

**Collection, Morphological and Molecular Characterization of Papaya Germplasm in
Kenya.**

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ABSTRACT

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. The objectives of this research were to collect, document and characterize the Kenyan papaya germplasm.

A survey conducted to garner information on papaya germplasm and production in six Kenyan provinces was based upon a structured questionnaire supplemented by oral interviews. The survey was carried out between June and September 2008. The papaya germplasm was collected from Coast, Nyanza, Western, Rift Valley, Eastern and Central provinces of Kenya and characterized in the field using IBPGR (International Board of Plant Genetic Resources) morphological descriptors based on fruit, flower, stem and leaf characteristics. The morphological characteristics were recorded and morphological data from sixty accessions submitted to principal component and Neighbor-Joining cluster analysis. The genetic diversity of 42 papaya accessions from the above named six provinces of Kenya was also investigated using seven simple sequence repeats (SSR) markers. The amplified DNA fragments were screened by capillary electrophoresis on the ABI 3730 genetic analyzer and analyzed using the Genemapper v3.7 software. Cluster and principal component analysis (PCA) were done using NTSYS-pc v2.2.

Data from the field survey indicated that majority of Kenyan papaya growers have medium sized farms (0.2-0.8 ha), upon which they conduct mixed cropping. While growers on small (less than 0.2 ha) and medium sized farms indicated no varietal preferences, the growers on large farms (larger than 0.8 ha) preferred specific varieties of known performance and traits such as Solo,

Sunrise, US, and Redlady. Most farmers produced papaya for both subsistence and market. Constraints to papaya production included seedling sex paradox, pests such as stink bugs and spider mites, viral diseases (papaya ringspot virus), and the lack of clean planting material.

Accessions from Coastal, Western, Rift Valley and Nyanza provinces showed the widest morphological diversity while those from Eastern and Central provinces showed the least diversity. In total, 7 SSR markers used in the analysis were highly polymorphic among the accessions and the polymorphic information content (PIC) varied from 0.75 to 0.852 with an average of 0.81. The number of alleles within the 42 papaya accessions across the seven loci ranged from 8 to 18 with an average of 11.93. The phylogenetic analysis clustered the 42 accessions into two main clusters A and B. Cluster A had four sub-clusters while cluster B had no sub-clusters. Microsatellite markers used therefore, showed limited genetic diversity among papaya accessions. However, the Coast province accessions showed the widest diversity, as they were scattered all over the dendrogram.

The morphological and genetic differences among the genotypes revealed by their clustering into distinct groups suggest the presence of different sources of variations among the papaya accessions. This could be attributed to their diversity, geographical locations and also due to exchange of plant genetic resources among farmers within and between the provinces. The high morphological diversity observed within the accessions points to ample possibilities of obtaining desirable trait combinations in Kenyan papaya. Knowledge of this diversity together with the documentation of cultural practices is also fundamental for the future improvement of Kenyan papaya germplasm. The wide diversity observed among accessions from Coastal, Western, Rift Valley and Nyanza provinces can be utilized in the selection of promising parents in hybrid

variety, inbred line development and estimating the potential of genetic gain in a breeding programme. There is also need for proper conservation of the different accessions reported as they could serve as raw material for the genetic improvement of different characters of the crop through recurrent selection after hybridisation.

Key words: Collection, diversity, documentation, germplasm, morphological markers, papaya, SSR markers.