Africa. Twelve of the verification accessions either shared names with accessions in the field genebank or were synonyms that had been collected from various parts of East Africa. The immediate question was whether the ITC accessions and the ones in the regional field collection (with the same names) were ramets and if so how much have the post-MTS accessions changed from the corresponding field accessions? The twelve pairs were surveyed for more than 50 morphological characters to assess the level of similarity between the field (non-MTS) accessions and those originally regenerated after MTS and thereafter transferred to the field collection. Results from the pair-wise estimation of resemblances between the 12 pairs of accessions indicated that the range of values of the correlation (0.75-0.98) and distance (0.04-014) coefficients between the pairs that shared names was smaller than the values between other pairs of accessions. This range was used as a measure to give an assessment standard of the levels of dissimilarity between other pairs of accessions. Results indicated that, on the basis of the standard assessment, several other pairs of accessions were found to be similar, differing only in their quantitative characters; hence more synonyms were worked out. This paper is describing the method used in estimating the dissimilarity levels among accessions that shared names and/or known to be synonyms from the field verification trial to those in the field genebank of east Africa. The value of the method is critically discussed.

Selection of Minimum Descriptors in Banana using Univariate and Multivariate Methods

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Keywords: Selection of descriptors, *Musa* spp., multivariate analysis

The objective of the present work was to quantify the genetic diversity between banana accessions at Embrapa Cassava and Fruits, Brazil, using a list of morpho-agronomic descriptors, as well as to provide a minimal number of descriptors capable of quantifying the diversity between accessions. The phenotypic characterization was carried out for 77 accessions, evaluated with 92 descriptors. The selection of the quantitative descriptors was carried out by principal components analysis and qualitative descriptors by entropy coefficient. The efficiency of elimination of descriptors was analyzed by a comparative study between the clusters formed, taking into consideration both

all 92 descriptors and only the selected ones. The selected descriptors were analyzed in combined fashion by the Ward-MLM procedure. The Ward-MLM method was used and the combined matrix formed by the Gower algorithm. In regard to the selection carried out for the quantitative and qualitative descriptors, it was possible to reduce the number of descriptors used for characterizing the banana germplasm by 51%. The correlation between the matrices, considering the 92 descriptors and the selected descriptors, was 0.82 showing that the reduction in the number of descriptors did not influence the estimation of the genetic variability between the banana accessions. The genetic diversity analysis by the Ward-MLM method demonstrated similarity between the accessions within the same group. However, between groups, it is possible to suggest the presence of variability for the minimal descriptors used, indicating that these genotypes can be used as parents in banana breeding programs.

Karyotype Analysis of Six A-Genome Banana Cultivars with Different Ploidy (AA or AAA)

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Keywords: *Musa* spp., chromosome features, karyotype analysis

The comparative analysis of karyotypes in various *Musa* species and clones contribute to the analysis of the evolution of cultivated clones. However, the analysis of the *Musa* karyotype is complicated by difficulties in identifying individual chromosomes. By using the method of wall degradation hypotonic, karyotype analysis was performed to investigate the chromosome features of six A-genome banana cultivars differing in ploidy, i.e. AA or AAA group. Results show that the diploid (AA) and triploid (AAA) cultivars had different karyotype characteristics. For example, the karyotype formula and type for 'Tianbaojiao' (AAA) is $2n = 3x = 33 = 3M + 27m$ (3SAT) + 3sm and "1A", respectively; and for 'Rose' (AA) is $2n = 2x = 22 = 2M + 18m$ (2SAT) + 2sm and "2A", respectively. The karyotype formula for 'Pisang Mas' (AA), 'Hainan Gongjiao' (AA), 'GCTCV-218' (AAA) and 'GCTCV-119' (AAA), is $2n = 2x = 22 = 4M + 16m$ (SAT) + 2sm, $2n = 2x = 22 = 2M + 18m$ (SAT) + 2sm, $2n = 3x = 33 = 6M + 15m$ (3SAT) + 12sm, and $2n = 3x = 33 = 6M + 15m$ (6SAT) + 12sm (3SAT), respectively. However, all these four cultivars exhibited a karyotype asymmetry of type "2B". Moreover, we also established the idiogram for the six banana cultivars.