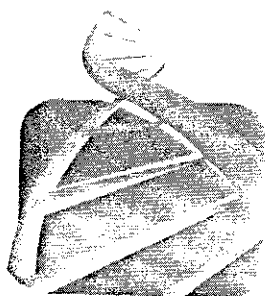


# SIMPÓSIO BRASILEIRO DE GENÉTICA

## MOLECULAR DE PLANTAS

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## PROGRAMA E RESUMOS

**DEVELOPMENT OF MICROSATELLITE MARKERS IN *Ilex paraguariensis* St. Hil., A NATIVE TREE SPECIES.**

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*Ilex paraguariensis* St. Hil., popularly known as "erva-mate", is a native tree species belonging to the family Aquifoliaceae and occurs in Brazil, Argentina and Paraguay. It plays an important economic role in this region. *I. paraguariensis* has been particularly used in the production of beverages, but has also used in medicines and cosmetics. Although the cultivation of *I. paraguariensis* has been implemented, with the aim of addressing the growing market demand, extraction of erva-mate still occurs for a large part in native populations. Knowledge of the genetic structure of a population may be applied to the conservation and management of biodiversity and can be acquired through the use of microsatellite molecular markers, which are powerful tools in determining genetic parameters, such as genetic diversity, analysis of paternity, gene flow and genetic drift, among others. Simple Sequence Repeats (SSR), based on polymorphic microsatellite loci, are codominant, multiallelic and widely distributed within eukaryotic genomes. A series of primers flanking microsatellite loci were developed from an *I. paraguariensis* random genomic library (shotgun). The fragments were cloned into the vector PCR4Blunt-TOPO (Invitrogen) and transformed into *E. coli* competent cells. The positive clones were sequenced using the BigDye Terminator v3.1 kit (Applied Biosystems) and ABI 3700 sequencer (Applied Biosystems). Approximately 1500 clones were sequenced using M13 Forward and Reverse primers. Fifty-two pairs of primers were designed and synthesized and are currently being optimized to assess the polymorphism of the loci, using denaturing polyacrylamide gels stained with silver nitrate. The most polymorphic primers will be selected for subsequent genetic studies in populations of *I. paraguariensis*. The molecular markers developed in this study represent a powerful tool for the generation of population genetic data, fundamental and essential to the conservation and collection activities in a breeding program.

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