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Research Article

Genetic variability and correlation in pigeonpea genotypes

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Abstract

Forty nine pigeon pea genotypes were evaluated at Agricultural Research Station Tandur during *kharif* 2015-16. Genotypes were grouped into six clusters based on Mahalonobis D^2 statistics. Days to maturity contributed to maximum genetic divergence followed by days to 50% flowering. Maximum inter cluster distance was observed between clusters II and VI and intra cluster distance in cluster I and II. Genotypes in cluster V recorded highest mean values for number of secondary branches/plant and number of pods/plant and seed yield. Broad sense heritability estimates were highest for days to maturity and days to 50% flowering. Significant and positive genotypic and phenotypic correlation was observed between seed yield and number of pods/plant and number of secondary branches/plant. The range of GCV observed was 4.55 to 22.07% for the traits under study indicating the extent of variability present among the pigeon pea genotypes. Path coefficient analysis revealed that days to maturity exhibited maximum direct effect followed by number of pods/plant.

Keywords
Pigeon pea, Genetic divergence, Correlation, Heritability

Introduction

Pigeon pea (*Cajanus cajan*) is the second important pulse crop after chickpea in India. India is the largest producer and consumer of pigeon pea. The crop suffers from yield losses due to various biotic stresses like wilt, Sterility Mosaic Disease, *Helicoverpa* pod borer *etc.* Therefore, it is necessary to increase the production of pigeon pea by developing pest resistant varieties. To develop high yielding varieties, knowledge on the existing genetic variability in the crop needs to be studied. Yield is a complex trait that is highly influenced by environment.

Genetic parameters like genotypic and phenotypic coefficient of variation, heritability and genetic advance are highly reliable making effective selection in the breeding material. The information on correlation of yield with yield attributes will assist the breeders in the identification of traits contributing to yield to make significant genetic gain. The present investigation was carried out to analyze the genetic divergence existing in the crop, phenotypic and genotypic variability, heritability in broad sense and genetic advance. This information is highly useful for breeders in the selection of parents and breeding material for the development of high yielding varieties of pigeon pea suited to rain fed conditions.

Materials and Methods

The experiment comprising of forty nine pigeon pea genotypes was carried out in randomized block design with three replications during *Kharif* 2015-16 at Agricultural Research Station, Tandur. The genotypes were sown in four rows of four meter length with 100 cm and 20 cm spacing between rows and plants respectively. All the recommended agronomical practices were followed for raising a good crop. Five plants were randomly selected for recording the data on days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/plant, 100-seed weight (g) and seed yield (kg/ha). Mahalonobis D^2 statistic (Rao, 1952) was used to analyze genetic divergence among pigeon pea genotypes. The data was subjected to statistical analysis to calculate genotypic (GCV) and phenotypic (PCV) coefficients of variation, heritability and genetic advance as per-cent of mean. Phenotypic coefficient of correlation was computed according to Al-Jibouri *et al*. (1958). The phenotypic correlation was partitioned into direct and indirect effects as suggested by Dewey and Lu (1959).

Results and Discussion

Analysis of variance revealed that significant differences existed among the genotypes for the characters studied. General mean, range and standard error are presented in Table. 1. Range of variation was highest for seed yield and lowest for number of primary branches/plant. The genetic parameters like genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance as percent of mean are also presented in Table 1. Phenotypic coefficient of variation was relatively high compared to corresponding genotypic coefficient of variation for all the characters studied, indicating environmental influence on the expression of these traits. The range of PCV observed was 6.58 to 27.13% for the characters which indicates the extent of phenotypic variability in the population. PCV observed was moderate for characters like seed yield (22.29%) and number of pods/plant (27.13%), whereas 100-seed weight (9.37%) and plant height (6.58%) exhibited low PCV. Genotypic coefficient of variation which indicates the extent of genetic variability ranged from 4.55% to 22.07%. Maximum GCV was observed for number of pods/plant (22.07%), followed by days to 50% flowering (17.71%) providing an opportunity for genetic improvement. Very low estimates of GCV and PCV were recorded for plant height and 100-seed weight. Genetic coefficient of variation along with heritability increases the efficiency of selection (Burton, 1952). GCV which measures the extent of genetic variability of a trait is considered in combination with heritability and genetic advance while assessing the effect of phenotypic selection. Yield attributing traits such as number of pods/plant and 100-seed weight exhibited higher heritability indicating that genetic improvement might be possible for these characters. High heritability values of more than 95% for number of pods/plant and 100-seed weight was earlier reported by Sharma *et al.,* 2012. Similar results were reported by Patel and Patel (1998) and Linge *et al*. (2010). High heritability though indicated 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. Johnson *et al.,* (1955) reported that heritability estimates along with the genetic gain are usually more useful. Number of pods/plant and days to 50% flowering exhibited moderate magnitude of genetic advance as a percentage of the mean, indicating that variations in these characters are attributable to additive gene effects to certain extent. High heritability coupled with genetic advance for the trait seed yield indicated the predominance of additive gene effect (Padi, 2003).

Genotypic correlation provides a measure of genotypic association among different traits and helps in identifying the traits in selection. Seed yield was found to be significantly and positively correlated with number of secondary branches/plant (0.5631***) and number of pods/plant (0.5214***) at the genotypic level, indicating that these traits contribute considerably towards seed yield in pigeon pea. 100-seed weight was negatively correlated with seed yield indicating that genotypes with bold seeds had lower seed yield. Similar such correlation among yield and 100 seed weight in pigeon pea as published earlier by Mittal *et al.,* 2010 and Patel and Acharya (2011). Phenotypic correlations estimated among forty nine genotypes for eight traits indicated inherent association between every two variables (Table 2). Seed yield was significantly and positively correlated with number of secondary branches/plant (0.3339***) and number of pods/plant (0.5243***) at phenotypic level. Days to maturity was significantly correlated with days to 50% flowering. This indicated that genotypes flowered earlier matured earlier. Seed yield was positively and significantly correlated with number of fruiting branches/plant and number of pods/plant (Sharma *et al.,* 2012). Similar results were earlier reported by Saroj *et al.,* 2013 except for one deviation that there was significant positive correlation of seed yield with 100-seed weight.

In the present study path coefficient analysis was carried out to estimate the direct and indirect contribution of various traits to seed yield. Days to maturity (8.4552) exhibited the highest magnitude of direct effects on seed yield followed by number of pods/plant (0.5224) (Table 3). The direct effects of number of pods/plant on seed yield were mainly due to indirect effects *via* number of primary branches/plant (0.0213) and secondary branches/plant (0.2377).

Also number of pods/plant is positively and significantly correlated with seed yield. These characters are principal components of seed yield and can be considered as selection criteria for increasing the seed yield of pigeonpea. Similar results were reported by Thanki and Sawargaonkar (2010). Number of secondary branches/plant had positive and significant correlation with seed yield (rg=0.3339***) and its direct effect on seed yield was 0.0946 which is mainly due to indirect effects *via* number of primary branches (0.0161) and number of pods/plant (0.0431)and100-seedweight (0.0100)

(Table 3). Earlier studies (Chandirakala and Subbaraman, 2010) indicated that number of pods/plant had negative direct effect on seed yield. The residual effect was found to be 0.8216 in path analysis. This indicated that other attributing characters were also important and may play a critical role in pigeon pea improvement. Kingshlin and Subbaraman, 1999 have reported that pod length and number of seeds/pod were the important yield contributing characters in pigeon pea. Previously Dahiya and Singh, 1994 have reported plant height, days to 50% flowering and number of pods/plant having both direct and indirect effect on seed yield of pigeon pea.

The Mahalonobis D^2 values grouped the forty nine pigeon pea genotypes into six distinct clusters. The average intra and inter cluster distances are depicted in (Table 4). The maximum intra D^2 value was 3.10 (cluster II). The maximum inter cluster distance was between cluster II and VI (99160.68). Optimum genetic distance between parents is a prerequisite for hybridization to increase the chances of isolation of transgressive segregants in the segregating generations. Cluster VI recorded early maturity (160) and maximum number of primary branches/plant while cluster I recorded highest days to maturity (200.77). Cluster V recorded more number of secondary branches (31.4), number of pods/plant (532.0) and highest seed yield (3149.3 kg/ha) (Table 5). Genotypes of cluster IV may be utilized for breeding early maturing varieties, while those of cluster II in the development of medium duration high yielding varieties. Maximum genetic distance was observed between genotypes of cluster II and VI. Thus genotypes in cluster IV and V can be utilized as parents for the development of early maturing and high seed yielding varieties. D^2 statistic indicated the characters contributing to divergence and is presented in Table 6. Maximum contribution towards genetic divergence is by days to maturity (50.51%) followed by days to 50% flowering (23.72%). These characters together recorded for more than 70% of the total divergence in the pigeon pea genotypes studied. Pandey *et al.,* 2013 reported that 100-seed weight and pods/plant contributed to 39.53% and 18.97% respectively towards genetic divergence among the parents of pigeon pea hybrids studied, while Muniswamy *et al.,* 2014 reported that 100-seed weight contributed to minimum genetic diversity (0.02%) and number of pods/plant to maximum genetic diversity (59.83%).

It is concluded that the yield components of pigeon pea *viz.*, number of secondary branches, number of pods/plant and days to maturity are important yield contributing traits since they have shown positive and significant correlation with seed yield. Number of pods/plant had significant positive correlation with seed yield coupled with high heritability and genetic advance.

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Table 1. Estimation of variability parameters in pigeonpea

Characters	Mean	Range	SE	Coefficient of variation		h^2_b (%)	GA (5%)	GA as % of Mean
				GCV (%)	PCV (%)			
Days to 50% flowering	124.5	94.6 - 157	4.38	17.71	18.73	89.4	42.95	34.48
Days to maturity	189.1	158.6 - 222	4.38	11.75	12.42	89.5	43.31	22.90
Plant Height	199.5	182.8 - 219.3	5.46	4.55	6.58	48.0	12.97	6.50
No. of primary branches/plant	4.6	3.7 - 5.8	0.42	15.59	22.11	49.7	1.05	22.64
No. of secondary branches/plant	29.1	22.2 - 44.8	2.46	12.38	19.21	41.5	4.78	16.43
No. of pods/plant	325	188.6 - 512	29.6	22.07	27.13	66.2	120.21	36.99
100-seed weight	10.25	8.3 - 11.8	0.34	7.36	9.37	61.7	1.22	11.92
Seed yield (kg/ha)	2324.8	1442 - 3812	213.61	15.60	22.29	49.0	523.24	22.51

Table 2. Estimates of genotypic and phenotypic correlation coefficients for yield related traits in pigeonpea

Characters	Days to maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/ plant	100-seed weight	Seed yield (kg/ha)
Days to 50% flowering gp	0.9998 0.9998	-0.2160 -0.1752	-0.2424 -0.1821	0.3073 0.2035	-0.0466 -0.0276	-0.0723 -0.0856	0.0628 -0.0178
Days to maturity gp		-0.2204 -0.1779	-0.2374 -0.1788	0.3021 0.2004	-0.0539 -0.0333	-0.0761 -0.0883	0.0626 -0.0176
Plant height gp			0.0759 0.0451	0.4295 0.2213	0.2922 0.2080	0.1368 0.0850	0.0356 0.1473
No. of primary branches/plant gp				-0.1560 0.1703	-0.1347 0.0407	-0.0792 -0.0321	0.1057 0.1424
No. of secondary branches/ plant gp					0.6724 0.4551	0.2586 0.1059	0.5631*** 0.3339***
No. of pods/plant gp						-0.1001 -0.0505	0.5214*** 0.5243***
100-seed weight gp							-0.1437 0.0236

Table 3. Phenotypic path coefficient showing direct and indirect effect of characters on grain yield in pigeonpea

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/ plant	100-seed weight (g)	Phenotypic correlation with seed yield (kg/ha)
Days to 50% flowering	**-8.4507**	-8.4490	1.4805	1.5391	-1.7201	0.2336	0.7236	-0.0178
Days to maturity	8.4534	**8.4552**	-1.5044	-1.5116	1.6945	-0.2817	-0.7464	-0.0176
Plant Height	-0.0057	-0.0058	**0.0328**	0.0015	0.0073	0.0068	0.0028	0.1473
No. of primary branches/plant	-0.0142	-0.0140	0.0035	**0.0781**	0.0133	0.0032	-0.0025	0.1424
No. of secondary branches/plant	0.0193	0.0190	0.0209	0.0161	**0.0946**	0.0431	0.0100	0.3339***
No. of pods/plant	-0.0144	-0.0174	0.1087	0.0213	0.2377	**0.5224**	-0.0264	0.5243***
100-seed weight	-0.0054	-0.0055	0.0053	-0.0020	0.0066	-0.0032	**0.0626**	0.0236

Figures in bold letters indicate the direct effects, Residual effect = 0.8216

Table 4. Average Inter and intra cluster distances (D^2) of six clusters in pigeonpea

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I	3.42	99160.8	4.52	4.72	4.71	5.5
II		3.10	99160.66	99160.65	99160.65	99160.68
III			0.0	4.77	4.92	5.36
IV				0.0	3.29	4.84
V					0.0	6.47
VI						0.0

Table 5. Cluster means of six clusters for eight characters in pigeonpea

Cluster	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/plant	100-seed weight (g)	Seed yield (kg/ha)
I	135.77	200.77	197.09	4.49	28.97	300.33	10.19	2311.25
II	116.59	180.59	202.12	4.53	29.59	351.44	10.41	2321.46
III	99	164	201.53	5.07	30.13	188.63	11.46	1442.0
IV	95	160	193.33	5.27	23.20	323.87	8.49	2991.0
V	103.67	168.67	201.67	4.87	31.40	532.0	9.26	3149.3
VI	117	182	197.8	9.2	23.60	241.07	9.65	2100.0

Table 6. Percent contribution of characters towards genetic diversity in pigeonpea

Characters	**Contribution %**	**Times Ranked 1st**
Days to 50% flowering	23.72	279
Days to maturity	50.51	594
Plant Height	3.74	44
No. of primary branches/plant	2.72	32
No. of secondary branches/plant	2.21	26
No. of pods/plant	4.08	48
100-seed weight	6.97	82
Seed Yield (kg/ha)	6.04	71