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A Study on Genetic Variability and Correlation in Pigeon Pea [*Cajanus cajan* (L) Millsp.]

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Abstract: ***Twenty varieties of pigeon pea were evaluated and a wide range of variation was found for almost all the traits under study. Phenotypic variance was higher than the genotypic variance for traits viz. plant height days to flower, days to maturity, number of branches/plant, number of fruiting branches/plant and seed yield/plant. High estimates of heritability along with high genetic advance was recorded for number seeds per plant, number of pods per plant, plant height, days to flowering and days to maturity. Correlation studies revealed that plant height, number of pods per plant, number of seeds per pod and 100 seeds weight are suitable selection criteria for seed yield improvement in pigeon pea.***

Keywords: pigeon pea, genotypic variance, phenotypic variance, correlation studies

1. Introduction

Pigeon pea [*Cajanus cajan* (L) Millsp.] is an important legume of the tropics, sub-tropics and warmer regions of the world. Pigeonpea is an often cross pollinated (20-70%) crop with 2n = 2x = 22 diploid chromosome number. India is considered as the native of pigeon pea **(Van der Maesen, 1980).** The major pigeon pea producing countries in the world are India, Eastern Africa, Central and South America, The Caribbean and West Indies. 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 plants have high nutritional, medicinal and economic values. It is contributes to improving the soil fertility **(Olawuyi and Fawole, 2005).** The leaves of pigeon pea are used in treatment of some skin and respiratory infections, while an aqueous infusion of seeds mixed with leaves are used in management of genetic disorder **(Owere et al., 2000)**. Pigeon pea play a singnifant role to full fill the need of Indian died nutritional requirement due to its high nutritional value with high protein content that ranges from 21% to over 25%. Besides its rich nutritional value, 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. The green revolution has been confined by and large to the cereals while the production of pulses has remained stagnant. Pigeon pea plays an important role by virtue of its multipurpose use in food, feed, fuel and farming.

Traditional varieties of pigeon pea are long duration types taking more then ten month to mature. They have little role to play in intensive agriculture as they cannot be fitted in multiple cropping system because of their longer duration. In order to make pigeon pea more profitable crop in irrigated farming it is essential that high yielding early maturing and relatively statured types are developed which can be suitable fitted in the newly developed multiple and inter cropping patterns **(Ramanujan and Singh 1981).**

Lack of genetic variability is one of the major constraints is any crop improvement programme. Correlation studies helps in determination of the interrelationship between various traits and give a better understanding of the contribution of each trait in the genetic makeup of the crop **(Kimani, 2000)**. The present study was carried out to estimate the genetic variability, heritability, genetic advance and correlation between yield and related characters in pigeon pea.

2. Materials and Methods

The materials for the present studies consists of 20 strains of pigeon pea *viz.* ICPL-4, ICPL-7, ICPL-384, ICPL-406, TAT-10, TATA-3, T-21, Pusa Ageti, UPAS-120 Gwalior-3, NP (WR)-15, 4-5-9, 4-16-12, P-861, Pusa Sweta-2 Corg-4, Corg-5, HY-8, HY-9 and Pant A-3. These strains were maintained in the Deptt. of Plant Breeding and Geenetics, RBS College, Bichpuri, Agra.

The experiment was conducted at, R.B.S. college research farm, Bichpuri, Agra in 2010-11. The accessions were grown on the field using randomized complete block design with three replicates. Each plot consisted of three rows spaced at 0.75m between and 0.5m within rows. Two seeds from each accession were planted at 2-3 cm depth from the soil, but thinned to one three weeks after planting. Agronomic practices were duly carried out. Observation were recorder on 5 randomly selected plants in each replication for 10 charterers *viz.* days to flowering, number of branches per plant, number of fruiting branches per plant, number of pods/plant, days to maturity, plant height (cm), Number of seeds/ plant, number of seeds per pods, seed yield/plant (gm) and 100- seed weight (gm)**.** The data were subjected to analysis of variance with Statistical Analysis System package **(SAS, 1999).** The formula given by **Robinsion and Comstock (1956)** was used for estimating the heritability in broad sense. Genetic advance under selection was calculated by the formula given **Robinson *et. al.*, (1949).** Correlation was calculated as per method suggested by **Searle (1961).**

3. Result and Discussion

The analysis of variance revealed that all the treatments were significantly different from each other (Table-1). The estimation of parameters of statistical and genetical variability *viz.* range, grand mean, Phenotypic and genotypic coefficient of variation, heritability and genetic advance in respect of all the ten attributes under study are presented in (Table-2).

A wide range of variation was found for almost all the traits. High estimates of coefficient of variation were number of pods/plant, number of seeds/plant, seed yield/plant, plant height and number of fruiting branches/plant. In general phenotypic coefficient of variation was found higher than the genotypic coefficient of variation. But differences were more for the traits viz. plant height, days to flower, days to maturity, number of branches and fruiting branches/plant and seed yield/plant. There by indicating the influence of environment. Higher phenotypic variance than genotypic variance in traits due to the interaction of environmental components as similarly observed by (**Oseni and Khadir., 1994 and Nguru., 1995).** High estimation of heritability was recorded for number of seeds/plant, 100 seed weight, number of pods/plant, number of seeds/pod plant height, days to maturity and days to flower. Heritability estimates was moderate for seed yield/plant and number of fruiting branches/plant while it was low for number of branches/plant. High estimation of genetic advance was number for number of pods/plant, number of seed/plant, plant height, 100 seed weight, seed yield and days to flower. Therefore selection would be beneficial for those characters having high heritability along high genetic advance.

The nature and magnitude of all possible correlation coefficients, both at genotypic, phenotypic levels, among the 10 attributes were worked out and are presented in table 3- form the correlation studies it is evident that seed yield was positively correlated with number of seeds/plant, plant height, number of pods/ plant and 100 seed weight. Therefore, these traits would be suitable selection criteria for improvement of seed yield in pigeon pea.

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Table 1: Analysis of variance for different characters in Pigeon pea

		Mean Sum of Squares (M.S.S.)									
Sources of variation	D.F.	Plant height (cm)	days of Flowering	Days of Maturity	Number of Branches per plant	Number of fruiting branches	Number of pods per plant	Number of Seeds per pod	100-seed weight (gm)	Seed yield per plant (gm)	Number of seeds per plant
Replication	2	51.04683	143.49415	110.06958	1.84512	0.57410	89.91583	01406	0.00949	72.14223	24.54408
Treatment	19	1996.92374*	581.55205*	623.07445*	11.98147*	7.49619*	3150.19949*	0.14023	3.27412*	206.5941*	43724.19294*
Error	38	97.99604	54.83003	42.80831	3.71922	1.29523	0.00600	0.00600	0.00509	33.39815	61.2271

Significant at 5% level.

Table 2: Mean range, Grand mean, Coefficient of variation, Standard error, Critical difference heritability, Genetic advance and G.A. in % of mean for ten characters in pigeon pea.

S. No	Characters	Mean range	Grand mean	Coefficient of variation		S.E.	C.D.	Heritability %	Genetic advance (K=2.06)	Genetic advance in % of mean
				Phenumbertypic	Genumbertypic					
1	Plant height (cm)	136.94-214.03	178.73	15.13	14.08	5.7154	15.8422	86.60	48.23	26.98
2	Days to flower	88.67-157.67	118.39	12.82	11.19	4.2751	11.8500	76.20	23.83	20.12
3	Days to maturity	125.74-168.15	160.24	9.59	8.68	3.7775	10.4707	81.88	25.93	16.18
4	Number of branches/plant	12.95-23.11	19.88	12.80	8.35	1.1134	3.0863	42.54	2.23	11.21
5	Number of fruiting branches /plant	7.70-14.95	12.21	15.01	11.17	0.6571	1.8213	61.48	2.32	19.00
6	Number of pods/plant	94.14-206.13	168.51	19.47	19.11	3.6080	10.0008	96.37	65.12	38.64
7	Number of seeds/pods	3.52-4.31	3.84	5.87	5.51	0.0447	0.01239	88.18	0.41	10.67
8	100- Seed weight (gm)	5.96-9.37	7.82	13.37	13.23	0.412	0.01142	97.79	2.10	26.85
9	Seed yield/plant (gm)	36.05-67.87	53.67	17.79	14.16	3.3366	9.2485	63.35	12.46	23.21
10	Number of seeds/plant	344.63-758.48	642.86	18.83	18.79	4.5175	12.5220	99.58	247.99	38.57

Table 3: Correlation between character combinations in Pigeon pea

parameter	Plant height	Days to flower	Days to maturity	No. of branches/ plant	No. of fruiting branches/plant	No. of pods /plant	Seeds /pod	100-seed weight	Seed yield/ plant	Seed/plant
Plant height G P		0.6304* 0.4948*	0.7432* 0.6247*	0.3712* 0.1855	0.3521* 0.2624*	0.6180* 0.5542*	-0.1204 -0.1031	-0.3092* -0.2814*	0.6464* 0.4902*	0.6267* 0.5814*
Days to flower G P			09944* 0.7359*	0.3405* 0.1993	0.5229* 0.3415*	0.1942 0.1894	-0.2741* -0.2343	-0.4043* -0.3482*	0.0155 -0.0015	0.1638 0.1517
Days to maturity G P				0.3116* 0.2945*	0.5283* 0.3281*	0.2940* 0.2552*	-0.2508* -0.1760	-0.3835* -0.3474	0.1815 0.1685	0.2538* 0.2314
No of branches/plant G P					0.8633* 0.4670*	0.0935 0.0533	0.1496 0.1725	-0.3533* -0.2360	-0.1676 -0.2010	0.1981 0.1268
No of fruiting branches/plant G P						0.0472 0.0463	0.2540* 0.1339	-0.1419 -0.1250	-0.1139 -0.0550	0.1517* -0.1102
No. of pods/plant G P							-0.4733* -0.4394*	-0.5246 -0.5137*	0.8345* 0.6646*	0.9535* 0.9323*
No. of seeds/pod G P								0.3642* 0.3344*	-0.1449 -0.0986	-0.1878 -0.1767
100 seeds weight G P									0.0500 0.0428	-0.5362* -0.5300*
Seed yield/ plant G P										0.8267* 0.6638*
No. of seeds/ plant G P										