



## **COMPARISON BETWEEN CLUSTER METHODS USING SIMULTANEOUS ANALYSIS OF QUALITATIVE AND QUANTITATIVE DATA IN BANANAS**

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Understanding the genetic variability in germplasm banks is essential to genetic breeding programs. Usually quantification of the variability is carried out using quantitative and qualitative data separately, which may not be enough to infer about the similarity between the genotypes evaluated. The objective of the present work is to compare methods of cluster analysis of banana genotypes considering quantitative and qualitative data, simultaneously and separately. Data from 19 banana genotypes using 23 quantitative and 67 molecular bands from SSR markers were used. The combined cluster analysis methods, INDOMIX, PCAMIX and PRINQUAL, were used. For the separate data, the cluster analysis considering the Mahalanobis distance was used for the quantitative data and the Nei and Li indice for the molecular data. The methods for the separate and combined data analysis were evaluated based on the proportion of erroneous classifications from the k-means cluster analysis, considering the classification of the genotypes in five pre-defined groups. In general, the three methods used presented lower probability of erroneous classification when compared to the methods separately. The INDOMIX, PCAMIX and PRINQUAL methods may be used to quantify the variability present in situations when quantitative and qualitative data are considered simultaneously and showed to be more efficient when the cluster analysis was used considering quantitative and qualitative data, separately.