

Phenotypic Characterization of Selected Kenyan Purple and Yellow Passion Fruit Genotypes Based on Morpho-Agronomic Descriptors

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Abstract

Phenotypic characterization is crucial in determination of variability of hybrid varieties and their parents. The objective of this study was to determine phenotypic variation among known genotypes of both parent and KPF hybrids, as well as genotypes collected mainly from Embu County which is one of the growing areas of hybrid varieties developed by KALRO. Analysis was done using Minitab 17.0 software. Six out of seven morpho-agronomic descriptors evaluated, showed significant differences among the genotypes under study. A dendrogram based on the 7 morpho-agronomic descriptors discriminated the genotypes into two main clusters with one main cluster (II) carrying only 2 genotypes. Principal component analysis corroborated the findings of the dendrogram, distantly placing the two genotypes further from the other genotypes.

Keywords: Phenotypic; Morpho-agronomic descriptors

Introduction

The passion fruit is considered a high value crop in Kenya, ranking third (8%) after avocado (62%) and mango (26%) in terms of foreign exchange earnings for the country [1]. Kenya is considered as the market leader of fruit juice exports in East Africa and is also listed among the large producers of passion fruit globally with its major regional market being Uganda [2,3].

If production is carried out efficiently, passion fruit enterprises have good returns, with a gross margin of Ksh. 629,850 per hectare (approximately 6298 USD) [4]. After orchard establishment, production is expected to increase subsequently from the first to the third year and can therefore be used productively during this period [5]. The relatively high gross margin makes passion fruit a high value crop with potential for poverty alleviation since it is mainly grown by farmers owning 0.5 - 2 acres of land [6,7]. Passion fruit farming is also preferred due to the fast maturity period of 9 months (flowering period) and the minimal labor and land space requirements [8].

The passion fruit is native to the Southern Brazil, Paraguay and North Argentina, thus this region is considered as the main center of genetic diversity of the *Passiflora species* [9,10]. The plant was introduced to Kenya by the white settlers in the early 20th century after which cultivation was limited to plantations owned by the European settlers [11,12]. The passion fruit only gained significant economic importance as an income generating crop in the 1990s when Kenya started bulk export of fruits and vegetables to the international markets [13].

Passion fruit production in Kenya had been increasing gradually from the beginning of the 21st century until 2007 when it started to decline. There was notable increase in production between 2005 and 2007 when production doubled after which it declined in 2008 with fluctuations in production through the subsequent years. This decline is attributed to perennial challenges that lead to the sector operating below potential and as such, lagging behind other global competing producers like Australia and South Africa [14,15].

Insufficient knowledge on good agricultural practices as well as pest and disease management as well as the inaccessibility of pathogen-free planting materials are some of the major challenges that face passion fruit production [16,17]. Changing climate patterns are also

contributing to the decline in passion fruit production by favoring population densities and emergence of new species of pests [16].

There is need to identify and document existing and new passion fruit varieties especially those perceived to have superior traits such as tolerance to *Fusarium*. A description of variety should help in resolution of identification conflicts that may arise during registration and protection of cultivars [18]. Morphological and agronomic characterization of germplasm as well as new varieties using descriptors is a key consideration in breeding programs. The term descriptor is used to refer to a character or attribute that is used to discriminate between varieties, with redundant descriptors being seen during evaluation of many traits and thus many descriptors are judged accordingly as unnecessary due to their low contribution to variability [18-20]. Elimination of redundant descriptors is an important strategy in that it ensures reduction of the work required to collect data without causing significant losses in genotype discrimination [20,21].

Some of the techniques used to determine the descriptors with high information content include regression [22], discriminant analysis [23] as well as principle components [24]. The distribution of variation is associated with the nature and number of characters that are used in the analysis and is concentrated in the first components only when few agronomically important traits are evaluated [25].

The current study aimed at characterizing hybrid cultivars that were recently developed by KALRO as well as their parents, using quantitative morpho-agronomic descriptors.

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Received April 07, 2016; Accepted May 25, 2016; Published June 05, 2016

Citation: Matheri F, Mwangi M, Runo S, Ngugi M, Kirubi DT, et al. (2016) Phenotypic Characterization of Selected Kenyan Purple and Yellow Passion Fruit Genotypes Based on Morpho-Agronomic Descriptors. Adv Crop Sci Tech 4: 226. doi:10.4172/2329-8863.1000226

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Materials and Methods

Collection of plant material

Fully ripe fruits and fully expanded leaves were collected from healthy vigorously growing vines of KPF 4, KPF 11, KPF 12, Brazil, and purple passion fruit genotypes in KALRO- Kandara. All samples were assigned to populations based on the variety. Samples were also collected from different geographic locations in Embu County, Kenya and Kenyatta University School of agriculture farms; all orchard ranging between 2-3 years since establishment. Replication was done five times per plant for each trait under study with three biological replicates covering the two main seasons in Kenya.

Morpho-agronomic descriptors

Seven quantitative morpho-agronomic traits developed by IPGRI (now Bioversity International) were evaluated in this study. These traits included; leaf length, leaf width, fruit length, fruit diameter and seed length whose data was recorded in centimeters. Fruit mass was recorded in grams.

Data management and analysis

The data for all the three biological replicates for each genotype were combined and analyzed statistically using Minitab 17.0 software. The differences in means of the 7 traits were separated through ANOVA followed by Tukey's post hoc. Cluster analysis was used to develop a dendrogram and scatter plot for examination of the phenotypic relatedness among the genotypes under study.

Results

The measurement of the leaf, fruit and seed traits for the 54 passion fruit genotypes and their mean values are shown in Appendix 1. From the tabulated results, KR4-1 which belongs to the KPF-4 variety, had the highest value of leaf length (14.82 cm) while KRC-3 which was a coastal yellow passion fruit variety had the lowest value (8.60 cm). In relations to the leaf width, there was no significant difference among all the genotypes although the data range indicated wide variation. KR4-1 had the highest mean value of leaf width (13.36 cm) while genotype JSE-N3 had the lowest mean value (9.62 cm) (Appendix 1).

On the other hand, longitudinal fruit length also had wide variations

ranging from 5.10 cm (PKS-TD1) to 10.58 cm (KR12-3). Equatorial fruit diameter ranged from 3.74 cm (KMD-TD1) to 10.18 cm (KR12-1). There was no significant difference among the mean fruit diameter for most genotypes. Fruit Rind thickness also had wide variation and ranged from, 0.52 (SGD-TD1) to 0.86 cm (KR12-1). In relations to seed length, there was variation among the genotypes, ranging from 0.36 cm (KR12-4) to 0.78 cm (PKS-TD1). There was also wide variation in fruit mass among the populations. The mean fruit mass ranged from 28.62 g (BMM-TD2) to 121.82 g (KR11-1) (Appendix 1).

Cluster analysis

The genotypes were discriminated into two major clusters; I and II with cluster I comprising two sub-clusters as shown in Figure 1. Each of the sub-clusters in cluster I was further been divided into several sub-clusters carrying various genotypes. From the dendrogram, most of the known genotypes were clustered together. For example, KRP-1, KRP-2, KRP-3 and KRP-4, all purple genotypes were clustered together. KR11-1, KR11-2, KR11-3 and KR11-4 were also clustered together at a similarity value close to 100%. However some of the known genotypes lacked homogeneity in clustering. For example, despite Brazil genotypes; KRC-2, KRC-3 and KRC-4 being clustered close together in the tree, KRC-1 which belonged to the same variety was clustered distantly. Other known varieties with non-homogeneity in clustering were KR12 (KPF-12) and KR4 (KPF-4). Genotypes belonging to the undetermined population were clustered together with those of known populations. For example, PKS-N3 which was an undetermined genotype, clustered with the coastal genotypes (KRC-2, KRC-3 and KRC-4). SGE-N1, SNV-N1, JSE-N3, MMN-N1 clustered together with KR4-4 and KR4-1 at a similarity value close to 100%, an indication that they may be related.

Principal component analysis (PCA)

The first three Eigen values were 3.5880, 1.6130 and 1.0062 respectively. The first principal component (PC1) accounted for 51.3% of total variance, while the second principal component (PC2) accounted for 23.0%. The third principal component (PC3) accounted for 14.4% variability for the 7 morpho-agronomic traits evaluated (Table 1). There was positive correlation between the Eigen values for PC1 while those of PC2 was negatively correlated to leaf length and leaf width and positively correlated to the remaining traits. The Eigen

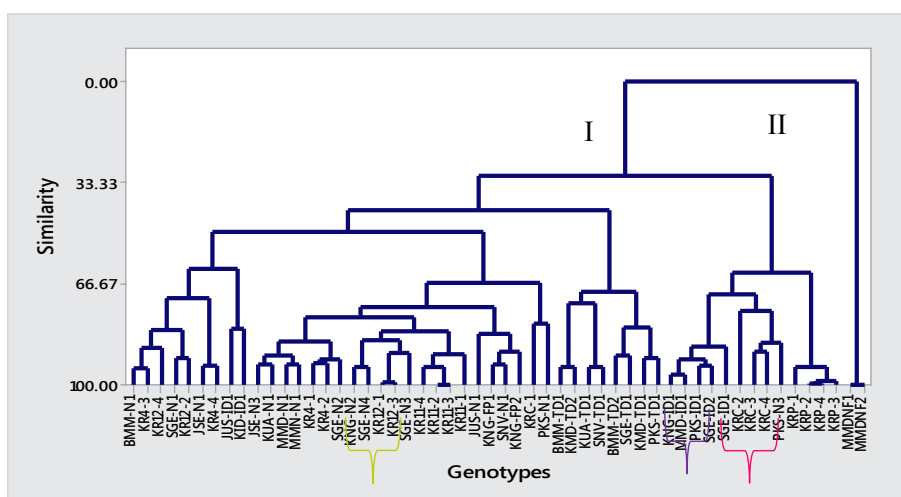


Figure 1: Euclidian distance based dendrogram developed from mean values of the 7 morpho-agronomic traits.

	PC1	PC2	PC3
Eigenvalue	3.5880	1.6130	1.0062
% Total Variance	51.3	23.0	14.4
%Cumulative	51.3	74.3	88.7
Traits	PC1	PC2	PC3
Leaf Length (cm)	0.119	-0.691	-0.015
Leaf Width (cm)	0.070	-0.597	-0.524
Fruit Length (cm)	0.511	0.036	0.095
Fruit Diameter (cm)	0.512	0.055	0.110
Rind Thickness (cm)	0.082	0.391	-0.824
Fruit Mass (g)	0.497	0.005	0.110
Seed Length (cm)	0.451	0.096	-0.118

Table 1: Eigen vectors, Eigen values, total variance and cumulative variance for 54 genotypes based on 7 morpho-agronomic traits.

value for PC3 was negatively correlated to leaf length, leaf width rind thickness as well as seed length. This value was however, positively correlated to the remaining morpho agronomic traits. The traits with negative correlation were retained in analysis since the all Eigen values for PC1 which accounted for much of the variation were positively correlated to the traits (Table 1).

Scatter plot

A scatter plot of the genotypes under study complemented the findings of the dendrogram that some of the genotypes had similarity value close or equal to 100%. For example, MMD-NF1 and MMD-NF2 which were clustered together on the dendrogram were also placed graphically on the scatter plot (Figure 2). The lack of homogeneity of clusters was also seen on the scatter plot with some of the known genotypes being on a far graphic location from the other genotypes of the same population.

Discussion

Measurement of genetic variability of passion fruit species by accessing markers such as morphological descriptors is a fundamental activity for both plant breeding and conservation programs of many species [26].

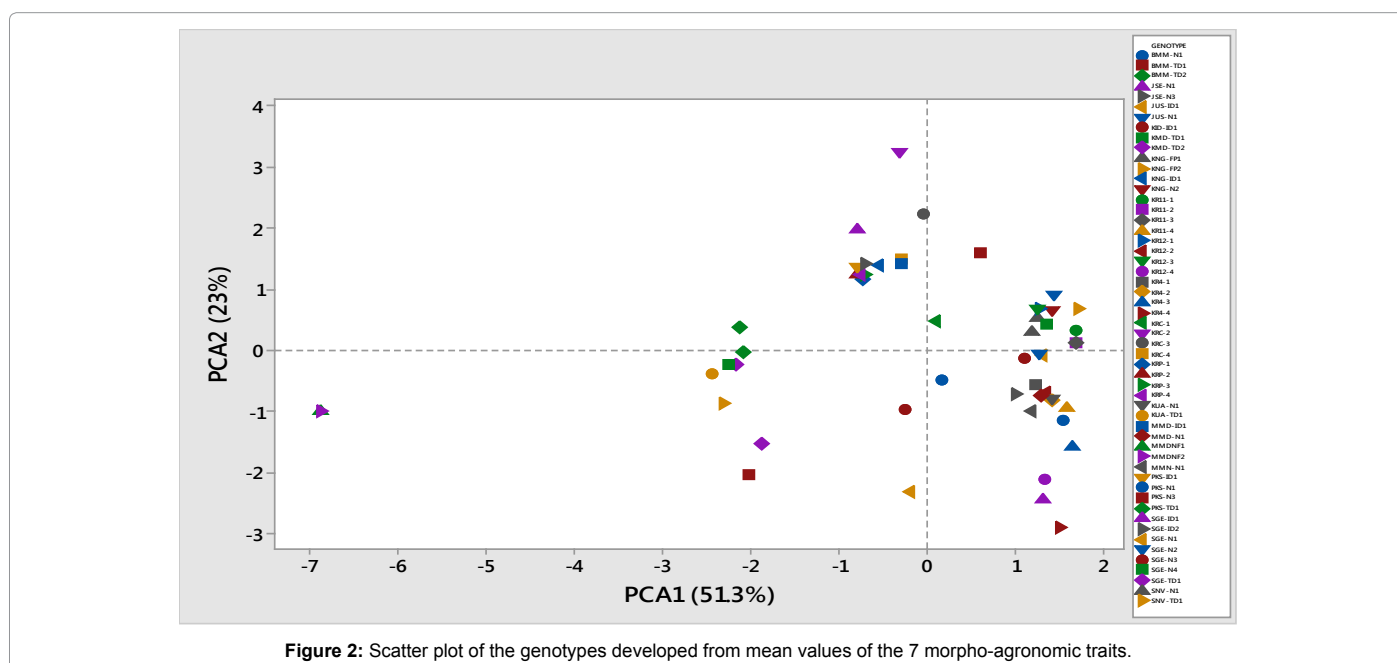
Such descriptors include fruit size, which can be described through fruit length and equatorial diameter. The size of fruit is important in the physical quality of the fruits destined for markets and industry [27].

From the tabulated results, the difference in leaf lengths of KR4-1 which belongs to the KPF-4 variety (14.82 cm) and KRC-3 which was a coastal yellow passion fruit variety (8.600 cm) can be explained by genotypic variation that is known to exist between hybrids and parent genotypes. Hybrid genotypes have been reported to have higher values for leaf length [28]. The lack of significant difference in leaf width of all the 54 genotypes indicates lack of agronomic and environmental influence on this trait.

The wide variation of seed length with an overall mean of 0.67 indicates a variation in seed fitness where the size of the seed affects fitness of the plant growing from it. This variation in seed length can be explained by difference in position on the inflorescence or the fruit [29,30]. The mean value for seed length was slightly higher than that obtained in related studies [28].

The mean value for rind thickness (0.48 cm) was lower than that obtained by Santos et al. [28]. The value was also slightly higher than that obtained in studies [30]. Conversely, the value was lower than that obtained by Silva et al. [31] and Cavalcante et al. [32]. Breeding programs seek to select genotypes with reduced rind thickness, which may be used to indicate greater amount of pulp which is regarded as a relevant factor in fruit ranking [28,33]. Therefore, based on these criteria, genotypes SGE-ID1 and SGE ID2 were favorable in terms of pulp and juice yield and can be adopted for crosses targeting higher juice and pulp yield. On the other hand, the wide variation in fruit diameter can be attributed to environmental and agronomic influence. The mean fruit diameter was equal to that obtained by Santos et al. [28] and close to that obtained by Silva et al. [31].

The wide variation in fruit length has also been reported in other studies [28,34]. The mean fruit length (8.06 cm) of the 54 genotypes was close to that obtained for *Passiflora edulis* (8.15 cm) [28] and slightly lower than the values obtained in function of the genotypes and fruit weight in passion fruit [31].



Fruit length and width are important attributes of passion fruit where higher length than in width, is the preferred fruit form for the consumer market [9]. The fruit form index is an important aspect that is useful in classification and standardization of passion fruit in the fruit market where it influences the acceptance and judgment of the product in some markets [35,36] and external aspect such as size and shape [9,37].

The results of principal component analysis indicated the contribution of each principal component to overall variation. The principal component technique is useful in phenotypic variability studies in that it allows the evaluation of importance of each trait/character of the accessions being studied over total variation, hence allowing elimination of less discriminating characters. The first principal component was responsible for much of the overall variation, having accounted for more than half (51.3%) and as such was reliable in discrimination of the genotypes based on the seven traits. The high cumulative variance obtained with only the first three principal components may be explained by the fact distribution of variation is associated with the nature and number of characters used in the study. This variation is concentrated in the first principal component especially when evaluating few agronomically important traits or certain groups such as flowers and fruits [25]. Quantitative descriptors should be discarded when they have high correlation with principal components of the lowest variance. However, none of the traits had a high correlation with the lowest variance (PC3) and as such not necessary to discard.

From the dendrogram in Figure 1; clustering of a majority of genotypes in cluster I is an indication of the great divergence among genotypes in the cluster. Discrimination of only two genotypes into main cluster II can be explained by their lack of fruit based traits, thus bringing wide variation between them and the rest of the genotypes. Their clustering at 100% similarity can be interpreted to mean that the two genotypes had common ancestry with a probability of being full siblings. The lack of homogeneity in clustering of the known genotypes can be attributed to underlying genetic basis, since the genotypes shared the same agronomic and environmental influence. Clustering of the undetermined genotype, PKS-N3, at a similarity of 100% could also be interpreted to mean that it belonged to the coastal variety.

The distribution of the genotypes on the scatter plot confirms the results of the dendrogram. The graphical position of genotypes, MMD-NF1 and MMD-NF2 confirms their wide variation compared to other genotypes. The graphical closeness of the two genotypes on the principal axis is an indication of their biological relatedness, which could be interpreted to indicate that they are biological replicates. Moreover, the graphical representation of the genotypes confirms the lack of homogeneity of the some of the known populations where some genotypes are clustering far from others.

Conclusion

Despite experiencing possible variation in environmental and agronomic conditions, this study was able to show existing morpho-agronomic variation existing between the genotypes under study. This is confirmed by the fact that the discrimination did not stratify the genotypes to the respective orchard and even plants in the same orchard could be separated. Moreover, that lack of significant difference in leaf width as well as the significant difference seen in the studied genotypes confirms, the little influence of environment and agronomic practice on the evaluated traits.

Acknowledgements

The authors wish to acknowledge the Kenya Agricultural Productivity and

Agribusiness Project (KAPAP) for funding this research work. We also thank the, Kenya Agricultural and Livestock Research Organization (KALRO) and MAKI farmers' group who provided the plant material.

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Citation: Matheri F, Mwangi M, Runo S, Ngugi M, Kirubi DT, et al. (2016) Phenotypic Characterization of Selected Kenyan Purple and Yellow Passion Fruit Genotypes Based on Morpho-Agronomic Descriptors. *Adv Crop Sci Tech* 4: 226. doi:[10.4172/2329-8863.1000226](https://doi.org/10.4172/2329-8863.1000226)

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