Phenotypic Divergence Analysis in Pigeonpea 
[Cajanus cajan (L.) Millspaugh] 
Germplasm Accessions

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Abstract: Pigeonpea (Cajanus cajan (L.) Millspaugh) is an important source of grain protein for low-income countries such as Malawi. Knowledge of the genetic diversity in pigeonpea is essential for an effective breeding program. The study objective was to assess the genetic diversity among diverse pigeonpea accessions to select complementary and unique genotypes for breeding. Eighty-one pigeonpea accessions were evaluated in six environments in Malawi using a 9 x 9 alpha-lattice design with two replications. The cross-tabulation analysis revealed a significant genotype variation on plant growth, flower, and seed traits. The combined analysis of variance identified genotypes MWPLR 14, ICEAP 01170, ICEAP 871091, and ICEAP 01285 as early maturing varieties, while Kachangu, MWPLR 16, TZA 5582, No. 40, and MWPLR 14 were identified as high-yielding genotypes. The correlation analysis revealed a significant positive correlation between grain yield and a hundred seed weight (HSWT) (r = 0.50, p < 0.01), suggesting the usefulness of this trait for selection. The nonlinear principal component analysis identified grain yield (GDY), days to 50% flowering (DTF), days to 75% maturity (DTM), number of pods per plant (NPP), number of racemes per plant (NRP), 100 seed weight (HSWT), leaf hairiness (LH), and number of seeds per pod (NSP) as the most discriminated traits among the test genotypes. The cluster analysis using morphological traits delineated the accessions into three clusters. The selected high-yielding and early-maturing genotypes may be recommended as parental lines for breeding and grain yield improvement in Malawi or similar agro-ecologies.

Keywords: agronomic performance; correlation analysis; malawi; pigeonpea; yield stability

1. Introduction

Pigeonpea (Cajanus cajan (L.) Millspaugh, 2n = 2x = 22) is an essential cash and food crop in the tropical and subtropical regions of the world. It is a multi-purpose crop that is cultivated mainly for its edible grains that are high in dietary protein and essential amino acids such as leucine (16.48 g/kg), tyrosine (14.77 g/kg), and arginine (13.51 g/kg) [1].

Pigeonpea is an essential component of the agriculture systems in semi-arid ecologies due to its adaptation to growing with relatively low rainfall and with poor soil fertility. It has a deep root system and a unique ability to maintain optimal osmotic adjustment under limited water conditions [2]. Pigeonpea can fix atmospheric nitrogen in the soils through symbiosis with species of Rhizobium bacteria depositing up to 200 kg of nitrogen per hectare in agricultural lands [3,4]. Thus, pigeonpea has important roles in enhancing food security and livelihoods, especially during drought years, and providing ecosystem services through nitrogen fixation and soil health improvement.
Pigeonpea accounts for 5% of the world’s pulse production [5]. India is the largest producer of pigeonpea, accounting for 25% of the world’s production, followed by Myanmar and Malawi [6]. In Malawi, pigeonpea accounts for more than 22% of total legume production and ranks as the 3rd most important legume crop after groundnut and common beans. The grain productivity of pigeonpea in Malawi is low (~700 kg ha\(^{-1}\)) compared to its potential yield of 2500 kg ha\(^{-1}\) [7]. The yield gap is due to various constraints, including insect pests and diseases, drought stress, and a lack of improved cultivars. The breeding and deployment of improved cultivars can enhance pigeonpea production and productivity. The successful development of improved cultivars with the client and market-preferred traits depends on the availability of adequate genetic variation.

Reportedly, modern pigeonpea cultivars and varieties exhibit relatively low levels of genetic diversity [8]. The loss of genetic diversity is due to continuous artificial selection and breeding for a few targeted economic traits to meet the market requirements [9]. Hence, there is a need to initiate pre-breeding programs in the target production environments through divergence breeding involving modern and obsolete cultivars, landraces, and wild relatives that possess desirable traits. This will broaden the genetic diversity of pigeonpea through gene recombination and effective selection [9]. The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and various national and regional improvement programs are actively involved in genetic improvement and conservation of the pigeonpea. Diverse pigeonpea collections are preserved globally, including by ICRISAT, the International Institute of Tropical Agriculture (IITA), and the Svalbard Global Seed Vault in Norway. These genetic resources can be used for pigeonpea improvement and breeding programs globally [10].

To date, only seven pigeonpea cultivars have been released in Malawi. These cultivars were introductions from ICRISAT [7] developed in Kenya with germplasm from eastern and southern Africa (ESA). The ESA region is recognized as a secondary center of genetic diversity for pigeonpea. The introduced cultivars are poorly adapted to local farming conditions in Malawi and lack farmer-preferred traits such as good cooking quality, resistance to pod borers, and high yield potential. Therefore, the development of high performance, locally adapted pigeonpea cultivars is an important target in Malawi. This requires a range of genetic resources and crosses to integrate adaptive and functional traits, according to the needs and preferences of farmers and the value chain. Introduced germplasm can provide useful genetic resources that can be introgressed into locally adapted germplasm to improve economic traits such as high yield, early maturity, and pest and disease resistance, among others [9]. Evaluating accessions maintained by the public and private breeding sectors within the ESA region provides an opportunity to identify stable and high-yielding genotypes for selection.

Many pigeonpea genotypes have been collected and maintained at the Department of Agricultural Services in Malawi for breeding purposes. The genotypes are adapted to the ESA region and possess valuable attributes including good cooking quality, insect pests, and disease resistance, but they are limited by their poor yield performance. The key traits present in the local and introduced germplasm should be assessed for pre-breeding and breeding purposes. Hence, the objectives of the study were to determine the genetic diversity among pigeonpea accessions in selected target production environments in Malawi to select complementary and unique genotypes for breeding.

2. Materials and Methods

2.1. Plant Materials

The study evaluated 81 pigeonpea genotypes comprising 28 landraces, 6 released cultivars, and 47 advanced elite lines (Table 1), which were sourced from the Department of Agricultural Research Services (DARS)/Malawi and the Tanzania Agriculture Research Institute (TARI) and the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)/Kenya. The landraces were included as checks for adaptation to local conditions and possessing farmers’ traits, while the elite lines provide important genetic resources, since Tanzania and Kenya have more advanced pigeonpea-breeding programs. The released cultivars provided a benchmark against commercial standards that are currently in production.
Table 1. Description of the pigeonpea genotypes used in the study.

| Code | Genotype Designation | Description | Source | Origin | Code | Genotype Designation | Description | Source | Origin |
|------|----------------------|-------------|--------|--------|------|----------------------|-------------|--------|--------|
| G1   | ICEAP 0673/1         | Breeding line | ICRISAT | Kenya  | G42  | ICEAP 87103          | Cultivar    | ICRISAT | Kenya  |
| G2   | ICEAP 00554          | Breeding line | ICRISAT | Kenya  | G43  | MWPLR 16             | Landrace    | GENE BANK | Malawi |
| G3   | ICEAP 01164/1        | Breeding line | ICRISAT | Kenya  | G44  | TZA 2496             | Landrace    | TARI    | Tanzania|
| G4   | MWPLR 19             | Landrace     | GENE BANK | Malawi | G45  | TZA 5582             | Landrace    | TARI    | Tanzania|
| G5   | MWPLR 22             | Landrace     | GENE BANK | Malawi | G46  | TZA 5596             | Landrace    | TARI    | Tanzania|
| G6   | ICEAP 01170          | Breeding line | ICRISAT | Kenya  | G47  | Chitedze Pigeonpea 2 | Cultivar    | DARS    | Malawi |
| G7   | ICEAP 01169          | Breeding line | ICRISAT | Tanzania | G48  | MWPLR 7             | Landrace    | GENE BANK | Malawi |
| G8   | TZA 2439             | Landrace     | TARI    | Tanzania | G49  | Babati               | Landrace    | TARI    | Tanzania|
| G9   | MWPLR 9              | Landrace     | GENE BANK | Malawi | G50  | TZA 5557             | Landrace    | TARI    | Tanzania|
| G10  | MWPLR 6              | Landrace     | GENE BANK | Malawi | G51  | MWPLR 14             | Landrace    | ICRISAT | Kenya  |
| G11  | MWPLR 17             | Landrace     | GENE BANK | Malawi | G52  | ICEAP 01101/1        | Breeding line | ICRISAT | Kenya  |
| G12  | TZA 253              | Landrace     | TARI    | Tanzania | G53  | TZA 2456             | Landrace    | TARI    | Tanzania|
| G13  | MWPLR 1              | Landrace     | GENE BANK | Malawi | G54  | TZA 5646             | Landrace    | TARI    | Tanzania|
| G14  | MWPLR 18             | Landrace     | GENE BANK | Malawi | G55  | ICEAP 01101/2        | Breeding line | ICRISAT | Kenya  |
| G15  | TZA 2464             | Landrace     | TARI    | Tanzania | G56  | ICEAP 01285          | Breeding line | ICRISAT | Kenya  |
| G16  | ICEAP 00604          | Breeding line | ICRISAT | Kenya  | G57  | MWPLR 25             | Landrace    | GENE BANK | Malawi |
| G17  | TZA 2509             | Landrace     | GENE BANK | Malawi | G58  | ICEAP 87091          | Breeding line | ICRISAT | Kenya  |
| G18  | ICEAP 01146/1        | Breeding line | ICRISAT | Kenya  | G59  | TZA 2692             | Landrace    | TARI    | Tanzania|
| G19  | MWPLR 11             | Landrace     | GENE BANK | Malawi | G60  | TZA 2807             | Landrace    | TARI    | Tanzania|
| G20  | TZA 5555             | Landrace     | TARI    | Tanzania | G61  | ICEAP 00006          | Breeding line | ICRISAT | Kenya  |
| G21  | No. 40               | Landrace     | TARI    | Tanzania | G62  | TZA 2785             | Landrace    | TARI    | Tanzania|
| G22  | ICEAP 01150          | Breeding line | ICRISAT | Kenya  | G63  | MWPLR 10             | Landrace    | GENE BANK | Malawi |
| G23  | MZ29                 | Breeding line | TARI    | Tanzania | G64  | ICEAP 00612          | Breeding line | ICRISAT | Kenya  |
| G24  | ICEAP 01172/1        | Breeding line | ICRISAT | Kenya  | G65  | MWPLR 21             | Landrace    | GENE BANK | Malawi |
| G25  | ICEAP 01103/1        | Breeding line | ICRISAT | Kenya  | G66  | TZA 2514             | Landrace    | TARI    | Tanzania|
| G26  | MWPLR 24             | Landrace     | GENE BANK | Malawi | G67  | TZA 2466             | Landrace    | TARI    | Tanzania|
| G27  | ICEAP 01155          | Breeding line | ICRISAT | Kenya  | G68  | ICEAP 01179          | Breeding line | ICRISAT | Kenya  |
| G28  | ICEAP 01180/2        | Breeding line | ICRISAT | Kenya  | G69  | MWPLR 13             | Landrace    | GENE BANK | Malawi |
| G29  | MWPLR 4              | Landrace     | GENE BANK | Malawi | G70  | MWPLR 2              | Landrace    | GENE BANK | Malawi |
| G30  | Kachangu             | Cultivar     | DARS    | Malawi | G71  | TZA 250              | Landrace    | DARS    | Malawi |
| G31  | Mwayiwathualimi      | Cultivar     | DARS    | Malawi | G72  | MWPLR 3              | Landrace    | GENE BANK | Malawi |
| G32  | MWPLR 8              | Landrace     | GENE BANK | Malawi | G73  | TZA 5541             | Landrace    | TARI    | Tanzania|
| G33  | ICEAP 01154/2        | Breeding line | ICRISAT | Kenya  | G74  | MWPLR 23             | Landrace    | GENE BANK | Malawi |
| G34  | Chitedze Pigeonpea 1 | Cultivar     | DARS    | Malawi | G75  | ICEAP 00979/1        | Breeding line | ICRISAT | Kenya  |
| G35  | ICEAP 01164          | Breeding line | ICRISAT | Kenya  | G76  | TZA 197              | Landrace    | TARI    | Tanzania|
| G36  | Bangili              | Landrace     | TARI    | Tanzania | G77  | MWPLR 20             | Landrace    | GENE BANK | Malawi |
| G37  | ICEAP 00053          | Breeding line | ICRISAT | Kenya  | G78  | HOMBOLO              | Landrace    | TARI    | Tanzania|
| G38  | MWPLR 12             | Landrace     | GENE BANK | Malawi | G79  | ICEAP 86012          | Breeding line | ICRISAT | Kenya  |
| G39  | TZA5463              | Landrace     | TARI    | Tanzania | G80  | ICEAP 01106/1        | Breeding line | ICRISAT | Kenya  |
| G40  | MWPLR 5              | Landrace     | GENE BANK | Malawi | G81  | Sauma                | Cultivar    | DARS    | Malawi |
| G41  | MWPLR 15             | Landrace     | GENE BANK | Malawi |        |                      |             |         |        |

ICRISAT = International Crops Research Institute for the Semi-Arid Tropics, DARS = Department of Agricultural Research Services, TARI = Tanzania Agricultural Research Institute.
2.2. Study Sites

Field experiments were conducted in Malawi at three sites, Bvumbwe, Chitedze, and Makoka Research Stations, during the 2017/18 and 2018/19 cropping seasons. The geographic location, altitude, weather, and soil characteristics of the study locations are presented in Table 2. Each season and site combination presented unique environmental conditions due to variations in temperature, rainfall, and agronomic practices. Therefore, due to site × season combinations, six environments were identified for evaluating the genotypes: Bvumbwe during 2017/18 (Environment 1), Bvumbwe in 2018/19 (Environment 2), Chitedze in 2017/18 (Environment 3), Chitedze in 2018/19 (Environment 4), Makoka in 2017/18 (Environment 5), and Makoka in 2018/19 (Environment 6).

Table 2. Physical and weather characteristics of the study locations.

| Site      | Latitude      | Longitude    | Altitude (Masl) | Soil Texture         | Rainfall (mm) | Min Temp (°C) | Max Temp (°C) |
|-----------|---------------|--------------|-----------------|----------------------|---------------|---------------|---------------|
|           |               |              |                 |                      | 2017/18 | 2018/19 | 2017/18 | 2018/19 | 2017/18 | 2018/19 |
| Bvumbwe   | 15°55′ S      | 35°04′ E     | 1228            | Sandy clay loam      | 975.2 | 1442 | 16.2 | 17.9 | 22.6 | 24.9 |
| Chitedze  | 13°59′ S      | 33°38′ E     | 1146            | Sandy clay           | 929.8 | 693.4 | 18.5 | 20.2 | 24.7 | 29.4 |
| Makoka    | 15°32′ S      | 35°11′ E     | 1029            | Sandy clay loam      | 566.6 | 1184.8 | 16.3 | 15.6 | 23.2 | 28.2 |

Masl = meters above sea level, mm = millimeters, min = minimum, max = maximum, temp = temperature, °C = degrees Celsius.

2.3. Experimental Design and Data Collection

The experiment at each site was laid out in an alpha-lattice design with two replications. Each genotype was planted on a plot consisting of two rows. The rows were 5 m in length and 0.90 m apart, giving a plot size of 4.5 m². Seeds were planted at 0.75 m apart within a row. Three seeds were planted per planting station and thinned to one plant two weeks after emergence. All agronomic practices were applied following standard practices for pigeonpea production in Malawi [7]. Both qualitative and quantitative phenotypic traits’ data were collected as presented in Table 3 according to pigeonpea descriptors of the International Board for Plant Genetic Resource (IBPGR) and International Centre for Research Institute for Semi-Arid Tropics (ICRISAT) [11].

2.4. Statistical Analysis

Data collected on qualitative traits (Table 3) were subjected to frequency distribution and cross-tabulation analyses using SPSS for Windows 25.0 [12].

The quantitative data from each variable were tested for homogeneity of variances using Bartlett’s test and data normality using the Shapiro–Wilkes test before the analysis of variance (ANOVA). Subsequently, the data were pooled across sites and subjected to a combined analysis of variance following the alpha lattice procedure in Genstat 18th edition [13]. The total variance was partitioned into genotype ($\sigma^2_g$), environment ($\sigma^2_e$), and genotype by environment ($\sigma^2_{ge}$) components based on the mean squares derived from the partial analysis of variance adapted from [14]. Correlation and principal component analyses were performed using Genstat 18th edition [13] to determine influential components and trait relationships. A nonlinear principal component analysis was conducted in SPSS (SPSS 2016). The nominal variables (qualitative traits) were transformed using the categorical principal component analysis (CATPCA) procedure described by [15]. The nonlinear PCA can standardize both quantitative and qualitative data to deduce their associations and identified the most important components.
Table 3. Descriptors for the pigeonpea qualitative and quantitative traits.

| Traits                  | Code | Description                                                                 |
|-------------------------|------|-----------------------------------------------------------------------------|
| **Qualitative Traits**  |      |                                                                             |
| Plant habit             | PH   | 1 = Compact (erect), 2 = semi-spreading (semi-erect) or 3 = spreading       |
| Flower streak pattern   | FSP  | 0 = no streaks, 1 = sparse, 2 = medium and 3 = dense streaks, 4 = uniform coverage of second color |
| Flower base/main color  | FBC  | 1 = ivory (green white), 2 = light yellow, 3 = yellow, 4 = orange, 5 = red, 6 = purple |
| Leaf shape              | LS   | 1 = ovate, 2 = triangular, 3 = trullate                                    |
| Leaf hairiness          | LH   | 1 = hairy, 2 = non-hairy                                                   |
| Pod form                | PF   | 1 = flat, 2 = cylindrical                                                  |
| Pod color               | PC   | 1 = green, 2 = purple, 3 = mixed (green +purple) and 4 = dark purple       |
| Seed color pattern      | SCP  | 1 = plain, 2 = mottled, 3 = speckled, 4 = mottled and speckled, 5 = ringed |
| Seed main color         | SMC  | 1 = white (yellow white), 2 = cream (gray white), 3 = orange, 4 = brown, 5 = grey, 6 = purple, 7 = black |
| Seed eye color          | SEC  | 1 = purple, 2 = light brown, 3 = reddish brown, 4 = gray/dark, 5 = cream/white |
| Seed shape              | SSH  | 1 = Oval, 2 = pea-shape, 3 = square/angular, 4 = elongate                  |
| **Quantitative Traits** |      |                                                                             |
| Plant height            | PH   | Measured in cm from plant base to the tip of the main stem                  |
| Days to 50% flowering   | DTF  | Number of days from sowing until when 50% of the plants have at least one open flower |
| Primary branches        | PBR  | The average number of primary branches of 10 randomly selected and tagged plants |
| Secondary branches      | NSB  | The average number of secondary branches of 10 randomly selected and tagged plants |
| Days to 75% maturity     | DTM  | Number of days from sowing until when 75% of the pods in a plot turn brown  |
| Number of seeds per pod | NSP  | The average number of pods per plant from 10 randomly selected and tagged pods |
| Number of pods per plant| NPP  | The average number of pods from 10 randomly selected and tagged plants      |
| Number of racemes per plant| NRP | The average number of racemes from 10 randomly selected and tagged plants   |
| Grain yield (t/ha)      | GYD  | Weight of the grain harvested in a plot extrapolated to t/ha                |
| 100 seed weight (g)     | HSWT | Weight of a random sample of 100 grain                                    |

3. Results

3.1. Genotype Variation Based on Qualitative Traits

Significant variations were exhibited among genotypes for all assessed qualitative traits ($p < 0.001$) such as growth habit, flower main color, flower streak pattern, pod color, and seed traits (Table 4, Figure 1A–D). A large proportion of test genotypes (61.9%) were semi-spreading, followed by spreading (26.6%) and compact (11.5%) in growth habits. A majority of the test genotypes (64.9%) had yellow flower color (Table 4, Figure 1A), while 16.8% had purple flowers, 13.6% had ivory flowers, and 7.4%
had light yellow flowers (Table 4, Figure 1A). A large population of the genotypes (60.5%) had no flower streaks, and the rest of the genotypes had sparse, medium, dense, and uniform coverage streaks at 8.1%, 1.9%, 14.5%, and 15%, respectively (Table 4, Figure 1B). About 48.7% of the genotypes had a green pod color, while 33.9% had a mixed pod color and 7.1% had purple pods (Table 4, Figure 1C). A majority of the genotypes (76.8%) had a cream seed coat color, while 11% had a brown seed coat color and the rest had gray, orange, and purple seed coat colors (Table 4, Figure 1D). About 70.2% of the test genotypes had a brown seed eye, and 20.7% had a purple seed eye, while the remainder had gray or cream seed eyes. The most common seed shape was square or angular shapes, which were exhibited by 69.3% of the test genotypes.

3.2. Genotype and Environment Variances for Quantitative Traits

The quantitative agronomic data were pooled across sites after applying tests for homogeneity of variance and normality. The genotype × environment interaction effects were significant ($p < 0.001$) for grain yield (GYD), days to 50% flowering (DTF), days to 75% maturity (DTM), plant height (PH), number of primary branches (NPB), number of pods per plant (NPP), number of racemes per plant (NRP), 100 seed weight (HSWT), and number of secondary branches per plant (NSB) (Table 5). The genotype and environment had significant ($p < 0.001$) effects on all assessed traits except the NSP. The site × environment interaction effects were significant ($p \leq 0.001$ and $p = 0.05$, respectively) for DTM, PH, and NSP (Table 6). The site × type interaction effects were only significant ($p = 0.01$ and $p = 0.05$) for DTM, NPP, NRP, and HSWT, respectively. However, season × type interaction effects were not significant for all the variables except for GYD, which was highly significant.
Table 4. Frequency distribution and significance tests among 81 pigeonpea genotypes assessed based on qualitative traits.

| Trait                        | Description                 | Frequency (%) | DF  | Chi-Square | Genotype Code               |
|------------------------------|-----------------------------|---------------|-----|------------|-----------------------------|
| Growth habit                 | Compact                     | 11.5          |     |            | G53, G2, G1, G27, G26       |
|                              | Semi-spreading              | 61.9          | 160 | 304.52 **  | G63, G50, G28, G70, G76, G80, G51 |
|                              | Spreading                   | 26.6          |     |            | G45, G41, G29, G49, G56, G64, G37, G60, G15, G11, G65, G75, G81, G44, G67, G11, G46 |
| Flower color                 | Ivory                       | 13.6          |     |            | G50, G45, G70, G53, G36, G12, G15, G37, G20, G60, G9, G54, G11, G66, G55, G80, G81 |
|                              | Light yellow                | 7.4           |     |            | G17, G53, G36, G22, G4, G58, G68, G18, G19, G17, G9, G62, G29, G32, G65, G21, G52, G1, G15, G66, G55, G80, G81 |
|                              | Yellow                      | 64.9          | 240 | 910.08 *** | G43, G26, G71, G44, G15, G67, G11, G69, G65, G75, G20, G43, G26, G71, G44, G15, G67, G11, G46, G65 |
|                              | Purple                      | 16.8          |     |            | G63, G28, G41, G56, G60, G25, G46, G54, G26, G42 |
| Flower streak pattern        | No streaks                  | 60.5          |     |            | G17, G53, G36, G12, G15, G37, G20, G60, G9, G54, G11, G66, G55, G80, G81 |
|                              | Sparse streaks              | 8.1           | 320 | 589.69 *** | G47, G61, G29, G60, G34, G40, G45, G67, G45, G68, G63, G77, G19 |
|                              | Medium sparse               | 1.9           |     |            | G79, G50, G76, G59, G25, G46, G78, G38, G51, G75, G26, G35, G52, G56, G41, G43 |
|                              | Dense streaks               | 14.5          |     |            | G73, G42, G1, G24, G74, G75, G52, G16, G65, G21, G18, G7, G13, G62, G17, G47, G61, G15, G20, G29, G44, G72, G60, G64, G9, G11, G66, G55, G80, G71, G58, G14, G27, G6, G57, G10, G8, G19 |
| Pod color                    | Green                       | 48.7          |     |            | G76, G45, G67, G38 |
|                              | Purple                      | 7.1           | 240 | 647.43 *** | G81, G70, G53, G36, G61, G43, G37, G34, G54, G79, G50, G40, G25, G23, G46, G42, G51, G4, G68, G26, G49, G3, G35, G32, G69, G2, G63, G22, G56, G77, G41, G30 |
|                              | Mixed (green + purple)      | 33.9          |     |            | G31, G28, G39, G48, G59, G43 |
|                              | Dark purple                 | 10.3          |     |            | G31, G28, G39, G48, G59, G43 |
Table 4. Cont.

| Trait                      | Description | Frequency (%) | DF | Chi-Square | Genotype Code #  |
|----------------------------|-------------|---------------|----|------------|------------------|
| Seed color pattern         | Plain       | 56.6          | 240| 841.57 ****| G59, G80, G5, G18, G6, G53, G65, G62, G35, G34, G4, G46, G60, G66, G21, G70, G36, G42, G40, G14, G50, G66, G20, G79, G49, G2, G3, G69, G56, G81, G47, G72, G15, G44 |
|                            | Mottled     | 15.3          |    |            | G41, G25, G34, G48, G28, G78, G23, G31, G9, G37, G57 |
|                            | Speckled    | 22.2          |    |            | G75, G68, G43, G38, G10, G19, G52, G58, G51, G73, G59, G76, G16, G29, G13, G33, G17, G8, G54, G1, G24, G7, G71, G27, G12, G22, G55, G77 |
|                            | Mottled + speckled | 5.9 |    |            | G46, G33, G30, 632, G39, G45, G26 |
| Seed main color            | Cream       | 76.8          | 320| 1049.31 ***| G75, G68, G59, G34, G5, G18, G6, G38, G10, G33, G65, G63, G35, G19, G34, 52, G72, G15, G44, G22, G55, G57, G77, G60, G38, G78, G32, G73, G51, G70, G36, G16, G29, G42, G40, G23, G14, G17, G8, G50, G66, G20, G49, G54, G2, G3, G69, G1, G24, G45, G7, G9, G71, G81, G12, G47 |
|                            | Orange      | 3             |    |            | G4, G46, G25 |
|                            | Brown       | 11            |    |            | G64, G76, G63, G30, G34, G48, G28, G31, G37, G26 |
|                            | Gray        | 6.2           |    |            | G80, G66, G67, G56, G39, G33, G41 |
|                            | Purple      | 3             |    |            | G80, G38, G63, G8, G7, G26 |
| Seed shape                 | Oval        | 30.7          | 80 | 480.21 *** | G75, G22, G5, G25, G38, G53, G35, G34, G28, G73, G51, G70, G36, G29, G42, G40, G31, G8, G18, G49, G3, G45, G37, G28, G27, G12, G55, G57 |
|                            | Square/angular | 69.3     |    |            | G15, G44, G22, G77, G68, G59, G43, G46, G80, G18, G33, G30, G41, G6, G10, G65, G62, G19, G34, G67, G4, G52, G48, G60, G38, G66, G32, G64, G76, G21, G16, G13, G23, G14, G63, G17, G39, G52, G66, G79, G54, G2, G69, G1, G24, G56, G67, G9, G71, G81 |
| Seed eye color             | Purple      | 20.7          |    |            | G68, G5, G34, G25, G60, G78, G51, G64, G76, G21, G16, G29, G42, G40, G31, G30, G49, G2, G69, G24, G81, G55, G37 |
|                            | Light brown | 70.2          | 240| 848.32 *** | G75, G39, G45, G46, G18, G33, G30, G41, G6, G10, G53, G65, G62, G35, G19, G34, G67, G52, G48, G58, G28, G66, G32, G73, G36, G23, G14, G17, G39, G74, G20, G79, G54, G1, G46, G45, G9, G71, G37, G27, G12, G47, G15, G44, G22 |
|                            | Gray/dark   | 1.2           |    |            | G25 |
|                            | Cream       | 7.5           |    |            | G80, G38, G63, G8, G7, G26 |

DF = degrees of freedom, ** and *** = significance at 0.01 and 0.001 levels, respectively; # see genotype codes (G1–G81) in Table 1.
Table 5. Mean squares and significant tests for grain yield and yield components measured in 81 pigeonpea genotypes across six environments in Malawi.

| Source of Variation | DF  | DTF | DTM | PH  | NPB | NSB | NRP | NPP | NSP | GYD | HSWT |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Location            | 2   | 9024.2 *** | 8735.4 *** | 54,965 *** | 114.4 *** | 93.7 * | 226.9 *** | 3236 ** | 22.5 *** | 5,968,860 *** | 1008.1 *** |
| Replication (Rep)   | 1   | 701.9 ns | 289 ns | 118 ns | 1.2 ns | 105.4 * | 14,646 ns | 9810 * | 0.45 ns | 1,663,232 * | 9.5 ns |
| Block (Rep)         | 8   | 3168.5 *** | 5703.4 *** | 7710.9 ns | 52.9 * | 93.7 * | 9099 * | 6433.6 ** | 2.4 * | 16,534,356.5 *** | 72.2 ** |
| Genotype (G)        | 80  | 879.2 *** | 1234.9 *** | 2137 *** | 12.5 * | 30.9 * | 5004.9 * | 1990.3 * | 0.8 ns | 351,745.3 * | 16.8 * |
| Season (S)          | 1   | 3370.5 ** | 2945.3 * | 447 ns | 409.6 *** | 650.1 *** | 2,023,492 *** | 437.5 *** | 31.5 *** | 30,308,789 *** | 50.2 * |
| G × L               | 160 | 243 * | 361.9 * | 1106 * | 18 * | 35.6 * | 6150.9 * | 1916.1 * | 0.9 * | 360,816.9 * | 20.7 ** |
| G × S               | 80  | 3610.3 ns | 606.9 ns | 1198 ns | 17.9 * | 34.7 * | 4642.7 ns | 1060.3 * | 0.9 ns | 400,468.2 * | 14.9 ns |
| Residual            | 469 | 345.4 | 585.8 | 1243.1 | 14.5 | 11.8 | 5822.9 | 5667.2 | 0.8 | 313,554 | 15.4 |

DF = degrees of freedom, Rep = replication, DTF = days to 50% flowering, DTM = days to 75% maturity, PH = plant height, NPB = number of primary branches, NSB = number of secondary branches per plant, NRP = number of racemes per plant, NPP = number of pods per plant, NSP = number of seeds per pod, GYD = grain yield, HSWT = 100 seed weight, *, ** and *** = significance at 0.05, 0.01 and 0.001 probability levels, respectively.

Table 6. Mean squares and significant tests for grain yield and yield components among the three categories of pigeonpea genotypes.

| Source of Variation | DF  | DTF | DTM | PH  | NPB | NSB | NRP | NPP | NSP | GYD | HSWT |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Site                | 2   | 9167 *** | 8020 *** | 55,114 *** | 108.6 *** | 93 * | 1,309,332 *** | 118,174 *** | 22.54 *** | 1.658 *** | 80.16 *** |
| Rep (Block)         | 16  | 123 | 82 | 9769 | 33.3 | 71 | 14908 | 21,509 *** | 1.35 | 0.206 | 11.78 |
| Season              | 2   | 3797 ** | 3625 * | 407 | 433.3 *** | 4627 *** | 2,043,617 *** | 440,237 *** | 31.51 *** | 3.092 *** | 0.04 |
| Type                | 2   | 1629 * | 4725 ** | 44,433 ** | 18.5 | 14 | 4686 | 5891 * | 40.2 *** | 2.087 *** | 20.09 |
| Site × Season       | 2   | 2523 ** | 700 | 55,081 *** | 910.5 *** | 253 *** | 1,018,464 *** | 149,039 *** | 36.09 *** | 6.38 *** | 39.42 * |
| Site × Type         | 4   | 114 | 4385 ** | 1257 | 17 | 29 | 988,914 * | 8167 *** | 0.41 | 0.078 | 45.83 * |
| Season × Type       | 2   | 161 | 388 | 3023 | 9.9 | 2 | 642 | 380 | 1.94 | 2.006 *** | 6.44 |
| Site × Season × Type| 4   | 676 | 7883 *** | 65,810 *** | 3.1 | 44 | 1771 | 2032 | 30.17 * | 0.2 | 1.82 |
| Residual            | 937 | 386 | 619 | 1177 | 15.5 | 31 | 5823 | 1682 | 0.79 | 0.149 | 12.45 |

DF = degrees of freedom, Rep = replication, DTF = days to 50% flowering, DTM = days to 75% maturity, PH = plant height, NPB = number of primary branches, NSB = number of secondary branches per plant, NRP = number of racemes per plant, NPP = number of pods per plant, GYD = grain yield, HSWT = 100 seed weight, *, ** and *** = significance at 0.05, 0.01 and 0.001 probability level.
3.3. Mean Performance of Pigeonpea Genotypes across the Test Environments

Tables 7–10 summarize the mean values and statistics for eight quantitative traits recorded from three locations in two seasons. The tables present the best ten, and the bottom five genotypes on DTF, DTM, PH, NPB, NRP, NPP and HSWT ranked on grain yield response. The mean DTF and DTM were 112 and 157 days, respectively (Table 7). Genotype MWPLR 14 was the earliest to attain 50% flowering and maturity at 74 and 113 days, which was followed by ICEAP 01170 at 87 and 133 days, and ICEAP 01169 at 91 and 137 days, respectively. Sauma was among the latest genotypes to flower and mature at 145 and 205 days, respectively. There were marked genotype differences in plant height that varied from 125.3 to 202.4 cm (Table 8). The mean plant height of the test genotypes was 167.5 cm. The shortest genotype across the testing environments was ICEAP 87105. The tallest genotypes with plant heights exceeding 180 cm were Kachangu, No. 40, ICEAP 01106/3, ICEAP 00068, TZA 5596, MWPLR 6, Sauma, and ICEAP 00053. The mean number of the primary branch of the test genotypes was 15 (Table 8). The most productive genotypes with many primary branches per plant were MWPLR 12, MWPLR 20, ICEAP 01170, and MWPLR 23, with 19, 18, 17, and 17 primary branches per plant, in that order. The mean number of pods per plant varied from 67 to 144, with a grand mean of 94 pods per plant (Table 9). The highest number of pods per plant was 144, 134, 126, 124, and 123 observed on the genotypes Kachangu, MWPLR 16, TZA 5582, No. 40, and MWPLR 14, in that order. The number of seeds per pod exhibited non-significant differences among the assessed genotypes. The mean number of grains per pod was five. There was a wide genetic variation for grain yield ranging from 0.5 to 1.8 t ha$^{-1}$ with a mean of 1.1 t ha$^{-1}$ (Table 10). Accessions No. 40, MWPLR 14, and MWPLR 16 were the three best performing genotypes with mean yields of 1.8, 1.7, and 1.7 t ha$^{-1}$, respectively. The lowest grain yield response was 0.5 t/ha recorded for the genotypes ICEAP 00604 and ICEAP 01285. The 100 seed weight ranged from 11.0 to 17.3 g/100 seed (Table 10). Accessions MWPLR 22, TZA 5582, and MWPLR 14 expressed the highest HSWT ≥ 17 g/100 seed.

Table 7. Mean values for 10 quantitative traits among the ten top best and five bottom performing genotypes after evaluating 81 genotypes in six environments in Malawi.

| Genotype | DTF | DTM |
|----------|-----|-----|
|          | YI  | YII | Mean | YI  | YII | Mean |
|          | S1  | S2  | S3   | S1  | S2  | S3   | S1  | S2  | S3   | S1  | S2  | S3   |
| Top Ten Genotypes |
| 21       | 129 | 131 | 141  | 124 | 131 | 132  | 131 | 173 | 191  | 211 | 158 | 176  |
| 43       | 125 | 119 | 117  | 105 | 105 | 113  | 113 | 177 | 166  | 172 | 156 | 161  |
| 51       | 63  | 65  | 64   | 87  | 67  | 98   | 74  | 95  | 105  | 102 | 127 | 116  |
| 30       | 100 | 97  | 118  | 128 | 116 | 118  | 113 | 113 | 150  | 164 | 159 | 159  |
| 45       | 107 | 96  | 91   | 128 | 101 | 124  | 108 | 143 | 138  | 146 | 170 | 153  |
| 81       | 163 | 127 | 135  | 132 | 165 | 130  | 145 | 215 | 201  | 254 | 171 | 211  |
| 17       | 147 | 120 | 125  | 109 | 120 | 106  | 121 | 182 | 167  | 156 | 160 | 147  |
| 66       | 120 | 95  | 115  | 116 | 108 | 116  | 111 | 135 | 151  | 170 | 154 | 161  |
| 74       | 118 | 78  | 123  | 113 | 118 | 110  | 110 | 163 | 145  | 166 | 153 | 163  |
| 20       | 116 | 120 | 129  | 122 | 120 | 127  | 122 | 143 | 163  | 175 | 160 | 172  |
| Bottom Five Genotypes |
| 39       | 113 | 90  | 131  | 85  | 90  | 88   | 99  | 149 | 144  | 195 | 127 | 150  |
| 13       | 126 | 117 | 109  | 116 | 107 | 115  | 115 | 167 | 166  | 153 | 145 | 155  |
| 50       | 117 | 77  | 107  | 116 | 77  | 115  | 101 | 141 | 136  | 156 | 155 | 137  |
| 42       | 114 | 102 | 127  | 120 | 102 | 120  | 114 | 145 | 154  | 172 | 164 | 166  |
| 79       | 124 | 101 | 122  | 117 | 127 | 119  | 118 | 168 | 153  | 165 | 152 | 179  |
| Mean     | 117.8| 102.8|115.5|110.6|106.1|113.1|110.6|154.7|156.5|163.2|148.7|155.7|155.3|
| STD      | 17.9| 18.2|15.1|13.0|16.9|12.3|10.5|22.0|22.0|21.1|13.7|18.4|14.9|
| SED±     | ±2.0|±2.0|±1.7|±1.4|±1.9|±1.4|±1.2|±2.4|±2.4|±2.3|±1.5|±2.0|±1.7|
| CV (%)   | 15.2|17.7|13.1|11.8|15.9|10.8|9.8|14.2|14.0|13.9|9.2|11.8|9.6|

STD = standard deviation, SED = standard error of difference, CV = coefficient of variation, S1 = site 1 (Bvumbwe), S2 = site 2 (Chitedze), S3 = site 3 (Makoka), YI = year 1 (2017/18), YII = year 2 (2018/19), DTF = days to flowering, DTM = days to 75% maturity, See genotype codes (G1–G81) in Table 1.
Table 8. Mean values for plant height and number of primary branches among the ten top best and five bottom performing genotypes after evaluating 81 genotypes in six environments in Malawi.

| Genotype | PH   | NPB  | S1  | S2  | S3  | Mean | Y1  | Y11 | Mean | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  |
|----------|------|------|-----|-----|-----|------|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|          |      |      |     |     |     |      |     |     |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Top Ten Genotypes |      |      |     |     |     |      |     |     |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 21       | 166.5 | 220.0 | 193.0 | 160.0 | 212.8 | 193.0 | 190.9 | 19 | 19 | 17 | 14 | 18 | 12 | 16 |
| 43       | 113.5 | 147.5 | 127.5 | 96.5 | 146.7 | 148.0 | 163.7 | 14 | 15 | 17 | 14 | 17 | 11 | 15 |
| 51       | 151.5 | 109.0 | 158.0 | 234.5 | 209.4 | 149.0 | 168.6 | 13 | 12 | 14 | 18 | 13 | 11 | 13 |
| 30       | 229.5 | 188.5 | 204.0 | 170.0 | 218.5 | 204.0 | 202.4 | 15 | 13 | 18 | 15 | 16 | 15 | 15 |
| 45       | 139.5 | 144.5 | 173.0 | 161.5 | 169.4 | 197.5 | 164.2 | 15 | 13 | 22 | 15 | 17 | 14 | 16 |
| 81       | 163.0 | 222.0 | 191.0 | 160.5 | 168.1 | 194.5 | 183.2 | 13 | 17 | 19 | 18 | 12 | 14 | 15 |
| 17       | 163.0 | 164.0 | 163.5 | 100.0 | 152.1 | 156.0 | 149.9 | 15 | 14 | 21 | 17 | 16 | 13 | 16 |
| 66       | 181.5 | 177.5 | 164.0 | 161.5 | 156.8 | 149.5 | 165.1 | 12 | 13 | 14 | 16 | 12 | 13 | 13 |
| 74       | 156.0 | 195.0 | 185.5 | 124.5 | 178.7 | 164.0 | 167.3 | 15 | 18 | 17 | 20 | 18 | 12 | 17 |
| 20       | 152.5 | 163.0 | 168.5 | 138.5 | 247.5 | 166.5 | 172.8 | 10 | 12 | 20 | 12 | 18 | 11 | 14 |

Mean 168.0 166.7 166.2 143.4 195.5 166.1 167.3 14.6 13.6 18.0 14.9 14.6 12.8 14.5
STD 23.9 34.5 22.1 23.0 27.0 23.1 12.6 2.7 4.4 2.7 2.4 3.2 2.0 1.3
CV (%) 14.2 20.7 13.3 16.0 13.8 13.9 7.5 18.7 32.1 15.0 16.3 22.0 15.6 9.1

STD = standard deviation, SED = standard error of difference, CV = coefficient of variation, S1 = site 1 (Bvumbwe), S2 = site 2 (Chitedze), S3 = site 3 (Makoka), Y1 = year 1 (2017/18), Y11 = year 2 (2018/19), PH = plant height (cm), NPB = number of primary branches, see genotype codes (G1–G81) in Table 1.

Table 9. Mean values for number of racemes and number of pods per plant among the ten top best and five bottom performing genotypes after evaluating 81 genotypes in six environments in Malawi.

| Genotype | NRP | NPP | S1  | S2  | S3  | Mean | Y1  | Y11 | Mean | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  | S1  | S2  | S3  |
|----------|-----|-----|-----|-----|-----|------|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Top Ten Genotypes |       |      |     |     |     |      |     |     |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 21       | 214  | 402  | 71  | 130 | 61  | 47   | 154 | 157 | 270  | 66  | 61  | 92  | 98  | 124 |
| 43       | 138  | 173  | 97  | 117 | 95  | 58   | 113 | 119 | 315  | 98  | 72  | 110 | 90  | 134 |
| 51       | 260  | 155  | 146 | 113 | 80  | 51   | 134 | 167 | 231  | 109 | 65  | 76  | 90  | 123 |
| 30       | 178  | 430  | 134 | 132 | 73  | 52   | 166 | 127 | 362  | 95  | 83  | 101 | 144 |
| 45       | 191  | 647  | 160 | 151 | 88  | 83   | 220 | 96  | 261  | 106 | 81  | 92  | 122 | 126 |
| 81       | 201  | 536  | 85  | 89  | 69  | 40   | 170 | 140 | 240  | 69  | 61  | 70  | 82  | 110 |
| 17       | 184  | 258  | 96  | 139 | 94  | 61   | 139 | 102 | 158  | 65  | 35  | 112 | 89  | 93  |
| 66       | 148  | 168  | 108 | 119 | 76  | 49   | 111 | 69  | 186  | 82  | 26  | 78  | 64  | 84  |
| 74       | 196  | 414  | 98  | 125 | 84  | 81   | 166 | 128 | 112  | 64  | 46  | 40  | 94  | 81  |
| 20       | 126  | 259  | 106 | 148 | 130 | 73   | 140 | 115 | 177  | 78  | 38  | 107 | 45  | 101 |

Mean 174.1 312.3 99.0 161.6 91.8 58.9 149.4 114.6 148.2 80.0 51.0 80.9 86.7 93.4
STD 43.9 146.5 27.7 39.8 30.0 12.1 26.2 30.5 56.7 22.1 16.1 33.4 19.7 14.1
CV (%) 25.2 46.9 28.0 47.2 32.7 20.6 17.5 26.6 38.2 27.7 31.5 41.3 22.8 15.1

STD = standard deviation, SED = standard error of difference, CV = coefficient of variation, S1 = site 1 (Bvumbwe), S2 = site 2 (Chitedze), S3 = site 3 (Makoka), Y1 = year 1 (2017/18), Y11 = year 2 (2018/19), NRP = number of racemes per plant, NPP = number of pods per plant, see genotype codes (G1–G81) in Table 1.
Table 10. Mean values for grain yield and hundred seed weight among the ten top best and five bottom performing genotypes after evaluating 81 genotypes in six environments in Malawi.

| Genotype | Y1 | Y11 | Mean | Y1 | Y11 | Mean |
|----------|----|-----|------|----|-----|------|
|          | S1 | S2  | S3   | S1 | S2  | S3   |
| Top Ten Genotypes | 21 | 0.9 | 2.3 | 2.4 | 1.3 | 1.7 | 1.8 | 16.0 | 16.5 | 10.0 | 10.5 | 12.5 | 15.5 | 13.5 |
|          | 43 | 1.7 | 1.6 | 1.8 | 1.6 | 1.9 | 1.7 | 17.0 | 14.0 | 14.0 | 17.0 | 22.5 | 13.0 | 16.3 |
|          | 51 | 1.8 | 2.1 | 2.1 | 1.7 | 1.7 | 1.7 | 16.5 | 17.5 | 14.5 | 18.5 | 21.5 | 13.5 | 17.0 |
|          | 30 | 2.3 | 1.6 | 1.2 | 1.2 | 1.4 | 1.8 | 17.5 | 17.0 | 15.0 | 16.0 | 16.0 | 12.0 | 15.6 |
|          | 45 | 1.5 | 0.9 | 1.4 | 1.5 | 2.3 | 1.9 | 18.4 | 19.0 | 15.5 | 16.0 | 16.5 | 18.0 | 17.2 |
|          | 81 | 1.3 | 0.5 | 1.6 | 1.5 | 2.3 | 2.3 | 16.9 | 15.0 | 19.0 | 15.0 | 11.0 | 14.0 | 15.5 |
|          | 17 | 1.1 | 0.7 | 1.4 | 2.5 | 3.0 | 1.5 | 18.5 | 14.0 | 11.0 | 17.5 | 20.0 | 15.5 | 16.1 |
|          | 66 | 2.4 | 1.5 | 1.2 | 1.2 | 1.4 | 1.5 | 15.5 | 15.0 | 17.5 | 15.0 | 17.5 | 13.5 | 15.8 |
|          | 74 | 2.2 | 1.6 | 1.1 | 1.0 | 1.1 | 1.8 | 15.4 | 14.5 | 15.5 | 16.9 | 20.0 | 13.5 | 15.8 |
|          | 20 | 1.2 | 0.9 | 1.7 | 1.7 | 1.2 | 1.4 | 16.0 | 12.5 | 15.0 | 18.5 | 15.0 | 14.0 | 15.2 |

| Bottom Five Genotypes | 39 | 0.4 | 0.4 | 1.1 | 1.1 | 1.2 | 0.9 | 0.8 | 15.5 | 14.5 | 14.5 | 16 | 15 | 16 | 15.3 |
|                       | 13 | 0.8 | 0.2 | 0.5 | 1.4 | 0.5 | 0.3 | 0.6 | 12.5 | 15 | 14 | 15 | 16.5 | 16 | 14.8 |
|                       | 50 | 0.9 | 0.5 | 0.4 | 0.5 | 0.4 | 0.7 | 0.6 | 13 | 10.5 | 7.5 | 21 | 19 | 14.5 | 15.9 |
|                       | 42 | 0.6 | 0.4 | 0.9 | 0.5 | 0.4 | 0.4 | 0.5 | 12 | 12.5 | 14 | 19 | 20 | 14.5 | 15.3 |
|                       | 20 | 0.8 | 0.3 | 0.4 | 0.5 | 0.3 | 0.5 | 0.5 | 13 | 16.5 | 14.5 | 17.5 | 15.7 | 14 | 15.5 |

Mean 1.1 0.6 1.3 1.3 1.5 1.3 1.2 15.9 13.9 13.5 17.6 12.9 14.2 14.7
STD = standard deviation, SED = standard error of difference, CV = coefficient of variation, S1 = site 1 (Bvumbwe), S2 = site 2 (Chitedze), S3 = site 3 (Makoka), Y1 = year 1 (2017/18), Y11 = year 2 (2018/19), GYD = grain yield (t ha⁻¹), HSWT = 100 seed weight (g), see genotype codes (G1–G81) in Table 1.

3.4. Correlation Analysis among Phenotypic Traits

Assessed traits exhibited variable degrees of associations with grain yield (Table 11). Grain yield was moderately correlated with HSWT (r = 0.50, p < 0.01). A number of secondary traits exhibited variable pairwise correlations. DTF and DTM exhibited the strongest correlation (r = 0.79, p < 0.01). There were moderate correlations between DTF and PH (r = 0.44, p < 0.01), NPB and NSP (r = 0.41, p < 0.01), and DTM and PH (r = 0.41, p < 0.01). Relatively, HSWT exhibited weak correlations (r < 0.30) with NPB and NPP.

Table 11. Phenotypic correlation coefficients among the ten quantitative traits of 81 pigeonpea genotypes evaluated in six environments.

| Trait | DTF | DTM | PH | NPB | NSB | NRP | NPP | NSP | GYD | HSWT |
|-------|-----|-----|----|-----|-----|-----|-----|-----|-----|------|
| DTF   | 1   | 0.787** | 0.442** | 0.069 | 0.006 | 0.063 | 0.121 | −0.134 | 0.232* | −0.021 |
| DTM   | 1   | 0.409** | 0.037 | 0.034 | 0.121 | −0.020 | 0.131 | 0.023 |
| PH    | 1   | 0.057 | 0.149 | 0.249* | 0.190 | −0.123 | 0.123 | 0.021 |
| NPB   | 1   | 0.044 | 0.261* | 0.145 | 0.406** | 0.174 | 0.350** |
| NSB   | 1   | 0.024 | 0.152 | −0.101 | 0.214 | 0.090 |
| NRP   | 1   | 0.191 | 0.262* | 0.177 | 0.124 |
| NPP   | 1   | 0.099 | 0.354** | 0.307** |
| NSP   | 1   | 0.051 | 0.173 |
| GYD   | 1   | 0.498** |
| HSWT  | 1   |       |

**. Correlation is significant at the 0.01 level, *. Correlation is significant at the 0.05 level (2-tailed), DTF = days to 50% flowering, DTM = days to 75% maturity, PH = plant height, NPB = number of pods per plant, NSB = number of secondary branches per plant, NRP = number of racemes per plant, NPP = number of primary branches per plant, GYD = grain yield, HSWT = 100 seed weight.
3.5. Nonlinear Principal Component (PC) and Cluster Analysis

The nonlinear principal component analysis was performed to identify the most discriminative variables among the pigeonpea genotypes. A total of 98% of the variation explained by the qualitative and quantitative traits were explained by the first three principal components (Table 12). In general, traits such as GYD, DTF, DTM, leaf hairiness (LH), leaf shape (LS), and NRP contributed much to the phenotypic variation in the PCs. However, GYD, LH, NPP, HSWT, and NSP were the highest contributors (with contributions of 0.86, 0.63, 0.63, 0.51, and 0.45, respectively) on PC1. The second principal component accounted for 73% of the total variation, with NRP and pod form (PF) being the highest (0.74 and 0.62) positive contributors. Conversely, traits including LS, flowering pattern (FP), and flower main color (FMC) negatively correlated with PC2 exhibiting negative (−0.63, −0.57, and −0.44, respectively) PC scores. DTF and DTM were the positive contributors to the observed phenotypic variation on PC3 with PC loadings of 0.83 and 0.79, respectively.

Table 12. Principal components showing variation and contribution by 24 phenotypic traits among 81 pigeonpea genotypes assessed in six environments in Malawi.

| Trait      | Dimension |
|------------|-----------|
|            | 1         | 2         | 3         |
| FMC        | −0.026    | −0.435    | −0.269    |
| FP         | 0.016     | −0.568    | 0.050     |
| FSC        | −0.101    | −0.172    | 0.291     |
| FSP        | 0.357     | −0.095    | −0.080    |
| GH         | −0.077    | 0.227     | 0.151     |
| LH         | 0.629     | −0.435    | −0.112    |
| LS         | −0.386    | −0.626    | 0.143     |
| PC         | 0.010     | 0.175     | −0.310    |
| PF         | 0.203     | 0.616     | 0.043     |
| SCP        | −0.050    | 0.327     | −0.235    |
| SEC        | −0.038    | 0.236     | −0.345    |
| SMC        | 0.020     | −0.144    | −0.060    |
| SSH        | 0.082     | −0.134    | 0.186     |
| STC        | −0.042    | 0.000     | 0.023     |
| DTF        | 0.186     | −0.069    | 0.827     |
| DTM        | 0.236     | −0.190    | 0.793     |
| PH         | 0.294     | −0.357    | 0.118     |
| NPB        | 0.037     | 0.208     | 0.239     |
| NSB        | 0.160     | 0.398     | 0.204     |
| NPP        | 0.626     | 0.086     | −0.073    |
| PL         | 0.252     | 0.353     | 0.104     |
| NRP        | 0.001     | 0.735     | −0.117    |
| NSP        | 0.476     | 0.076     | −0.075    |
| HSWT       | 0.508     | 0.219     | −0.084    |
| GYD        | 0.863     | 0.146     | −0.109    |
| Eigen value| 3.404     | 2.967     | 2.163     |
| Variance % | 39        | 34        | 25        |
| Cumulative | 39        | 73        | 98        |

DTF = days to 50% flowering, DTM = days to 75% maturity, PH = plant height, NPB = number of primary branches, NSB = number of secondary branches per plant, NRP = number of racemes per plant, NPP = number of pods per plant, GYD = grain yield, HSWT = 100 seed.

Figure 2 shows the variable correlation plot showing positive association between PC1 and DTF traits such as DTM, GYD, HSWT, NRP, plant height (PH), and pod length (PL). Conversely, seed eye color (SEC), pod color (PC), number of secondary branches per plant (NSB), and FMC exhibited negative associations with PC1. Quantitative traits such as plant habit (PH), NPP, HSWT, DTF, DTM, NRP, and GYD were positively correlated to each other as exhibited by their vectors, which were in the same direction and separated by acute angles between them. Similarly, the qualitative traits such as SEC, PC, and FMC were positively correlated to each other. However, the quantitative traits were positively correlated with GYD, while the qualitative traits were negatively correlated with GYD.
Assessment of the phenotypic diversity using morphological attributes delineated the genotypes into three distinct clusters (Figure 3). The first cluster had the highest number (51) of genotypes. The second cluster had 27 genotypes, and the third cluster had three genotypes. However, the composition of genotypes in all the three clusters consisted of mixtures of landraces, breeding lines, and cultivars.
4. Discussion

The current study evaluated 81 pigeonpea genotypes across six environments to assess the genetic diversity and yield stability, and to select complementary and unique genotypes for breeding. The genotypes exhibited wide and significant variation in qualitative traits (Table 4), which indicated that the tested germplasm could harbor important genetic variation that underpins the morphological variation. Similarly, [16] reported significant variation in qualitative traits among pigeonpea accessions sourced from ICRISAT’s international genebank. The variation in qualitative traits such as growth habit and seed color is important for breeding cultivars that meet farmer expectations. For instance, the variation present in growth habit is important to identify genotypes with compact growth habit for intercropping to maximize space utilization and productivity in moisture-limited environments. Farmers often intercrop pigeonpea with cereal crops such as maize and sorghum, and legumes such as groundnuts. Hence, pigeonpea genotypes with a spreading growth habit may not be suitable for mixed cropping systems [17]. The diversity in pigeonpea seed color helps to identify genotypes that are preferred by local farmers. For instance, farmers in Malawi prefer pigeonpea varieties with a cream seed color, which they associate with good cooking quality. Similar findings were reported by [18], who reported a predominance of cream and light gray pigeonpea varieties in Benin, reflecting the farmers’ color preferences. Knowledge of variability in qualitative traits among the accessions and understanding farmer preferences are important as a basis for the development of direct breeding objectives and appropriate breeding strategies.

The significant genetic variation exhibited in the quantitative traits (Table 5) highlights the genetic diversity available for exploitation during cultivar development. The genotype performances were also affected by significant genotype \( \times \) environment interactions, suggesting that genotype performances were not consistent in all the environments. Genotypic variation is underpinned by differences in genetic constitution among the genotypes, which is important for crop improvement [19]. The environment influences phenotypic expression through variation in factors such as temperature, humidity, and soil fertility. The significant impact of the environment on phenotypic expression is known to reduce genotype–phenotype correlation [20], which complicates the identification of stable and superior genotypes. However, significant genotype \( \times \) environment interaction on yield and yield components of legumes such as common bean, cowpea, and pigeonpea has been previously reported [21–23]. In the present study, the genotypes that matured early were shorter with low numbers of branches and pods per plant and low grain yields compared to the medium to late maturing genotypes that grew taller, produced more branches and pods per plant, and had higher grain yields. Similarly, [24] reported that cultivars with higher numbers of primary branches, secondary branches, number of pods per plant, and taller plant height had higher grain yields.

There was limited genetic variation among pigeonpea landraces, cultivars, and breeding lines in this study (Table 6). This could be attributed to gene flow arising from the exchange of germplasm between Malawi and Tanzania. In addition, there could be high level of genotype relatedness since the breeding lines and cultivars were developed from the landraces collected from Malawi and Tanzania by ICRISAT. However, the genotype performance in terms of days to maturity and plant height were affected by significant genotype \( \times \) environment interactions (Tables 7 and 8), suggesting that genotype performances were not consistent in all the environments. This could be because the landraces, cultivars, and breeding lines belong to three maturity groups: early, medium, and late duration. The early maturity exhibited by the ICRISAT genotypes could be a result of selection for earliness at ICRISAT in Kenya, which has advanced pigeonpea breeding programs and has developed a number of elite breeding lines that have been distributed in several East and Southern African countries for evaluation. The TARI and DARS genotypes are comprised of landraces and cultivars that are medium to late maturing. Similarly, [21] also reported that traditionally grown pigeonpea cultivars and landraces are represented by varieties from medium to long maturity groups (150 to 280 days), which are high yielding but very sensitive to photoperiod.
The positive and moderate correlation between GYD and HSWT ($r = 0.50$, $p < 0.01$) (Table 11) indicated that HSWT could be used for the direct selection for GYD. The moderate positive correlation between DTF, DTM, and PH revealed that selection for earliness can be based on the plant height. Although pigeonpea is relatively drought-tolerant, there is a need to develop early flowering and maturing cultivars to fit in the cropping cycles of sub-Saharan Africa, which are becoming progressively shorter due to climate change. The positive correlations exhibited by most secondary traits show that multiple trait selection would be possible. However, the weak correlations among the traits would result in an inefficient selection or low genetic gains. A strong correlation ($r = 0.858$) between grain yield and the number of pods per plant was reported by [25]. In addition, [26] reported moderate to weak correlations between grain yield and days to 50% flowering ($r = 0.58$), days to maturity ($r = 0.59$), and plant height ($r = 0.42$). Conversely, [27] and [28] reported a negative association between 100 seed weight and grain yield. The significant relationship between DTF, DTM, HSWT, PH, NPP, and GYD is useful when selecting for high grain yield [16]. Direct selection for these traits would result in yield improvement in pigeonpea.

The nonlinear principal component analysis enabled the identification of important traits with high variability among the genotypes. In this study, GDY, DTF, DTM, NPP, NRP, LH, HSWT, and NSP were identified as the most important traits due to their high contribution on PC1 and PC2 (Table 12). This suggests that these traits are useful for selection. Accessions that exhibit high and desirable mean performances based on the target traits would be selected for improvement. Other reports indicated that trait contribution to different PCs varies with genetic diversity within the tested germplasm and the number of traits evaluated [16,25]. The results further revealed that DTF, NPP, NPB, NSB, PH, PL, and HSWT are important secondary traits for the indirect selection for GYD due to their positive association with GYD and their high contribution on the PCs.

The cluster analysis delineated the accessions into three groups (Figure 3), suggesting the presence of considerable genetic variation among the genotypes. However, a mixture of breeding lines, landraces, and cultivars in each group could be attributed to the geographical proximity between Malawi and Tanzania (where some of the landraces were collected). The level of natural outcrossing in pigeonpea is very high and varies from 5 to 70% depending on the prevailing weather conditions and insect activities for pollination [29]. In addition, the breeding lines from ICRISAT were developed using some parents selected from the landraces from Tanzania and Malawi. East Africa is known as a center of diversity for pigeonpea—hence the close genetic relatedness. The present finding is in agreement with [30], who reported little variation among the cultivated pigeonpea collected in Africa based on diversity array technology (DArT) markers.

5. Conclusions

The study examined 81 pigeonpea genotypes for their diversity and yield stability. The genotypes exhibited a wide genetic variation in qualitative traits such as growth habit, flower main color, flower streak pattern, pod color, and seed traits. The combined analysis revealed significant genotype × environment interaction effects for most traits, suggesting the need for selection for specific adaptation. A lack of significant variation in quantitative traits among landraces, cultivars, and breeding lines indicate that there is potentially high gene flow among the different categories of germplasm, which could present genetic bottlenecks during breeding. Traits such as GDY, DTF, DTM, NPP, NRP, HSWT, LH, and NSP with high scores on PC1 and PC2 are useful selection indices for pigeonpea improvement. Accessions that exhibited high and desirable mean performances in the target traits such as early maturing (MWPLR 14, ICEAP 01170, ICEAP 871091, ICEAP 01285) and high yielding (Kachangu, MWPLR 16, TZA 5582, No. 40, and MWPLR 14) would be recommended as parental lines for the breeding program. The genetic diversity analysis using morphological traits has enabled the identification of promising parents and heterotic clusters for breeding.

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the experiments and wrote up the manuscript. All authors have read and agreed to the published version of the manuscript.

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