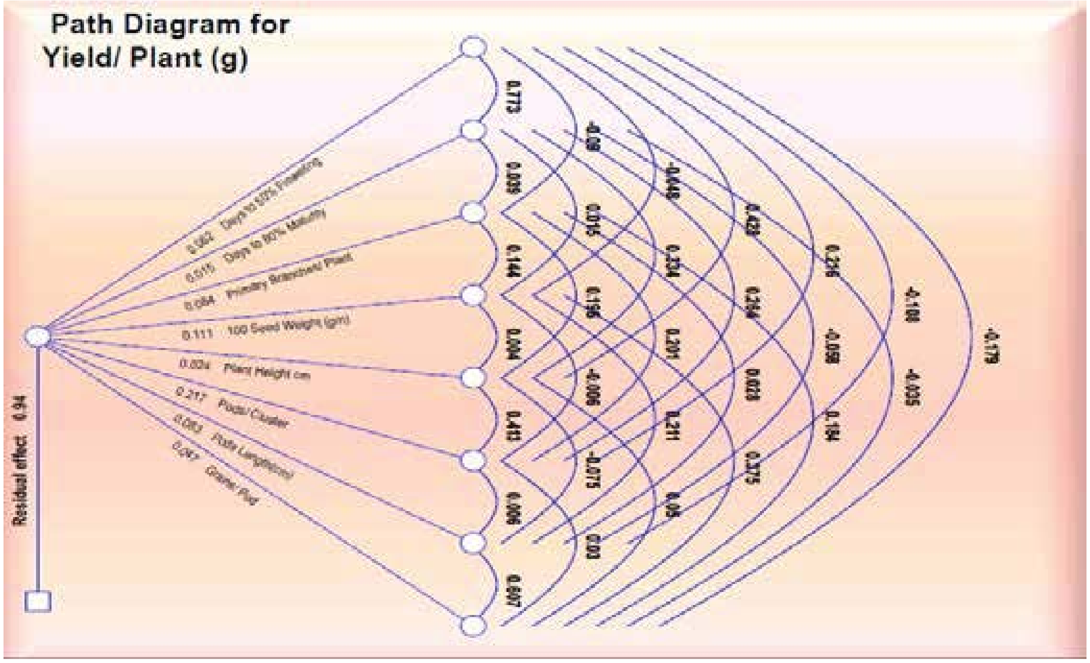

Fig. 1. Path diagram for yield per plant (R^2= 0.1168 Residual effect = 0.94)

by estimating Euclidean inter-cluster and intra-cluster standard distances. The dendrogram based on Ward's minimum variances (Ward, 1963) was constructed which grouped all accessions under study into 11 distinct non-overlapping clusters. The number of clusters and the inter-cluster distances indicated presence of significantly high genetic diversity in the collected germplasm accessions. Cluster I comprised of 14 genotypes which were maximum in any cluster followed by cluster V and X with 13 genotypes each, cluster VIII and IX with 10 genotypes each, cluster III, IV and XI with 9 genotypes each and cluster II, VI and VII with 6, 5 and 4 genotypes respectively. The cluster means for the studied nine quantitative traits were estimated and based on it the desirable accessions were selected from cluster II which had accessions with lowest mean for days to maturity (211.38) and cluster VII which had accessions with maximum mean yield per plant (153.08). The inter-cluster distance was maximum between cluster II and VI (38.13) and minimum between clusters VIII and IX (11.65). The intra-cluster distance was minimum in cluster XI (6.61) and maximum in cluster VI (11.30). Both Bahar and NDA-1, used as checks were grouped in the same cluster in the present study. Different genotypes of the same geographic origin were found to be scattered across different clusters and thus the geographic site of collection and genetic divergence were found to lack a definite relationship in the present study. The main factor behind the presence of high genetic diversity in the collected accessions appeared to be due to genetic drift and selection in differing environments rather than the geographic origin of the germplasm. The free movement of the germplasm across different environments represented by the collection sites could also be a reason of the lack of a definite relationship between the geographic site of collection and genetic identity of the accession. The experimental findings of cluster analysis are in general agreement with the findings of Sharma and Roy (1994), Mahamad *et al.* (2006), and Pandey *et al.* (2015). Kumari *et al.* (2014) have reported similar results in an SSR primer based genetic diversity study in pigeonpea. The inter-cluster distances were greater than the intra-cluster distances revealing that considerable amount of genetic diversity existed among the accessions. It is assumed that maximum amount of heterosis would be manifested in cross combinations involving the parents belonging to the most divergent clusters. The percent contribution of different traits for genetic divergence showed that the contribution of complex trait yield per plant was maximum (47%) towards genetic divergence followed by that of plant height (40%). The traits days to 50% flowering and days to 80% maturity contributed 6% each while primary branches per plant contributed only 1% to the total genetic divergence. These findings are in agreement with those of Kumara *et al.* (2014) who reported that yield is the biggest contributing trait towards genetic divergence in pigeonpea. In the present study, the parents having traits contributing maximum towards genetic divergence, for example, yield per plant and plant height were successfully identified for further use in the pigeonpea improvement programmes.

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