

## MICROSATELLITE DATASET REVELS NEW INSIGHTS OF *CEDRELA*(MELIACEAE) VARIABILTY IN NORTHEN MINAS GERAIS STATE, BRAZIL.

Juan M Díaz-Soto <sup>1,23</sup>, Alexander Huamán-Mera<sup>1,4</sup>, Luiz Orlando de Oliveira <sup>1,5\*</sup>.

1. Laboratório de Biologia Molecular e Filogeografia, Instituto de Biotecnologia Aplicada à Agropecuária– BIOAGRO, Universidade Federal de Viçosa, 36570-900 Viçosa (MG), Brasil; 2. Programa de Biología, Universidad de Sucre, Cra 28 No 5-267 Barrio Puerta Roja, Sincelejo, Colombia; 3. Departamento de Genética e Melhoramento, Universidade Federal de Viçosa, 36570-900 Viçosa (MG), Brazil4. Departamento de Biologia Vegetal, Universidade Federal de Viçosa, 36570-900 Viçosa (MG), Brazil5. Departamento de Biologia Molecular, Universidade Federal de Viçosa, 36570-900 Viçosa (MG), Brasil; 5. Departamento de Biologia Molecular, Universidade Federal de Viçosa, 36570-900 Viçosa (MG), Brasil; \*Correspondence to luiz.ufv@hotmail.com

Tema/Meio de apresentação: Filogeografia/Poster

Cedrela P. Browne (Meliaceae) is a tree genus, widely distributed throughout the Neotropics, from Mexico to Argentina. The genus has 18 species taxonomically accepted. In Brazil, Cedrela is widely represented by Cedrela fissilis, which consists of two genealogical lineages that occupy the Chiquitano and Atlantic ranges, respectively. Each range occurs at the west and east of the Cerrado of central Brazil. This study aimed to identify the genealogical origin of Cedrela from Northern Minas Gerais. Seven populations of Cedrela were sampled and genotyped with 11 fluorescent microsatellites. For comparative analyses, we added microsatellite information from additional 15 populations from the east and west lineages of Cedrela fissilis from a wide geographic range in Brazil. Descriptive and Bayesian statistics uncovered details of multilocus genetic diversity and population structure. Bayesian analysis in Structure indicated the best K is K = 3, which suggested three distinct genetic groups were present in our dataset. AMOVA showed that the genetic differentiation by allele frequencies was 4% among groups (East, West, and Northern Minas Gerais), 4% within groups, and 92% within populations. However, the contribution to genetic differentiation among and within groups, due to the variability of the allele frequencies, was less than attributed to the effect at the number of repeats of the microsatellite motif. AMOVA for microsatellite size variation showed that the contributions range from 27.0% among groups to 8.0% within groups and within populations 65.0%. Analyses of Nei genetic distance confirmed the separation and differentiation of these three genetic groups. Those groups comprised the west and east lineages of C. fissilis, in addition to a third, newly identified lineage from Northern Minas Gerais. Gene flow studies through progeny tests will provide further support for the taxonomic status of the newly described lineage in northern Minas Gerais.

Acknowledgements: The authors thank Universidad de Sucre for providing grand for JMDS and CAPES for AHM, as well FAPEMIG by funding the project APQ-03504-15.