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Morphological diversity of Kenyan papaya germplasm

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Papaya is one of the major fruit crops of the tropical regions of the world. It shows considerable phenotypic variation in morphological and horticultural traits that can be utilized in its genetic improvement. In Kenya, wide range of papaya germplasm exists and has not been characterized. Therefore, there is difficulty in differentiating the papaya accessions in the different regions of Kenya. Characterization of papaya germplasm is normally accomplished by use of morphological descriptors, hence as a first step, a germplasm collection from within Kenya was gathered and its morphological diversity was assessed. The papaya germplasm was collected from Coast, Nyanza, Western, Rift Valley, Eastern and Central provinces of Kenya and characterized in the field using morphological descriptors based on fruit, flower, stem and leaf characteristics. The morphological characters were recorded and morphological data from sixty accessions were submitted to principal component and Neighbor-Joining cluster analysis. Accessions from Coastal, Western, Rift Valley and Nyanza provinces showed the widest morphological diversity with those from Eastern and Central provinces showing the least diversity. Fruit shape, fruit diameter, tree habit, leaf size and flower color showed the greatest variation in principal component analysis. The high diversity observed within the accessions points to ample possibilities of obtaining desirable trait combinations in specific cultivars.

Key words: Kenya, papaya, germplasm, morphological characterization.

INTRODUCTION

Papaya (*Carica papaya L.*) belonging to the *Caricaceae* family (Samson, 1986; Nakasone and Paull, 1998) is a medium sized fruit crop with a potential to produce fruits throughout the year. It is a small normally unbranched quick-growing soft-wooded tree 'almost an herb' (Chandler, 1958) with latex vessels in all parts. It is an important crop in Kenya both for local and export markets

(Imungi and Wabule, 1990). It is a polygamous species with three basic sex types: female, male and hermaphrodite (Storey, 1938; Hofmeyr, 1938; Janick, 1986). Both females and hermaphrodites are commercially useful for fruit production, while the males are solely used as a pollen source. The ripe fruits are popularly used as dessert or processed into jam, puree or wine, while the green fruits are cooked as vegetables (Samson, 1986; Nakasone and Paull, 1998). Latex from green fruits contains papain, a proteolytic enzyme, which is used in pharmaceutical, cosmetics and garment industries (Ali and Lazan, 1998; Nakasone and Paull, 1998). Thus

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papaya is also a good source of nutritious food as well as income for the producers. Due to its nature as a single stemmed tree, it can be economically produced in any size of land.

Morphologically, the stem is hollow between the nodes, except in young plants, consisting mainly of wood parenchyma and bears large triangular scars. The peltate leaves are arranged in a 2/5 spiral, having large long hollow petioles and large, deeply-lobed blades except in some cultivars (Samson, 1986). Female flowers which are 3 to 5 cm long, sit alone or in small groups in the leaf axils. The ovary is 2 to 3 cm long and has five fan-shaped stigmas on top. The male flowers, with ten stamens each, are found on long hanging panicles. Hermaphrodite flowers have either five or ten stamens and some of these may become carpelloid (fruit-like), in which case the fruits have a 'cat-face' appearance and are unmarketable. Different types of hermaphrodite flowers may occur on the same tree, depending on the season, or on the age of the tree.

The fruit is a large, fleshy and hollow berry. Fruits formed from female flowers are oblong to nearly spherical, but if formed from bisexual flowers, they are pear-shaped, cylindrical or grooved. Marketable fruits weigh from 0.5 to 2 kg (Samson, 1986) and are 10 to 20 cm long. The thin green skin turns yellow at the bottom when maturity sets in. The flesh is yellow to orange, in some cultivars reddish, and has a pleasant flavour. Around the cavity lie a thousand or more black seeds, but seedless fruits occur too. Twenty air-dried seeds weigh about one gram.

The fruit crop is believed to have been introduced into Kenya more than 50 years ago. The major varieties were possibly introduced from Hawaii, Philippines, India and Indonesia (Kamau et al., 1993). Papaya is commercially propagated by seed (Griesbach, 1992). Since it is open pollinated, a lot of changes have occurred resulting in loss of identity of the introduced varieties. Indeed, it is possible that many new genotypes have arisen owing to many years of uncontrolled open pollination. Thus, it is difficult to distinguish papaya accessions from different regions of Kenya. Additionally, wild relatives of the commercial papaya like *Vasconcella* spp. that grow naturally in some parts of the Kenya highlands, contribute to the local papaya germplasm.

Like most Caricaceae, the common papaya is a diploid (2n = 18), dioecious species (Arumuganathan and Earle, 1991). Many landraces and cultivars present hermaphrodite plants, which are generally preferred for production. They display considerable phenotypic variation for many morphological and horticultural traits (Ocampo et al., 2006). However, despite this considerable phenotypic variation in morphological and horticultural traits, there are no published studies on morphological diversity of papaya species in Kenya. A better knowledge of the morphological and genetic diversity of Kenyan papaya is therefore, desirable. The objective of this study is therefore to assess the morphological diversity in the papaya germplasm in Kenya and to find out if there are variations for their improvement.

MATERIALS AND METHODS

Collection of papaya germplasm in Kenya

The plant materials (Table 1) were obtained from locally available papaya varieties and landraces from six major producing provinces of Kenya namely, Coast (Kilifi and Taita districts), Nyanza (Rongo and Nyamira districts), Western (Vihiga, Bungoma and Kakamega districts), Rift Valley (Baringo, Keiyo and Nakuru districts), Eastern (Tharaka and Embu districts) and Central (Kirinyaga and Maragua districts) provinces (Figure 1). Different papaya accessions in fields were sampled. The collection was undertaken over the period of June to September 2008. The papaya germplasm collected consisted of 65 papaya accessions, representing 29 accessions from Coast, 4 from Central, 10 from Eastern, 9 from Nyanza, 5 from Western and 8 accessions from Rift Valley provinces of Kenya (Table 1).

Morphological characterization of papaya germplasm

Morphological characterization was done in the field during the collection using a descriptor list from IBPGR (1988). Fifteen descriptors were used in the characterization (Table 2).

Data collection

The data collected from the papaya germplasm surveys included stem diameter, internode length, petiole length and leaf length. Plant internode length was determined as the mean length of five internodes measured 10 cm above the ground. The color of mature leaf petioles was determined by visual appraisal based on the guidelines of IBPGR (1988). Length of mature petioles was determined as the average length of five mature leaf petioles measured from every observed petiole. Leaf length represented the average length of five mature leaf petioles measured tree. The habit of the trees were also recorded as either single or multiple stemmed. The length of flower buds was determined. Flower bud length was determined as the length measured from observed flowers. The color of flowers was also recorded as determined by visual appraisal on fully developed open flowers.

The fruits used for quality analysis were harvested and collected depending on the availability at the time of collection in the fields. Data for fruit length, fruit weight, fruit width, flesh thickness and cavity volume were taken. Longitudinal sections of the harvested fruits per tree were made, and then the fruit length was determined from pole to pole of the fruits. Fruit width was determined from the equator of the sectioned fruit.

Data analysis

Only the female and hermaphrodite plants were included in the subsequent analysis of the morphological diversity. Quantitative data were submitted to principal component analysis (PCA), using the XLSTAT 2008 statistical package. Cluster analyses were carried out on the principal components with Eigenvalues 0f 0.988 to 3.147 using the Neighbor Joining method (Nei, 1973) or hierarchic ascendant analysis (HAC) and Euclidian average distance.

Code	Local/ variety name	District of collection	Province	Sexual type	Morphological analysis(*)
MIG1	Papayi	Kilifi	Coast	Female	*
MIG2	Papayi	Kilifi	Coast	Female	*
MIG3	Papayi	Kilifi	Coast	Female	*
MIG4	Papayi	Kilifi	Coast	Female	*
ST1	Papayi	Kilifi	Coast	Female	*
ST2	Papayi	Kilifi	Coast	Female	*
KLF2	Papayi	Kilifi	Coast	Hermaphrodite	*
KOS1	US	Kilifi	Coast	Hermaphrodite	*
KOS2	Redlady	Kilifi	Coast	Hermaphrodite	*
KOS3	Sunrise	Kilifi	Coast	Female	*
KOS4	US	Kilifi	Coast	Hermaphrodite	*
IMA1	Mountain	Taita	Coast	Hermaphrodite	*
IMA2	Papayi	Taita	Coast	Hermaphrodite	*
IMA3	Papayi	Taita	Coast	Female	*
IMA4	Papayi	Taita	Coast	Hermaphrodite	*
IMA6	Papayi	Taita	Coast	Female	*
IMA0 IMA7	Papayi	Taita	Coast	Female	*
IMA7 IMA8		Taita			*
	Papayi		Coast	Hermaphrodite Female	*
VOI1	Papayi	Taita	Coast		*
VOI2	Papayi	Taita	Coast	Female	+
VOI4	Papayi	Taita	Coast	Female	÷
VB1	Papayi	Taita	Coast	Female	+
VB2	Papayi	Taita	Coast	Hermaphrodite	*
VB3	Papayi	Taita	Coast	Hermaphrodite	*
MAN1	Papayi	Taita	Coast	Female	*
MAN2	Papayi	Taita	Coast	Female	*
GAV1	Papayi	Vihiga	Western	Hermaphrodite	*
GAV2	Papayi	Vihiga	Western	Hermaphrodite	*
GAV3	Papayi	Vihiga	Western	Female	*
GAV4	Papayi	Vihiga	Western	Female	*
SCC	Kiru	Bungoma	Western	Hermaphrodite	*
RAP1	Ароуо	Rongo	Nyanza	Female	*
KIZ1	Ароуо	Rongo	Nyanza	Hermaphrodite	*
KIZ2	Ароуо	Rongo	Nyanza	Female	*
KIZ3	Ароуо	Rongo	Nyanza	Female	*
KIZ4	Ароуо	Rongo	Nyanza	Female	*
KIZ5	Ароуо	Rongo	Nyanza	Hermaphrodite	*
KIZ6	Ароуо	Rongo	Nyanza	Female	*
KIZ7	Ароуо	Rongo	Nyanza	Female	*
KAN1	Papayi	Nakuru	Rift Valley	Hermaphrodite	*
MUT1	Papayi	Nakuru	Rift Valley	Hermaphrodite	*
REB1	Sunrise	Tharaka	Eastern	Hermaphrodite	*
REB2	Sunrise	Tharaka	Eastern	Female	*
REB3	Mountain	Tharaka	Eastern	Female	*
REB4	Sunrise	Tharaka	Eastern	Hermaphrodite	*
THK2	Local	Tharaka	Eastern	Female	*
TMJ1	Sunrise	Tharaka	Eastern	Hermaphrodite	*
TMJ2	Sunrise	Tharaka	Eastern	Female	*
EMB1	Sunrise	Embu	Eastern	Hermaphrodite	*
				Female	*
EMB2	Sunrise	Embu	Eastern	remale	

 Table 1. Papaya accessions and districts of collection.

MF1	Mountain	Kirinyaga	Central	Female	*	
MF2	Local	Kirinyaga	Central	Hermaphrodite	*	
KIB1	Papayi	Kirinyaga	Central	Hermaphrodite	*	
MR1	Papayi	Maragua	Central	Female	*	
MR2	Papayi	Maragua	Central	Hermaphrodite	*	
MRG1	Sunrise solo	Baringo	Rift Valley	Hermaphrodite	*	
PKR1	Kiru	Baringo	Rift Valley	Female	*	
PKR2	Solo	Baringo	Rift Valley	Female	*	
CHP1	Honey dew	Keiyo	Rift Valley	Female	*	
CHP2	Solo	Keiyo	Rift Valley	Hermaphrodite	*	
KLF1	Papayi	Kilifi	Rift Valley	Female	-	
IMA5	Papayi	Taita	Coast	Male	-	
VOI3	Papayi	Taita	Coast	Female	-	
THK1	Local	Tharaka	Eastern	Male	-	
PKR3	Kiru	Baringo	Rift Valley	Male	-	

Table 1. Cont.

RESULTS

Morphological diversity in the papaya germplasm in Kenya

Kenyan papaya accessions displays a wide variation in all aspects of the fruit tree characteristics, including leaf size, leaf shape, leaf color, fruit size, shape of the fruit, flesh color, stem pigmentation and tree habit (Plate 1). The variability of these characteristics of different papaya accessions is indicated in Table 3.

Principal component analysis

In the principal component analysis (PCA), the first seven principal components took into account 72.9% of the total variance (Table 4). The first principal component was related to fruit length, fruit diameter, tree habit, petiole length, flower color and leaf size, the second one was to fruit shape, fruit skin texture, flower length and sexual or tree type, the third one was to fruit diameter and uniformity of fruit distribution, the fourth one was to petiole color, the fifth one was to uniformity of fruit distribution and fruit skin color at maturity and the sixth one was to fruit skin color at maturity. The seventh principal component was related to internode length.

The correlation among characters showed four main clusters of characters (Figure 2). The first cluster comprised traits associated with fruit shape, uniformity of fruits distribution, fruit skin color at maturity, flower color, fruit length and leaf size; the second cluster comprised traits associated with the tree habit, fruit diameter, internode length, stem diameter, petiole length and flower length; the third cluster comprised characters related to petiole color and fruit skin texture and the fourth cluster comprised only sexual or tree type.

Cluster analysis

The agglomerative hierarchical clustering dendrogram illustrates the relationship among the accessions (Figure 3). At 4.899 level of dissimilarity, almost all the sixty accessions were distinct from each other, while at 20 levels and above, larger numbers of the accessions were similar to each other. The cluster analysis separated the sixty accessions as different genotypes with Euclidean dissimilarity distance ranging from 4.9 to 57.

The dendrogram (Figure 3) was divided into four main branches: C1, C2, C3 and C4 based on the major morphological characters associated with them. The first cluster represented five accessions, the second one contained twenty five accessions, the third one contained twelve accessions and the fourth one contained eighteen accessions. At higher similarity levels, the above clusters were further divided into smaller sub-clusters.

DISCUSSION

Morphological analysis based on fifteen selected papaya descriptors (IBPGR, 1988) showed significant diversity within the cultivated papaya. As expected, not all the accessions collected corresponded to distinct cultivars. US, Redlady, Mountain, Papayi, Apoyo, Local, Sunrise, Kiru, Solo, Honey dew and Sunsise solo were recorded (Table 1). Each locality has its own unique set of names for different cultivars, with even very different cultivars sometimes referred to by the same name. This linguistic polymorphism constitutes an obstacle to reliable identification of cultivars and therefore their eventual use for different research programmes (Dansi et al., 1999). This shows, as expected, some challenges in the utilization of plants including papaya.

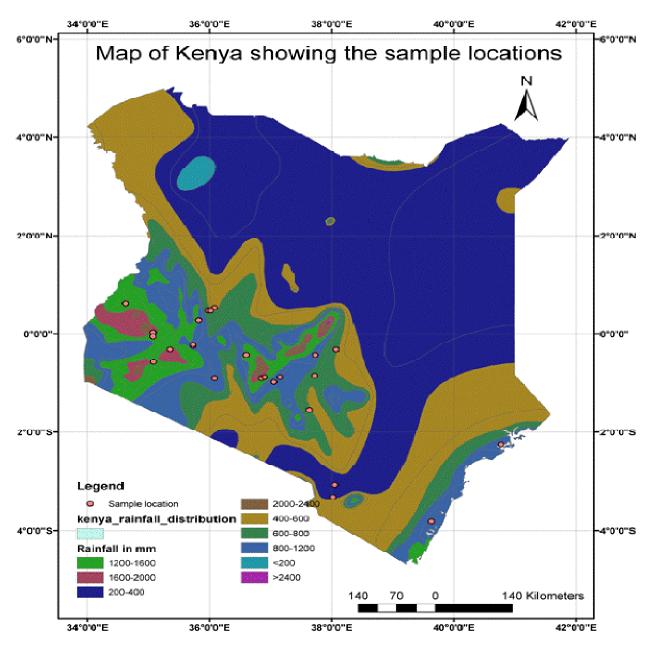


Figure 1. Map of Kenya showing the sample sites and the climatic conditions.

 Table 2. Morphological descriptors used in characterization of Kenyan papaya germplasm.

Plant part	Quantitative trait	Qualitative trait
Stem	Internode length, diameter (cm)	Tree habit
Petiole	Length (cm)	Color
Leaf	Length (cm)	-
Flower	Length (cm)	Color
Florescence	-	Sexual type
Fruit peduncle	Length (cm)	-
Fruit	Length (cm), diameter (cm), weight (kg), flesh density, sugar content (%)	General shape, uniformity of fruit distribution, skin texture, color at maturity.

Source: IBPGR (1988).

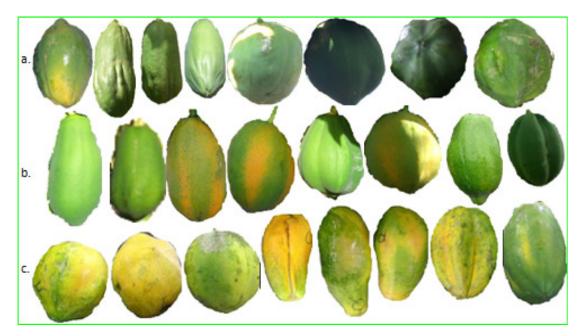


Plate 1. Morphological diversity observed in the Kenyan papaya germplasm; (a) Fruits collected from Central and Eastern provinces; (b) from Coast province and (c) from Rift Valley, Western and Nyanza provinces.

Variable	Minimum	Maximum	Mean	Std. deviation
Fruit length (cm)	7.000	30.000	17.828	5.616
Fruit diameter (cm)	5.000	28.000	14.118	5.641
Fruit shape	1.000	17.000	6.350	3.974
Uniformity of fruit distribution	1.000	3.000	2.333	0.951
Fruit skin colour at maturity	1.000	5.000	1.133	0.566
Fruit skin texture	0.000	7.000	5.050	1.731
Internode length (cm)	4.000	14.000	9.067	2.524
Stem diameter (cm)	6.000	50.000	19.900	9.559
Tree habit	1.000	2.000	1.583	0.497
Petiole colour	1.000	2.000	1.983	0.129
Petiole length (cm)	0.500	3.000	1.453	0.614
Flower length (cm)	1.000	6.000	3.217	1.144
Flower colour	1.000	2.000	1.900	0.303
Leaf size (cm)	15.000	58.000	36.217	9.042
Sexual/ tree type	1.000	2.000	1.433	0.500

Table 3. The standard deviation calculated comparing the measured morphological characteristics.

Table 4. Principal component analysis (PCA) performed using the XLSTAT 2008 statistical package showing the correlations of the first seven principal components with the variables observed on papaya accessions.

Principal component	Eigen value	Variability (%)	Cumulative (%)
PC1	3.147	20.978	20.978
PC2	1.842	12.28	33.259
PC3	1.417	9.449	42.708
PC4	1.272	8.479	51.187
PC5	1.142	7.613	58.800
PC6	1.128	7.517	66.317
PC7	0.988	6.585	72.902

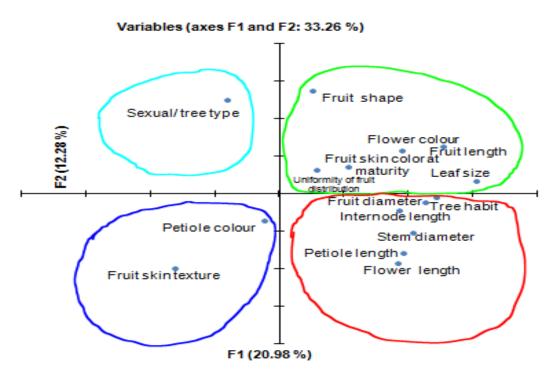


Figure 2. Correlation among characters associated with the first and second principal components. The closer the attributes are to each other in the PCA plot, the higher the correlation (that is, the smaller the angle between the attributes, the higher the correlation).

Morphological traits were the major criteria used by farmers in distinguishing and naming the papaya accessions. In the different production zones, factors influencing farmers' variety of choice and determining the level of diversity that is maintained included social, cultural, economic, abiotic and biotic factors.

The assumption in the multivariate analysis is based on the use of genotypes with maximum genetic divergence (Bhatt, 1970). Knowledge of correlations among characters is useful in designing an effective breeding programme for any crop. There are several reasons for using indirect selection. Sometimes the main character is expressed late or measurement of the indirect character is much easier than for the direct character. Moreover, complex plant characters such as yield are quantitatively inherited and influenced by genetic effects, as well as by genotype and environmental interaction. Therefore, identification and use of highly correlated characters are appropriate. Strong correlations were observed between traits related to fruit characteristics, petiole length and leaf size, confirming the results of Ocampo et al. (2006) who showed correlation between these traits. This indicates presence of diverse variable arrangements at the individual genotype level pointing to ample possibilities of obtaining desirable trait combinations in specific cultivars. Broad trait variation apparent among the tested papaya accessions entails the presence of ample opportunities and prospects for genetic improvement of these characters through selection either directly or following recombination through intraspecific hybridisation of desirable genotypes. This would be crucial in meeting the demand of the farmers, researchers and consumers of this fruit crop.

Substantial morphological variation within and between the various accessions may be attributed to pollination, sexual recombination and perhaps mutation followed by intensive selection by isolated human communities in diverse environments (Martin, 1976). Problems in pollination, fruit set and production are intimately associated with sex expression resulting from genotype-environment interactions. Cultivar and environmental differences have also produced a wide array of modified forms, so the number and types of modifications have varied in reports by various researchers (Nakasone and Paull, 1998). Consequently, special breeding programs and experimental designs are needed to distinguish genotypic from phenotypic variation (Weising et al., 2005).

From the dendrogram, however, the first cluster (C1) comprised all accessions from Taita and Kilifi representing Coast province. The second (C2) and the third (C3) clusters were characterized by cultivars from Rift Valley, Nyanza, Western and Coast provinces showing possibility of frequent exchange of planting materials among farmers from different zones. The fourth cluster (C4) was however, characterized by cultivars from Central, Eastern, Rift Valley and Western provinces. In the dendrogram obtained, using quantitative and qualitative traits, a small part seems to include accessions from the

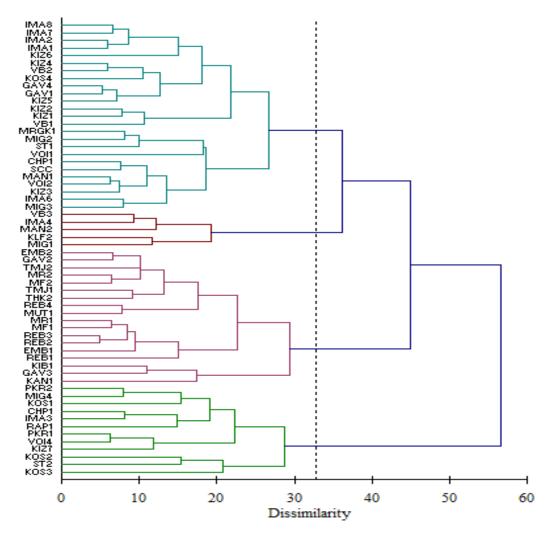


Figure 3. Dendrogram constructed based on morphological characters of 60 papaya accessions from six provinces of Kenya using the Neighbor Joining method (Nei, 1973) and Euclidian average distance. C1, C2, C3 and C4 are the clusters (1 to 4) generated in the cluster analysis.

same geographical location as indicated by first cluster (C1). In both cases, the germplasm from Coast and Rift Valley provinces presented the highest variation, being scattered all over the tree, with little differentiation of accessions from other provinces. Apart from showing great phenotypic variation among the accessions, the study has also found characteristics such as the fruit shape, flesh, texture, color and fruit shape that can be useful as markers for classifying the accessions and can be employed in achieving papaya breeding objectives.

This study has shown significant variation in morphological traits (fruit length, fruit diameter, tree habit, petiole length, flower color, leaf size, fruit shape, fruit skin texture, flower length, sexual or tree type, uniformity of fruit distribution in the tree, petiole color, fruit skin color at maturity and internode length) among the different accessions of papaya morphotypes. The analysis using morphological characters revealed considerable amount of diversity among 60 papaya accessions that can be used in selecting diverse parents in breeding programme. This is also crucial in utilizing the genetic potential of these genotypes for improvement of traits needed for adaptation to various conditions. However, there is the need for complementing similar work with other techniques such as DNA genetic markers to further accurately classify papaya germplasm existing in Kenya.

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