Phenotyping of Selected Kenyan *Passiflora edulis* Varieties and Their Hybrids Based on Quantitative Morpho-agronomic Traits

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Abstract

The passion fruit was introduced to Kenya through Europe in the 1920s, and only gained significant economic importance in the 1990s. Several species of the genus Passiflora present potential superior characteristics for genetic breeding of the passion fruit germplasm. Quantitative morpho-agronomic traits are important in passion fruit breeding since they allow for discrimination of varieties for important parameters that are useful in selection of fruit for market. The present study aimed at evaluating existing phenotypic variation between the Purple and Brazil varieties as well as their hybrids, developed by the Kenya Agricultural and Livestock Research Organization (KALRO). Seven quantitative morpho-agronomic traits were targeted with replication per plant and variety. Principal component technique and cluster analysis statistical tools of Minitab 17.0 software were used to discriminate the accessions under study based on the morpho-agronomic traits. Both the dendrogram and scatter plot clustered accessions based on their respective varieties, an indication of phenotypic relatedness within varieties. The results of this study will supplement the current body of knowledge on Kenyan passion fruit breeding.

Introduction

The passion fruit belongs to the Passifloraceae family which comprises of about 530 species. The Passifloracea family originated from tropical regions of America such as Brazil which has a distribution of approximately 150 species of this family [1]. The passion was introduced to Kenya through Europe, and only gained significant economic importance in the 1990s when bulk export of fruits and vegetables to the international markets was commenced [2,3].

Passion fruit farming is faced with low productivity due to factors such as pests and pathogens, inadequate techniques of cultivation, heterogeneity of the orchards and reduced number of improved accessions available to the producers [4,5]. Several species of the genus *Passiflora* present potential superior characteristics for genetic breeding of the passion fruit germplasm. Such characteristics include resistance to pathogens such as Cowpea aphid-borne mosaic virus(CABMV), self-compatibility, better adaptation to adverse climatic conditions, desirable physical-chemical characteristics for the fruits market [6,7]. Other factors affecting breeding programs include incapability to maintain germplasm banks as well as, the lack of both agronomic and biological information [8].

Quantitative morpho-agronomic traits are important in passion fruit breeding since they determine important parameters for selection of passion fruit for market. For example, the fruit form index which is an important aspect of classification and standardization in passion fruit market, is determined by longitudinal fruit length and equatorial diameter. The fruit form index influences the acceptance and judgment of produce in some markets [9]. For fresh consumption, passion fruit is classified by size and external aspect, given that consumers prefer oval fruits [10-12].

Studies of morphological diversity of the genus *Passiflora* are relatively new with previous studies being limited to taxonomic descriptions [13]. Characterization of a segregating population using morpho-agronomic descriptors is crucial to breeding because of availability of wide variability that remains unknown or exploited. Furthermore, it allows the identification of superior accessions for advanced generations in the breeding program [14].

Multivariate methods, such as the Canonical variables, Principal components, and Cluster analyses are useful in predicting genetic divergence of different accessions. The choice of the multivariate method to use depends on the desired breeder precision as well as the ease of analysis and data acquirement [15,16]. Despite the global gains in phenotypic studies of passion fruit, there is no existing information on morphological studies of Kenyan passion fruit varieties especially considering that several varieties are new. This study employed principal component technique and cluster analysis to evaluate existing phenotypic variation existing between the Purple and Brazil varieties as well as their hybrids, developed by the Kenya Agricultural and Livestock Research Organization (KALRO).

Materials and Methods

Fully ripe fruits as well as fully expanded leaves were collected from hybrid passion fruit accessions belonging to the following varieties; KPF 4, KPF 11, KPF 12 and parent varieties; Brazil, and purple. These materials were collected from the KALRO orchards at the Centre for Horticultural Crops-Kandara. Replication was done, with five samples

per plant and three biological replicates spread across fifteen weeks and all samples assigned to populations based on the respective variety.

Leaf and fruit based agronomic descriptors developed by CARIAD, IPGRI (now Bioversity International) for phenotypic characterization of *Passiflora edulis* were used in this study. The morpho-agronomic traits used in this study were; leaf length (LL), leaf width (LW), fruit length (FL), fruit diameter (FD) and seed length (SL) whose data was recorded in centimeters, with all measurements being taken using a digital caliper. The other trait studied was fruit mass (FM) which was taken using an analytical balance at Kenyatta University Plant Transformation Laboratory and recorded in grams. Seed length was measured after extraction of seed and drying with paper towel under shade. The recorded data was tabulated on a spread sheet and used for phenotypic analysis using the Minitab software version 17. The mean values for all the replicates per plant were computed and used for further analysis in-order to discriminate the various accessions to the respective varieties as well as to determine how closely or distantly related the accessions and varieties were from each other. Eigen values, contribution of each component to total variation and a scatter plot were generated using the principal component tool while a dendrogram was constructed using Eucledian distance tool of the Minitab 17 software.

Results

Principal component analysis (PCA)

The principal component technique was used to indicate the contribution of each trait to total variation of the various accessions. The first three principal components had eigen values of 3.94, 1.61 and 0.77 respectively. These principal components accounted for a cumulative more than 90% variation in the studied accessions and as such were sufficient for among the seven traits under study. The respective contribution of the first three principal components to total variation was 56.3%, 23.1% and 11.0%. There was positive correlation of all eigen values of each trait for the first three principal components and thus the agronomic traits were useful in discrimination of various accessions. The most positive correlation was that for seed length in the second principal component while the lowest correlation value was for the same trait on the first principal component (Table 1).

Cluster observation through a scatter plot

Cluster observation through a scatter plot was used to distinguish the various accessions and varieties based on the overall influence of all the seven quantitative traits. The scatter plot of the accessions under study based on the two main principal components; PC1 (56.3%) and PC2 (23.1%) discriminated accessions into various populations. The graphical analysis of the two main coordinates revealed genetic dissimilarity among accessions belonging to the population KR11 (KPF-11). However two accessions from this population were located on the same graphical location, but graphically far from the remaining accessions in this population. This was the similar scenario on accessions of KR12 (KPF-12). One accession was closer to accessions of KPF-11 compared to other accessions within KPF-12. On the other hand, there was homogeneity in clustering amongst accessions of the purple variety. The other population that had close clustering on the scatter plot was the coastal variety (KRC). From the scatter plot, it was also observed that accessions from both parent varieties (Coastal and Purple) were closer compared to the hybrid accessions (Figure 1).
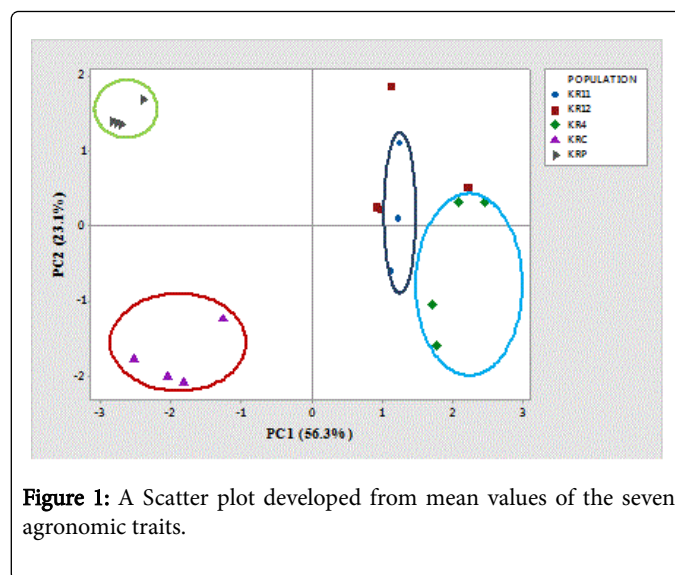

Figure 1: A Scatter plot developed from mean values of the seven agronomic traits.

TRAIT	PC1	PC2	PC3
Eigen value	3.94	1.61	0.77
% Variance	56.3	23.1	11
Cumulative Variance	56.3	79.4	90.4
Leaf Length	0.4	0.39	0.23
Leaf Width	0.31	0.28	0.2
Fruit Length	0.48	0.34	0.24
Fruit Width	0.47	0.19	0.21
Rind Thickness	0.36	0.48	0.08
Fruit Mass	0.41	0.21	0.4
Seed Length	0.05	0.7	0.2

Table 1: Results of principal component analysis for the accessions under study, targeting 7 agronomic descriptors.

Phylogenetic analysis

The accessions were discriminated into two major clusters; I and II each comprising two sub-clusters (Figure 2). Each of the sub-clusters in cluster I was further been divided into several phylogenetic divisions carrying various accessions. From the dendrogram, all accessions in each population were clustered closer together. However, despite clustering closer to each other, some accessions were placed in clusters bearing accessions from other populations. For example, despite clustering next to other accessions in the population (KPF-11), accession KR11-4 was in the same cluster with KR12-4, which belongs to the KPF-12 population. This closeness of these two accessions confirms the findings of the scatter plot. The accessions from the Coastal population are closer to those of the Purple population on the dendrogram. These results are similar to those in the scatter plot. Some accessions have similarity values closer to 100%. Such combinations include KR11-2 vs. KR11-3; KR12-1 vs. KR12-3; KRP-4 vs. KRP-3 (Figure 2).
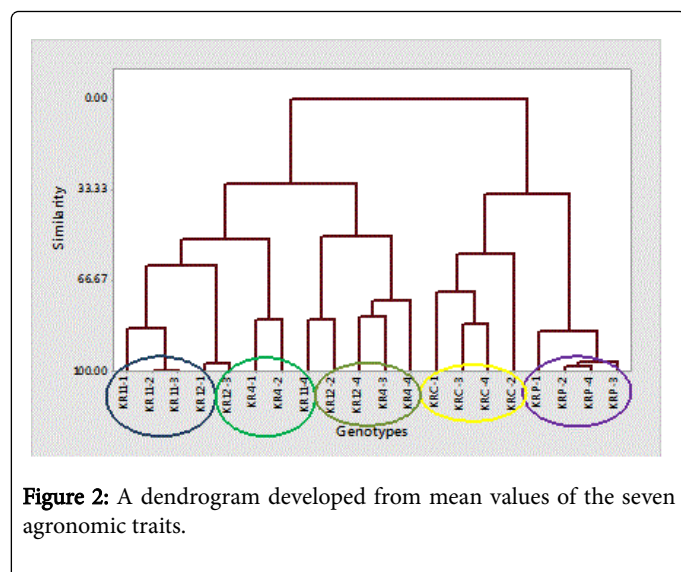
Figure 2: A dendrogram developed from mean values of the seven agronomic traits.

Discussion

Plant breeding requires proper knowledge of the underlying genetic variation among the varieties involved. Phenotyping is one useful method that has been used over time in the understanding of the genetic variations among the respective varieties.

The finding that the first principal component was responsible for much of the total variation (56.3%) is an indication that much the phenotypic differences of the accessions under study were mainly contributed by this component. The principal components analysis is useful in that it allows the evaluation of importance of each agronomic trait under study, over total variation. This enables identification and elimination of less discriminating characters [17]. In the current study, all the traits under evaluation had positive correlation with the first three main principal components and were therefore useful and effective in discrimination of the accessions under study. The highest correlation value of seed length (0.7) indicates that this trait was the most reliable for phenotypic discrimination of the accessions under study. The finding that this value was in the second principal component can be interpreted to mean that the variation based on this trait resided in the second principal component. Further, the relatively higher correlation value of this trait in the second principal component compared to that in the first principal component can be interpreted to mean the reliability of the second component in discrimination based on this trait. The overall low values for the each trait eigen can be attributed to the low number of traits under evaluation [18].

On the other hand, clustering of related accessions together on the scatter plot indicates their genetic relatedness, and sufficiency of the seven agronomic traits in discrimination of the various populations. Clustering of accessions from the purple variety closer to the Coastal accessions is evidence of the underlying phenotypic relatedness of the two varieties, despite their underlying genetic variability [19]. The closer graphical existence of accessions of the two parent varieties also indicates that they were phenotypically unique compared to the hybrid accessions. This could be attributed to known phenotypic variation, where hybrids are known to have higher measurements of agronomic traits such as leaf length and fruit length [20].

Conclusion

From the current study, there was sufficient discrimination based on the seven morpho-agronomic descriptors. The study also confirmed the findings by Santos et al. [20] that on average, hybrids gain higher quantitative agronomic values compared to parents.

Acknowledgement

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