

Genetic Variability, Correlation Coefficient and Path Analysis for Yield and its Attributing Characters in Some Early Genotypes of Pigeon pea [*Cajanus cajan* (L.)]

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ABSTRACT

The present investigation was carried out during *kharif* season, 2017-17 on ten genotypes with a check variety in Randomized Block Design to study the phenotypic and genotypic variances, heritability, genetic advances, correlation and path coefficient. Results revealed maximum genotypic coefficient of variation and phenotypic coefficient of variation was recorded for number of secondary branches per plant (35.90). Heritability in broad sense ranged from 57.00 per cent (seeds per pod) to 96.00 per cent (days to 50 per cent flowering). High genetic advance was observed for number of secondary branches per plant (135.07) followed by plant height (80.70) indicating the prevalence of additive gene action for inheritance of these traits. Seed yield per plant showed highly significant and positive correlation with plant height (0.943), primary branches per plant

(0.924) and secondary branches per plant (0.915) at both genotypic and phenotypic levels. The higher positive direct effect on seed yield per plant was exerted by secondary branches per plant (2.288) and highest negative direct effect on seed yield per plant was exhibited by plant height (-1.776). The inter-relationship among the characters identified above may be utilized in the breeding program to exploit the field potential and to find out the most elite genotype.

Keywords Pigeon pea, Genetic variance, Heritability, Correlation, Path analysis.

INTRODUCTION

Pigeon pea is an important multi-use shrub legume of the tropics, subtropics and warmer regions of the world between 30N and 35S latitude. Unlike other grain legumes, pigeon pea production is concentrated in developing countries, particularly in South and South East Asia and Eastern and Southern African countries. Pigeon pea is rich in starch, protein, calcium, manganese, crude fiber, fat, trace elements, and minerals. It also helps in sustaining the soil productivity through symbiotic fixation of atmospheric nitrogen into the soil as well as the leaf fall helps in recycling of nutrients in the soil.

India is the largest producer of pigeon pea and

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accounts about 80% of the global area and production. It is one of the most widely cultivated pulse crops in India next to chickpea. At present, the world production of pigeon pea sums up to 3.25 million tonnes in an area of 4.3 million hectares. Production of pigeon pea in India stands at 41.80 lakh tonnes from 44.59 lakh ha areas (DES 2017). In spite of the huge area under this crop in India, there is no proportionality in its production and consumption, as the per capita availability of pigeon in India has been declining due to various biotic and abiotic stress. Pigeonpea is also known as a crop that can tolerate long-term water-stress conditions during its growth cycle and produce reasonable yield. Therefore, the introduction of early maturing hybrids with these characteristics will facilitate growing of pigeon pea in water deficient areas. The earliness of such high yielding hybrids will also help in escaping terminal drought and therefore will have good adaptation to environments with a short growing season basically 3-4 months. Considering the importance of pigeon pea in the world economy and its potential for future economy, it is imperative to increase its productivity and other important traits through genetic manipulation. For genetic improvement of any crop plant, it is prerequisite to know the nature and magnitude of variability present in the available germplasm of the crop. Therefore, the present study was undertaken to estimate phenotypic and genotypic variability, phenotypic and genotypic coefficient of variation, heritability in broad sense, expected genetic advance, correlation coefficient, path analysis and to find out the most promising type and genetic variability of the early maturing genotype pigeon pea.

MATERIALS AND METHODS

The present investigation on “Evaluation of early genotypes of pigeon pea [*Cajanus cajan* (L.) Mill-

sp.]” was carried out at the experimental farm of Department of Genetics and Plant Breeding, School of Agricultural sciences and Rural Development, Nagaland University, Medziphema Nagaland during the kharif season 2016-2017. The experiment was carried out following Randomized complete Block Design in three replications with eleven genotypes. Plot size was 3 × 2.4 m consist of four rows of row to row distance 60 cm and plant to plant distance of 20 cm respectively. All recommended agronomical practices were followed for raising the good crop.

The observation were recorded on five randomly selected plants from each plot in each replication for the following characters viz 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/ plant, number of seeds/pod, 100-seed weight (g) and seed yield/plant (g). The mean values over replications were subjected for analyzing the various parameters. The genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation and heritability were estimated as suggested by earlier, while genetic advance was computed as per the procedure of Johnson et al. (1955). The data were also analyzed for estimating the correlation coefficient (Al-Jibouri et al. 1958) and path analysis as per Dewey and Lu (1959) for grain yield and its component characters.

RESULTS AND DISCUSSION

The analysis of variance among the genotypes differed significantly for all the quantitative characters (Table 1), indicating the presence of considerable amount of variability among the genotypes. The analysis of variance revealed significant differences among genotypes for secondary branches (1956.43), number of pods per plant (6188.89), plant height

Table 1. Analysis of variance for nine characters of pigeon pea. **significant at 1%.

Source of variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches	Secondary branches	No. of pod per plant	No. of seeds per pod	Test weight (g)
Replication	2.00	3.12	18.76	397.32	6.29	532.34	1053.90	0.02	2.28
Genotypes	10.00	1289.52**	650.98**	5598.98**	217.93**	19560.43**	6188.89**	0.38**	5.72**
Error	20.00	14.09	18.19	256.31	9.74	1981.21	975.22	0.07	0.83

Table 2. Mean performance of pigeon pea genotypes for yield related traits.

Geno- types	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches	Secondary branches	No. of pods per plant	No. of seeds per pod	Test weight (g)	Yield per plant (g)
ICPL-88039	78.00	169.67	167.47	27.07	233.20	164.80	3.49	18.69	33.53
AL-1849	112.00	171.33	186.93	29.80	217.60	135.13	2.80	17.80	31.06
AL-2021	137.00	187.67	186.20	32.00	198.33	134.07	3.06	17.30	34.08
AL-1871	109.67	171.33	170.53	24.23	136.20	87.33	3.26	17.20	27.09
AL-17605	80.00	173.00	187.40	31.33	191.53	113.73	3.46	21.34	30.40
AL-2025	99.00	173.00	207.87	39.93	268.67	157.80	2.86	18.58	34.20
ICPL-161	114.00	195.00	204.87	36.33	216.60	131.20	3.06	19.67	32.25
AL-1756	107.67	168.33	229.4	38.00	244.87	122.47	3.63	20.10	33.10
ICPL-20338	63.00	135.00	69.45	9.00	34.00	41.60	2.87	17.10	8.31
AL-1758	104.33	169.00	221.13	35.40	357.40	196.20	3.55	19.32	35.02
UPAS-120	114.00	171.00	209.33	32.80	248.87	197.53	2.55	19.88	35.69
G.Mean	101.69	171.3	185.5	30.52	213.38	134.93	3.14	18.81	30.43
CD-55	6.39	7.26	27.29	5.31	75.81	53.19	0.47	1.52	3.86
CD-1%	8.72	9.91	37.22	7.24	103.40	72.54	0.67	2.07	5.27
SE	2.16	2.46	1.80	2.25	25.69	18.02	0.15	0.51	1.31

(5598.98) and days to 50 percent flowering (1289.52) indicating high degree of variability present in the material.

The mean performance of eleven genotypes and the range of variance for yield and yield related traits are presented in Table 2. All the genotypes varied significantly for the traits seed yield per plant. The highest seed yield per plant was recorded in genotype UPAS (35.69 g) followed by AL-1758 (35.02 g), whereas the genotype ICPL-20338 (8.31 g) recorded the lowest seed yield per plant. The high yield of the genotype UPAS 120 was attributed by high number of pod/plant and test weight. The genotype ICPL-20338 was the earliest to flowering (63.00 days) followed by ICPL-88039 (78.00 days). Whereas, maximum

period for flowering (137.00 days) was taken by genotype AL-2021 followed by ICPL-16 (114.00) and UPAS (114.00 days). Genotype ICPL-30338 took the shortest duration of time (135.00 days) for maturity followed by AL-1756 (168.33 days). AL-1756 recorded the tallest plant height (229.40 cm) followed by AL-1758 (221.13 cm). The highest primary branches were observed in genotype AL-2025 (39.93) followed by AL-1756 (38.00) while, the lowest was observed in genotype ICPL-20338 (9.00). However, highest number of secondary branches was recorded in genotype AL-1758 (357.40) followed by AL-2025 (268.67). The highest seed per pod was observed in the genotype AL-1756 (3.63) and the lowest was observed in genotype UPAS (2.55). The maximum seed weight was 21.34 gin genotype AL-1760 followed by AL-

Table 3. Genetics parameters for nine quantitative characters of pigeonpea.

Characters	Mean	Range	Components of variance		Coefficient of variance		Heri- tability (%)	Genetic advance	Genetic advance as % mean
			PV	GV	PCV	GCV			
Days to 50% flowering	101.72	63.00-137.00	439.22	425.13	20.63	20.27	96.00	41.04	40.72
Days to maturity	171.34	135.00-195.00	229.11	210.92	8.83	8.47	92.00	28.69	16.74
Plant height (cm)	185.51	69.0-229.40	2028.50	1771.74	24.23	22.65	87.00	80.70	43.50
Primary branches	30.53	9.00-39.93	79.14	69.41	29.14	27.29	87.00	15.94	52.21
Secondary branches	213.39	34.00-357.40	7851.57	5870.36	41.52	35.90	74.00	135.07	63.29
No. of pods per plant	134.93	41.60-197.53	2713.11	1737.89	38.60	30.89	64.00	68.67	50.89
No. of seeds per pod	3.14	2.53-3.55	0.17	0.10	13.41	10.20	57.00	0.48	15.38
Test weight (g)	18.82	17.20-21.34	2.43	1.64	8.29	6.80	67.00	2.15	11.42
Yield per plant (g)	30.43	8.31-35.69	63.13	57.98	26.11	25.02	91.00	14.89	48.93

Table 4. Genotype and phenotypic correlation coefficient of yields and its contributing characters. * significant at 5% level, ** significant at 1% level.

Characters	Days to 50% flowering	Days to maturity	Primary branches	Plant height (cm)	Secondary branches	No. of pods per plant	No. of seeds per pod	Test weight (g)	Yield per plant (g)
Days to 50% flowering		0.739**p	0.590*	0.6652**	0.439	0.437	-0.199	-0.12	0.634**
Days to maturity		0.725**	0.557*	0.596*	0.341	0.332	-0.155	-0.071	0.598*
Primary branches			0.771**	0.746**	0.546*	0.538*	0.074	0.324	0.819**
Plant height (cm)			0.690**	0.656**					
Secondary branches					0.419	0.354	0.074	0.205	0.705**
No. of pods per plant				0.981**	0.868**	0.731**	0.206	0.601*	0.924**
No. of seeds per pod				0.913**	0.81**	0.683*	0.147	0.487	0.853**
Test weight (g)					0.894**	0.759**	0.306	0.612*	0.943**
					0.806**	0.715**	0.173	0.481	0.891**
						0.937**	0.309*	0.566*	0.915**
						0.877**	0.216	0.351	0.775**
							0.001	0.461	0.902**
							0.008	0.338	0.773**
								0.475	
								0.186	0.2320.118
									0.471
									0.434

1756 (20.10 g). This variability among genotypes may be considered for inclusion in the breeding program to develop high yielding varieties.

The various genetic parameters like phenotypic and genotypic variance (PV and GV), phenotypic and genotypic coefficient of variance (PCV and GCV), heritability and genetic advance as percent mean are presented in Table 3. A considerable range of variation was observed for all the characters under study. Genotypic coefficient of variation, which expresses a picture of the extent of genetic variability in the population, ranged from 6.80 to 35.90. The maximum GCV was observed for secondary branches (35.90), followed by pods/plant (30.89) and primary branches/plant (27.29). These findings are in agreement with Rekha et al. (2013). Thus, these traits further provided an opportunity for genetic improvement. Maximum phenotypic variance was observed for secondary branches per plant (41.52), followed by number of pods per plant (38.60) and plant height (29.14). The moderate phenotypic variance was observed for days to 50 percent flowering (26.11) and the lowest PVC was observed for number of seeds per pod (13.41). The analysis of genotypic and phenotypic coefficient of variation showed that GCV estimates were closer to the PCV estimate for days to 50 percent flowering

and days to maturity, indicating lesser influences of environment in the expression of the characters. This seems to be valid since the heritability estimates for these characters are high. On the other hand, for the character number of seeds per pod, 100-seed weight and seed yield per plant, PCV was of much higher magnitude than the GCV, indicating that, the character is much prone to environmental fluctuation. Thus, it can be suggested that, a large magnitude of variability is present in these genotypes, which can be exploited for genetic improvement.

The estimate of broad sense heritability exhibited high heritability (more than 50 percent) among all the traits ranging from 57.00 percent for number of seeds per pod to 96.00 percent for days to 50 percent flowering. The estimate of broad sense heritability was the highest for days to 50% flowering (96%), followed by seeds/pods, days to maturity (92.00 percent), seed yield per plant (91.00 percent), primary branches (87.00 per cent), plant height (87.00 percent), secondary branches (74.00 percent) whereas, 100 seed weight (67.00 percent), number of pods per plant (64.00 percent) and number of seeds per pod (57.00 percent) exhibited the lowest heritability among the various character under studied. These results are in conformity with the findings of Parmar and Kathiria

Table 5. Direct and indirect effect for the seed yield per plant. Residual effect=0.280.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches	Secondary branches	No. of pods per plant	No. of seeds per pod	Test weight (g)	Correlation with yield per plant (g)
Days to 50% flowering	0.645	0.396	0.165	-1.159	1.005	-0.386	0.023	-0.055	0.634
Days to maturity	0.477	0.536	0.125	-1.326	1.249	-0.475	-0.008	0.149	0.819
Plant height (cm)	0.412	0.400	-1.776	0.274	2.047	-0.670	-0.035	0.282	0.943
Primary branches	0.381	0.413	-1.744	0.279	1.986	-0.645	-0.024	0.277	0.924
Secondary branches	0.283	0.293	-1.590	0.242	2.288	-0.827	-0.036	0.261	0.915
No. of pods per plant	0.282	0.289	-1.354	0.204	2.145	-0.882	-0.000	0.212	0.902
No. seeds per pod	-0.129	0.039	-0.544	0.057	0.707	-0.001	-0.116	0.219	0.232
Tests weight (g)	-0.077	0.174	-1.087	0.168	1.296	-0.407	-0.055	0.461	0.471

(2016) suggesting that the highly heritable characters were least affected by environmental variation and selection for these characters based on phenotypic performance may be more effective for pigeonpea improvement. However, high heritability associated with moderate genetic advance was observed in primary branches per plant and seed yield per plant, which indicate that these characters were under control of complex nature of inheritance. Similar findings were reported by Gowda (1999) and Arshad et al. (2003).

In general, genotypic correlations exhibited higher magnitude than the corresponding phenotypic correlations for all the characters under study (Table 4). This indicated that there was inherent association among the characters. At both phenotypic and genotypic level seed yield per plant showed significantly and positive correlation with days to 50 percent flowering, days to maturity, primary branches per plant, plant height, secondary branches and number of pods per plant. Among yield components, at phenotypic and genotypic level the trait days to 50 percent flowering was recorded to have significant and positive correlation with days to maturity, primary branches per plant, plant height and yield per plant. The results are in agreement with, Kumara et al. (2013) and Ojwang et al. (2016). Similarly, days to maturity exhibited and positive correlation with primary branches per plant, plant height and yield per plant at phenotypic level. At genotypic level it exhibited significant correlation with primary branches per plant, plant height, secondary branches, number of pods per plant and yield per plant. Primary branches exhibited significantly

and positive correlation with plant height, secondary branches, number of pods per plant and yield per plant at phenotypic level. At genotypic level it was recorded positive and significantly correlation with plant height, secondary branches, number of pods per plant, 100-seed weight and yield per plant. However, 100-seed weight was negatively associated for all the characters at both genotypic and phenotypic levels. The critical analysis of characters association revealed that number of plant height, primary branches, secondary branches, number of pods per plant, days to maturity and days to 50 percent flowering are the major yield contributing characters traits as they have positive association with grain yield. Hence, selection of these traits will be more reliable for obtaining high yielding early genotypes of pigeon pea.

Seed yield is a complex character and exhibits low heritability. Moreover, it is also affected by interactive effects of various traits and influenced by environmental factors, thus selection will be more effective based on these traits than seed yield per se. The path coefficient analysis provides a more realistic picture of the interrelationship, as it considers direct as well as indirect effects of the variables by partitioning the correlation coefficients. In the present investigation, the path analysis revealed that secondary branches (2.288), primary branches per plant, days to 50 percent flowering (0.645), days to maturity (0.536) and 100 seed weight (0.461) (Table 4) exhibited positive direct effect indicating a true relationship among the traits. Birhan et al. (2013) and Saroj et al. (2013) had reported similar type of

results. High order of negative direct effect on yield was contributed by plant height (-1.776), number of pods per plant (-0.882) and number of seeds per plant (-0.116). Similar findings were reported by Mahajan et al. (2007). It was also observed that high indirect contribution was also exhibited by most of the yield components and hence traits may be given emphasis while selecting high yielding pigeon pea genotypes. This investigation suggests that for getting higher seed yield there should be a greater number of primary branches and secondary branches. Similar result was reported by Mittal et al. (2010). The residual effect estimated was 0.280 indicating that the traits under study are not sufficient to account for variability and there might be a few more characters other than those studied in the present investigation thus inclusion of some more characters are necessary. The present study suggested that while selection emphasis should be given to secondary branches, primary branches per plant, days to maturity, and days to 50 percent flowering and 100 seed weight for improvement of early genotype in pigeon pea.

So, among all the genotypes studied AL-2025 can be used as a promising genotype since, it exhibited earliness in flowering, high primary and secondary branches and high yield traits. The genotypes ICPL-20338, ICPL-88039 and AL-1760 earliest to flowering and maturity can also be considered as potential genotypes for incorporation in pigeon pea breeding program.

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