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Estimation of genetic variability and character association for development of selection criteria in pigeonpea [*Cajanus cajan* (L.) Millspaugh]

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Abstract

The present study was conducted with an aim to estimate genetic variability parameters and to develop suitable selection criteria in pigeonpea. The experiment consisted of eleven elite pigeonpea genotypes sown in Randomized block design with three replications during *kharif* 2017 and 2018 crop season at G.B.P.U.A. & T., Pantnagar and the observations were recorded on nine different yield and yield attributing traits. The analysis of variance (ANOVA) indicated significant mean sum of squares (MSS) for all the characters under study indicating preponderance of sufficient genetic variability. In general, the PCV was found higher than the corresponding GCV estimates. The characters, number of secondary branches per plant and number of pods per plant exhibited high direct effects on seed yield along with significant and positive correlation with seed yield. It can be concluded that these two traits (number of secondary branches per plant and number of pods per plant) can be used as selection criteria in pigeonpea for bringing improvement in seed yield.

Keywords: Pigeonpea, variability, association and selection criteria

Introduction

Pigeonpea is a major *kharif* pulse crop and second most important pulse after chickpea in India. It plays a major role in securing nutritional security along with crop diversification. Globally, India is the largest producer as well as consumer of pulses. Pigeonpea [*Cajanus cajan* (L.) Millspaugh] commonly known as *Arhar* or *Tur* is an important multipurpose pulse crop. During 2017-18, the production of pigeonpea is about 4.25 mt from an area of 4.43 m ha at productivity level of 960 kg/ha (Anonymous, 2018) [2]. Due to adoption of improved varieties and cultivation practices, the productivity of pigeonpea has increased from 689 kg/ha (1980-81) to 960 kg/ha (2017-18). Now the major challenge is to break the yield plateau in pigeonpea as it remains stagnant in the last decade. In this context, the study of variability parameters becomes very important as these parameters are an indicator of amount of variability present in populations that can be acted upon by selection for crop improvement. For selection to be effective there must be the presence of sufficient genetic variability in the population and the variability must be heritable. The high heritability along with high genetic advance indicates the presence of additive gene effects and hence selection for such traits will be effective and responsive. It is more useful to use heritability along with genetic advance than heritability alone in the prediction of resultant effect of selection Johnson *et al.* (1955) [7]. Hence, for selection of improved and high yielding genotypes, knowledge on variability parameters like heritability and genetic advance is must.

Yield is complex trait governed by a number of genes, each having a small but cumulative effect and hence the direct selection for yield may be misleading. Therefore, it is important to find out the direct and indirect contribution of each component trait on seed yield in order to identify important component characters influencing seed yield. The knowledge about the extent of relationship between crop yield and its attributing traits facilitate selection of improved genotypes. The study of correlation between yield and other morphological traits gives an indication about the degree and direction of association but does not provides information about extent of relationship (direct and indirect effects). Hence, variability parameters and correlation studies alone are not effective.

In such situations, path coefficient analysis is an important tool in the hands of plant breeders for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable Saroj *et al.* (2013) [9]. By using correlation and path coefficients suitable selection criteria can be developed in pigeonpea to identify yield attributing traits to be used in crop improvement programme and therefore, the present study was conducted to estimate the variability parameters, correlation at genotypic and phenotypic level and direct and indirect effects of different traits on seed yield.

Materials and Methods

The experimental material consisted of eleven pigeonpea genotypes sown in Randomized Block Design (RBD) with three replications during *kharif*, 2017-18 and 2018-19 crop seasons at N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The observations were recorded for nine different morphological characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g) and seed yield/plant (g). The row to row distance of 60 cm and plant to plant distance of 20 cm was maintained. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period. The observations recorded for all the traits were subjected to the analysis of variance. The genotypic and phenotypic coefficient of variability were calculated by using the formula of Burton and De Vane (1953) [3], heritability and genetic advance by using formula of Burton and De Vane (1953) [3] and the genetic advance as per cent of mean was evaluated as per the formula provided by Johnson *et al.* (1955) [7]. The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance as given by Searle (1961) [11]. Direct and indirect effects of various characters on seed yield were estimated with the help of path coefficient analysis as suggested by Wright (1921) [13] and Dewey and Lu (1959) [4].

Results and Discussion

Study of ANOVA and genetic variability parameters

The analysis of variance (ANOVA) for the year 2017 and 2018 revealed that mean sum of squares for all the traits under study were highly significant indicating the considerable amount of genetic variability in the experimental material Table 1. The presence of sufficient genetic variability is an indication that selection would be effective to improve the traits. The significance of ANOVA for these traits was earlier also reported by Pandey *et al.* (2016) [8], Gaur *et al.* (2018) [5] and Pal *et al.* (2018).

Variability parameters

A close perusal of Table 1 indicated that in all the studied traits, estimates of Phenotypic Coefficient of Variation (PCV) were in, general, higher than the corresponding Genotypic Coefficient of Variation (GCV). During both years number of primary branches and secondary branches per plant recorded high PCV (>20%) while high GCV (>20%) was reported only for number of secondary branches per plant during both the years. The high estimates of PCV and GCV were an indication of variability in the experimental material. The high estimate of heritability (>60%) in both the years were reported for days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, number of seeds per pod and 100-seed weight. High estimates of heritability for these characters were earlier also recorded by Verma *et al.* (2018) [12]. In both the year, moderate heritability estimates (30-60%) were recorded for number of primary branches per plant. Seed yield per plant reported moderate heritability in 2017 while high heritability in 2018. The high estimates of genetic advance as percent of mean (>20%) in both the years for number of primary branches per plant, number of secondary branches per plant, number of pods per plant earlier by Hemavathy *et al.* (2019) [6]. Moderate estimates (10-20%) of genetic advance as per cent of mean in both the year were reported by days to 50% flowering, days to maturity and 100 seed weight. Seed yield per plant reported moderate estimates of genetic advance as per cent of mean in 2017 while high estimates in 2018. High estimates of heritability along with high genetic advance in both the year were reported for number of secondary branches per plant and number of pods per plant indicating the presence of additive gene action for these traits and hence selection would be effective for improvement in these traits. High heritability along with high genetic advance as per cent of mean for number of secondary branches per plant and pods per plant were also reported by Bhadru (2010) [10] and Hemavathy *et al.* (2019) [6].

Association Studies (Correlation and Path analysis)

Correlation coefficients measure the relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences. In general, for all the traits under study estimates of genotypic correlation coefficients were higher than the corresponding phenotypic correlations. Perusal of Table 2 revealed that number of secondary branches per plant and number of pods per plants reported with significantly positive correlation with seed yield per plant in both the years. Similar results showing positive correlation of secondary branches per plant and number of pods per plants with seed yield per plant was also reported by Saroj *et al.* (2013) [9]. The high estimates of genotypic correlations than the corresponding phenotypic ones during both the years indicates the strong association between these two traits genetically, however the phenotypic values are lessened by the significant environmental interactions. The traits like days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of seeds per pods reported significant positive correlation with seed yield per plant only in year 2017 while in 2018 correlation generally remains non-significant for these traits. The study of path analysis indicates the direct and indirect contribution of different component traits towards the seed yield. The traits showing high direct effects on seed yield per plant during both the year were plant height, number of secondary branches per plant and number of pods per plant Table 3. Similar results were also reported by Saroj *et al.* (2013) [9] and Verma *et al.* (2018) [12]. Among these traits number of secondary branches per plant and number of pods per plant also showed significant positive correlation with seed yield per plant indicating the true relationship of number of secondary branches per plant and number of pods per plant with grain yield and hence an improvement in these two traits will bring an improvement in seed yield through selection and therefore number of secondary branches per plant and number of pods per plant may be used as selection criteria in pigeonpea for seed yield improvement.

Table 1: Analysis of variance (ANOVA) and variability parameters of RBD for the year 2017 and 2018

Source of variation	***d.f.***	**Year**	**Mean Sum of Squares**								
			Days to 50% flowering	**Days to maturity**	**Plant height (cm)**	**No. of primary branches**	**No. of secondary branches**	**No. of pods/ plant**	**No. of seeds/ pods**	**100-seed weight (g)**	**Yield/ plant (g)**
Replication	2	2017	0.21	1.30	54.94	0.48	1.09	1.57	0.17	0.10	17.45
		2018	4.03	0.27	4.45	0.81	0.48	5.54	0.01	0.04	53.30*
Genotypes	10	2017	150.49**	154.03**	414.09**	9.95**	24.81**	1182.98**	0.45**	0.95**	89.83**
		2018	172.21**	173.95**	693.29**	15.05**	24.25**	1521.25**	0.78**	0.72**	135.87**
Error	20	2017	1.54	1.50	53.10	2.05	3.69	52.24	0.05	0.09	19.72
		2018	2.16	0.93	57.68	2.71	2.61	20.74	0.62	0.04	13.73
General Mean		2017	77.00	133.00	210.20	8.80	11.40	152.90	3.60	8.10	41.30
		2018	78.00	132.50	224.20	12.00	13.20	168.10	3.70	8.20	44.50
CD		2017	2.13	2.10	12.49	2.47	3.29	12.39	0.39	0.52	7.61
		2018	2.52	1.66	13.02	2.82	2.77	7.81	0.42	0.35	6.35
CV		2017	1.61	0.92	3.46	16.13	16.64	4.71	6.27	3.78	10.73
		2018	1.88	0.73	3.38	13.43	12.38	2.70	6.64	2.52	8.31
PCV		2017	9.27	5.42	6.26	24.38	28.37	13.51	11.67	7.57	15.87
		2018	9.85	5.76	7.31	21.29	24.01	13.56	14.66	6.32	16.55
GCV		2017	9.13	5.34	5.22	18.27	22.98	12.66	9.84	6.56	11.68
		2018	9.66	5.71	6.48	16.52	20.56	13.29	13.06	5.79	14.31
Heritability		2017	96.98	97.12	69.38	56.21	65.61	87.83	71.15	75.04	54.23
		2018	96.32	98.39	78.59	60.21	73.36	96.02	79.43	83.99	74.77
Genetic Advance		2017	14.29	14.47	18.82	2.51	4.43	37.48	0.63	0.95	7.33
		2018	15.22	15.51	26.58	3.24	4.74	45.14	0.9	0.9	11.36
GA as (%) of mean		2017	18.52	10.86	8.95	28.23	38.35	24.43	17.1	11.7	17.73
		2018	19.54	11.68	11.84	26.41	36.28	26.82	23.98	10.93	25.49

Table 2: Phenotypic (r_p) and genotypic (r_g) correlation coefficients among various characters

Traits	**YEAR**		**DF**	**DM**	**PH**	**NPB**	**NSB**	**NPP**	**NSP**	**100-SW**	**Y/P**
DF	2017	r_p	1.000	0.92**	0.22	0.51**	0.57**	0.47**	0.40*	0.64**	0.45**
		r_g	1.000	0.958**	0.26	0.70**	0.68**	0.50**	0.52**	0.72**	0.60**
	2018	r_p	1.000	0.92**	-0.01	-0.33	0.07	0.06	0.06	0.67**	0.01
		r_g	1.000	0.94**	-0.0	-0.44*	0.10	0.06	0.09	0.72**	-0.02
DM	2017	r_p		1.000	0.25	0.51**	0.50**	0.45**	0.39*	0.70**	0.48**
		r_g		1.000	0.31	0.67**	0.63**	0.51**	0.51**	0.83**	0.65**
	2018	r_p		1.000	0.01	-0.24	0.18	-0.06	0.19	0.69**	-0.08
		r_g		1.000	0.03	-0.31	0.21	-0.06	0.19	0.75**	-0.12
PH	2017	r_p			1.000	0.32	0.42*	0.62**	0.36*	0.00	0.65**
		r_g			1.000	0.59**	0.77**	0.79**	0.56**	0.01	0.98**
	2018	r_p			1.000	0.14	-0.03	0.15	0.16	-0.46**	0.06
		r_g			1.000	0.17	0.09	0.15	0.23	-0.56**	0.08
NPB	2017	r_p				1.000	0.64**	0.34	0.35*	0.13	0.40*
		r_g				1.000	1.00**	0.43*	0.54**	0.31	1.05**
	2018	r_p				1.000	-0.42*	-0.31	-0.16	-0.43*	-0.32
		r_g				1.000	-0.43*	-0.44**	-0.22	-0.59**	-0.50**
NSB	2017	r_p					1.000	0.63**	0.56**	0.28	0.54**
		r_g					1.000	0.82**	0.80**	0.23	1.06**
	2018	r_p					1.000	0.21	0.16	0.01	0.37*
		r_g					1.000	0.30	0.28	0.13	0.47**
NPP	2017	r_p						1.000	0.49**	0.34	0.64**
		r_g						1.000	0.56**	0.37*	0.90**
	2018	r_p						1.000	0.42*	-0.00	0.72**
		r_g						1.000	0.47**	-0.01	0.88**
NSP	2017	r_p							1.000	0.32	0.38*
		r_g							1.000	0.36*	0.78**
	2018	r_p							1.000	0.34	0.18
		r_g							1.000	0.30	0.20
SW	2017	r_p								1.000	0.15
		r_g								1.000	0.30
	2018	r_p								1.000	-0.03
		r_g								1.000	-0.14
Y/P	2017	r_p									1.000
		r_g									1.000
	2018	r_p									1.000
		r_g									1.000

Table 3: Phenotypic path showing direct and indirect effects

Traits	Years	Correlation with seed yield/plant	Direct effects	Indirect effects Via							
				DF	DM	PH	NPB	NSB	NPP	NSP	100-SW
DF	2017	0.45**	-0.125		0.511	0.074	-0.041	0.095	0.119	-0.001	-0.180
	2018	0.01	0.156		-0.404	-0.002	-0.031	0.026	0.044	-0.015	0.242
DM	2017	0.48**	0.552	-0.115		0.085	-0.041	0.084	0.113	-0.000	-0.197
	2018	-0.08	-0.438	0.143		0.003	-0.023	0.068	-0.042	-0.045	0.247
PH	2017	0.65**	0.339	-0.027	0.138		-0.025	0.069	0.155	-0.001	0.000
	2018	0.06	0.162	-0.002	-0.008		0.013	-0.010	0.111	-0.039	-0.165
NPB	2017	0.40*	-0.081	-0.063	0.285	0.107		0.107	0.087	-0.001	-0.030
	2018	-0.32	0.094	-0.052	0.108	0.022		-0.156	-0.222	0.039	-0.155
NSB	2017	0.54**	0.167	-0.071	0.278	0.141	-0.051		0.158	-0.001	0.079
	2018	0.37*	0.371	0.011	-0.080	-0.004	-0.039		0.150	-0.039	0.005
NPP	2017	0.64**	0.251	-0.059	0.249	0.211	-0.027	0.106		-0.001	0.094
	2018	0.72**	0.717	0.009	0.026	0.025	-0.029	0.077		-0.101	-0.000
NSP	2017	0.38*	-0.001	-0.050	0.219	-0.080	-0.028	0.093	0.126		0.090
	2018	0.18	-0.241	0.010	-0.083	0.026	-0.015	0.060	0.301		0.120
100-SW	2017	0.15	-0.279	-0.080	0.390	0.000	-0.010	0.047	0.084	-0.00	
	2018	-0.03	0.359	0.105	-0.302	-0.074	-0.040	0.005	-0.001	-0.080	

Conclusion

On the basis of results obtained it can be concluded that sufficient genetic variability was present in the experimental material. Further, studies on variability parameters, character association and path coefficients concluded that number of secondary branches per plant and number of pods per plant can be used as most suitable selection criteria for developing the improved high yielding genotypes of pigeonpea.

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