

GENETIC VARIABILITY OF CAMU-CAMU (*MYRCIARIA DUBIA*) ACCESSIONS DETERMINED BY *INTER SIMPLE SEQUENCE REPEAT* MARKERS

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Camu-camu has great potential yet to be explored in Brazil. The identification and characterization of genetic diversity and population structure preserved in germplasm banks this species is fundamental to the evolution of breeding programs. The objective of this study was to evaluate the genetic variability of 94 accessions of camu-camu, obtained from 10 populations found on the shores of Lago do Rei (LR), located in the municipality of Caracaraí, Roraima / RR. 14 ISSR primers were used with genetic analysis performed using the 'Convert' applications 'GenAlex 6', 'Popgene 32' and 'Structure 2.3.4'. By molecular analyzes, accessions were grouped within and between existing populations, revealing that individuals within populations exhibit greater genetic diversity. The total number of alleles identified was 108, and the VBV, GCV, UBC 810 and UBC 827 loci were those with the highest numbers of alleles, ranging from 4 to 10. Greater genetic diversity and percentage of polymorphism was verified by populations LR02, LR15 and LR04, respectively. According to the results of the PCoA analysis and 'Structure', observed the separation of 3 groups, showing little variability among populations, with greater variability within the population. ISSR markers used showed suitability and efficiency in discriminating individuals 94 and the corresponding populations, separating them into three different groups and revealing the genetic variability of each population and its individuals. Genetic diversity within populations of camu-camu may be useful for selection of new individuals with higher performance in the field, as well as for the conservation of germplasm.

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