Mysore J. Agric. Sci., 59 (2) : 390-399 (2025)

Genetic Variability and Diversity Studies in Medium duration Pigeonpea [*Cajanus cajan* (L.) Millsp.] Genotypes

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Received : November 2024
Accepted : December 2024

Abstract

Pigeonpea is an important grain legume of tropical and sub-tropical regions of the world and play a vital role in meeting the growing demand of food and nutrition of these regions, largely owing to its high nutritional status. The improvement in grain yield and in turn to achieve higher production, genetic variability is a pre-requisite for selection of superior genotypes. Hence, the present study was designed to assess the presence of genetic variation for grain yield and its attributes among thirty-seven medium duration pigeonpea genotypes along with three checks (ICP 8863, ICPL 87119 and a local check) were evaluated in five environments (Badnapur, Tandur, GKVK, Patancheru and Ranchi) in an alpha lattice design with three replications. The combined analysis of variance depicted significant ($P< 0.001$) mean squares for genotypes, environments and genotype × environment interaction. Furthermore, high estimates of GCV and PCV revealed the presence of maximum variability for grain yield and minimum variability for hundred seed weight. The principal component analysis for the traits studied has shown significance of two PCs accounting for 70.69 per cent of cumulative variation. Traits like hundred seed weight and grain yield had higher estimates of heritability and genetic advance as per cent mean revealing the effectiveness of selection. Correlation coefficient further showed that the grain yield and hundred seed weight are positively correlated suggesting for the possibility of simultaneous improvement. In addition, the path coefficient analysis deciphered the positive direct effect of hundred seed weight on grain yield indicating that it can be used as an index to select for complex traits like grain yield.

Keywords : Heritability, Genetic variability, PCV (phenotypic coefficient of variance), GCV (genotypic coefficient of variance), Correlation and path coefficient analysis

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is an important grain legume crop of tropical and subtropical regions of the world (Varshney *et al.,* 2012). It is a diploid (2n=2x=22) originated from India. Pigeonpea is rich in protein, dietary fiber and vitamins, making it valuable for food security and balanced diets. Globally, pigeonpea covers an area of 6.09 million hectares, producing 5.01 million tonnes with productivity of 822 kg ha^{-1} (FAOSTAT, 2020). India contributes 90 per cent of the global pigeonpea production with Maharashtra being the leading producer, followed by Karnataka and Madhya Pradesh. However, Karnataka's pigeonpea productivity is relatively low (591 kg ha^{-1}) compared to the national average. Pigeonpea yield is influenced by various biotic, abiotic and agronomic elements, which should be optimized to obtain maximum grain yield (Dash *et al.,* 2024).

Yield is a complex trait influenced by multiple genes, each with a small but cumulative effect. Direct selection for yield can be misleading as it is a quantitative trait and is significantly influenced by environment. Therefore, it is crucial to determine the direct and indirect contributions of each component trait to grain yield in order to identify key factors that influence yield. Correlation studies provide insight into the degree and direction of association between yield and other morphological traits, but they do not reveal the extent of the relationship (direct and indirect effects). Therefore, relying solely on variability parameters and correlation studies is not sufficient. Principal component analysis (PCA) (Jeffers, 1967), is an explanatory tool for multi dimensional data which reduces large set of data into relatively small number of components. Reduction of dimension was done by forming groups with strong inter-correlation in a set of variables and each component explains varied per cent variation to the total variability (Das *et al.,* 2017) and thus revealing the pattern of different traits and eliminates redundancy in large data sets.

For selection to be effective, sufficient genetic variability should be present in the population and the variability must be heritable. Genetic parameters such as GCV (Genotypic Coefficient of Variation), PCV (Phenotypic Coefficient of Variation), heritability and genetic advance are important measures and estimates of such parameters that contribute to exploit the available genetic variability in the population (Hossain *et al.,* 2015). GCV and PCV assess the amount of genetic variability present in the experimental material, while heritability and genetic advance decides the effectiveness of selection. Heritability sheds light on the extent of a character that will be transmitted to subsequent generations (Bello *et al.,* 2012). For effective selection, along with heritability, high genetic advance and GCV is important. Additive gene action underlies the characters with high heritability, genetic advance and GCV. Thereby, improvement can be achieved by selection methods (Ibrahim and Hussein, 2006). Thus, the selection efficiency for certain traits can be broadened using estimates of genetic parameters, which are fundamental for plant breeding.

MATERIAL AND METHODS

The genetic material of the present study comprised of 40 pigeonpea genotypes among which 37 genotypes were developed at ICRISAT, Patancheru and three checks were included *viz.,* ICP 8863, ICPL 87119 and a local check (Table 1). The experimental material was evaluated for yield and its attributing traits in five environments *viz.,* Patancheru, Tandur, GKVK (Bengaluru), Badnapur and Ranchi. Genotypes were sown in alpha lattice design with three replications

TABLE 1

Detailed list of genotypes used in the study

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	ICPL 19394	11	ICPL 19407	21	ICPL 19419	31	ICPL 19430
2	ICPL 19395	12	ICPL 19408	22	ICPL 19420	32	ICPL 19432
3	ICPL 19396	13	ICPL 19410	23	ICPL 19421	33	ICPL 20201
4	ICPL 19399	14	ICPL 19411	24	ICPL 19422	34	ICPL 20202
5	ICPL 19401	15	ICPL 19412	25	ICPL 19423	35	ICPL 20203
6	ICPL 19402	16	ICPL 19414	26	ICPL 19424	36	ICPL 20204
7	ICPL 19403	17	ICPL 19415	27	ICPL 19425	37	ICPL 20205
8	ICPL 19404	18	ICPL 19416	28	ICPL 19426	38	ICPL 87119 (C)
9	ICPL 19405	19	ICPL 19417	29	ICPL 19427	39	ICPL 8863 (C)
10	ICPL 19406	20	ICPL 19418	30	ICPL 19428	40	Local Check

during *kharif* 2021. Data was recorded on five randomly selected plants and observations were recorded on traits such as days to 50 per cent flowering, days to maturity, plant height (cm), hundred seed weight (g) and grain yield (kg ha^{-1}).

Data from five environments was subjected to the combined analysis of variance. Main and interaction effects of genotypes and environments were assessed by combined analysis of variance (ANOVA) across five environments. The combined ANOVA for alpha lattice design over environments was constructed using R software v4.1.3 (Butler *et al.,* 2017). BLUPs (Best Linear Unbiased Predictors) values calculated for genotypes across environments were further used for analysis. A pooled data analyses across environments was performed using R software v4.1.3 to obtain genetic variability parameters, principal component analysis, correlation and path coefficient analysis.

RESULTS AND DISCUSSION

Combined Analysis of Variance

The combined analysis of variance revealed significant mean squares ($P < 0.001$) for all the traits studied showing the presence of substantial variations between the genotypes. Furthermore, significant mean square was also observed for the traits for environments and genotype × environment (Table 2) indicating that the genotypes differed in their expression under the influence of varied environmental conditions.

The significant mean squares for these traits were formerly reported by Pandey *et al.* (2016); Pal *et al.* (2018) and Gaur *et al.* (2020). The existence of genetic variability is a necessary aspect for the crop improvement, as it allows for the selection of superior genotypes in plant breeding programmes. Hence, further studies are conducted to study the extent of genetic variability in the experimental material.

Estimates of Genetic Parameters for Yield and its Attributes

The significant mean squares for all the traits for genotypes indicated the presence of substantial variation among genotypes for traits studied. The magnitude of variation among genotypes for each trait further can be depicted through estimates of mean, range, PCV and GCV, heritability and genetic advancement as a percentage of the mean (Table 3). The result revealed that the maximal variability was recorded for grain yield (375 – 2893.3 kg ha^{-1}), whereas the minimal range was noticed for hundred seed weight (6.50 – 16.10 g).

Higher PCV compared to GCV was recorded for all traits evaluated in this study, showing the influence of the environment on the genotypes for the traits studied (Saroj *et al.,* 2013). The variation of GCV and PCV for different traits is depicted in Fig. 1. PCV was slightly higher than GCV for traits like days to

TABLE 2

Combined analysis of variance for yield and its attributing traits in pigeonpea

Source of variation	df	DFF	DTM	PHT	HSW	GY
Genotype	39	642.1 ***	728 ***	1062.5 ***	14.72 ***	423087 ***
Environment	4	7000.6 ***	40445 ***	29518.0 ***	14.38 ***	4923223 ***
Replication (Environment)	10	3.0	16 **	300.5 **	0.82	197911 ***
Block (Replication * Environment)	60	6.1	10 *	73.8 *	0.77	42836 *
Genotype * Environment	156	145.4 ***	149 ***	661.5 ***	2.72 ***	242198 ***
Residuals	330	3.74	5.25	63.7	0.52	28973

DFF: Days to 50% flowering; DTM: Days to maturity; PHT: Plant height; HSW: Hundred seed weight; GY: Grain yield; NS: not significant; *,**,***: significant at 5%, 1% and 0.1%, respectively

TABLE 3

Estimates of genetic variability parameters for yield and its attributing traits in pigeonpea

Genetic parameters	DFF	DTM	PHT	HSW	GY
Maximum	144	230	242	16.1	2893.3
Minimum	81	140	128	6.5	375
Mean	114.4	177.03	173.57	10.32	1329.05
Standard error of mean	5.58	10.58	12.2	0.65	205.82
Genotypic variance	182.78	130.64	205.22	4.48	98666
Phenotypic variance	276.49	466.64	652.05	5.75	225755
GCV	11.82	6.45	8.25	20.51	23.63
PCV	14.53	12.2	14.71	23.24	35.75
Heritability (%)	66	59	32	77	44
Genetic advance as percentage of mean (%)	19.8	7.47	9.53	37.3	32.18
CV	2.03	1.52	5.81	8.55	12.89

DFF: Days to 50% flowering; DTM: Days to maturity; PHT: Plant height; HSW: Hundred seed weight; GY: Grain yield

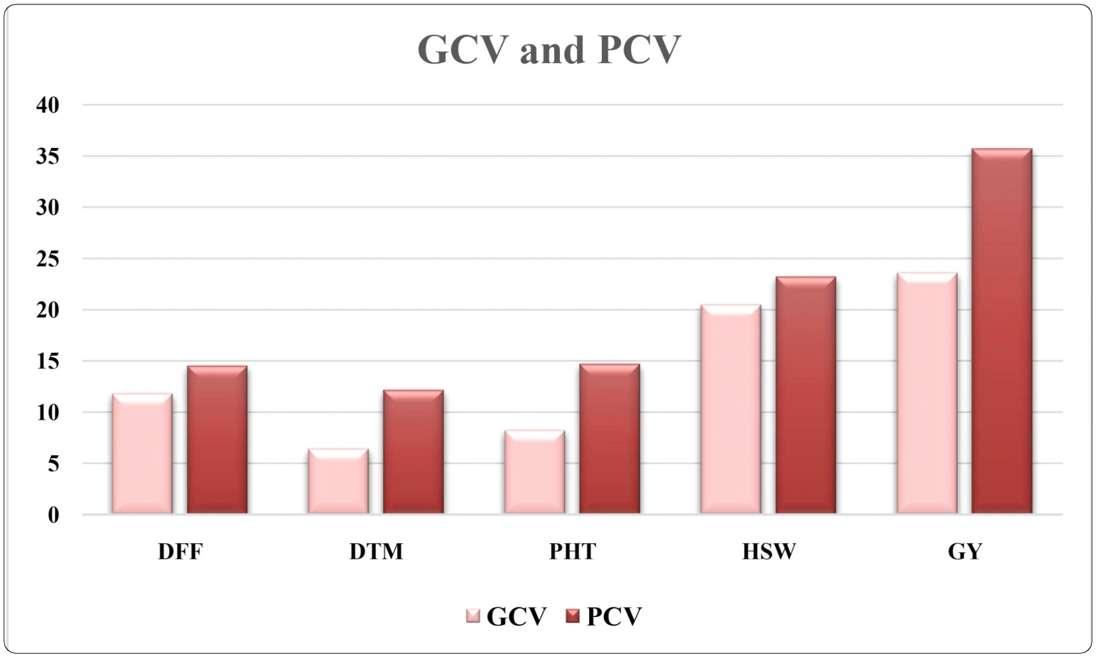

Fig. 1 : Graphical representation of GCV and PCV estimates for the traits studied

maturity, plant height, hundred seed weight and grain yield, indicating that the influence of environment was less on the experimental material (Singh *et al.* 2013). As a result, direct selection can be followed for the improvement of the trait. The difference between PCV and GCV was more for grain yield, indicating the influence of environment for the trait to be much higher. Grain yield had the highest GCV (23.63) and PCV (35.75) estimates. Singh *et al.* (2013) reported higher GCV and PCV for grain yield in pigeonpea. Traits like days to 50 per cent flowering (11.82, 14.53) days to maturity (6.45, 12.2) and plant height (8.25, 14.71) showed low GCV and PCV estimates, respectively. Relatively low variability was observed for the traits, days to 50 per cent flowering and days to maturity. Similar lower estimates of GCV and PCV for the above-mentioned traits were also reported previously by Birhan *et al.,* 2013 and Parre & Raje, 2022. Similar results on genetic variability parameters on yield are reported by Jambagi & Savithramma, 2020 and Shilpa *et al.,* 2023 (Groundnut).

Heritability and Genetic Advance as a Percentage of the Mean

Heritability estimates were categorized into three groups *viz.,* low (<30%), medium (30% – 0.50%) and high (> 0.50%). Among the five traits studied, days to 50 per cent flowering (66%), days to maturity (59%), and hundred seed weight (77%) had higher estimates of heritability, indicating the effectiveness of selection in the genetic improvement of these traits. Traits like plant height (32%) and grain yield (44%) showed moderate heritability (Table 3). Pushpavalli *et al.,* (2018) and Kumar *et al.,* (2022) also reported different levels of heritability for yield attributing traits.

Genetic advance is a good measure of selection in the relevant population. Based on the genetic advance over per cent mean (GAM), genotypes can be grouped into three classes such as low (<10%), moderate (10-20%) and high (>20%). Out of five traits under investigation, hundred seed weight (37.30%) and grain yield (32.18) showed high GAM estimates. The remaining traits such as plant height (9.53%) and days to maturity (7.47%) showed low GAM values, whereas days to 50 per cent flowering had moderate genetic advance over per cent mean (19.8%).

High genetic advance coupled with high heritability estimates offer the most suitable condition for selection and indicate a more reliable index of selection value (Johnson *et al.,* 1955). The variation observed for heritability and GAM for different traits are graphically depicted in Fig. 2. Days to maturity and days to 50 per cent flowering had high heritability and low/moderate genetic advance, indicating the possibility of preponderance of non-additive gene action in the expression of these traits.

Consequently, selection would be ineffective as the response to selection would be poor. Plant height showed lower/moderate estimates of both heritability and genetic advance over per cent mean. Traits such

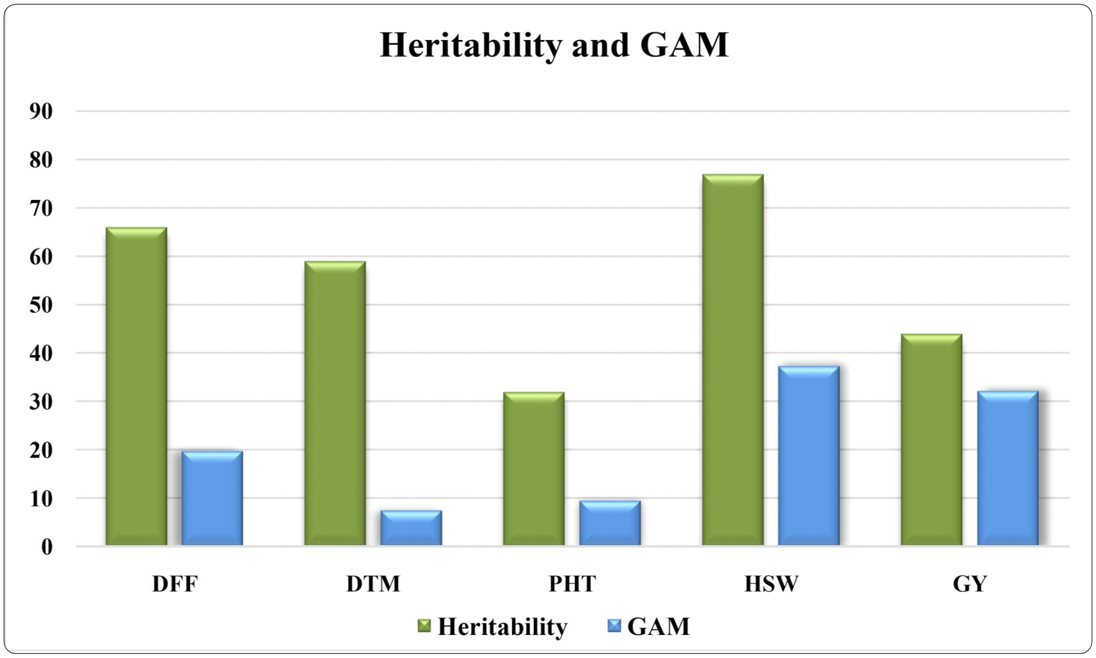

Fig. 2 : Variation in heritability and genetic advance for different traits

TABLE 4

Genotypic and phenotypic correlation coefficients in pigeonpea

		DFF	DTM	PHT	HSW	GY
DFF	G	1.000 **				
	P					
DTM	G	0.931 **	1.000 **			
	P	0.9081 **				
PHT	G	-0.2734 $^{\text{NS}}$	-0.166 $^{\text{NS}}$	1.000 **		
	P	-0.2514 **	-0.115 $^{\text{NS}}$			
HSW	G	-0.3452 *	-0.3172 *	-0.102 $^{\text{NS}}$	1 **	
	P	-0.2451 **	-0.2155 *	-0.0846 $^{\text{NS}}$		
GY	G	-0.381 *	-0.3242 *	-0.1597 *	0.3406 **	1 **
	P	-0.3651 **	-0.3106 **	0.125 $^{\text{NS}}$	0.242 **	

DFF: Days to 50% flowering; DTM: Days to maturity; PHT: Plant height; HSW: Hundred seed weight; GY: Grain yield. NS: not significant; *,**,***: significant at 5%, 1% and 0.1% respectively

as hundred seed weight and grain yield showed high/ moderate heritability along with high genetic advance as percentage of mean, indicates the effectiveness upon selection practiced. Similar results were also reported by Bhadru (2010) and Hemavathy *et al.* (2019).

Correlation Between Grain Yield and its Attributes

Correlation coefficient envisages relationship among yield and its attributing traits that form selection index to simultaneously improve more than one trait (Ningwal *et al.,* 2023). Genotypic and phenotypic correlation estimates between traits are represented in Table 4. The significant and positive genotypic correlation (r= 0.340, P< 0.01) was noticed between hundred seed weight and grain yield. It emphasizes that hundred seed weight and grain yield can be improved simultaneously. On contrary, traits like days to 50 per cent flowering (r=0.381, P< 0.01), days to maturity (r= 0.324, P< 0.05) and plant height (r= 0.159, P< 0.05) showed significant negative genotypic correlation with grain yield. Similar results were also obtained by Saroj *et al.,* 2013. Similarly, phenotypic correlation also showed significant and positive relationship (r= 0.242, P< 0.01) between hundred seed weight and grain yield. However, days to 50 per cent flowering (r= 0.365, P< 0.01) and days to maturity (r= 0.310, P< 0.01) showed significant negative phenotypic correlation indicating that the late flowering and maturity will not increase the grain yield of genotypes.

Path Coefficient Analysis

The significance of the correlation coefficient further necessitates to partition the correlation coefficient into direct and indirect effects. Path coefficient analysis thus estimates the influence of independent traits on dependent traits. It is used to assess the direct and indirect effects of component traits on grain yield. The direct and indirect effects on grain yield are represented in Table 5. Under genotypic path coefficient estimates, the highest positive direct effect on grain yield was showed by hundred seed weight (0.2590). While, days to 50 per cent flowering

TABLE 5

Direct (diagonal) and indirect (non-diagonal) effects of four traits on grain yield in pigeonpea

	DFF	DTM	PHT	HSW
DFF	**-0.4083**	0.1441	-0.0274	-0.089
DTM	-0.3801	**0.1548**	-0.0167	-0.0821
PHT	0.1116	-0.0258	**-0.0265**	-0.0265
HSW	0.1409	-0.0491	-0.0103	**0.2590**

Residual effect: 0.79

TABLE 6

Per cent variability explained by five eigen vectors

	PC1	PC2	PC3	PC4	PC5
Eigen values	2.41	1.12	0.99	0.46	0.01
% Variance explained	48.28	22.41	19.80	9.27	0.21
% Cumulative variance	48.28	70.69	90.50	99.78	100.00
DFF	0.611	-0.161	-0.161	0.281	-0.703
DTM	0.610	-0.204	-0.131	0.253	0.709
PHT	0.475	0.373	0.072	-0.793	-0.005
HSW	0.034	0.884	-0.195	0.419	0.039
GY	-0.158	-0.097	-0.955	-0.227	0.012

DFF: Days to 50% flowering; DTM: Days to maturity; PHT: Plant height; HSW: Hundred seed weight; GY: Grain yield

(-0.4083) showed negative direct effects on grain yield followed by plant height (-0.0265). Similar direct and indirect effects on grain yield were reported by Tharageshwari and Hemavathy (2020) and Yadav *et al.* (2024) in pigeonpea.

Principal Component Analysis

Principal Component Analysis (PCA) is a technique used to identify the linear combination that captures the maximum variability in the data. In this study, PCA was performed on the data of 39 pigeonpea genotypes of medium duration group. The eigen values of the five principal component axes and the percentage of variation derived from the principal component analysis are shown in Table 6. Out of five principal components, only two had more than 1.00 eigen value exhibited about 70.69 per cent of cumulative variance. The percentage variability of PC1 was 48.28 and PC2 was 22.41 for the traits under investigation. It elucidates the predominance of the first two PCs in capturing the variability present in the experimental material.

Contribution of Individual Trait to Total Variability

The number of PCs having significant effect on the trait is noted using a graphical approach utilizing a scree plot, it tells about the optimum number of PCs to be further considered. After the first PC, the plot steeply fell downward initially and then became approximately horizontal line. The point at which the curve first began to straighten out was considered to indicate the maximum number of components (Kumawat *et al.,* 2021). The contribution of different traits towards the genetic diversity varied across PCs (Table 6). The first two PCs showed significant contribution to the genetic diversity (Fig. 3). Positive contribution towards PC1 of genetic divergence was witnessed for traits like DFF (0.611), DTM (0.610), PHT (0.475) and HSW (0.034). For PC2, traits like

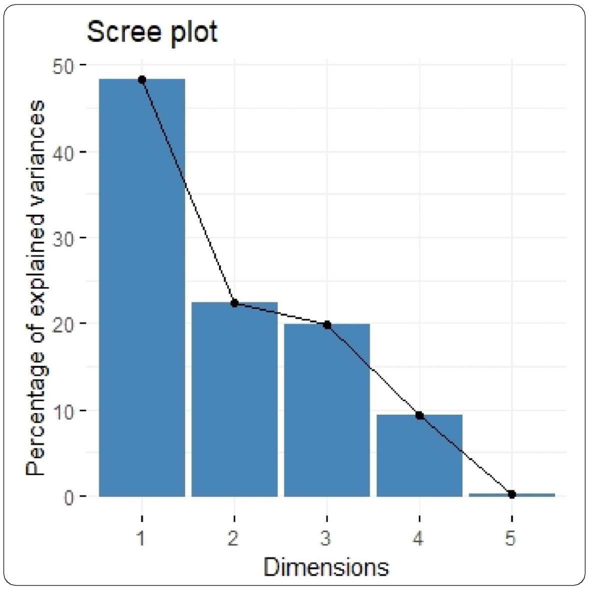

Fig. 3 : Scree plot displaying percentage of explained variances corresponding to five extracted principal components

PHT (0.373) and HSW (0.884) showed positive contribution to the genetic divergence. Akshaya *et al.* (2023) used PCA to categorize traits of pigeonpea that contributed for most of the variance in the data.

Genotype by trait biplot diagram between PC1 and PC2 explains the distribution and the nature of diversity for both variables and the genotypes (Fig. 4). The location of genotypes in the biplot tells about the contribution of them to the genetic variance. The genotypes occupied the biplot close to the origin contributed less to the total genetic variance, whereas those genotypes deviating from the origin contributed more to the total variance. Genotypes G39, G5, G6 and G15 were found close to origin with less variation and genotypes G2, G3, G4, G31 and G34 with much deviation from the origin contributed to the major part of the genetic variance. Similar contribution of genotypes to the total genetic variance was reported by Kumar *et al.* (2022) and Tharageshwari & Hemavathy (2020). Traits under consideration were represented as lines projecting from the origin. Acute angle was noticed between DFF and DTM indicating that they were positively associated and were found to be independent of GY, PHT and HSW. The bi-plot diagram exhibited high variability among the genotypes and between the parameters (Hemavathy *et al.,* 2019). This variability can be exploited further to achieve significant genetic improvement for the traits studied.

The genotypes evaluated in five environments have shown significant differences for genotypes and environments for yield and its attributing traits. The components contributing to the total variance was reduced by using a multi dimensional approach to few

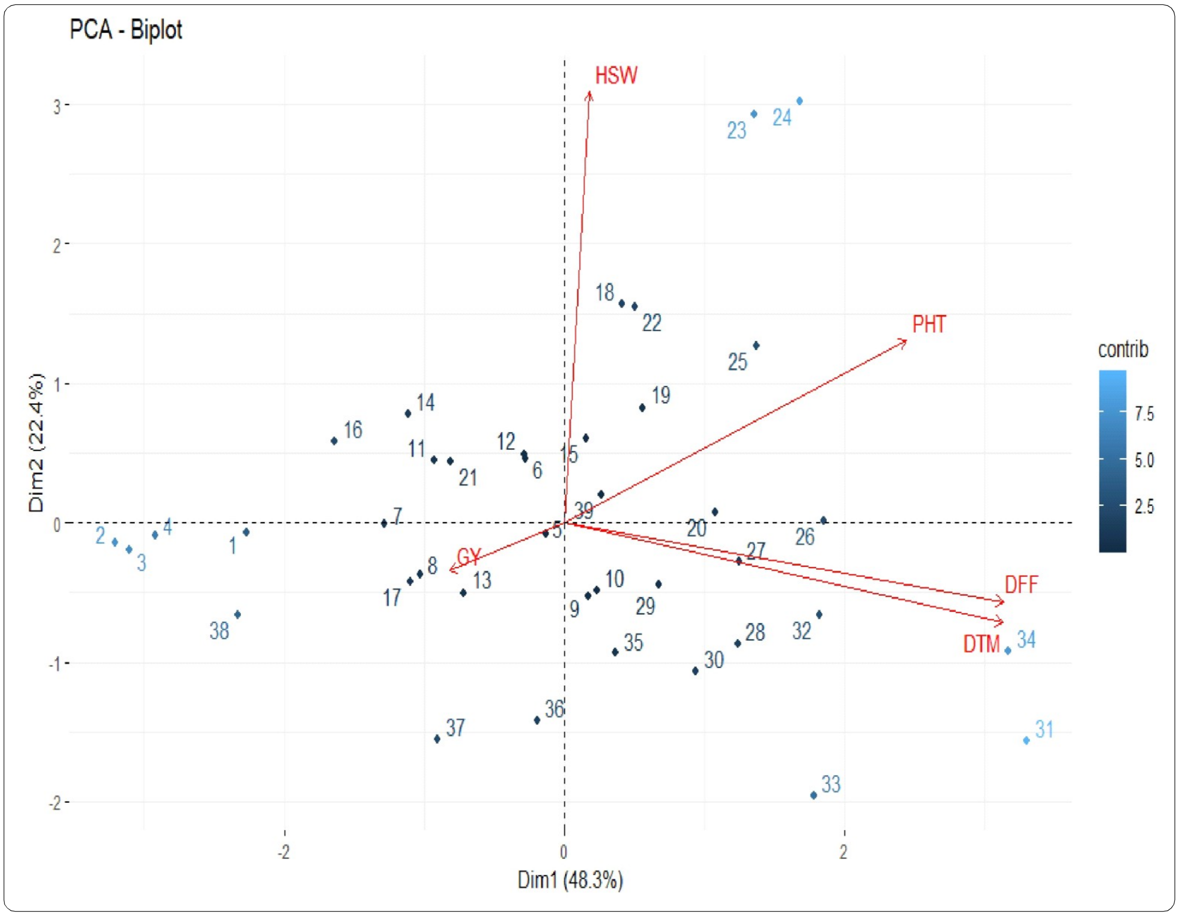

Fig. 4 : Genotype by trait biplot representing medium-duration pigeonpea genotypes

principal components. A total of five PCs were calculated, among them first two PCs were significant and accounted for 70.69 per cent of total variability. The traits like DFF, DTM and PHT contributed majorly to the genetic diversity that was captured by PC1 in the positive direction. The higher variability, along with estimates of genetic parameters like GCV, PCV, heritability and genetic advance over per cent mean together determine the effectiveness of the selection towards the trait under improvement. Thus, higher estimates of GCV and PCV for grain yield in the present study emphasizes the presence of huge variability in the experimental material. Further hundred seed weight and grain yield showed higher estimates of heritability and genetic advance over per cent mean envisages the role of additive gene action in its heritance. Thereby, selection for these traits will be rewarding for genetic improvement of pigeonpea.

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