



**Full Length Article**

## Morphological Plasticity of Economical Traits in Pigeonpea Genotypes Grown in South Africa

Maletsema Alina Mofokeng<sup>1</sup>, Zaid Bello<sup>1</sup>, Kingstone Mashingaidze<sup>1</sup> and Abe Shegro Gerrano<sup>2,3\*</sup>

<sup>1</sup>Agricultural Research Council-Grain Crops, Private Bag X 1251, Potchefstroom, 2520, South Africa

<sup>2</sup>Agricultural Research Council - Vegetables, Industrial and Medicinal Plants, Private Bag X 293, Pretoria, 0001. South Africa

<sup>3</sup>Food Security and Safety Focus Area, Faculty of Natural and Agricultural Sciences, North-West University, Mmabatho, South Africa

\*For correspondence: [agerrano@arc.agric.za](mailto:agerrano@arc.agric.za); ORCID: <http://orcid.org/0000-0001-7472-8246>

Received 09 May 2022; Accepted 16 July 2022; Published 25 August 2022

### Abstract

Pigeonpea (*Cajanus cajan*) is a leguminous crops cultivated in tropical and sub-tropical region of the world. This crop is one of underutilized and future food security plant species grown southern Africa. The objective of the study was to assess morphological variability among nineteen tested pigeonpea genotypes using multivariate analysis. The experimental trial was conducted at Mafikeng and Nelspruit sites located in Northwest and Mpumalanga Provinces of South Africa. A randomized complete block design with three replications at all sites. Data were recorded on quantitative and qualitative traits and analysed using univariate (ANOVA), and multivariate analysis tools. Significant genotype effect was observed for plant height (PH), pod bearing (PDB) and seed number per pod (SNP) among the studied genotypes. Seed yield (SY) was positively correlated with seed number per pod (SNT), seed number per plant (SNP) and pod weight (PWT), whereas PBD was negatively associated with hundred seed weight (HSW). Principal component analysis (PCA) revealed five significant principal components (PCs), which accounted for 84.70% of phenotypic variation among the studied genotypes. The Shannon Weaver diversity indices ranged from 0.98–1.00, indicating the presence of variation among the qualitative traits measured. The clustering analysis grouped genotypes into three main groups, with ICEAP00554, ICEAP000979-1, ICEAP00540, and Karatu-1 being the most diverse and singletons. Hence, use of multivariate analyses revealed the existence of morphological variation among the test pigeonpea genotypes for breeding population. These identified genotypes could be used as potential parental lines in a pigeonpea breeding programme for direct production and development of new high yielding varieties in the country. © 2022 Friends Science Publishers

**Keywords:** Agro-morphology; Characterization; Pigeonpea; Similarity; Variation

### Introduction

Pigeonpea (*Cajanus cajan*) is a diploid ( $2n = 2x = 22$ ) legume (Maesen 1990) grown in tropical and subtropical regions of the world. It is underutilised crop species, despite its contribution to food and nutritional security (Lin-Qi 2014). The crop improves the fertility of the soil through atmospheric nitrogen fixation and increase production and productivity of the crop (Adebowale and Maliki 2011; Choudhary *et al.* 2013; Saidia *et al.* 2019). Pigeonpea can be intercropped with cereal-based cropping system (Lin-Qi 2014). It is sources of macro- and micronutrients, vitamins and phytochemical compositions (Saxena *et al.* 2010; Gerrano *et al.* 2022). It is considered as climate smart crop in tropical and sub-tropical regions. It has the ability to withstand drought and give good economic benefits when planted under dryland farming conditions and sustain the

livelihood of resource poor rural populations in tropical and sub-tropical regions of the African continent including South Africa. Furthermore, the crop helps in protecting the environment from soil erosion and degradation, improve the fertility of the soil, increase crop production and productivity at marginal crop lands towards soil and food security strategies. It is climate smart crop that adapt to the current climate change, which is tolerant to heat, drought, diseases and insect pests (Odeny 2007).

The seed of the crop can be eaten as a green vegetable and dry pulse and is an important source of nutritional components (Faris *et al.* 1987; Choudhary *et al.* 2013). The green pods and foliage of the plant can be used as animal feed (Mallikarjuna *et al.* 2011). The crop is cultivated by the resource poor small scale farmers with the low input agriculture in South Africa. Hence, identification of potential candidate genotypes and development of improved

cultivars for increased production and productivity of the crop is important.

For an efficient evaluation and utilisation of the plant genetic resources, understanding and knowledge of genetic diversity, genetic background information, collection and classification are important and the basis for crop improvement programs (Khan *et al.* 2014; Syafii *et al.* 2015), which is elucidated through different marker systems such as agro-morphological, biochemical and molecular markers. Among these, morphological characterisation is considered as the initial step for designing breeding programs (Smith and Smith 1989; Khan *et al.* 2014), it is influenced by the growing environmental condition unlike that of DNA-based markers. Yohane *et al.* (2020) reported the existence of widest variability among test pigeonpea based on their morphological performance in Malawi. Assessing genetic variability helps to study heterosis (Virk *et al.* 2003), selection of transgressive breeding segregants and genes of novelty, and has a role in collection and maintenance of germplasm for crop improvement (Duran *et al.* 2009) in the gene bank for future use.

Potential parental lines were identified for improvement (Malik *et al.* 2014; Syed *et al.* 2019) through using multivariate statistical analysis. It is effective statistical tool for studying the differences and similarities between and within the genotypes (Peeters and Martinelli 1989; Kovacic 1994; Rachovska *et al.* 2002; Mondal 2003; Mohammadi and Prasanna 2003; Ajmal *et al.* 2013; Immad *et al.* 2018), which can help to generate new breeding population in the breeding programme. The knowledge and understanding of the crop species and their respective descriptors are necessary for informed breeding strategy (Upadhyaya *et al.* 2007; Gbaguidi *et al.* 2018). The assessment of phenotypic plasticity using morphological characters in pigeonpea is importance in order to determine the existing variability in the population which will finally enable the identification and selection of potential and superior lines of the genotypes for production and breeding. Therefore, the objective of the current study was to assess the variability and their interrelationship in pigeonpea genotypes using morphological traits.

## Materials and Methods

### Plant material and trial sites

The 19 pigeonpea genotypes were evaluated on the field during the summer season of 2019–2020. The origins of the pigeonpea genotypes used in the study are listed in Table 1.

The experimental trials were conducted at the North West University research farm at Mafikeng (25°48' S, 45°38' E; 1012 m. a. s. l.) in North West Province and the Agricultural Research Council – Tropical and Subtropical research station in Nelspruit (25.49°89' S, 31.35°37' E; 670 m. a. s. l.) in Mpumalanga Provinces during 2019/2020 cropping season in South Africa. Pigeonpea is widely grown

predominantly in this two Province in South Africa and have extreme variations in agro-climatic conditions. The soils on the North West University farm belongs to the Hutton series, with sandy loam and a yellow sand alternating (Molope 1987; Kasirivu *et al.* 2011), while the Nelspruit research station field consisted of sandy loam soil. During the season, Mafikeng received a summer total rainfall, with a mean of 571 mm during the cropping season. The mean maximum temperature is 37°C, while the mean minimum temperature is 9°C during this cropping season. The field in Nelspruit is characterised by mean maximum temperature of 28°C. The mean minimum temperature is 12.5°C with a precipitation of about 796 mm during the cropping season in 2019/2020.

### Trial design and management

The trials were laid out in a randomized complete block design replicated three times with a plot consisting of two rows of 4 m length. The inter- and intra-row spacing's were 90 and 60 cm, respectively. The experiment was conducted during summer cropping season in rainfed condition based on the farmers practice. Weeding was done manually. No fertilizer was applied to simulate low input cropping system in the region (Gerrano *et al.* 2015).

### Data collection

Data were recorded according to standard descriptor list for pigeonpea (IBPGR 1994). Data were recorded from three randomly selected plants in the middle of each row per replications. The qualitative data recorded included base flower colour, second flower colour, vigour at 50% flowering, pod form, seed colour pattern, seed shape, and pattern of streaks. The list of quantitative traits studied and their data collection method is presented in Table 2.

### Statistical data analysis

The recorded quantitative data were analysed using analysis of variance (ANOVA), principal component analysis (PCA), and Pearson correlations. The qualitative data were analysed using frequencies, spearman correlations, and Shannon Weaver diversity index. The biplots were generated using principal coordinate analysis in SAS version 9.6 (SAS Institute 2021). A dendrogram was constructed using Genstat 18<sup>th</sup> edition (VSN International, Hempstead, UK) (2020).

## Results

### Genetic variability and genotype by environment interaction

The univariate analysis of variance (ANOVA) result depicted that there were highly significant ( $P \leq 0.01$ ) genetic

**Table 1:** Pigeonpea germplasm used in the study

| Entry number | Genotype Name   | Origin/source |
|--------------|-----------------|---------------|
| 1            | ICEAP 01147     | Kenya         |
| 2            | ICEAP 01154-2   | Kenya         |
| 3            | ICEAP 01150-1   | Kenya         |
| 4            | ICEAP 01179     | Kenya         |
| 5            | ICEAP 00979-1   | Kenya         |
| 6            | ICEAP 01172-2-4 | Kenya         |
| 7            | ICEAP 01159     | Kenya         |
| 8            | ICEAP 01544-2   | Kenya         |
| 9            | ICEAP 00540     | Kenya         |
| 10           | ICEAP 00554     | Kenya         |
| 11           | ICEAP 00557     | Kenya         |
| 12           | ICEAP 00850     | Kenya         |
| 13           | Ilonga 14-M1    | Tanzania      |
| 14           | Mali            | Tanzania      |
| 15           | Ilonga 14-M2    | Tanzania      |
| 16           | Karatu-1        | Tanzania      |
| 17           | Kiboko          | Tanzania      |
| 18           | Kombo           | Tanzania      |
| 19           | Tumia           | Tanzania      |

**Table 2:** A list of economical traits measured, abbreviations and definitions

| Trait                 | Abbreviation | Measurement/definitions  |
|-----------------------|--------------|--|
| Plant height (cm)     | PHT          | Height of a plant from the base of the stem to the tip of the plant at harvest |
| Days to 50% flowering | DFP          | Number of days from planting until 50% of the plants have flowered in a plot   |
| Pod bearing (cm)      | PDB          | Distance from lowest to the top most of the plant                              |
| Leaf length (mm)      | LFL          | Length from the tip of the leaf to the leaf petiole                            |
| Leaf width (mm)       | LFW          | Length in the middle of the leaf from one tip to the other tip                 |
| Branch number         | BRN          | Number of branches per plant   |
| Stem diameter (cm)    | STD          | Diameter of plant stem   |
| Pod length (mm)       | PDL          | Length of the pod from bottom end to top end at harvest                        |
| Pod width (mm)        | PDW          | Length at the centre of the pod from one end to the other end/diameter         |
| 100 Seed weight (g)   | HSW          | Weight of 100 seed picked randomly for each genotype                           |
| Pod weight (g)        | PWT          | Weight of dry pods harvested from each genotype                                |
| Seed number per pod   | SNT          | Number of seeds in a pod (average of 10 pods)                                  |
| Seed number per plant | SNP          | A number of seeds produced by a single plant.                                  |
| Seed yield (g)        | SYD          | Weight of seeds produced per plant   |

DFP = Days to 50% flowering; PHT = Plant height; BRN = Branch number; LFL = Leaf length; LFW = Leaf width; PDB = Pod bearing; 100SW = hundred seed weight; PDL = Pod length; PDW = Pod width; SNP = Seed number per pod; PWT = Pod weight; SEP = Seed number per plant; STD = Stem diameter; SYD = seed yield per plant

variability observed among the tested genotypes for pod length (PDL) and pod weight (PWT) ( $P \leq 0.01$ ) (Table 3). Furthermore, the ANOVA mean squares showed genotype (G), site (S), and genotype  $\times$  site interaction (GEI) effects on quantitative traits is presented in Table 3. Furthermore, the agronomic characteristics of the pigeonpea genotypes showed variability in different environments due to the significant genotype  $\times$  environment interaction (Table 3) for plant height (PHT) ( $P \leq 0.01$ ), pod bearing (PDB) ( $P \leq 0.05$ ) and seed number per pod (SNP) ( $P \leq 0.05$ ). There were significant ( $P \leq 0.05$ ) differences between sites based on days to flowering (DFP), plant height, branch number (BRN), stem diameter (STD), pod bearing, pod length, pod weight and significant differences for seed number per pod. There was a significant ( $P \leq 0.05$ ) site  $\times$  genotype interaction effect based on plant height, pod bearing and seed number per pod (Table 3).

### Pearson correlation analysis

Pearson's correlations ( $r$ ) of 14 quantitative traits measured

in the study are shown in Table 4. Days to flowering was significantly and positively correlated with plant height, branch number, stem diameter, and hundred seed weight. Similarly, days to flowering was significantly and positively correlated with pod weight and negatively correlated with pod bearing. Plant height was highly significant and positively correlated with branch number per plant, stem diameter, and hundred seed weight, and negatively associated with pod bearing. Branch number had a negative and significant association with stem diameter and pod bearing, and a positive correlation with hundred seed weight. Stem diameter had a significant and positive correlation with leaf length, whereas pod bearing showed a negative association with hundred seed weight. Leaf length showed positive and significant correlations with leaf width and pod bearing. Leaf width had a negative association with seed number per pod. Pod bearing had a highly significant negative correlation with hundred seed weight. Pod length showed a positive association with seed number per pod, pod weight, seed number per plant, seed yield. Pod width showed a positive and highly significant correlation with

**Table 3:** Combined analysis of variance for quantitative traits among the studied pigeonpea genotypes in terms of means squares

| SOV         | d.f | DFE       | PHT        | BRN      | STD       | LLT | LWT   | PDB       | 100 SW | PDL      | PDW  | SNP    | PWT     | SEP | SYD  |
|-------------|-----|-----------|------------|----------|-----------|-----|-------|-----------|--------|----------|------|--------|---------|-----|------|
| Site (S)    | 1   | 85323.9** | 175005.4** | 1141.9** | 11556.7** | 0.2 | 722.6 | 41198.2** | 83.4   | 1957.3** | 10.9 | 138.3* | 142.2** | 1.3 | 45.9 |
| Genotype(G) | 18  | 76.2      | 1908.7     | 15.6     | 13.5      | 1.9 | 327.2 | 1417.3    | 163.3  | 507.8**  | 3.7  | 57.0   | 46.0**  | 8.0 | 20.0 |
| S × G       | 18  | 72.9      | 2867.6**   | 16.7     | 14.7      | 2.1 | 325.4 | 2733.8*   | 165.9  | 322.2    | 4.0  | 61.2*  | 30.8    | 8.9 | 17.9 |

SOV = Sources of variation; d.f. = degree of freedom; DFE = Days to 50% flowering; PHT = plant height; BRN = Branch number; LLT = Leaf length; LWT = Leaf width; PDB = Pod bearing; 100SW = hundred seed weight; PDL = Pod length; PDW = Pod width; SNP = Seed number per pod; PWT = Pod weight; SEP = Seed number per plant; STD = Stem diameter; SYD = seed yield per plant; \* = significantly different from zero at  $P \leq 0.05$ ; \*\* = significantly different from zero at  $P \leq 0.01$

**Table 4:** Pearson correlations for quantitative traits among the studied pigeonpea genotypes

| Variable | DFE              | PHT              | BRN              | STD             | LLT             | LWT            | PDB              | 100 SW | PDL             | PDW             | SNP             | PWT             | SEP             |
|----------|------------------|------------------|------------------|-----------------|-----------------|----------------|------------------|--------|-----------------|-----------------|-----------------|-----------------|-----------------|
| DFE      | 1.00             |                  |                  |                 |                 |                |                  |        |                 |                 |                 |                 |                 |
| PHT      | <b>0.701***</b>  | 1.00             |                  |                 |                 |                |                  |        |                 |                 |                 |                 |                 |
| BRN      | <b>0.625***</b>  | <b>0.751***</b>  | 1.00             |                 |                 |                |                  |        |                 |                 |                 |                 |                 |
| STD      | <b>-0.900***</b> | <b>-0.667***</b> | <b>-0.492***</b> | 1.00            |                 |                |                  |        |                 |                 |                 |                 |                 |
| LLT      | -0.089           | 0.017            | 0.040            | <b>0.241</b>    | 1.00            |                |                  |        |                 |                 |                 |                 |                 |
| LWT      | -0.034           | -0.019           | 0.075            | 0.169           | <b>0.672***</b> | 1.00           |                  |        |                 |                 |                 |                 |                 |
| PDB      | <b>-0.498***</b> | <b>-0.405***</b> | <b>-0.341***</b> | <b>0.504</b>    | <b>0.190*</b>   | -0.056         | 1.00             |        |                 |                 |                 |                 |                 |
| 100SW    | <b>0.525***</b>  | <b>0.431***</b>  | <b>0.296**</b>   | <b>-0.574**</b> | -0.053          | -0.003         | <b>-0.353***</b> | 1.00   |                 |                 |                 |                 |                 |
| PDL      | 0.183            | 0.046            | -0.011           | -0.136          | 0.117           | 0.095          | -0.010           | 0.159  | 1.00            |                 |                 |                 |                 |
| PDW      | 0.063            | 0.083            | 0.114            | -0.024          | 0.003           | -0.110         | 0.014            | -0.060 | 0.018           | 1.00            |                 |                 |                 |
| SNP      | 0.086            | 0.133            | 0.089            | -0.076          | -0.085          | <b>-0.202*</b> | 0.020            | -0.063 | <b>0.436***</b> | 0.135           | 1.00            |                 |                 |
| PWT      | <b>0.189*</b>    | 0.068            | 0.013            | -0.139          | 0.102           | 0.055          | -0.006           | 0.135  | <b>0.986***</b> | 0.161           | <b>0.526***</b> | 1.00            |                 |
| SEP      | 0.183            | 0.107            | 0.064            | -0.130          | 0.060           | -0.037         | 0.005            | 0.072  | <b>0.858***</b> | <b>0.453***</b> | <b>0.669***</b> | <b>0.932***</b> | 1.00            |
| SYD      | 0.183            | 0.096            | 0.042            | -0.136          | 0.065           | -0.013         | 0.001            | 0.092  | <b>0.928***</b> | <b>0.248**</b>  | <b>0.694***</b> | <b>0.974***</b> | <b>0.976***</b> |

DFE = Days to 50% flowering, PHT = plant height, BRN = Branch number, LLT = Leaf length, LWT = Leaf width, PDB = Pod bearing, 100 SW = hundred seed weight, PDL = Pod length, PDW = Pod width, SNP = Seed number per pod, PWT = Pod weight, SEP = Seed number per plant, STD = Stem diameter, SYD = seed weight per plant.

Bold value represent significant association \* =  $P < 0.05$ , \*\* =  $P < 0.01$ , \*\*\* =  $P < 0.001$

**Table 5:** Factor loadings of the most important PCs for agro-morphological traits among the studied pigeonpea genotypes

| Traits                  | PC1    | PC2    | PC3    | PC4    | PC5   |
|-------------------------|--------|--------|--------|--------|-------|
| DFE                     | 0.57   | -0.72  | 0.05   | -0.02  | 0.01  |
| PHT                     | 0.47   | -0.70  | 0.12   | 0.24   | -0.25 |
| BRN                     | 0.37   | -0.64  | 0.19   | 0.37   | -0.31 |
| STD                     | -0.52  | 0.74   | 0.12   | 0.13   | -0.07 |
| LLT                     | -0.00  | 0.21   | 0.87   | 0.18   | -0.04 |
| LWT                     | -0.04  | 0.08   | 0.91   | -0.02  | 0.07  |
| PDB                     | -0.27  | 0.58   | -0.01  | 0.17   | -0.22 |
| HSW                     | 0.37   | -0.54  | 0.09   | -0.35  | 0.32  |
| PDL                     | 0.82   | 0.42   | 0.13   | -0.30  | 0.03  |
| PDW                     | 0.27   | 0.11   | -0.15  | 0.78   | 0.53  |
| SNP                     | 0.612  | 0.31   | -0.26  | 0.15   | -0.45 |
| PWT                     | 0.87   | 0.44   | 0.07   | -0.17  | 0.06  |
| SEP                     | 0.88   | 0.44   | -0.05  | 0.14   | 0.10  |
| SYD                     | 0.89   | 0.45   | -0.02  | -0.07  | -0.02 |
| Eigenvalue              | 4.62   | 3.50   | 1.78   | 1.163  | 0.82  |
| Explained variance (%)  | 32.97  | 24.96  | 12.694 | 8.307  | 5.87  |
| Cumulative variance (%) | 32.968 | 57.931 | 70.625 | 78.932 | 84.80 |

DFE = Days to 50% flowering, PHT = plant height, BRN = Branch number, LLT = Leaf length, LWT = Leaf width, PDB = Pod bearing, 100 SW = hundred seed weight, PDL = Pod length, PDW = Pod width, SNP = Seed number per pod, PWT = Pod weight, SEP = Seed number per plant, STD = Stem diameter, SYD = seed weight per plant

seed number per plant and seed yield. Seed number per pod was positively correlated with pod weight, seed number per plant, and seed yield. Pod weight had positive correlations with seed number per plant and seed yield. Seed number per plant was highly significant and positively correlated with seed yield (Table 4).

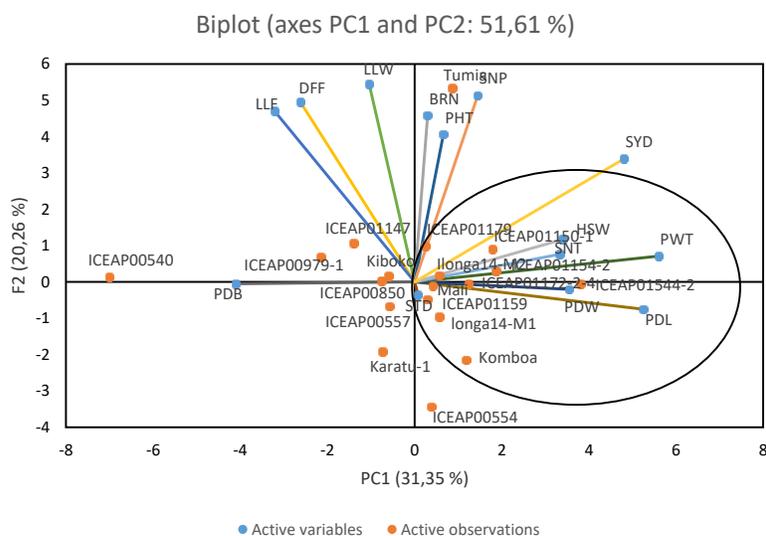
### Principal component analysis

Five most important PCs were identified contributing 32.9, 24.9, 12.7, 8.3 and 5.9%, to the total variation of 84.7%, respectively (Table 5). The first PC had pod length, pod

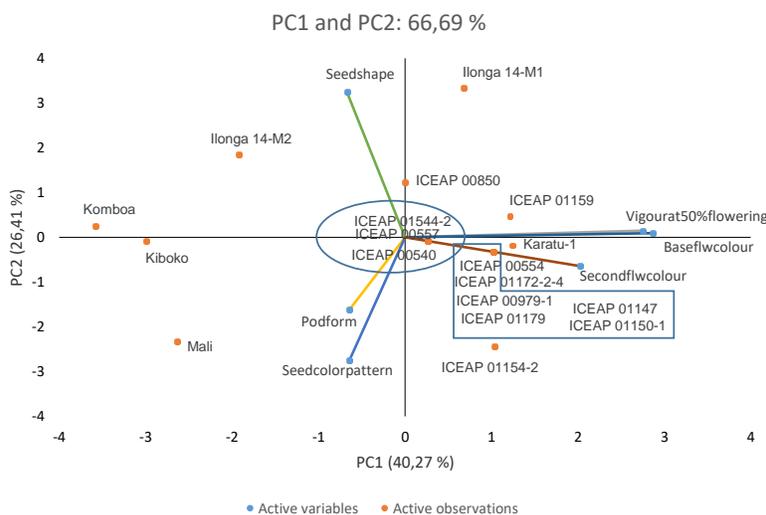
weight, seed number per plant and seed yield contributing to this variation. In the second PC, days to flowering, plant height, branch number, stem diameter contributed the most to variation. Leaf length and leaf width contributed the most variation in third PC. In the fourth PC, pod width was the most contributors to variation whereas in the fifth PC, pod width and seed number per pod was the traits that contributed the most variation.

### Principal coordinate analysis

The principal component (PC) biplot of the quantitative



**Fig. 1:** PC biplot for quantitative traits among the studied pigeonpea genotypes. PC1=first principal component; PC2=second principal component



**Fig. 2:** PCA biplot for qualitative traits among the studied pigeonpea genotypes.

traits showing grouping of genotypes superimposed with traits is presented in Fig. 1, PC1 had 31.35% and PC2 had 20.26% variances with the total contributing variation of 51.61%. Gerrano *et al.* (2022) reported that the angles lesser than 45° between the vector lines of the two respective variables indicate positive and high trait correlation and revealed the ability to discriminate the test genotypes for breeding. Genotypes ICEAP01150-1, ICEAP01154-2, Ilonga14-M2, ICEAP01172-2-4, ICEAP01544-2, Mali, ICEAP04459 and Ilonga14-M1 were grouped together based on high SYD, HSW, SNT, PWT, PDW and PDL. Further, ICEAP01179 and Tumia were identified as best genotypes for BRN, PHT and SNP. The genotype ICEAP01147, Kiboko, and ICEAP00850 were associated with the variables LLF, DFF, and LLW, while the

genotypes ICEAP00557, Karatu-1, ICEAP00554 and Komboa revealed less association to the variables recorded indicating that the genotypes were less responsive to the variables. Genotype ICEAP00850 was associated to PDB. Genotype ICEAP00540 is peculiar genotypes that was found far from the rest of genotypes from the scatter biplot (Fig. 1), which can be considered for further evaluation in the breeding program. Stem diameter and pod bearing were negatively correlated with plant height, branch number, seed yield, and 100 seed weight. Seed number per pod, pod length, pod width, pod weight, seed yield, and seed number per plant were positively correlated with hundred seed weight, while branch number and plant height were highly positively correlated. The same traits were also correlated with stem diameter, pod bearing, leaf width and leaf length.

**Table 6:** Frequency percentages of qualitative traits for medium duration pigeonpea

| Trait                   | Score                            | Frequency (%) | Cumulative frequency (%) | H'   |
|-------------------------|----------------------------------|---------------|--------------------------|------|
| Vigour at 50% flowering | Low                              | 5.36          | 5.36                     | 0.99 |
|                         | Intermediate                     | 23.21         | 28.57                    |      |
|                         | High                             | 71.43         | 100                      |      |
| Base flower colour      | Light yellow                     | 19.65         | 19.65                    | 0.97 |
|                         | Yellow                           | 51.78         | 71.43                    |      |
|                         | Orange-yellow                    | 28.57         | 100                      |      |
| Second flower colour    | Red                              | 71.43         | 71.43                    | 0.96 |
|                         | Purple                           | 28.57         | 100                      |      |
|                         |                                  |               |                          |      |
| Pattern of streaks      | Sparse                           | 35.09         | 35.09                    | 0.97 |
|                         | Medium amount                    | 15.79         | 50.88                    |      |
|                         | Dense                            | 22.81         | 73.68                    |      |
|                         | Uniform coverage of second color | 26.32         | 100                      |      |
| Flowering pattern       | Determinate                      | 100           | 100                      | 1.00 |
| Stem Thickness rating   | Thick (>13 mm)                   | 100           | 100                      | 1.00 |
| Growth habit            | Erect and compact                | 22.81         | 22.81                    | 0.98 |
|                         | Semi spreading                   | 1.75          | 24.56                    |      |
|                         | Spreading                        | 75.44         | 100                      |      |
| Stem color              | Green                            | 63.16         | 63.16                    | 0.98 |
|                         | Sun Red                          | 36.84         | 100                      |      |
|                         |                                  |               |                          |      |
| Pod form                | Flat                             | 3.64          | 3.64                     | 0.99 |
|                         |                                  |               |                          |      |
| Seed color pattern      | Cylindrical                      | 96.36         | 100                      | 0.99 |
|                         | Plain                            | 3.57          | 3.57                     |      |
|                         | Mottled                          | 7.14          | 10.71                    |      |
|                         | Speckled                         | 71.43         | 82.14                    |      |
|                         | Mottled and speckled             | 17.86         | 100                      |      |
| Seed shape              | Oval                             | 21.43         | 21.43                    | 0.98 |
|                         | Globular                         | 64.29         | 85.71                    |      |
|                         | Square                           | 14.29         | 100                      |      |
|                         |                                  |               |                          |      |

H' = Shannon Weaver Index

The biplot for the qualitative traits, the PC1 showed 40.27% and F2 had 26.41% (Fig. 2). The first quadrant showed base flower colour and vigour at 50% flowering, which are positively correlated in this quadrant and are associated with the genotypes Ilonga 144-M1, ICEAP 00850, and ICEAP 01159, while the second quadrant showed seed shape that was associated with the genotypes positioned in this quadrant. The third quadrant had pod form and seed colour pattern that are positively correlated to each other. The genotypes Kiboko and Mali had similar pod form and seed colour pattern in this quadrant. The 4th quadrant consists of only second flower colour. All the genotypes scattered in this quadrant were grouped together based on this trait (Fig. 2). In Fig. 2, the genotypes that are circled have similar values for PC1 and PC2 scores, which made them to be positioned on one dot.

### Frequencies of qualitative traits

The frequencies of eleven qualitative traits measured are shown in Table 6. Vigorousness at flowering was high with 71.4% of plants being vigorous and intermediate was 23.2%. The base flower colour was dominated by yellow flowers followed by orange-yellow. The second flower colour was predominantly composed of red flowers (71.4%). The pattern of streaks was dominated by sparse streaks (35.1%), followed by uniform coverage of second colour and dense streaks. All plants

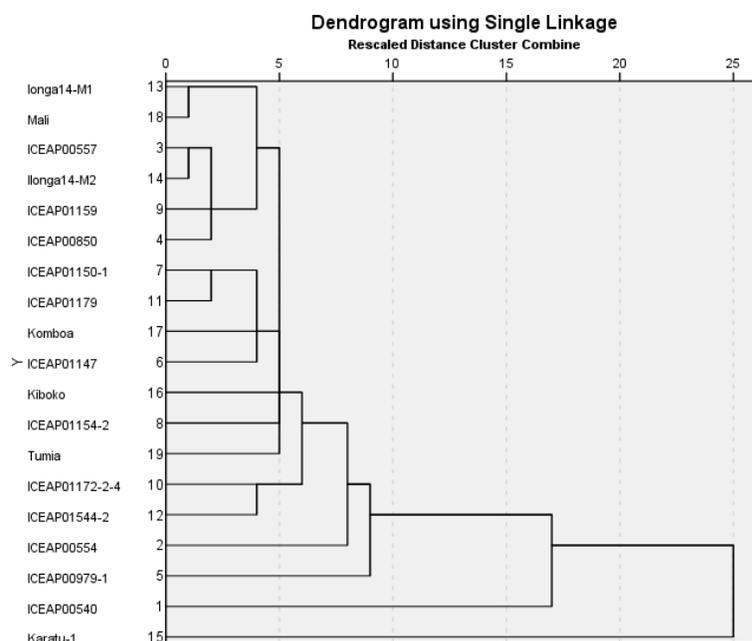
of various genotypes had 100% stems thicker than 13 mm with green stems dominating (63.2%). The growth habit of the crop was predominantly composed of spreading types (75.4%) followed by erect and compact at 22.8%. The genotypes were dominated by cylindrical pods 96.40 with speckled seed colour pattern at 71.4% followed by mottled and speckled at 17.9%. The shape of the seed was predominantly globular (64.3%) with oval shape being 21.4%.

### Shannon weaver diversity

Shannon weaver diversity indices are shown in Table 6. The diversity indices range from 0.96 (second flower colour) to 1.00 (flowering pattern and stem thickness). All traits showed significant variation except for flowering pattern and stem thickness.

### Hierarchical clustering

A dendrogram was constructed using hierarchical clustering to present differences and interrelationships among the studied pigeonpea genotypes (Fig. 3). The dendrogram grouped genotypes into three clusters and four singletons. The first cluster was composed of six genotype, Longa14-M1, Mali, ICEAP00557, Ilonga14-M2, ICEAP01159, and ICEAP00850. The second cluster was composed of four genotypes, ICEAP0050-1, ICEAP01179, kmboa and



**Fig. 3:** A dendrogram showing interrelationships and divergence among nineteen pigeonpea genotypes based on quantitative traits

ICEAP01147. The genotypes, Kiboko, ICEAP01154-2, Tumia, ICEAP01172-2-4 and ICEAP01544-2 were grouped in third cluster. Four genotypes were identified as most divergent and grouped as singletons (ICEAP00554, ICEAP000979-1, ICEAP00540, and Karatu-1). These genotypes were far and distantly related with the rest of the test genotypes.

## Discussion

The significant difference observed among the pigeonpea genotypes showed the existence of genetic variation with respect to the measured morphological characteristics. The knowledge of morphological variation for a trait and trait correlations are important components of any breeding objective. There were highly significant differences for sites based on days to flowering, plant height, branch number, stem diameter, pod bearing, pod length, pod weight and significant differences for seed number per pod (Table 3). This indicates that the expression of the significant traits varied with the growing environmental conditions they were tested in. Their performance was not stable across sites. The presence of highly significant differences in genotypes based on pod length and pod weight highlights the presence of genotypic variation among the genotypes evaluated based on the two traits which can be exploited for cultivar improvement in future breeding programmes. The significant differences on genotype  $\times$  site interaction could be attributed to the different reactions of the genotypes to sites or due to differences between the sites. In each environment, phenotypic manifestation is the result of the action of the genotype under the influence of the

environment. However, when considering a series of growing environments, in addition to the genetic and environmental effects, an additional effect can be detected from their interaction (Marais *et al.* 2013; Nunes *et al.* 2014). Significant genotype  $\times$  environment interaction on yield and yield components in this study concur with the results reported previously (Vales *et al.* 2012; Kimaro 2016; Gerrano *et al.* 2020).

The positive and significant correlation observed among the quantitative characters indicated that direct selection for any of these traits could lead to simultaneous improvement in the other characters of pigeonpea for increased production and productivity. Yohane *et al.* (2020) reported the existence of positive correlations for most of secondary traits that revealed multiple trait identification and selection for simultaneous trait improvement, while the weak correlations among the traits would result in an inefficient selection or low genetic gains that will take long time to fix the traits of interest. In this study seed yield was positively correlated with seed number per pod, seed number per plant and pod weight whereas pod bearing was negatively associated with hundred seed weight. The positive and significant correlations in the current study indicated the importance of simultaneous improvement for the traits of interest in the crop (Sodavadiya *et al.* 2009; Linge *et al.* 2010; Prasad *et al.* 2013; Saroj *et al.* 2013; Ojwang *et al.* 2016; Kinhoégbè *et al.* 2020; Yohane *et al.* 2020).

The Principal component analysis over sites revealed five most important PCs with pod length, pod weight, seed number per plant, seed yield, leaf length, leaf width, days to flowering, plant height, and stem diameter being the most contributing traits to the total variation observed. This suggests

that these traits are useful for selection. Other reports have indicated that trait contribution to different PCs varies with genetic diversity within the tested germplasm and the number of traits evaluated (Upadhyaya *et al.* 2007). The biplot also showed the different grouping of pigeonpea genotypes based on specific traits. These findings suggested that both agromorphological traits revealed variability among the tested genotypes but complementary information for breeding.

The most of pigeonpea genotypes in the current study showed a tendency to spreading growth habit, yellow based flower colour, with red second flower colour, sparse pattern of streaks, green stems, with globular and speckled seed color pattern. Similar results have been reported for qualitative traits (Rupika and Bapu 2014). Shannon Weaver indices also confirmed the presence of genetic divergence based on qualitative traits. Thus, in spite of the influence of prevalent environmental factors, qualitative variables can be used to characterize pigeonpea genetic resources.

The pigeonpea genotypes were clustered into three major groups, indicating that these genotypes in the three groups are distantly related. The genotypes in the same cluster group are closely related and they maybe of the same source or origin. Hence, selection of genotypes within these clusters may not be desirable to get higher yield and economic benefits (Muniswamy *et al.* 2014; Rupika and Bapu 2014). Therefore, for the crop hybridization programs, the choice of suitable diverse parents based on their genetic differentiation would be more fruitful than the choice based on the geographical distances. ICEAP 00540, ICEP00979-1, Karatu-1 and ICEAP00554 would be the ideal genotypes for use as parents in any pigeonpea breeding programme for agronomic improvement. The genotypes clustered in the same group showed their genetic similarities that might be due to free exchange of similar materials with different names that may have overlapped in the previous diversity distribution pattern of the domesticated species (Jaradat and Shahid 2006; Aghaee *et al.* 2010). Reddy and Jayamani (2019) as well as Niranjana *et al.* (2014) reported the existence of genetic diversity in pigeonpea using multivariate analysis. Singh *et al.* (2014); Qutadah *et al.* (2019); Kinhoégbè *et al.* (2020) further reported different grouping of genotypes for the agronomic traits in the assessment of genetic variability.

## Conclusion

In conclusion, there was sufficient genetic variability existed among pigeonpea genotypes that would help the improvement through identification and selection of parental lines for the traits of interest with greater chances of success in pigeonpea breeding. The study revealed the presence of genetic diversity among the pigeonpea genotypes studied based on the analysis of variance and multivariate tools used for analyses. The results indicated that the higher level of genetic diversity observed within the acquired genotypes from ICRISAT collection in Kenya and

Tanzania would enable efficient utilisation and pigeonpea improvement in breeding programs in South Africa and other countries. The variability among the genotypes also will help to identify and select the potential parents for hybridization. The selection for single trait and improvement for this trait would require more breeding work to fix the trait, therefore it is suggested that selection of genotypes for multiple traits as well as directly correlated traits would accelerate pigeonpea breeding for improvement of traits of interest simultaneously. Further characterization this crop using molecular techniques should be conducted to elucidate the environmental factor for utilization in the future breeding programs.

## Acknowledgements

The first author would like to thank the Department of Agriculture, Land Redistribution and Rural Development for funding. Additionally, the authors would like to thank the technical assistance and trial management of Paul Rantso, Dinah Scott, Deon Du Toit, and Theodora Mathobisa.

## Author Contributions

Dr. Maletsema Alina Mofokeng is a Researcher in Plant Breeding at the Agricultural Research Council-Grain Crops, Potchefstroom, South Africa. Contribution: Conceptualization, experimental design, planting, trial monitoring, data recording, analysis and drafting of the manuscript. Dr. Zaid Bello is a Researcher in Agronomy department of Agricultural Research Council-Grain Crops, Potchefstroom, South Africa. Contribution: trial management, and review the manuscript. Dr Kingstone Mashingaidze is a Senior Research Manager in the Agricultural Research Council-Grain Crops, Potchefstroom, South Africa. Contribution: review, supervision and edition inputs into the manuscript. Dr Abe Shegro Gerrano is a Senior Research Specialist in the Agricultural Research Council-Vegetables, Industrial and Medicinal Plants, Pretoria, South Africa. Contribution: Conceptualization, experimental design, data analysis and review the manuscript.

## Conflicts of Interest

The authors have not declared any conflict of interests.

## Funding Source

This work was supported by the Department of Agriculture, Land Redistribution and Rural Development.

## In Loving Memory

This article is dedicated to our colleague Dr. Maletsema Alina Mofokeng who passed away on 21 April 2022.

## Data Availability

All new research results were presented in this article.

## Ethics Approval

Not applicable.

## References

- Adebowale OJ, K Maliki (2011). Effect of fermentation period on the chemical composition and functional properties of pigeonpea seed flour. *Int Food Res J* 18:1329–1333
- Aghae M, R Mohammadi, S Nabovati (2010). Agro-morphological characterization of durum wheat accessions using pattern analysis. *Aust J Crop Sci* 4:505–514
- Ajmal SU, MN Minhas, A Hamdani, A Shakir, M Zubair, Z Ahmad (2013). Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) germplasm. *Pak J Bot* 45:1643–1648
- Choudhary AK, S Kumar, BS Patil, JS Bhat, M Sharma, S Kemal, TP Ontagodi, S Datta, P Patil, SK Chaturvedi, R Sultana, VS Hedge, S Choudhary, PY Kamannavar, AG Vijaykumar (2013). Narrowing yield gaps through genetic improvement for *Fusarium* wilt resistance in three pulse crops of the semi-arid tropics. *Sabrao J Breed Genet* 45:341–370
- Duran C, N Appleby, D Edwards, J Batley (2009). Molecular genetic markers: Discovery, applications, data storage and visualisation. *Curr Bioinform* 4:16–27
- Faris DG, KB Saxena, S Mazumdar, U Singh (1987). *Vegetable Pigeonpea: A promising crop for India*. ICRISAT, Patancheru, India
- Gbaguidi AA, A Dansi, I Dossou-Aminon, DSJC Gbemavo, A Orobiyi, F Sanoussi, H Yedomonhan (2018). Agromorphological diversity of local Bambara groundnut (*Vigna subterranea* (L.) Verdc.) collected in Benin. *Genet Res Crop Evol* 65:1159–1171
- Gerrano AS, A Moalafi, HA Seepe, S Amoo, H Shimelis (2022). Nutritional and phytochemical compositions and their interrelationship in succulent pods of pigeon pea (*Cajanus cajan* L.) Millsp.). *Heliyon* 8:1–7
- Gerrano AS, WSJV Rensburg, I Mathew, AIT Shayanowako, MW Bairu, SL Venter, W Swart, A Mofokeng, JJ Mellem, M Labuschagne (2020). Genotype and genotype x environment interaction effects on the grain yield performance of cowpea genotypes in dryland farming system in South Africa. *Euphytica* 216:80–90
- Gerrano AS, WSJV Rensburg, PO Adebola (2015). Genetic diversity of amaranthus species in South Africa. *S Afr J Plant Soil* 32:39–46
- IBPGR (1994). *International Board for Plant Genetic Resources*. Rome, Italy
- Immad AS, KV Imran, AM Shakeel, MS Pukhta, AD Zahoor, L Ajaz (2018). Genetic Diversity by Multivariate Analysis Using R Software. *Intl J Pure Appl Biosci* 6:181–190
- Jaradat AA, MA Shahid (2006). Patterns of phenotypic variation in a germplasm collection of (*Carthamus tinctorius* L.) from the Middle East. *Genet Res Crop Evol* 53:225–244
- Kasirivu J, S Materechera, M Dire (2011). Composting ruminant animal manure reduces emergence and species diversity of weed seedlings in a semi-arid environment of South Africa. *S Afr J Plant Soil* 28:228–235
- Khan SA, J Iqbal, H Khurshid, N Saleem, MA Rabbani, M Zia, ZK Shinwari (2014). The extent of intra-specific genetic divergence in *Brassica napus* L. population estimated through various agro-morphological traits. *Eur J Acad Res* 2:2255–2275
- Kimaro D (2016). Genetic improvement of pigeonpea (*Cajanus cajan* (L.) Millsp.) for fusarium wilt resistance in Tanzania. *Ph.D. Thesis* University of Kwazulu-Natal, Pietermaritzburg, South Africa
- Kinhoégbè G, G Djèdatin, LEY Loko, RI Agbo, RK Saxena, RK Varshney, C Agbangla, A Dansi (2020). Agro-morphological characterization of pigeonpea (*Cajanus cajan* L. Millspaugh) landraces grown in Benin: Implications for breeding and conservation. *J Plant Breed Crop Sci* 12:34–49
- Kovacic Z (1994). *Multivariate analysis*, p:293. Faculty of Economics, University of Belgrade, Serbian
- Linge SS, HV Kalpande, SL Sawargaonkar, BV Hudge, HP Thanki (2010). Study of enetic variability and correlation in interspecific derivatives of pigeonpea (*Cajanus cajan* (L.) Millsp.). *Electr J Plant Breed* 1:929–935
- Lin-Qi X, TT Li, Z Wei, N Guo, M Luo, W Wang, Y Zu, Y Fu, X Peng (2014). Solvent-free microwave extraction of essential oil from pigeonpea leaves and evaluation of its antimicrobial activity. *Ind Crops Prod J* 58:322–328
- Maesen LGJVD (1990). Pigeonpea: Origin, history, evolution and taxonomy. In: *The pigeonpea*, pp:15–46. Nene L, SD Hall, VK Sheilla (Eds), pp:15–46. C.A.B. International, Wallingford, UK
- Malik R, H Sharma, I Sharma, S Kundu, A Verma, S Sheoran S, R Kumar, R Chatrath (2014). Genetic diversity of agro-morphological characters in Indian wheat varieties using GT biplot. *Aust J Crop Sci* 8:1266–1271
- Mallikarjuna N, KB Saxena, DR Jadhav (2011). *Cajanus*. In: *Wild Crop Relatives: Genomic and Breeding Resources, Legume Crops and Forages*, pp:21–33. Kole C (Ed). Springer-Verlag, Berlin, Heidelberg, Germany
- Marais LDD, KM Hernandez, E Juenger (2013). Genotype-by-environment interaction and plasticity: Exploring genomic responses of plants to the abiotic environment. *Annl Rev Ecol Evol Syst* 44:5–29
- Mohammadi SA, BM Prasanna (2003). Analysis of genetic diversity in crop plants-salient statistical tools and considerations. *Crop Sci* 43:1235–1248
- Molope M (1987). Soil aggregate stability. The contribution of biological and physiological processes. *S Afr J Plant Soil* 4:121–126
- Mondal MAA (2003). Improvement of Potato (*Solanum Tuberosum* L.) through hybridization and *in vitro* culture technique. *Ph.D. Thesis*. Rajshahi University, Rajshahi, Bangladesh
- Muniswamy S, R Loksha, P Dharmaraj, S Yamanura, JR Diwan (2014). Morphological characterization and assessment of genetic diversity in minicore collection of igeon pea (*Cajanus Cajan* (L.) Millsp.). *Eur J Pharm Biopharm* 5:179–186
- Niranjana KB, PS Dharmaraj, VB Wali (2014). Genetic diversity and variability studies of advanced breeding lines of pigeonpea (*Cajanus cajana* L.). *Intl J Adv Pharm Biol Sci* 3:404–409
- Nunes HF, FFH Freire, VQ Ribeiro, RLF Gomes (2014). Grain yield adaptability and stability of blackeyed cowpea genotypes under rainfed agriculture in Brazil. *Afr J Agric Res* 9:255–261
- Odeny DA (2007). *The potential of pigeonpea (Cajanus cajan (L.) Millsp.) in Africa*. Natural resources forum. Wiley Online Library
- Ojwang JD, RO Nyankanga, OM Olanya, DO Ukuku, J Imungi (2016). Yield components of vegetable pigeonpea cultivars. *Trop Subtrop Agric Environ* 67:1–12
- Peeters J, JA Martinelli (1989). Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theor Appl Genet* 78:42–48
- Prasad Y, K Kumar, SB Mishra (2013). Studies on genetic parameters and interrelationships among yield and yield contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Bioscan* 8:207–211
- Qutadah SM, S Mehandi, IP Singh, F Singh (2019). Assessment of Genetic Diversity for Polygenic Traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Intl J Curr Microbiol Appl Sci* 8:1581–1588
- Rachovska G, D Dimova, B Bojinov (2002). Application of cluster analysis and principal component analysis for evaluation of common winter wheat genotypes. In: *Proceedings of the Scientific Session of Jubilee*, Vol. 3, pp:68–72. Sadovo, Bulgaria
- Reddy DSE, P Jayamani (2019). Genetic diversity in land races of pigeonpea (*Cajanus cajan* (L.) Millsp.). *Electr J Plant Breed* 10:667–672
- Rupika K, KJR Bapu (2014). Assessment of genetic diversity in pigeonpea germplasm collection using morphological characters. *Eur J Pharm Biopharm* 5:781–785
- Saidia PS, F Asch, AA Kimaro, J Germer, FC Kahimba, F Graef, JM Semoka, CL Rweyemamu (2019). Soil moisture management and fertilizer micro-dosing on yield and land utilization efficiency of inter-cropping maize-pigeon-pea in sub humid Tanzania. *Agric Water Manage* 223:105712

- Saroj SK, MN Singh, R Kumar, T Singh, MK Singh (2013). Genetic variability, correlation and path analysis for yield attributes in pigeonpea. *Bioscan* 8:941–944
- SAS Institute (2021). *SAS/STAT user's Guide*, version 9.2 SAS Institute, Cary, North Carolina, USA
- Saxena KB, RV Kumar, R Sultana (2010). *Quality Nutrition through Pigeonpea-Review*, Vol. 2, pp:1335–1344. ICRISAT, Hyderabad, India
- Singh AK, S Swain, RK Gautam, PK Singh, AK Betal, T Bharathimeena, N Kumar, SD Roy (2014). Agro-morphological characterization of Bay Islands pigeonpea (*Cajanus cajan*) landraces and advanced lines using under Islands conditions. In: *3<sup>rd</sup> International Conference on Agriculture and Horticulture, October 27–29, 2014* Hyderabad International Convention Centre, India
- Smith JSC, OS Smith (1989). The description and assessment of distance between inbred lines of maize. The utility of morphological, biochemical and genetic descriptors and a scheme for the testing of distinctiveness between inbred lines. *Maydica* 34:151–161
- Sodavadiya MS, JJ Pithia, AG Savaliya, A Pansuriya, VK Korat (2009). Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp.). *Leg Res* 32:203–205
- Syafii M, I Cartika, D Ruswandi (2015). Multivariate analysis of genetic diversity among some maize genotypes under maize-albizia cropping system in Indonesia. *Asian J Crop Sci* 7:244–255
- Syed MQ, M Suhel, IP Singh, S Farindra (2019). Assessment of Genetic Diversity for Polygenic Traits in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Intl J Curr Microbiol Appl Sci* 8:1581–1588
- Upadhyaya HD, KN Reddy, CLL Gowda, S Singh (2007). Phenotypic diversity in the pigeonpea (*Cajanus cajan*) core collection. *Genet Res Crop Evol* 54:1167–1184
- Vales M, R Srivastava, R Sultana, S Singh, I Singh, G Singh, S Patil, K Saxena (2012). Breeding for earliness in pigeonpea: Development of new determinate and non-determinate lines. *Crop Sci* 52:2507–2516
- Virk PS, GS Khush, SS Virmani (2003). Breeding strategies to enhance heterosis in rice. In: *Hybrid Rice for Food Security, Poverty Alleviation and Environmental Protection*, pp:21–29. Virman SS, CX Mao, B Hardy (Eds). International Rice Research Institute Los Banos, Philippines
- VSN International (2020). *Genstat for Windows*, 20<sup>th</sup> edn. VSN International, Hemel Hempstead, UK
- Yohane EN, H Shimelis, M Laing, I Mathew, A Shayanowako (2020). Phenotypic Divergence analysis in pigeonpea [*Cajanus cajan* (L.) Millspaugh] germplasm accessions. *Agronomy* 10:1682–1699