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Multivariate Analysis for Selection of High Yielding and Early Genotypes in Pigeonpea [*Cajanus cajan* (L.) Millsp.] for North Western Plain Zone of India

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ABSTRACT

Background: Pigeonpea [*Cajanus cajan* (L.) Millsp] is the second most important pulse crop in India after chickpea. The crop is cultivated during *kharif* in the arid and semi-arid regions of India. The present study aims to evaluate the genetic variability of the population in small scale trial (SST) through multivariate, principal component and cluster analysis so as to identify superior high yielding early maturing genotypes that fit in cropping systems suitable for the North Western Plain Zone of India.

Methods: The plant material comprised of thirty advanced pigeonpea genotypes along with three checks evaluated in small scale trial (SST) during in randomized complete block design with three replications.

Result: High GCV and PCV along with high heritability and GA as percent of mean was recorded for the characters PPP and SYPP indicating the preponderance of additive gene action for the expression of these traits. Seed yield per plot (SYPP) was found to be positively correlated with DF (0.30) and HSW (0.37). Path coefficient analysis revealed that PPP, DF and HSW had significant positive and direct effect on seed yield per plot. Principal component analysis further substantiated the variability of the population wherein three components explained 65.8% of variation. Cluster analysis classified the 33 genotypes into eight different clusters thereby highlighting sufficient divergence in the population. Cluster VI and VIII showed the highest distance, which is suggestive of prospective utilization of heterosis from their crosses. Two genotypes AH 20-10 and AH 20-23 were identified as the most genetically distant and hence could be forwarded in future breeding programme.

Key words: Genetic variability, Multivariate analysis, Pigeonpea.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.], is often cross pollinated crop propagated through seeds. It is mostly cultivated in the tropical semi-arid regions of the world and belongs to the family fabaceae. Being India's second most significant pulse crop after gram or chickpea the crop holds immense potential in contributing to the Indian food basket. Seeds are important sources of dietary proteins (21%), lipids (2.3%) and carbohydrates (67%) (Sodavadiya *et al.,* 2009) along with vitamins like riboflavin, niacin, thiamine and minerals like calcium, magnesium, zinc, copper and iron (Talari and Shakappa, 2018). Apart from dietary supplements the crop also finds other uses as feed, fodder and fuel. Being a legume the deep tap root system of the crop enables fixation of atmospheric nitrogen thereby enhancing the soil fertility (Rao *et al.,* 2016). Biometrical analysis of a population through genotypic and phenotypic coefficient of variances, correlation study, path coefficient analyses, heritability and genetic advance explicates the underlying variability existing in a population empowering plant breeders to identify the reliable yield attributing characters for which selection would be effective (Singh *et al.,* 2019). This further helps in selecting potentially better performing lines from the population on the basis of the reliable yield and yield attributing characters as identified from the biometrical analyses (Pushpavalli *et al*., 2017 and Sharma *et al*., 2021).

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Pigeonpea being a long duration pulse crop takes 160-180 days to mature and hence finds low acceptance in different cropping systems in India. Hence identification of early maturing short duration genotypes, along with high seed yielding traits are desirable for crop intensification programmes. In this context, the current investigation highlights the study of different genetic variability parameters in pigeonpea genotypes evaluated in small scale trial to identify superior high yielding and early maturing pigeonpea lines which could be utilized in further crop improvement fitting in cropping systems suitable for the North West Plain zones of India.

MATERIALS AND METHODS

The trial was conducted during *Kharif* 2020-21 at the crop research field of Pulses Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Experimental design followed was randomized complete block design with three replications. The experimental materials consisted of thirty genotypes along with three check varieties *viz.* Manak, Pusa 992 and PAU 881 (Table 1). The observations regarding days to flowering, days to maturity, number of branches per plant, number of pods per plant, 100 seed weight, plant height and yield were recorded from five randomly collected plants in each replication for each genotype. The planting system consisted of four rows per genotype. The row to row and plant to plant spacing was 45 × 10 cm. The mean data obtained was subjected to analysis of variance as laid down by Panse and Sukhatme (1989). The estimation of genotypic and phenotypic correlation coefficients from the phenotypic and genotypic components of variances were carried out as per the methodologies put forward by Fisher (1954) and Al-Jibouri *et al.* (1958). Similarly, broad-sense heritability, genetic advance and genetic advance as percentage of mean, genotypic and phenotypic coefficient of variation (GCV and PCV) were also analyzed (Lush, 1940; Burton, 1952;

Table 1: Mean performance of advance pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes in *kharif* 2020-21.

Genotype	Pedigree	PH	Days to		BPP	Pods/	100 seed	Yield	Yield
		(cm)	Flowering	Maturity		plant	weight (g)	gm/plot	Kg/ha
AH 20-01	Paras × Manak	190	81	143	13	243	9	2292.33	3182
AH 20-02	Manak × CORG 9701	214	84	141	12	176	9	1674.67	2324
AH 20-03	-do-	244	87	138	13	213	9	2195	3047
AH 20-04	-do-	234	88	142	14	256	10	2080	2887
AH 20-05	-do-	237	92	140	15	287	10	2144	2976
AH 20-06	-do-	247	88	138	14	231	10	1951.67	2709
AH 20-07	-do-	238	81	140	13	222	9	1713.33	2378
AH 20-08	Manak × ICPL 88039	206	81	138	16	360	9	1718.00	2385
AH 20-09	-do-	225	86	142	12	210	10	1696.67	2355
AH 20-10	-do-	246	85	138	15	251	10	2579.67*	3581*
AH 20-11	-do-	229	81	136	14	198	9	2199	3052
AH 20-12	-do-	247	81	145	12	258	9	1719	2386
AH 20-13	AH 09-38 × Paras	214	92	142	15	274	9	2026.67	2813
AH 20-14	-do-	248	88	140	14	259	9	1391.67	1932
AH 20-15	-do-	225	80	148	15	346	9	1661.33	2306
AH 20-16	ILRG 30 × AL 1189	245	92	151	14	301	9	1365.67	1896
AH 20-17	-do-	262	91	151	13	290	10	1643	2280
AH 20-18	-do-	230	85	138	16	269	9	1255.33	1742
AH 20-19	P2001-6 × ILRG-30	238	86	141	12	289	10	1721.33	2389
AH 20-20	-do-	243	82	139	14	313	9	1614.00	2240
AH 20-21	-do-	232	87	144	13	265	10	1936.33	2688
AH 20-22	AL 1743 × ICP5028	252	80	140	15	275	10	1681	2333
AH 20-23	-do-	251	92	141	13	361	9	2474.6*	3435*
AH 20-24	P2001/5/2 × JBP-110B	243	93	140	12	227	9	1959.67	2720
AH 20-25	P 2002 × ICPL 20339	240	78	141	11	256	10	1924	2671
AH 20-26	P 2002 × ICPL 88039	212	80	142	13	226	9	1507.33	2092
AH 20-27	-do-	224	79	137	12	249	9	1714.33	2379
AH 20-28	ICPL 20339 × P2002	209	85	137	15	237	9	1681	2333
AH 20-29	-do-	236	76	138	13	290	9	1702	2362
AH 20-30	AH 16-36A (AL 1484 × ICPL 85024)	232	76	136	12	296	9	1284.33	1783
Manak (C)		244	80	137	12	231	9	1719.33	2386
Pusa 992 (C)		235	81	140	12	209	9	1935.33	2686
PAU 881 (C)		226	88	141	13	235	9	2117	2938

*Significantly higher than the best check.

C: Control; DF: Days to flowering, DM: Days to maturity; BPP: Branches per plant; PH: Plant height; PPP: Pods per plant; HSW: 100 seed weight; SYPP: Seed yield per plot.

Allard, 1960 and Johnson *et al.,* 1955). Path co-efficient analysis was worked out to estimate the direct and indirect effects of different traits on the yield (Dewey and Lu, 1959). Cluster analysis was carried out as per Tocher's method (Rao, 1952). Group distances based on multiple characters was carried out as per Mahalanobis (1936) utilizing the D^2 statistic. Data analyses were carried out in INDOSTAT software (https://www.indostat.org). Principle component analysis was carried out using PAST4.02 software package (Hammer *et al.,* 2001).

RESULTS AND DISCUSSION

Mean performance of advance pigeonpea genotypes is depicted in Table 1 and analysis of variance was done for the seven different quantitative characters. The variation among the thirty-three genotypes for the seven quantitative characters was highly significant ($p<0.01$) which justified subsequent biometrical analysis. All the seven different quantitative morphological and phenological characters significant variability was evident across the genotypes under study. Such divergence also justifies the variation in the population for the characters which could be utilized for crop improvement. Sufficient variability in pigeonpea has been in a number of published findings (Aswini *et al.,* 2021; Fousiya *et al.,* 2021; Sharma *et al.,* 2021).

Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance

The estimates of heritability, genetic advance and the coefficients of variation enable prediction and assessment of gain under selection (Sahu *et al.,* 2015). In the current investigation highest values for GCV and PCV were found in case of seed yield per plant (16.67, 17.40) followed by pods per plant (14.76, 16.95). Similar findings were reported by Patel *et al.* (2021) in seed yield and pods per plant having high GCV and PCV. For all the characters, values of PCV exceed the values of GCV slightly except for the trait branches per plant where sufficient difference between GCV and PCV is observed (Table 2). This shows that the effect of environment in the manifestation of that character is high and plant selection on basis of this character would not be effective. For fruitful selection high heritability is desirable with high genetic advance (GA). The broad sense heritability for almost all the characters were high *viz.* plant height (PH) (90.8%), days to flowering (DF) (96.8%), days to maturity

Table 2: Heritability, GCV, PCV, genetic advance and genetic advance as percent of mean for quantitative characters.

Traits	Heritability (bs) (%)	GCV (%)	PCV (%)	Genetic advance 5%	Genetic advance percent of mean
PH	90.8	6.27	6.58	28.72	15.78
DF	96.8	5.71	5.80	9.76	14.82
DM	90.8	2.50	2.61	6.88	6.26
BPP	40.3	6.40	10.45	1.14	11.12
PPP	75.8	14.76	16.95	69.03	33.93
HSW	92.3	3.87	4.03	0.72	9.82
SYPP	91.7	16.67	17.40	600.71	42.15

PH: Plant height; DF: Days to flowering; DM: Days to maturity; BPP: Branches per plant; PPP: Pods per plant; HSW: 100 seed weight; SYPP: Seed yield per plot.

Table 3: Estimates for genotypic and phenotypic correlation coefficients for different characters in pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes in SST during *kharif* 2020.

Traits		PH	DF	DM	BPP	PPP	HSW
PH	G		0.241*	0.224	-0.280**	0.178	0.334**
	P		0.240*	0.186	-0.160	0.144	0.310**
DF	G			0.395**	0.333**	0.070	0.282**
	P			0.374**	0.200	0.062	0.264
DM	G				0.179	0.317**	0.069
	P				0.062	0.249	0.072
BPP	G					0.616**	-0.071
	P					0.473**	-0.108
PPP	G						-0.047
	P						-0.056
SYPP	G	0.002	0.300**	-0.136	-0.545**	-0.141	0.365**
	P	-0.012	0.279	-0.127	-0.329*	-0.115	0.329

*Significant at 5% level; **Significant at 1% level.

PH: Plant height; DF: Days to flowering; DM: Days to maturity; BPP: Branches per plant; PPP: Pods per plant; HSW: 100 seed weight; SYPP: Seed yield per plot.

(DM) (90.8%), 100 seed weight (HSW) (92.3%) and seed yield per plant (SYPP) (91.7%). Correspondingly, high values of GA and genetic advance as percent of mean (GAM) was noticed for the characters PPP and SYPP. This is implicative of underlying additive gene action for the traits. This also means that the characters are fixable and hence selection for such traits would be effective. The character DM showed high heritability but low GAM (Table 2). This implies underlying non-additive gene action and hence scope for heterosis breeding. The lowest heritability was noticed in case of branches per plant (BPP) (40.3%), whereas pods per plant (PPP) depicted moderate heritability (75.8). Similar results for high heritability for PH, DF, HSW were found in the published results of Saroj *et al.* (2013), Vanniarajan *et al.* (2021).

Correlation analysis

Correlation study elucidates the direction and magnitude of association which reveal the relative contributions of the characters to yield and thereby facilitate the criteria for the selection of high yielding genotypes (Sharma *et al.,* 2022). In the present study it was seen that the values of genotypic correlations were higher than phenotypic correlations. This means that environment does influence the character association negatively. Although the value reduction for the characters DF and HSW is low which justifies their degree of character stability and association with SYPP. Such results are in correspondence to the findings of Almeida *et al.* (2010) and Verma *et al.* (2018) who also testified the character correlations of DF and HSW with yield. Table 3 represents the values of correlation coefficients for the different characters with seed yield. Positive and significant correlations were found for SYPP with DF (0.300) and HSW (0.365). This indicates that earliness to flowering would contribute to increase in seed yield. As the traits show high heritability along with genetic advance so these characters provide reliable factors for effective selection. Similarly, higher test weight of seeds indicates bold seeds which ensures better crop establishment. Negative correlations were seen in case BPP to SYPP at both genotypic and phenotypic levels. This is implicative environmental effects for this character expression is more and hence the character should be avoided for improved plant selections. Ranjani *et al.* (2018) also reported the negative correlation of BPP with seed yield.

Path coefficient analysis

Path coefficient analysis is carried out which divides the correlation into direct and indirect effects quantifying the relative importance of each character (Khan *et al*., 2016). With yield per plot being considered as the dependent variable and the other six characters as the independent variables path coefficient analysis was carried out. At genotypic level highest positive direct effect was observed in case of PPP (1.35) followed by DF (1.22) and HSW (0.34) (Fig 1). Similar results of significant high positive direct effects of PPP on SYPP were mentioned by Bishnoi *et al.* (2019); Hemavathy *et al.* (2019); Devi *et al.* (2020). The residual effect of 0.191 pointed out that the independent characters played significant role in expression of the dependent character. PPP showed high positive indirect effect on seed yield through BPP. Similarly, DF exhibited positive indirect effect on DM. Although negative direct effect on seed yield was seen in case of BPP (-1.975), PH (-1.089) and DM (-0.469). The findings are in concurrence to the reports of Sharma *et al.* (2021) wherein it was emphasized that selection for yield enhancement could be made through direct selection for DF and indirect selection for BPP. The results are suggestive that the above morphological *i.e.* HSW and PPP and phenological characters *i.e.* DF are effective indicators for direct selection of high yielding genotypes in pigeonpea.

Principal component analysis

Principal component analysis (PCA) study was carried out to decipher the underlying factors contributing mostly to the variability in the population. The population under the present study is highly variable and hence the PCA analysis has revealed that 65.8% of variation could be explained by the first three principal components. Trait biplot (Fig 2) revealed that for SYPP had high correlation with HSW and DF. First principal component displayed high contribution to divergence for the characters DF, PH, HSW and SYPP. Correspondingly the genotypes AH 20-10 and AH 20-23 explicated the variability for SYPP and DF. Hence hybridization between these genotypes for the concerned

Table 4: Grouping of pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes into different clusters using between-group method (Tocher's method).

Cluster	No. of genotypes	Name of genotypes
Cluster I	11	AH 20-07, Pusa 992, Manak, AH 20-20, AH 20-25, AH 20-22, AH 20-27, AH 20-11, AH 20-29, AH 20-26, AH 20-30
Cluster II	11	AH 20-4, AH 20-21, PAU 881, AH 20-03, AH 20-19, AH 20-06, AH 20-05, AH 20-09, AH 20-14, AH 20-24, AH 20-13
Cluster III	1	AH 20-18
Cluster IV	4	AH 20-02, AH 20-28, AH 20-08, AH 20-01
Cluster V	2	AH 20-16, AH 20-17
Cluster VI	1	AH 20-10
Cluster VII	2	AH 20-12, AH 20-15
Cluster VIII	1	AH 20-23

characters could be rewarding. PC2 substantiated the divergence for the characters BPP, PPP and DM. Such results also found in the published works of Hussain *et al.* (2021) wherein PC2 showed positive correlation with PPP and BPP. Thus the above characters were identified to be the key components of variability in the population and henceforth could be forwarded for in breeding programmes as significant factors of selection.

Cluster analysis

Mahalonobis D^2 method is an effective tool enabling the classification of a population into clusters based upon their genetic divergence. Genotypes with diverse genetic architecture provide for increased chances of genetic recombination manifesting hybrid vigour. Cluster analysis of the population segregated the thirty-three genotypes under study into eight clusters indicating sufficient divergence in the population. The clustering pattern displayed that cluster I and II have the most number of genotypes (11), whereas cluster III, VI and VIII have only one genotype each (Table 4). The genotypes in cluster VI, VII and VIII were found to be outstanding in terms genetic distance. Upon correlation with the yield values as shown in Table 1 genotypes AH 20-10 and AH20-23 from clusters

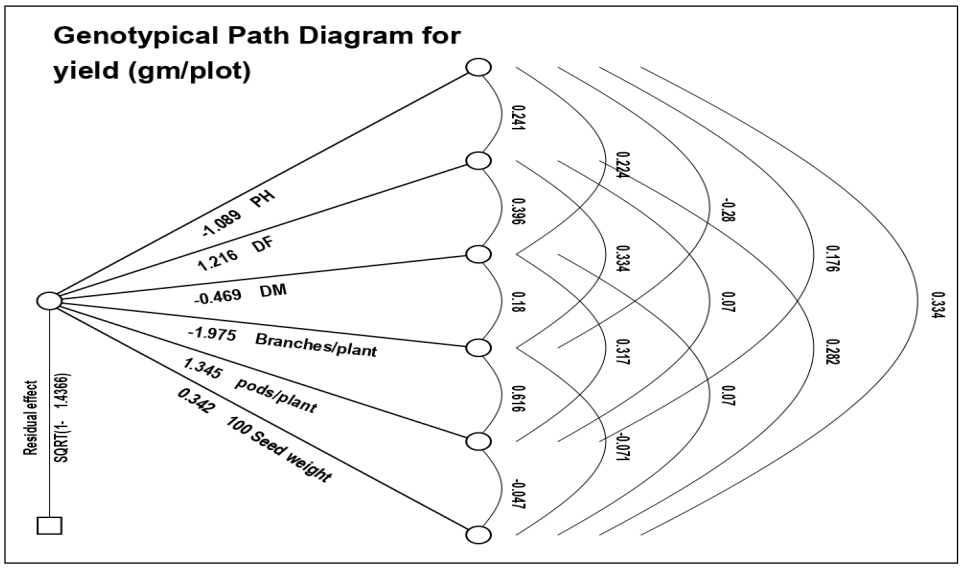


Fig 1: Genotypic path diagram for the characters in pigeonpea [*Cajanus cajan* (L.) Millsp.].

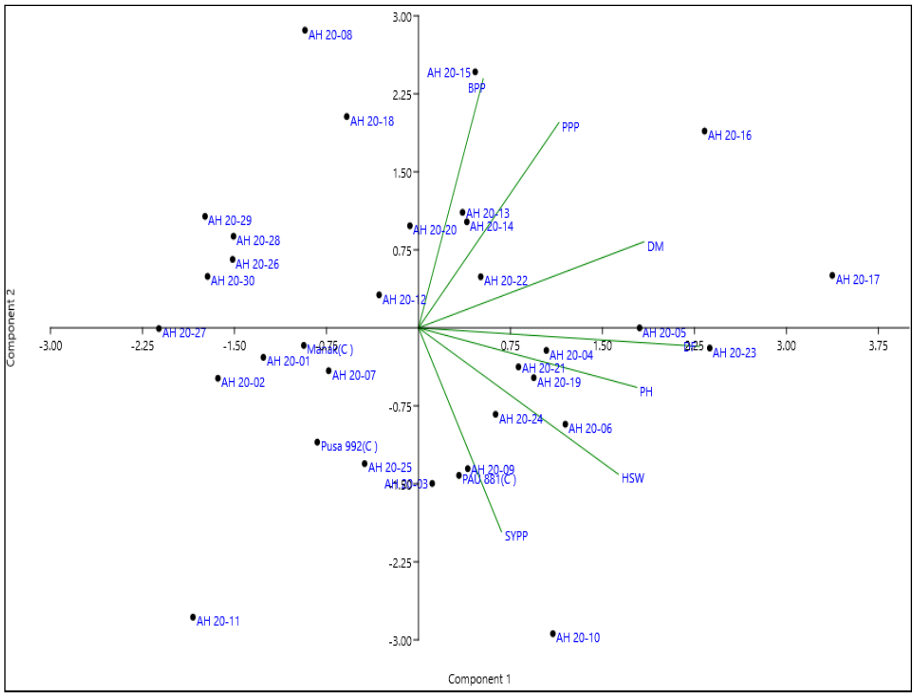


Fig 2: Trait biplot ordination depicting the association among quantitative traits in 33 pigeonpea genotypes.

VI and VIII showed highest yield compared to the checks. Hence, considering the genetic heterogeneity these clusters could be well utilized in hybridization programmes to develop superior recombinants. Among the recent investigations cluster analysis to decipher the diversity of pigeonpea populations were carried out by Hemavathy *et al.* (2019) and Sandeep *et al.* (2020).

CONCLUSION AND FUTURE PROSPECTS

Multivariate analyses provide idea about the racial likelihood of a population. The present investigation highlights character assessment, its association with yield and identification of superior genotypes in pigeonpea evaluated in small scale trial. Significant variability among the genotypes was observed. There is positive association between the seed yield per plot with DF and HSW. Similarly, path coefficient analysis revealed that PPP, DF and HSW had significant positive and direct effect on seed yield per plot at both genotypic and phenotypic levels. Hence significantly the characters HSW, DF and PPP turn out to be prominent traits aiding improved plant selection. Direct selection for the above traits would be suitable for yield improvement. This is suggestive that earliness in flowering along with bold seeded in pigeonpea contributes to yield enhancement. The population exhibited sufficient divergence as evident from the principal component analysis revealing three significant components which explained 65.8% of the total variation and cluster analysis which classified the 33 genotypes into eight different clusters. High inter cluster distance between Cluster VI, VII and VIII is reflective of potential possibilities of hybridization between these clusters for fruitful crop improvement. The genotypes AH 20-10 and AH 20-23 present from the respective clusters were identified as the sufficiently productive with respect to DF, PPP and SYPP. Thus the results are further suggestive of a correlated response of earliness to increased seed yield. Henceforth future crop breeding programmes for pigeonpea improvement should target early duration and high yielding genotypes as highlighted in the present investigation. The identified genotypes could thus be further evaluated in advanced breeding trials in further generations.

Conflict of interest: None.

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