



Analysis of genetic diversity of Laeliinae (Orchidaceae) in the State of Sergipe using ISSR markers

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ABSTRACT. The Orchidaceae represent one of the largest and most diverse families on the planet. However, this family is constantly threatened by predators and by the advancement of urban centers over its natural habitats. The objective of this study was to use inter-simple sequence repeat markers to evaluate the genetic diversity between orchid accessions of the Laeliinae subtribe, which comprise part of the Orchidaceae study collection at the Department of Agronomic Engineering of the Federal University of Sergipe. DNA was extracted from each specimen by using an adapted 2% cetyltrimethyl ammonium bromide protocol. Similarity between individuals was calculated using the Jaccard method. Clustering was carried out by the unweighted pair group method with arithmetic mean method, with resampling and 10,000 bootstraps. Eighty-seven fragments were obtained, all of which were polymorphic, revealing high variability between accessions. The mean similarity was 35.77% between *Encyclia* sp individuals,

and 35.90% between specimens of *Cattleya tigrina*. For *Epidendrum secundum*, a relationship between geographic and genetic distances was observed, and the accession collected in the southern part of the State of Sergipe (Serra de Itabaiana National Park) was more divergent than that of the other parts of the state. The data generated in this study will guide further research aimed at the *ex situ* conservation of these materials.

Key words: *Cattleya tigrina*; Conservation; Genetic diversity; *Encyclia* sp; *Epidendrum* sp; ISSR