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Survey of differentially methylated and expressed genes in vegetative and reproductive organs of two Ilex species

Jimena Cascales, Mariana Julia Garberoglio and Alexandra Marina Gottlieb

University of Buenos Aires, Argentina

Ilex paraguariensis and *I. dumosa* (Aquifoliaceae) are dioecious perennial trees native to southern Brazil, northwestern Argentina, northeastern Paraguay and Uruguay. The aerial parts of *I. paraguariensis* the 'yerba mate' are used to prepare the 'mate' infusion which has a great cultural and socio-economic value in many southern South American countries. This species produces several secondary metabolites, many with nutraceutical properties. *Ilex dumosa* is a valuable gene/allelic reservoir as it produces significantly lower contents of such compounds and shows resistance to an *I. paraguariensis*' hemipteran plague. The mechanisms of sex determination are unknown in *Ilex*, while metabolic and defense pathways have been proposed only for *I. paraguariensis*. The knowledge derived from intra- and interspecific comparisons could be applied in genetic improvement programs of the 'yerba mate' crop, as well as to enhance the harvest period. The present comparative study focused in detecting epigenetic and gene expression differences between sexes and species, by screening flower buds and vegetative organs (young and adult leaves). For this, MSAP Methylation Sensitive Amplified Polymorphism and cDNA-AFLP techniques

were used. A total of 103 isolated differential fragments were effectively characterized with bioinformatic tools, considering $\leq 10^{-5}$ E-value. Of these, 46.6% derive from *I. paraguariensis* and 53.4% from *I. dumosa*; 63% were recovered from reproductive and 37% from vegetative organs. Thirty-five percent of the fragments were identified as related to: metabolism (7.8%), regulation of gene expression (7.8%), biotic/abiotic stress resistance (3.9%), and other cellular processes (15.5%). Additionally, three groups of genes were distinguished: a) potentially involved in sexual determination (9 sequences), b) secondary metabolite production (3 sequences), and c) biotic stress resistance (6 sequences). The methodological approach allowed detecting differentially represented genes, which would be worth validating in qPCR studies.

Biography

Jimena Cascales is a postdoctoral scholar with expertise in population genetics, epigenetics and gene expression analysis of *Ilex paraguariensis* and *I. dumosa*.

jcascales@ege.fcen.uba.ar