IDENTIFICATION OF INDEPENDENT LINEAGES FOR *CLUSIA CRIUVA* CAMBESS. *S.L.* COMPLEX BASED ON MOLECULAR DATA AND ECOLOGICAL NICHE MODELING

Maria Beatriz Cortez[1], João de Deus Vidal[2], Danilo Augusto Sforça[1], José Elvino do Nascimento Júnior[1], Volker Bittrich[3], Maria do Carmo Estanislau do Amaral[1] & Anete Pereira de Souza[1]

[1] Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas – UNICAMP, Campinas, SP, Brasil.
[2] Departamento de Botânica, Instituto de Biociências de Botucatu, Universidade Estadual Paulista "Júlio de Mesquita Filho" – UNESP, Botucatu, SP, Brasil
[3] R. Mário de Nucci, 500, Cidade Universitária, Campinas, SP

Clusia criuva Cambess. *s.l.* is a species complex that occupies two Brazilian biomes: Cerrado and Atlantic forest. The plants are dioecious and present mimetic flowers that are beetle-pollinated. The fruit of *C. criuva* consists of a septifragal capsule, primarily dispersed by different bird species. Recently, this complex underwent a taxonomical reorganization. Previously recognized *C. parviflora* Engl. (nom. illeg.) was reduced to subspecies status with *C. criuva* being currently divided into two subspecies: *C. criuva* ssp. *criuva* and *C. criuva* ssp. *parviflora* Vesque. Morphologically, these subspecies can only be distinguished by stamen/staminode morphology which combined with non-overlapping distributions serves as an indicator that these lineages are evolving separately. Multiple lines of evidences are necessary to test and evaluate the degree of such isolation since different stages of lineage diversification result in distinct effects of isolation. In this study we combined molecular and ecological evidences to test population structure between subspecies. We developed a set of polymorphic nuclear microsatellite markers combining population genetics data with species distribution modeling. Chloroplast SSR markers previously described were also tested for polymorphism and six markers were chosen to characterize populations. To test if the subspecies presented distinct genotypic clusters we calculated F-statistics (FSTAT), genetic distance (TFPGA) and performed population structure analyses. Putative phylogeographic breaks were also identified using the software ´Barrier´. We were able to identify 41 alleles across 10 loci in 289 samples with an average of 4.1 alleles per loci and 23.8 alleles per population. F_{ST} values produced an elevated average of 0.330 across loci while the average found for F_{IS} was of -0.342 across loci, demonstrating that genetic differences are mainly between populations rather than within. AMOVA percentages corroborate F_{ST} results with 82% of differentiation found among populations and 18% found within populations. Distribution models pointed to a retraction of the distribution area between the Last Glacial Maximum and the Mid-Holocene. Our results indicate clustering between populations and distributional range retractions during Quaternary climatic fluctuations. These data may assist a further taxonomic treatment supporting the re-establishment of two distinct species instead of subspecies. (FAPESP 2012/51781-0)(CAPES)

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