



Genetic Variability, Character Association And Path Analysis In Pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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ABSTRACT

To studies that genetic variability, heritability, genetic advance, correlation and path coefficient analysis was studied for grain yield in 45 diverse genotypes of pigeon pea genotypes. The analysis of variance estimated that the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes. Observed the genotypic and phenotypic coefficient of variation were high for grain yield per plant followed by number of pod per plant, 100-grain weight, number of primary branches per plant and number of secondary branches per plant. High heritability were revealed for plant height, days to 50% flowering, days to maturity, 100- grain weight, number of pod per plant, pod length and grain yield per plant. High genetic advance observed that number of pod per plant, plant height and days to maturity. Genotypic coefficients of correlation were generally, higher than corresponding phenotypic coefficients of correlation for most of the characters. Green yield exhibited significant stable and positive correlation with number of pod per plant, number of secondary branches per plant, plant height and number of secondary branches per plant at genotypic and phenotypic level. Thus, it can be inferred that selection based on any one of these characters either alone or in combination, will result in identifying high grain yielding strains. Path coefficient analysis of genotypic and phenotypic exhibited high positive and direct effect of number of pod per plant, days to maturity, 100- grain weight, number of seed per pod, number of chambers per pod and number of primary branches per plant towards grain yield. Thus any selection based on these characters will enhance performance and improvement grain yield in pigeonpea.

Key words: wheat, Genetic variation, heritability, genetic advance, correlation, path analysis.

Received 20.10.2017

Revised 07.12.2017

Accepted 21.01.2018

INTRODUCTION

Pigeon pea [*Cajanus cajan* L. Millsp.], ($2n=2x=22$) is the second most important pulses crop after chickpea in India and fifth rank in the world. It is major producer and consumer of pigeon pea in the world and presently occupies an area of about 27 million hectares with an annual total production of 18.5 million tonnes and mean productivity of 730 kg/hectare (Anonymous, 2014). As 'dal', pigeon pea is an important constituent of the Indian meal. It contains 20-21% protein. The per capita availability of protein in the country is 28 g/ day, while WHO recommended it should be 80 g/day, consequently most serious problem of the malnutrition existing among the poor people, where most of the people have vegetarian diet and avoid the animal protein. It is needs fulfill its demand through pulses protein. Therefore, it is necessary to increase the production of pigeon pea, which could be done opting suitable, breeding methods. To overcome such situation, genetically stable genotypes having high yield potential are urgently needed. It may be important tools for the breeder to enhancing the production and productivity of the pigeon pea [1, 8].

MATERIAL AND METHODS

Forth five diverse accession of pigeonpea were evaluated for grain yield and its component traits in randomized block design with three replications at crop research center, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each entry was sown in a single row of 5 m length with inter and intra row spacing of 75 cm and 25 cm, respectively. The recommended agronomic practices and plant protection measures were followed timely for the successful raising of the crop. Five

random plants were selected from each plot for recording the observations on grain yield per plant and its component traits. The coefficient of variation, heritability genetic advance, correlation coefficients and path analysis were calculated as per the method suggested by [4, 5, 6 and 9]. Observation were recorded on five competitive plants for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, pod length, number of chambers per pod, number of seeds per pod, 100- grain weight, and grain yield per plant.

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant different among genotypes for all the eleven characters, *i.e.* days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pod per plant, pod length, number of chambers per pod, number of seeds per pod, 100- grain weight, and grain yield per plant indicating wide spectrum of variation among the genotypes (Table-1).

Table-1: Analysis of variance for 11 characters in 45 pigeonpea genotypes

Source of variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branches per plant	No. of secondary branches per plant	No. of pods per plant	Pod length (cm)	No. of Chambers per pod	No. of seeds per pod	100-grain weight	Grain yield per plant (g)
Replication	2	2.50	1.75	45.75	1.78	4.39	454.50	0.19	0.66	0.86	0.28	13.21
Treatment	44	241.21**	451.66**	2993.98**	59.60**	110.94**	12670.73**	0.76**	0.89**	0.69**	11.17**	405.78**
Error	88	0.59	1.30	1.56	1.82	5.35	247.38	0.15	0.31	0.39	0.65	9.63

*, ** Significant at 5% and 1% level, respectively

The overall range of phenotypic variation was high than genotypic coefficient of variation for all of the traits considered (Table-2), indicating that all these traits were influenced by environment. These finding are similar in agreement with earlier reported by [3].

Table-2: Estimates of variability parameter for eleven characters in pigeonpea genotypes

Characters	Heritability (%)	Genetic advance	GA (%) of Mean	GCV	PCV
Days to 50 % flowering	99.30	18.38	13.84	6.74	6.77
Days to maturity	99.10	25.13	13.28	6.47	6.50
Plant height (cm)	99.80	65.01	32.59	15.83	15.84
No. of primary branches per plant	91.40	8.64	47.94	24.35	25.47
No. of secondary branches per plant	86.80	11.39	43.55	22.69	24.35
No. of Pods per plant	94.40	128.77	54.29	27.13	27.93
Pod length (cm)	94.20	1.00	25.53	12.77	13.16
No. of chambers per pod	90.00	1.03	31.17	15.91	16.76
No. of Seeds per pod	73.70	0.59	19.54	10.99	12.79
100-grain weight	98.30	3.93	53.03	25.96	26.19
Grain yield per plant (gm)	93.20	22.85	58.63	29.48	30.54

The genotypic coefficient of variation ranged from 6.47 to 29.48 per cent for various characters under study. The highest phenotypic of variation (PCV) was highly showed for grain yield per plant (30.54) followed by number of pod per plant (27.93), 100-grain weight (26.19), number of primary branches per plant (25.47) and number of secondary branches per plant (24.35), whereas minimum recorded for days

to 50% flowering (6.77), days to maturity (6.50) indicating that these traits can be effectively selected for improvement. The GCV was higher found in grain yield per plant (29.48) followed by number of pod per plant (27.13), 100-grain weight (25.96), number of primary branches per plant (24.35) and number of secondary branches per plant (22.69) whereas minimum recorded for days to 50% flowering (6.74), days to maturity (6.47) indicating that these traits are important for pigeon pea improvement. Contrary finding has been reported by [2, 3 and 7] for pods per plant and seed yield per plot in mung bean which had high genotypic and phenotypic coefficients of variation. The efficiency of selection not only depends on the magnitude of genetic variability but also on the heritability of the desirable traits. The high heritability in broad sense (Table-2) was noted for most of the characters viz., plant height, days to 50% flowering, days to maturity, 100- grain weight, number of pod per plant, pod length, grain yield per plant and number of primary branches per plant. This is conformity with the finding of (2). The high heritability donated high proportion of genetic effects in the determination of these traits and can be adopted for improving grain yield in pigeonpea. In the present study, estimates of genetic advance as percent of mean at 5% selection intensity ranged from 13.28% for days to maturity to 58.63% for grain yield per plant. The genetic advance as per cent of mean maximum grain yield per plant (58.63) followed by number of pod per plant (54.29), 100- seed weight (53.03), number of primary branches per plant (47.94) and number of secondary branches per plant (43.55) whereas, it was minimum for number of chamber per pods (31.17), and plant height (32.59). This result is similar finding by [2] also reported high genetic advance for seed yield per plot, harvest index and number of pods per plant in pigeon. However, similar high genetic advance as percent of mean value was reported by (10) for pods per plant, seed yield per plot, harvest index and 100-seed weight in pigeon pea. High heritability accompanied with high genetic advance as percent of the mean in case of grain yield per plant, 100-seed weight, pods per plant, number of secondary branches per plant, number of primary branches per plant and plant height indicate that these are simply inherited traits and most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. However, days to maturity, days to 50% flowering and seeds per pod had high heritability coupled with low genetic advance indicates non-additive gene effects. Genotypic correlations (Table-3) were higher in magnitude than the phenotypic correlation indicating strong inherent relationship among the characters except few, which could be due to modifying effects in the environment studied. Similar findings were reported by [8]. The character grain yield per plant was found to be significant stable and positive association with number of pod per plant (0.743, 0.732) followed by number of secondary branches per plant (0.367, 0.347), plant height (0.357, 0.344) and number of primary branches per plant (0.318, 0.277) at genotypic and phenotypic level (Table-3) These results were in agreement with those reported by [8,10]. The results of correlation in present investigation revealed that grain yield per plant, primary branches per plant, pods per plant and plant height were the most important attributes and may contribute considerably towards higher grain yield. But grain yield is a complex trait which is influenced by its various components directly and indirectly via other traits, which creates a complex situation at the selection time. Results on the phenotypic and genotypic path coefficient exhibited high positive direct contribution of number of pod per plant (1.017, 0.976) followed by days to maturity (0.417, 0.328), 100- grain weight (0.378, 0.374), number of seed per pod (0.259, 0.139) number of chambers per pod (0.207, 0.081) and number of primary branches per plant (0.122, 0.101) towards grain yield (Table-4). It is evident that the highly significant and positive correlation of pods per plant had found with grain yield per plant due to their maximum direct and indirect effect via number of chamber per pods and days to 50 % flowering respectively. Plant height showed medium positive direct effect and their genotypic correlation with grain yield was significant. Therefore, these traits would be suitable selection criteria for improvement of seed yield in pigeon pea. Therefore, it can be concluded from variability parameters, correlation and path coefficient analyses that pods per plant, number of secondary branches per plant, plant height and number of primary branches per plant are the most important yield contributing traits and due emphasis should be given to these characters for genetic improvement of grain yield in pigeonpea.

Table-3: Genotypic and phenotypic correlations among 11 characters in pigeonpea genotypes

yield/plant (gm)	0.073 0.072	0.088 0.086	0.357** 0.344**	0.277** 0.318**	0.347** 0.367**	0.732** 0.743**	-0.045 -0.042	0.056 0.045	0.078 0.076	0.107 0.093	1.000 1.000
100-grain weight	-0.150 -0.148	-0.064 -0.064	-0.246 -0.242	-0.324* -0.315*	-0.335* -0.323*	-0.360* -0.354*	0.126 0.118	-0.034 -0.026	0.053 0.048	1.000 1.000	
No. of seeds per pod	-0.017 -0.018	-0.040 -0.034	0.250 0.213	0.061 0.068	0.057 0.074	-0.026 -0.013	0.114 0.095	0.696** 0.586**	1.000 1.000		
chambers per pod	0.061 0.056	0.189 0.181	0.265 0.248	-0.141 -0.129	-0.057 -0.056	0.044 0.031	0.477** 0.435**	1.000 1.000			
Pod length (cm)	0.143 0.141	0.175 0.164	0.094 0.091	-0.278 -0.260	-0.279 -0.259	-0.100 -0.096	1.000 1.000				
No. of pods per plant	0.212 0.207	0.095 0.094	0.550** 0.534**	0.452** 0.481**	0.547** 0.574**	1.000 1.000					
Secondary branches/ plant	0.060 0.056	-0.040 -0.031	0.352** 0.326**	0.832** 0.837**	1.000 1.000						
branches/ plant	0.005 0.005	-0.151 -0.141	0.175 0.165	1.000 1.000							
Plant height (cm)	0.168 0.167	0.178 0.177	1.000 1.000								
Days to maturity	0.834** 0.828**	1.000 1.000									
Days to 50 % flowering	1.000 1.000										
Correlation	G P	G P	G P	G P	G P	G P	G P	G P	G P	G P	G P
Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of Pods per plant	Pod length (cm)	No. of chambers per pod	No. of Seeds per pod	100-grain weight	Grain yield per plant (gm)

G= Genotypic correlation; P= Phenotypic correlation

G= Genotypic path; P= Phenotypic path

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CITATION OF THE ARTICLE

A Kumar, A Singh, R Kumar and B Singh: Genetic Variability, Character Association And Path Analysis in Pigeonpea [*Cajanus Cajan* (L.) Millspaugh]. *Bull. Env. Pharmacol. Life Sci.*, Vol 7 [3] February 2018 : 63-68