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Research Note

Genetic analysis for yield and its components in hybrid pigeonpea

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Abstract:
Mahalanobis D^2 statistics was applied to assess the divergence among the 36 hybrids and three checks of pigeonpea. The hybrids were grouped into nine clusters, where cluster I was the largest containing twenty one hybrids followed by cluster II with seven hybrids. The inter cluster distance was maximum between cluster III and VIII followed by III and VI and seed yield contributed the most (22.2) towards genetic divergence. High heritability coupled with high genetic advance as per cent of mean was noticed for seed yield, number of primary branches per plant and secondary branches per plant suggesting additive gene action controlling these traits. Seed yield showed positive correlation with all the characters studied except 100-seed weight. Genotypic path analysis revealed that the maximum direct effect on seed yield was exhibited by number of primary branches per plant, days to 50% flowering and number of pods per plant.

Key words: Hybrid pigeonpea, divergence, variability

Pigeonpea is a drought tolerant legume crop in tropical and sub tropical regions of Asia, Africa, Latin America and Caribbean. It plays an important role in subsistence agriculture because, it produces protein rich food with fewer inputs and can be grown in diverse cropping systems. India has the largest pigeonpea area (3.5 m.ha) with an estimated production of 2.5 m. tons. To meet the protein needs of population, it is essential to increase the production of pulses. A number of varieties has been released and the area also increased but the yield has remained unacceptably low because of several biotic and abiotic constraints. Hence these hybrid breeding technology is expected to enhance the production by a margin of 30% or more, thereby breaking the yield barrier in pigeonpea. Development of hybrid pigeonpea with diversified genetic base of the male sterile and fertility restorers has increased emphasis on disease and insect resistance, stability and yield. The present investigation has been carried out to understand the extent of genetic variation for various characters, to know the extent of correlation for yield and component characters and direct and indirect effects of various characters on yield.

The experimental material comprised of 36 hybrids of pigeonpea received from ICRISAT, Patancheru, Hyderabad. The material was sown in randomized block design with two replications during *kharif* 2010 at Agricultural Research Station, Tandur. Each line was accommodated in three rows of 5m length spaced at 100 cm apart with plant to plant spacing of 20 cm. The recommended packages of practices were followed to raise a healthy crop. Data were recorded on days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100- seed weight (g) and seed yield (g) on five randomly selected plants in each replication. Data were subjected to statistical analysis to work out genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance as per cent of mean as per Johnson *et al*, 1955. The analysis of genetic divergence was carried out using Mahalanobis D^2 statistics. Thirty six hybrids studied were grouped into clusters by the Tocher's method as described by Rao (1952). Genotypic and phenotypic correlation coefficients were calculated as per Johnson *et al.*, (1955). The direct and indirect contribution of various characters to yield were calculated through path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959).

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on D^2 statistics, the 36 pigeonpea hybrids were grouped into 9 clusters with variable numbers of genotypes revealing the presence of considerable amount of genetic diversity in the material. Cluster I the maximum number of hybrids (21) followed by cluster II with 7 hybrids and cluster III with 2 hybrids. Clusters I and II together included 28 hybrids reflecting a narrow genetic diversity among them while clusters IV, V VI, VII, VIII and IX were solitary clusters demonstrating the impact of selection pressure in increasing thegenetic diversity (Table 4).

The intra cluster distance ranged from 0.00 to 2.98 with highest intra cluster distance in cluster II (2.98) followed by I and III. Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past history of selection in developmental traits and degree of general combining ability (Table1). The inter cluster D^2 values ranged from 2.63 to 8.73, the maximum inter cluster distance was observed between the clusters III and VIII (8.73) followed by III and VI (8.51) and III and IX (8.21). The minimum inter cluster distance was observed between cluster IV and VII (2.63) indicating the close relationship among the hybrids in these clusters.

The cluster mean of each trait towards genetic divergence are presented in Table 2. The data revealed that considerable differences existed among the clusters for most of characters studied. The cluster VI (ICPH 3759) recorded the highest mean values for days to 50% flowering, plant height and seed yield whereas IX (ICPH 2751) showed highest mean values for primary branches per plant, secondary branches per plant and pods per plant. Similarly, cluster VIII exhibited high mean values for days to maturity and 100 seed weight. The data on inter cluster distances and *per se* performance of hybrids were used to select genetically diverse and agronomically superior hybrids. The characters contributing to most of the divergence should be given more importance for the purpose of effective selection (Table 3). Among the eight characters studied seed yield contributed the most (22.2) towards genetic divergence of hybrids followed by days to 50% flowering, plant height and secondary branches per plant whereas, test weight contributed the least divergence indicating narrow diversity for this character among the hybrids under study.

The range of variation was maximum for seed yield (391 – 2656 kg/ha), number of pods per plant (97-505), plant height (126-228 cm) and days to maturity (159-208 days), while it was lowest in the case of 100 seed weight (9.44 – 13.54 g) and number of primary branches per plant (6.1 to 23.2). PCV values were higher than the GCV values for all the characters studied (Table 5) indicating the role of environment in their expression. The magnitude of variation was maximum for number of secondary branches per plant (38.65), number of pods per plant (35.73), seed yield (32.56) and number of primary branches per plant (29.87). These results are in accordance with the results of Sameer Kumar (2006).

In the present investigation all the characters expressed high heritability estimates ranging from 55.5(100 seed weight) to 87.7 (days to maturity). The genetic advance was highest for secondary branches per plant (64.31%) followed by number of pods per plant (59.98%), seed yield (56.10%) and number of primary branches per plant (52.07%) and rest of the characters recorded medium to low genetic advance as per cent of mean. The variability and genetic advance as per cent of mean were higher for number of primary branches, number of secondary branches, number of pods per plant and seed yield while, high heritability coupled with high genetic advance as per cent of mean was noticed for the characters *viz.*, seed yield, number of primary branches per plant and secondary branches per plant suggesting the presence of additive gene action controlling these traits. Similar results were reported by Baskaran and Muthaiah (2006). However, high heritability with low genetic advance as per cent of mean indicates the influence of environment on the traits which will result in unstable expression of traits. Hence, breeder should not rely on the estimates of heritability alone.

Correlation studies provide better understanding of interrelations of yield components which helps the plant breeder during selection. Seed yield showed positive correlation with all the characters studied except 100-seed weight (Table 6). 100-seed weight showed negative association with all the traits except number of primary branches per plant. Seed yield has high positive correlation with number of primary branches per plant, days to 50% flowering, number of pods per plant and days to maturity. Rahman *et al.,* (1999) reported similar results in pigeonpea. 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. The perusal of the results obtained in genotypic path analysis revealed that the maximum direct effect on seed yield was exhibited by number of primary branches per plant, days to 50% flowering and number of pods per plant (Table 7). The negative direct effect on seed yield was exhibited by plant height, number of secondary branches per plant and 100-seed weight. These results are in agreement with the earlier findings of Lal *et al.,* (2002) and Viridi *et al.,* (2004). Hence, number of pods per plant, number of primary branches per plant and days to 50% flowering appear to be major components for seed yield and selection for them will lead to increase in seed yield in hybrid pigeonpea.

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Table 1: Estimates of mean, range, phenotypic and genotypic coefficient of variability, heritability and genetic advance for eight characters in pigeonpea hybrids

Character	Mean	Range		Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (%)	Genetic advance	Genetic advance as % of mean
		Min.	Max.					
Days to 50 % flowering	129	96	148	8.66	9.49	83.3	21.02	16.29
Days to maturity	191	159	208	6.23	6.66	87.7	22.93	12.03
Plant height (cm)	196	126	228	10.76	12.12	78.8	37.98	19.68
No. of primary branches / plant	12.1	6.1	23	29.87	35.30	71.6	6.30	52.07
No. of secondary branches / plant	20.36	19	41	38.65	47.86	65.2	13.05	64.31
No. of pods/ plant	240	97	505	35.73	43.85	66.4	142.16	59.98
100 seed weight (g)	11.33	9	13	7.93	10.65	55.5	1.38	12.18
Seed yield / plant (g)	1256	391	2656	32.56	38.88	70.2	706.95	56.19