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Variability and Association Studies for Yield and Yield Related Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT

Background: Study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) reveals the extent of phenotypic and genotypic variability in given population, respectively. Correlation and path analysis helps in identifying suitable selection criteria for improving the crop yield.

Methods: Plant material comprised of 68 genotypes belongs to early maturity group of pigeonpea and experiment conducted during *Kharif* 2015-16 in randomized complete block design with two replications.

Result: Traits, seed yield per plant (GCV= 51.56%, h^2= 97.13%, GAM= 104.67%) and number of pods per plant (GCV= 49.01%, h^2= 99.07%, GAM= 100.49%) had high values of genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as % of the mean (GAM) which indicated their additive genetic control. Plant height and number of seeds per pod recorded moderate to low heritability coupled with low GAM, indicating non-additive genetic control for these characters. Correlation analysis has revealed significant and positive association of seed yield per plant with number of pods per plant, plant height, secondary branches per plant, 100-seed weight and primary branches per plant. Path coefficient analysis identified number of pods per plant, secondary branches per plant and 100-seed weight as major traits affecting seed yield per plant directly and indirectly. The number of pods per plant and 100-seed weight should be given greater emphasis for improvement of seed yield in pigeonpea.

Key words: Correlation, Genetic variability, Heritability, Path coefficient, Pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is a drought tolerant pulse crop of semi-arid tropical regions of the world. Like other pulses, pigeonpea grain is an important source of protein (21%), carbohydrates (67%) and lipids (2.3%) (Sodavadiya *et al.,* 2009). It is a good source of water soluble vitamins (thiamine, riboflavin, niacin) and minerals (Ca, Mg, Cu, Fe and Zn) (Talari *et al*., 2018). By utilizing its extensive deep root system, pigeonpea corrects the quality and structure of soil through fixing atmospheric nitrogen. Being an often-cross pollinated crop, pigeonpea has moderate to high genetic variability but still has low yield potential as compared to cereal crops. Seed yield in pigeonpea is a complex trait like in other crops, it influenced by pods per plant and fruiting branches per plant (Singh *et al*., 2018). It is therefore important to analyse the extent and nature of variability and inheritance pattern of various yield amplifying traits (Singh *et al*., 2019). Currently, studies on pigeonpea are orchestrated towards exploration of its morphological and molecular diversity (Sharma *et al*., 2018a; Sharma *et al*., 2018b), hunt for stable fertility restorers and maintainers (Sharma *et al*., 2018c) and mapping of fertility restorer gene (Sharma *et al*., 2019). Along with it, biotic and abiotic stresses concerning pigeonpea yield are under research quist (Rao *et al*., 2003; Srivastava *et al*., 2006; Saxena, 2008, Pande *et al*., 2011; Ramu *et al*., 2012; Krishnamurthy *et al*., 2012; Saxena *et al*., 2017; Singh *et al*., 2020). The study of parameters such as phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) reveals the extent of phenotypic and genotypic variability in given population, respectively. The effect of selection can be further enhanced by classifying variability into heritable and non-heritable components. In addition, genetic up-gradation of a new population over the present population can be defined by genetic advance analysis. In addition to this, level of relationship among various plant characters can be well defined by correlation coefficient analysis. Path coefficient analysis is a standardized partial regression coefficient, which divides the correlation into direct and indirect effects (Singh *et al*., 2018). Correlation and path analysis thus help in identifying suitable selection criteria for improving the yield. The present investigation was undertaken to assess the genetic variability, correlation and direct and indirect effects of different influencing characters on seed yield in pigeonpea.

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MATERIALS AND METHODS

Present experiment was conducted during *Kharif* 2015-16 at experimental field area of Pulses Section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana in randomized complete block design with two replications. Experimental material comprised of 68 genotypes belongs to early maturity group (Table 1). Selfed seeds of each genotype were grown in a single row of 4 m length with a spacing of 50 cm between the rows and 25 cm between the plants within rows. The observations were recorded on plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per pod, 100-seed weight and seed yield per plant on five randomly taken competitive plants in each genotype in each replication. The mean data were subjected for analysis of variance (Panse and Sukhatme, 1989) and various genetic parameters *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were estimated as per Lush, 1940; Burton, 1952; Allard, 1960 and Johnson *et al.* (1955). The procedures suggested by Fisher (1954) and Al-Jibouri *et al*. (1958) were used in the estimation of genotypic and phenotypic correlation coefficients from the phenotypic and genotypic components of variances and co-variances. Path co-efficient analysis was worked out to estimate the direct and indirect effects of different traits on the yield (Dewey and Lu, 1959).

RESULTS AND DISCUSSION

The analysis of variance was done for all the seven characters and their mean square values are mentioned in Table 2. The mean sum of squares due to genotypes showed significant differences for all the studied traits excluding number of seeds per pod and 100-seed weight. Significant differences were reported in five traits (plant height, primary branches per plant, secondary branches per plant, pods per plant, seed yield per plant) indicating the presence of significant genetic variability in the experimental material that can be further utilized for pigeonpea improvement.

Genotypic coefficient of variation

Genotypic coefficient of variation (GCV) was found to be high for seed yield per plant (51.56%) followed by pods per plant (49.01%), primary branches per plant (32.88%) and secondary branches per plant (31.95%). The GCV was moderate for 100-seed weight (13.44%) and low in case of plant height (9.10%) and number of seeds per pod (4.01%) (Table 3). Presence of variability for different traits was also reported by Rangare *et al*. (2013); Singh *et al*. (2014); Ram *et al*. (2016); Mallesh *et al*. (2017) and Reddy and Jayamani, (2019) in cultivated pigeonpea. The expression of variable characters was found to be influenced by environment as genotypic coefficient of variation was reported to be less than respective phenotypic coefficient for all the traits.

Heritability and genetic advance

Pods per plant recorded highest heritability (99.07%) followed by seed yield per plant (97.13%), 100-seed weight (95.64%), secondary branches per plant (94.71%) and primary branches per plant (91.25%). Phenotypic expression can reliably recognize the genotypic character which was concluded from high magnitude of heritability these traits except seeds per pod. Singh *et al.* (2019) also reported the high magnitude of heritability for all the traits expect seeds per pod in BC_1F_3 generation of pigeonpea. Moderate heritability was observed for plant height (48.26%) and low for number of seeds per pod (23.67%).

Genetic advance as % of the mean (GAM) was found to be high (>20%) for all traits, except the plant height (13.03%) and number of seeds per pod (9.11%). The highest genetic advance was recorded (Table 3) for seeds yield per plant (104.67%) followed by number of pods per plant (100.49%), primary branches (64.71%) and secondary branches (64.07%). Saroj *et al.* (2013) also reported the higher genetic advance (more than 100%) for yield component traits in pigeonpea. The genetic advance coupled with heritability as % of the mean provides a better explanation of the nature of inheritance and effectiveness of selection for traits of interest (Johnson *et al.,* 1955).

In the present experiment, the traits *viz*., seed yield per plant and pods per plant had higher values of GCV (%), heritability and GAM showing that these traits are under the control of additive gene action and will give response to phenotypic selection. High heritability coupled with moderate genetic advance was observed for 100-seed weight, primary branches per plant and secondary branches per plant. However, plant height had moderate heritability with high genetic advance and number of seeds per pod has lower heritability as well as lower genetic advance. These results depict that phenotypic selection for such traits is not effective as there is predominance of non-additive gene actions.

Correlation and path coefficient analysis

Correlation and path analysis used to estimate the nature and magnitude of association between different characters affecting yield. These analyses help to understand the causes of association which is further exploited in the formulation of selection criteria for yield improvement.

In general, correlation analysis revealed that genotypic correlations were higher than phenotypic correlations and the directions of genotypic and phenotypic correlations were also similar for most of the character combinations. According to Almeida *et al.* (2010), demonstrates that genetic factors contributed more than the environmental factor to the correlations, so that genetic correlation were greater than phenotypic correlations. Masking and modifying effects of the environment on association of traits could be the cause of lower phenotypic correlations then genotypic correlations (Saroj *et al*., 2013). Correlation coefficients among all the traits are presented in Table 4. Seed yield per plant was found to have highly significant and positive correlation with pods per plant (0.944), plant height (0.398), secondary branches per plant (0.289), 100-seed weight (0.2876) and primary branches per plant (0.2602). However, seeds per pod exhibited positive but non-significant

correlation with seed yield per plant. Pandey *et al*. (2016), Pushpavalli *et al*. (2017), Baldaniya *et al*. (2018) and Singh *et al*. (2019) also reported significant and positive correlation between seed yield per plant and number of pods per plant. As it is well known that yield is a complex trait and it depends upon number of yield contributing traits. Selection for specific trait will also bring change in the other related trait. So, the knowledge related to direction and magnitude of association between the components traits is desirable for improvement in the desirable direction.

Table 1: List of pigeonpea genotypes used for present study.

S. no.	Genotype	Origin	S. no.	Genotype	Origin
1	AL 2092	PAU, Ludhiana	35	ICPL 88031	ICRISAT, Hyderabad
2	AL 301	PAU, Ludhiana	36	ICPL 92045	ICRISAT, Hyderabad
3	AL 302	PAU, Ludhiana	37	ICPL 93081	ICRISAT, Hyderabad
4	AL 1476	PAU, Ludhiana	38	ICPL 20340	ICRISAT, Hyderabad
5	AL 1599	PAU, Ludhiana	39	Pant A 37	GBPUAT, Pantnagar
6	AL-15	PAU, Ludhiana	40	Pant A 151	GBPUAT, Pantnagar
7	H-93-2	HAU, Hisar	41	Pant A 163	GBPUAT, Pantnagar
8	H-93-13	HAU, Hisar	42	Pant A 169	GBPUAT, Pantnagar
9	H-05-62	HAU, Hisar	43	Pant A 174	GBPUAT, Pantnagar
10	H-94-6	HAU, Hisar	44	Pant A 251	GBPUAT, Pantnagar
11	AH -06-1	HAU, Hisar	45	Pant A 252	GBPUAT, Pantnagar
12	AH-06-3	HAU, Hisar	46	P A 342	GBPUAT, Pantnagar
13	AH-06-7	HAU, Hisar	47	PUSA 991	IARI, New Delhi
14	AH-06-8	HAU, Hisar	48	P 226	IARI, New Delhi
15	H-93-22	HAU, Hisar	49	PUSA 2001	IARI, New Delhi
16	H-93-32	HAU, Hisar	50	P2002	IARI, New Delhi
17	Manak	HAU, Hisar	51	P 971	IARI, New Delhi
18	Paras	HAU, Hisar	52	PUSA 992	IARI, New Delhi
19	CORG 6012	TNAU, Coimbatore	53	Pusa 84	IARI, New Delhi
20	CORG 105	TNAU, Coimbatore	54	P 2012-1	IARI, New Delhi
21	CORG 108	TNAU, Coimbatore	55	P 951-1	IARI, New Delhi
22	CORG 169	TNAU, Coimbatore	56	P 954	IARI, New Delhi
23	CORG 111	TNAU, Coimbatore	57	T-21	CSAUK, U.P.
24	CORG 9704	TNAU, Coimbatore	58	VRG- 62	ARS, Vamban
25	IC 245183	ICRISAT, Hyderabad	59	1371- A	ARS, Vamban
26	IC 245186	ICRISAT, Hyderabad	60	MN-1	Minisota
27	IC 245219	ICRISAT, Hyderabad	61	TAT-108	BARC(MH)
28	IC 245132	ICRISAT, Hyderabad	62	AF 352	RRS, Faridkot
29	IC 245139	ICRISAT, Hyderabad	63	AF 370	RRS, Faridkot
30	IC 245273	ICRISAT, Hyderabad	64	MTH 103	Unknown
31	ICP 3977	ICRISAT, Hyderabad	65	GAYT 110	Unknown
32	ICPL 8947	ICRISAT, Hyderabad	66	ULA 11	Unknown
33	ICPL 9008	ICRISAT, Hyderabad	67	CIPB S1 20	Unknown
34	ICPL 85035	ICRISAT, Hyderabad	68	SP 2-2	Unknown

Table 2: Analysis of variance (ANOVA) for different traits in pigeonpea.

Source of variation	D.F.	Plant height (cm)	Primary branches	Secondary branches	Number of pods per plant	Seeds per pods	100 seed weight (g)	Seed yield per plant (g)
Replications (MSS)	1	23.35	4.60	3.24	28.19	0.26	0.07	3.61
Treatments (MSS)	67	1248.44**	48.64**	85.35**	8862.44**	0.17	1.87	498.03**
Error (MSS)	67	104.49	2.22	2.26	40.53	0.18	0.04	7.25
P.M.± S.E.		245.79±3.37	14.59±0.59	20.39±0.79	135.49±8.01	3.58±0.05	7.12±0.12	30.55±1.84
CD 5%		20.40	2.98	3.00	12.71	0.84	0.41	5.37
CV (%)		4.16	10.51	7.52	4.71	12.99	2.87	8.86

D.F. = Degree of freedom; MSS = Mean sum of square; P.M. = Population mean; S.E. = Standard error; CD = Critical difference and CV = Coefficient of variation. *Significant at 5% and **Significant at 1% level of significance.

Table 3: Parameters of genetic variability for different traits in pigeonpea.

Traits	PCV (%)	GCV (%)	h^2 (%)	GA	GA as % of mean
Plant height (cm)	13.10	9.10	48.26	31.88	13.03
Primary branches	34.42	32.88	91.25	9.44	64.71
Secondary branches	32.83	31.95	94.71	13.06	64.04
Number of pods per plant	49.23	49.01	99.07	136.15	100.49
Seeds per pods	17.23	4.01	23.67	0.33	9.11
100 seed weight (g)	13.74	13.44	95.64	1.93	27.07
Seed yield per plant (g)	52.31	51.56	97.13	31.80	104.67

PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation; h^2=heritability in broad sense; GA = Genetic advance.

Table 4: Correlation coefficients among all possible combinations of traits.

Traits		Primary branches	Secondary branches	Number of pods per plant	Seeds per pods	100 seed weight (g)	Seed yield per plant (g)
Plant height (cm)	G	0.0495	0.1042	0.3513	0.0001	0.0788	0.3984
	P	0.1001	0.0347	0.2824**	0.0369	0.1584	0.3116**
Primary branches	G		0.3245	0.3799	0.0012	-0.1234	0.2602
	P		0.3040**	0.3563**	-0.1369	-0.1012	0.2427**
Secondary branches	G			0.3720	0.0001	-0.1200	0.2898
	P			0.3554**	-0.0798	-0.1160	0.2786**
Number of pods per plant	G				0.0013	0.0444	0.9443
	P				-0.0201	0.0407	0.9338**
Seeds per pods	G					0.0014	0.0011
	P					0.0338	0.1089
100 weight (g)	G						0.2876
	P						0.2844**

Critical value of r at 5% = 0.1669 and at 1% = 0.2172. *Significant at 5% and **Significant at 1% level of significance.

Table 5: Direct and indirect effects of various traits on seed yield per plant.

Traits		Plant height (cm)	Primary branches	Secondary branches	Number of pods per plant	Seeds per pods	100 seed weight (g)	Correlation with seed yield per plant
Plant height (cm)	G	**0.0866**	-0.0028	-0.0153	0.0108	-0.0004	0.0015	0.3984**
	P	**0.0091**	-0.0054	-0.0002	0.2669	0.0041	0.0372	0.3116**
Primary branches	G	0.0016	**-0.0493**	-0.0048	0.0051	-0.0019	-0.0081	0.2427**
	P	0.0009	**-0.0544**	-0.0015	0.3367	-0.0153	-0.0237	0.2602**
Secondary branches	G	-0.0242	0.0133	**0.1366**	0.0208	0.0306	0.0002	0.2898**
	P	0.0003	-0.0165	**-0.0050**	0.3359	-0.0089	-0.0272	0.2786**
Number of pods per plant	G	0.0609	-0.0506	-0.0743	**0.4879**	0.0280	-0.0473	0.9443**
	P	0.0026	-0.0194	0.0018	**0.9451**	-0.0022	0.0095	0.9338**
Seeds per pods	G	-0.0010	0.0071	0.0416	0.0107	**0.1860**	0.0038	0.0011
	P	0.0003	0.0074	0.0004	-0.0190	**0.1118**	0.0079	0.1089
100 weight (g)	G	0.0045	0.0420	0.0003	-0.0248	0.0052	**0.2552**	0.2876**
	P	0.0014	0.0055	0.0006	0.0385	0.0038	**0.2347**	0.2844**

Residual effect = 0.0503. *Significant at 5% and **Significant at 1% level of significance.
Bold figure indicated direct effect.

Correlation analysis depicts the kind of relationship among the traits but does not give information regarding direct or indirect effects. Path coefficient analysis was worked out to understand the extent of relationship by considering seed yield per plant as dependent variable and rest of the traits are considered as independent variables. Results of path coefficient analysis with direct and indirect effects are mentioned in Table 5. Highest positive direct effect on seed yield per plant was exhibited by number of pods per plant (0.48) followed by 100-seed weight (0.25), seeds per pod (0.18) and secondary branches per plant (0.13). Pods per plant also exhibited positive indirect effect on seed yield per plant *via* secondary branches and 100-seed weight. Present results clearly indicated that selecting for high yield focus should be given on number of pods per plant, secondary branches per plant and 100-seed weight which

shows high direct positive effect along with positive correlation. Negative direct effect on seed yield per plant was shown by primary branches per plant. The association of pods per plant, secondary branches per plant, plant height and 100-seed weight with seed yield per plant was positive due to positive direct effects. Similar outcomes were also reported by Kothimbire *et al*. (2016), Ram *et al*. (2016), Kumar *et al*. (2017), Ranjani *et al*. (2018) and Singh *et al*. (2019). Above results indicated that indirect selection for higher seed yield can be achieved through secondary branches per plant.

CONCLUSION

Outcomes of various genetic variability parameters, correlation and path analysis identified pods per plant, secondary branches per plant and 100-seed weight as the main yield components. Selection for these traits will be helpful to improve of seed yield of pigeonpea.

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