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Association studies in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract

The present investigation was conducted during the *kharif* season of 2018 to obtain the knowledge of nature and magnitude of genetic parameters and its utilization in development of superior varieties of pigeonpea [*Cajanus cajan* (L.) Millsp.]. The results indicated that the genotypes showed significant variability for all the traits studied. The moderate estimates of genotypic coefficient of variation (GCV) were observed for pods per plant, yield per plot, days to 50% flowering, test weight, pod length and days to maturity, while the traits branches per plant, seed per pod and plant height exhibited low estimates of GCV. High heritability accompanied along with high genetic gain was recorded for days to 50% flowering, days to 80% maturity, test weight and grain yield. Grain yield showed positive correlation with pods per plant and branches per plant. Path analysis revealed that pods per plant and branches per plant were the major component of grain yield. Over all study showed that selection may effective for the pods per plant, branches per plant, test weight, days to 50% flowering and days to 80% maturity for development of early maturing and high yielding genotypes in pigeonpea.

Keywords: Correlation, genetic variability, heritability, path analysis, pigeonpea

Introduction

Pulses are the major source of proteins and are consumed worldwide to meet the protein requirement of the growing population. Among the legume crops of the tropics and sub-tropics pigeonpea [*Cajanus cajan* (L.) Millsp.] is recognized as an important crop for subsistence agriculture due to its drought tolerance, ability to recover from the losses caused by various stresses, high protein (20-22%) grains, quality fodder and fuel wood. Pigeonpea is the second most important pulse crop next to chickpea in India.

A complete understanding of the correlation between yield and yield components is a must for a plant breeder towards the improvement of any crop. Similarly path analysis determines the direct and indirect effects of these characters towards the yield. As emphasized by Pandey *et al.*, (2015) [8] the optimum combination of yield contributing traits can be accumulated in a particular genotype only by understanding the inter relationships of various traits using correlation and path coefficients. Seed yield is a dependant character and whenever plant breeder goes for selection for yield it always misleads because it depends on various characters and to some extent to the environmental conditions. An attempt has been made in this study to know the relationship between yield and different yield attributing characters and their direct and indirect effects on yield in pigeonpea.

Materials and Methods

Eighteen genotypes of pigeonpea were evaluated under rainfed conditions at Agricultural Research Station, Ummedganj, Kota, Agriculture University, Kota, Rajasthan during *Kharif*, 2018. The genotypes were grown in 6 rows of 4m length spaced 60 cm apart with the plant to plant distance of 20 cm. Each genotype was planted in three replications in Randomized Block Design. Observations were recorded on days to 50% flowering, days to 80% maturity, plant height (cm), branches per plant, pods per plant, 100-seed weight (g), pod length (cm), seed per pod and seed yield (g) per plot. Recommended and uniform agronomical practices as well as plant protection measures were followed to raise the healthy crop. The variability parameters were estimated. Correlation between nine characters was estimated according to the method given by Singh and Chaudhary (1985) [13]. Direct and indirect effects were estimated as described by Dewey and Lu (1959) [4].

Results and Discussion

Mean squares due to genotypes revealed that genotypes had significant differences for the all the characters in pigeonpea. These results indicated that the genotypes exhibited sufficient amount of variability for grain yield and related traits.

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The genotypic variance reflects the magnitude of genotypic variability, while the genotypic coefficient of variance (GCV) provides a direct comparison of variability between different traits. In general for all the characters estimates of GCV indicating that genetic factor were predominantly responsible for these characters. The overall range of phenotypic coefficient variation (PCV) revealed relatively high values in comparison to corresponding genotypic coefficient of variation (GCV) for all the traits studied, indicating that all these traits were influenced by environment (Table 1). These findings are similar in agreement with earlier reported by Kumar *et al.* (2018) [5]. The moderate estimates of genotypic coefficient of variation (GCV) were observed for pods per plant, yield per plot, days to 50% flowering, test weight, pod length and days to maturity, while the traits branches per plant, seed per pod and plant height exhibited low estimates of GCV. Baldaniya *et al.* (2018) [2] also reported moderate GCV for yield per plant and low for branches per plant and plant height. The high value of PCV was recorded for pods per plant. Similar finding has also been reported by Kumar *et al.* (2018) [5].

Higher heritability was observed for the characters like days to 50% flowering, days to 80% maturity, pod length, test weight and grain yield, 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. Similar results were also reported by Birhan *et al.* (2013) [3], Saroj *et al.* (2013) [11] and Kumar *et al.* (2018) [5]. Singh *et al.* (2013) [12] also reported similar finding for days to 50% flowering, grain yield and days to maturity. While, higher genetic gain was observed in days to 50% flowering, grain yield, pods per plant, test weight, days to 80% maturity and pod length. In the present study, high heritability accompanied along with high genetic gain (GG) was recorded for days to 50% flowering, days to 80% maturity, test weight

and grain yield. Similar finding were also reported by Kumar *et al.* (2018) [5] for test weight and grain yield. The characters showing high heritability estimates coupled with high genetic gain (GG) indicates the preponderance of additive gene action and greater scope for improvement in these traits through selection.

Association analysis provides measures of relationship among the traits and serves to assess the opportunity of mutual improvement of two desirable traits by common selection programme. Knowledge about inter-relationship between yield and yield contributing characters facilitates the choice of an efficient breeding method to be adopted and selection of parents for crop improvement. Association estimates revealed that in general there was a close agreement between genotypic correlations. Grain yield showed positive correlation with pods per plant and branches per plant (Table 2). Similar findings of positive association were also reported by Baldaniya *et al.* (2018) [2] and Kumar *et al.* (2018) [5] for pods per plant and branches per plant; Bal *et al.* (2018) [1], Narayanan *et al.* (2018) [6] and Pal *et al.* (2018) [7] for pods per plant.

The associations among yield and its contributing characters were further substantiated by path coefficient analysis. The genotypic correlation coefficient between seed yield and other yield attributing traits were partitioned into direct and indirect effect (Table 2). Path analysis revealed that pods per plant and branches per plant were the major component of grain yield (Rao *et al.* 2013, Ram *et al.*, 2016, Verma *et al.* 2018) [10, 9, 14]. Over all study showed that selection may effective for the pods per plant, branches per plant, test weight, days to 50% flowering and days to 80% maturity for development of early maturing and high yielding genotypes in pigeonpea. Therefore, selection for these traits would be effective for genetic improvement in pigeonpea as these traits may exhibit additive gene effects.

Table 1: Estimates of variability parameters for seed yield and its component traits in pigeonpea

S. No	Characters	Mean	GCV (%)	PCV (%)	ECV (%)	Heritability h ² (%)	GA	GG
1	Days to 50% flowering	108.87	15.06	15.12	1.29	99.27	33.66	30.91
2	Days to 80% maturity	180.13	10.35	10.37	0.60	99.66	38.33	21.28
3	Plant height(cm)	197.00	7.28	9.01	5.31	65.32	23.89	12.13
4	Branches/plant	6.13	7.92	10.62	7.09	55.50	0.74	12.15
5	Pods/plant	167.98	17.38	21.28	12.29	66.65	49.09	29.22
6	Seed/Pod	4.52	7.73	9.69	5.85	63.60	0.57	12.69
7	Pod Length (cm)	4.74	11.07	12.09	4.85	83.90	0.99	20.89
8	Test weight (g)	9.79	12.00	12.95	4.85	85.95	2.25	22.92
9	Yield (g)/Plot	1120.00	16.41	18.80	9.17	76.19	330.45	29.50

Table 2: Genotypic path coefficients showing direct and indirect effects of different characters on yield (g)/plot in pigeonpea

Character	Days to 50% flowering	Days to 80% maturity	Plant height(cm)	Branches/plant	Pods/plant	Seed/Pod	Pod Length (cm)	Test weight (g)	r
Days to 50% flowering	1.56	-0.97	0.91	0.08	-0.34	0.49	-1.72	-0.14	-0.14
Days to 80% maturity	1.39	-1.09	0.90	0.02	-0.53	0.31	-1.11	-0.18	-0.30
Plant height(cm)	0.69	-0.48	2.05	0.30	-0.40	1.13	-3.13	-0.49	-0.31
Branches/plant	-0.15	0.03	-0.78	-0.79	0.29	0.28	0.96	0.56	0.41
Pods/plant	-0.42	0.47	-0.65	-0.19	1.25	0.11	-0.38	0.89	1.07
Seed/Pod	0.24	-0.11	0.73	-0.07	0.04	3.17	-4.27	0.16	-0.10
Pod Length (cm)	0.55	-0.25	1.33	0.16	0.10	2.80	-4.84	0.19	0.04
Test weight(g)	0.17	-0.15	0.77	0.34	-0.86	-0.39	0.72		-0.68**

Residual = 0.3647; r = Genotypic correlation of seed yield with yield components

*, ** Significant correlation with dependent character at 5% and 1% respectively

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