Received: 12 Apr 2021 | Revised: 28 May 2021 | Accepted: 01 Jun 2021

Electronic Journal of Plant Breeding

Research Article

Genetic variability of agronomic traits in extra-early maturing Introgression Lines (ILs) of pigeonpea [*Cajanus cajan* (L.)]

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Abstract

A study was designed with a total of 20 pigeonpea extra- early introgression lines along with the checks in RCBD for genetic variability and other genetic parameters for 10 agronomic traits. Data was recorded on days to flower, days to 50% flowering, days to maturity, plant height, the number of primary branches, the number of secondary branches, the number of pods per plant, pod weight per plant, hundred seed weight and grain yield per plant. Considerable variation was observed for all the traits studied. High heritability coupled with high genetic advance was observed for days to flowering, days to 50% flowering, days to maturity, plant height, the number of pods per plant, pod weight per plant, and grain yield per plant, signifying that these traits governed by additive gene action. Simple selection may be useful for these traits. Further, using PCA analysis, it was found that these traits are ideal for pigeonpea improvement through the selection. Promising lines viz., ICPP 171540, ICPP 171541, ICPP 171542, ICPP 171546, ICPP 171556, ICPP 171559, ICPP 171561, ICPP 171564, ICPP 171566, ICPP 171578, ICPP 171579, and ICPP 171581, and ICPP 171578 were identified in extra-early determinate groups. These promising lines should be evaluated in multi-season/location for further utilization.

Key words

Pigeonpea ,Genetic variability, introgression lines, indeterminate,determinate, PCA

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] 2n=22 is a vital legume crop with 833.07 Mb genome size, grown extensively in the South Asia and Africa regions under limited moisture content. Globally, it occupies of 6.9 m.ha with a production of 5.9 m. t. and an average yield of 852.4 kg/ha (FAO, 2018). Pigeonpea is also known as redgram and widely used for different purposes viz., food, fodder, fuel, firewood, thatch, fencing material, for

https://doi.org/10.37992/2021.1202.071

soil improvement through N fixation (Mapfumo *et al.*, 1999). Pigeonpea grain is usually consumed as split dhal. It is also preferred as dry whole grain or green peas. It is a good source of human dietary protein (Amarteifio *et al.,* 2002). It also enriches the soil by improving water infiltration and conserving valuable nutrients and water. It can flourish well in drought-prone depleted soil (Kumar *et al.*, 2011).

Pigeonpea grown at higher latitude faces sensitivity to temperature and photoperiod. (Silim *et al.*, 2006). This sensitivity affects mostly plant height, vegetative biomass and grain yield Whiteman *et al*., 1985). Additionally, delayed flowering and maturity will cause exposure to terminal drought. Thus, cultivating late-maturing long-duration types poses several challenges for smallholder farmers. Expanding pigeonpea in crop diversification, flowering, and maturity within a given time frame is essential to the varieties. Growing photoperiod insensitive cultivars beyond 35º latitudes will improve the adaptation of pigeonpea (Wallis *et al.,* 1981 and Wallace *et al.,* 1993). Earliness is directly linked to photo insensitivity (Turnbull *et al.,* 1980 and Wallis *et al.*, 1981). Therefore, it necessitates breeding for earliness traits in the pigeonpea improvement program.

The narrow genetic base of cultivated pigeonpea leads to the utilization of wild relatives in the crossing program to broaden the genetic base and introduce useful traits. These includes insensitive to photoperiod, prolific flowering and podding and biotic stresses tolerance such as pod borer (Sujana *et al.,* 2008), wilt, phytophthora blight (Ariyanayagam and Spence 1978; Pundir and Singh 1987; Dundas 1990), nematodes (Sharma, 1995), sterility mosaic (Kumar *et al.,* 2005). Considering these extra-early maturing cultivars were developed to fit the ecological niches where pigeonpea was never grown previously.With the myriad of advantages, an attempt to study the genotypic variability in 20 introgression lines of pigeonpea for yield and yield attribute traits was done for future crop improvement in early introgression lines pigeonpea.

MATERIALS AND METHODS

The experimental materials consisted of 20 extra-early pigeonpea introgression lines (ILs) consisting of 16 determinate types (DT) and with two DT checks ICPL 11255, ICPL 85010 and two IDT check ICPL 20325 and ICPL 88039. These 16 ILs are derived from an interspecific cross between a popular pigeonpea cultivar ICPL 85010 and *C. volubilis* accession ICP 15774 (Mallikarjuna, 2014). These ILs in F_{10} generation were used in this study. The trial was evaluated for agronomic traits in field trials at ICRISAT, Patancheru, Hyderabad in vertisols during the 2019 rainy season. Each trial was conducted in a randomized complete block design with three replications. The field layout was designed to have a two-row plot of 2 m length with 0.75 m row to row spacing. Manual weeding and spraying of insecticides were done to control the insect-pest damage. All standard agronomic practices were followed for raising healthy crops. A total of 10 agronomic traits were evaluated for trial. Plant height was measured from the ground to the uppermost plant part at pod maturity. Days to flowering were recorded on a plot basis when the first flower in bloom. Days to 50% flowering were recorded when 50% of the plant has at least one flower open. Days to Maturity were recorded when 75% of pods become matured. Plant height, the number of branches, the number of pods, pod weight, hundred seed weight and grain yield per plant were recorded on five randomly selected representative plants per plot following pigeonpea descriptors (IBPGR and ICRISAT,1993). Data collected were analyzed using residual maximum likelihood (REML) in GenStat 15 (https://www.vsni.co.uk/) in a mixed model approach considering genotypes as random effect and replication as a fixed effect. For agronomic traits, the best linear unbiased predictors (BLUPs) were obtained, and the range and mean were calculated based on BLUPs. Phenotypic correlations were estimated for the determination of trait associations using R package corrplot. Using the R package "prcomp" principal component analysis was performed to analyze trait variations. Genotypic coefficient of variation and phenotypic coefficient of variation was calculated according to the procedures given by Burton, (1952). Heritability and genetic advance was estimated utilizing the methodology by Lush, (1940) and Johnson *et al.*(1955), respectively.

RESULTS AND DISCUSSION

The REML analysis showed significant variations among pigeonpea introgression lines (σ^2_g) for all the ten agronomic traits indicating substantial variability among the introgression lines. A considerable variation was observed amongst the introgression lines for all the agronomic traits (**Table 1**). The phenotypic coefficient of variation (PCV) values of all the traits was higher than the corresponding genotypic coefficient of variation (GCV). Five traits showed large phenotypic and genotypic variations, with PCV and GCV values greater than 10 per cent. Two traits had PCV exceeding 20 per cent, three ranged from 10 to 20 per cent, and five less than 10 per cent. The number of secondary branches per plant and plant height had the largest PCV values of 28.14 and 22.71 per cent, respectively (**Table1**). Phenological traits viz., days to flowering, days to 50% flowering and days to maturity had very low variation (less than 6%). This result indicates the presence of genetic variation in the introgression lines of the pigeonpea, which, through selection, may provide opportunities for genetic improvement in component traits (Pal *et al*.,2018).

Broad sense heritability of a phenotype is the degree to which the environment and experimental error influence genotypes, a measurement that helps breeders to consider the precision or repeatability of phenotypic

Table 1. Variance component due to genotypes (σ^2g) their standard errors (SE), summary statistics and estimates of genetic parameters for various traits in the extra –early pigeon pea

Traits	σ^2_g	SE	Mean	Range	GCV (%)	PCV (%)	GA	GAM (%)	H^2 (%)
DF	11.55**	0.70	59.1±0.70	50-70	5.75	5.86	6.90	11.60	96.40
DFF	12.44**	0.60	63.03±0.60	54-75	5.60	5.67	7.20	11.40	97.20
DM	11.28**	0.62	108.6±0.62	104-125	3.09	3.14	6.80	6.30	96.70
PH	373.81**	3.48	86.5±3.48	61.40-159.4	22.35	22.71	39.20	45.30	96.90
NPB	0.51*	0.61	9.78±0.61	7-12.40	7.30	9.59	1.10	11.34	57.90
NSB	1.08**	1.00	4±1	2.0-7	25.76	28.14	2.00	48.60	83.80
PPP	186.35**	8.00	98.98±8	61.20-161	13.79	15.97	24.30	24.50	74.60
PWPP	32.96**	3.01	38.75±3.01	23.60-63.73	14.82	16.73	10.50	27.00	78.50
HSW	0.21**	0.21	10.69±0.21	9.42-11.64	4.27	4.70	0.90	8.00	82.70
SYPP	19.27**	2.54	26.53±2.54	13.38-43.88	16.55	19.11	7.80	29.50	74.90

DF: Days to flowering, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height (cm), NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NPP: Number of pods per plant, PWPP: Pod weight per plant (g), HSW:Hundred seed weight (g), SYPP: Grain yield per plant (g).

GCV: Genotypic coefficient of variation ,PCV: Phenotypic coefficient of variation, GA: Genetic advance, GAM: Genetic advance as percent of mean, H^2: Broad sense heritability

** Signfiicant at P ≤ 0.01; * Signfiicant at P ≤ 0.05.

breeding selection (You *et al*., 2016). It ranged from 57.9 to 97.2 per cent. High H^2 values (>60%) were found in all traits except for the number of primary branches per plant. H^2 values were found highest for the trait days to 50% flowering (97.20%) followed by plant height (96.90%), days to maturity (96.70%), and days to flowering (96.40%), suggesting that these traits may be controlled by additive gene action, and simple selection for these traits may be successful. The trait number of primary branches per plant showed moderate heritability (57.90 %). The trait number of primary branches per plant showed moderate heritability (57.90 %). Similar findings were also reported by Bhadru (2010) for the number of pods per plant. Results for high heritability along with high genetic advance for various traits have also been reported earlier for the number of pods per plant and seed yield (Magar, 2003 and Pushpavalli *et al.,* 2017).

Expected genetic advance as perc ent of the mean (GAM) showed that high potential selection gains were expected in traits *viz*., plant height (45.30%), the number of secondary branches per plant (48.60%), grain yield per plant (29.50%), pod weight per plant (27 %) and the number of pods per plant (24.50 %). Moderate GAM was found for days to flowering (11.6%), days to 50% flowering (11.40%) and the number of branches (11.34%). However, the low GAM was found for days to maturity (6.30%) and hundred seed weight (8%). These findings are consistent with Obala *et al.* (2018). Higher GAM was also reported for plant height, the number of pods per plant, grain yield per plant, the number of branches per plant by Ranjani *et al.* (2018). Pushpavalli *et al.* (2017) and Verma *et al.* (2018) also reported similar findings for days to 50% flowering, plant height, and the number of primary branches. Due to high variability and transmissibility, these traits that embody high heritability and genetic advance values emerge as ideal development traits through selection.

A large flowering variation ranged from (50-70 days) was observed. All introgression lines showed earlier flowering than popular early check variety ICPL 85010, which took 62 days to flower. The earliness in flowering would have been inherited from the *Cajanus volubilis* wild type which have been introgressed and stabilized in these lines. Large variation was also noted amongst the ILs for plant height (75-86 cm) compared with ICPL11255 (average 75 cm tall). Similarly, the number of pods per plant was also higher in the ILs (up to 110 pods per plant) compared to check ICPL11255 (70 pods per plant). Similarly, grain yield per plant was also higher (up to 30 g in ILs compared to 18 g in ICPL11255). Twelve ILs showed on par grain yield per plant (19 -30 g) when compared to 32 g in ICPL 85010. One of the reasons for reduction in yield might be linkage drag (Mallikarjuna *et al.,* 2005).

Correlation analysis between different agronomic traits showed that there is a significant positive association between days to flowering (r=0.66, p=0.01) with grain yield. Days to 50% flowering (r=0.75, p=0.01) showed a significantly high positive correlation with grain yield. Days to maturity (r=0.43) showed a non-significant correlation with seed yield. Similarly, plant height also had a significant positive correlation (r=0.69, p=0.01) with grain yield. On the other hand, primary branches (r=0.48, p=0.05) showed a significant low positive correlation with grain yield. There was a negligible correlation between secondary branches (r=0.20) with seed yield. The number of pods per plant emerged as one of the most essential

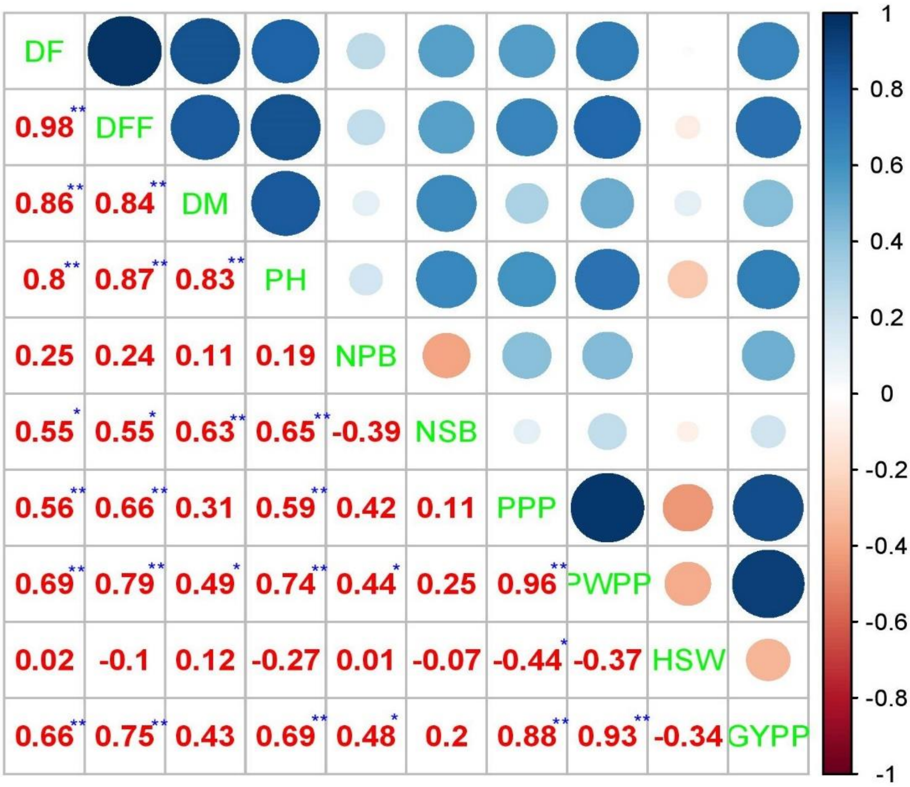

Fig. 1. Correlation analysis of various agronomic traits in pigeon pea

Significant at P ≤ 0.01; * Significant at P ≤ 0.05.

DF: Days to flowering, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NPP: Number of pods per plant, PWPP: Pod weight per plant, HSW:Hundred seed weight, GYPP: Grain yield per plant.

traits for selecting a high yielding line as it had a correlation (r=0.88, p=0.01) on grain yield. Similarly, pod weight per plant also showed its importance in determining grain yield with a correlation value (r=0.93, p=0.01). Non-significant and negative correlation with grain yield was observed for a hundred seed weight (r=-0.34) (**Fig.1)**.

Among the yield contributing traits, the number of primary branches per plant had a significant correlation (r=0.42, p=0.01) with the number of pods per plant. Similarly, plant height also showed a significant positive correlation (r=0.59, p=0.01) with the number of pods per plant. A significant negative correlation (r=-0.44, p=0.05) was observed between a hundred seed weight and the number of pods per plant. The number of primary branches also showed a non-significant negative correlation (r= -0.40) with secondary branches (**Table 2)** and (**Fig. 1)**. Selecting any of these traits would offer the opportunity for the simultaneous improvement of contributing characters. Thus, it should be kept in thought for enhancing yield potential in pigeonpea (Ojwang *et al*., 2016). No significant correlation between hundred seed weight and grain yield per plant indicates an excellent opportunity for independent improvement of both the traits. Similar results were also obtained by Bal *et al*. (2018).

The principal component analysis was performed based on means for the quantitative traits of ILs (**Table 3**). The result of PCA revealed that out of ten, only three principal components (PCs) exhibited more than 1.00 Eigenvalue and showed about 90.18 per cent of the total phenotypic variability.The PC1 had the highest variability (58.20 %), followed by PC2 (19.84 %) and PC3 (12.13 %) for traits. The first two principal components accounted for (78.05 %) of total phenotypic variability. The PC1 explained 58.20 per cent for the first axis and PC2 explained 19.8 per cent for the second axis. In **Fig.2** (biplot), it is possible to see the dispersion of characteristics according to score and correlation between them. The first principal component was positively correlated with all the characters studied except a hundred seed weight. Grain yield per plant, the number of pods per plant, pod weight per plant, days to 50% flowering were the main contributing traits in PC1. The second principal component (PC2) was positively correlated with grain yield per plant, the number of pods per plant, pod weight per plant, and the number of branches per plant whereas negatively correlated with days to 50% flowering, plant height, days to flowering, the number of secondary branches and days to maturity. The biplot explains that the ILs in this experiment could be categorized into two groups: A and B. The ILs found in group viz., ICPP 171541, ICPP17146, ICPP 171556, and ICPP 171561genotype had higher values for grain yield, the number of pods and the number of branches. Similarly, ILs found in group B viz., ICPP 171540 and ICPP 171579 had higher values for a hundred seed weight. Hundred seed weight vector is far from seed yield per plant, showing a negative correlation between these traits and contributes less towards variability. Similar findings were reported by (Manyasa *et al.,* 2009 and Hemavathy *et al.,* 2017). Rekha *et al.* (2013) also observed the largest participation of the number of pods and plant height. This will help breeders choose trait-specific and diverse ILs for use in a breeding program to introduce new useful alleles derived from wild species into their working collection and newly developed cultivars/varieties.

This study of evaluation of pigeonpea ILs for variability and identification of promising lines revealed a considerable genetic variation. High genetic gain for this crop would be possible in this region to improve traits such as single plant

Table 2. Correlation matrix among quantitative traits.

Traits	DF	DFF	DM	PH	NPB	NSB	PPP	PWPP	HSW	SYPP
DF	1									
DFF	0.98**	1.00								
DM	0.87**	0.84**	1.00							
PH	0.81**	0.87**	0.84**	1.00						
NPB	0.26	0.25	0.12	0.19	1.00					
NSB	0.55*	0.55*	0.64**	0.65**	-0.40	1.00				
PPP	0.56**	0.66**	0.32	0.6**	0.42	0.12	1.00			
PWPP	0.7**	0.79**	0.5*	0.74**	0.44*	0.25	0.97**	1.00		
HSW	0.02	-0.10	0.12	-0.27	0.01	-0.08	-0.44*	-0.37	1.00	
GYPP	0.66**	0.75**	0.43	0.69**	0.49*	0.20	0.88**	0.93**	-0.34	1.00

DF: Days to flowering, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NPP: Number of pods per plant, PWPP: Pod weight per plant, HSW:Hundred seed weight, SYPP: Grain yield per plant.

** Signfiicant at $P \le 0.01$; *Signfiicant at $P \le 0.05$.

Table 3. Principal Component (PC) analysis of 10 quantitative traits

Parameters	PC1	PC2	PC3
Eigen vector (loadings)			
DF	0.373239	-0.18843	0.196515
DFF	0.395114	-0.13145	0.095134
DM	0.321385	-0.35971	0.201163
PH	0.378089	-0.15362	-0.09404
NPB	0.143145	0.441476	0.520459
NSB	0.212018	-0.50471	-0.30433
PPP	0.33253	0.348528	-0.12935
PWPP	0.376606	0.248471	-0.06292
HSW	-0.1074	-0.2925	0.720112
SYPP	0.359101	0.275357	-0.01659
Eigenvalue	5.820769	1.984252	1.213607
Proportion of variance	58.20769	19.84252	12.13607
Cumulative variance	58.20769	78.05021	90.18628

DF: Days to flowering, DFF: days to 50% flowering, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NPP: Number of pods per plant, PWPP: Pod weight per plant, HSW:Hundred seed weight, SYPP: Grain yield per plant.

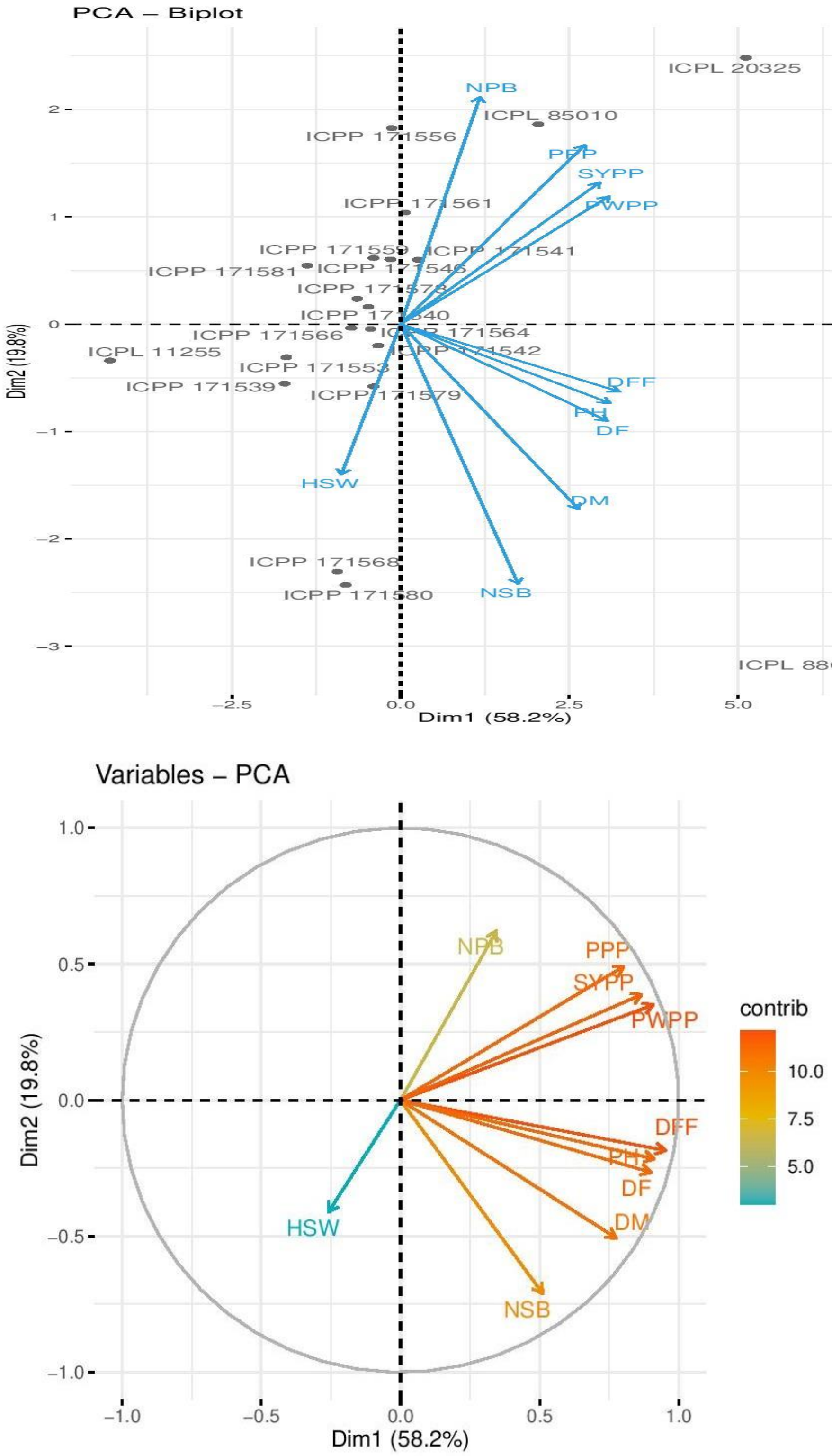

Fig. 2. Projection of 10 quantitative characters on the first two components (axis 1 and axis 2) of the PCA.

DF: Days to flowering, DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NPP: Number of pods per plant, PWPP: Pod weight per plant, HSW:Hundred seed weight, SYPP: Grain yield per plant.

yield, the number of pods per plant, and pod weight per plant. This study identified 12 promising lines *viz.,*ICPP 171540, ICPP 171541, ICPP 171542, ICPP 171546, ICPP 171556, ICPP 171559, ICPP 171561, ICPP 171564, ICPP 171566, ICPP 171578, ICPP 171579 and ICPP 171581, that have the potential to be used as parents in breeding programs and released as a variety after evaluation across multi-location over the years. Further, these lines possess earliness and could be grown in rice fallows and fit into rotation with wheat expanding the pigeonpea cultivation.

ACKNOWLEDGMENT

The financial support provided by Global Crop Diversity Trust and the CGIAR Research Program on Grain Legumes and Dryland Cereals (GLDC) is duly acknowledged.

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https://doi.org/10.37992/2021.1202.071