

SP 19758j
Id 31929

A multi-gene phylogeny of the Brazilian Cerrado genus *Diplusodon* Pohl (Lythraceae)

Inglis, PW¹; Azevedo, VCR¹; Ciampi, AY¹ and Cavalcanti, TB²

¹ Laboratório de genética vegetal, Embrapa Recursos Genéticos e Biotecnologia, Parque Estação Biológica, Brasília-DF, CEP 70770-900, C.P. 02372, Brazil.

² Herbario CEN, Embrapa Recursos Genéticos e Biotecnologia

The genus *Diplusodon* comprises 85 species, which are almost exclusively restricted to the Brazilian Cerrado. The genus is therefore an interesting model for the study of plant evolution and phylogeography. A multi-gene phylogeny was inferred using data collected from direct sequencing of PCR amplified DNA markers from 50 *Diplusodon* species. The DNA loci studied were: a. the nuclear ribosomal RNA internal transcribed spacers, ITS; b. the nuclear ribosomal RNA external transcribed spacer, ETS; c. two introns of the nuclear low copy number *waxy* gene; d. the chloroplast *PsbA-TrnH* intergenic spacer; and e. the chloroplast *TrnL* intron. Phylogenetic relationships were estimated using maximum parsimony and Bayesian analysis of individual and combined data sets using sequences from some other genera of Lythraceae for rooting of trees. The chloroplast *TrnL* intron was found to be almost invariant in *Diplusodon* and was excluded from further analysis. The chloroplast *PsbA-TrnH* intergenic spacer was found to contain relatively few phylogenetically informative base substitutions, although the region appeared to be highly prone to genetic rearrangements, manifested as a high frequency of indel accumulation, most prominent of which were a conserved 30bp inverted repeat and a 25bp direct repeat, independently present in many species. However, many of the *PsbA-TrnH* intergenic spacer characters were highly homoplasious. Of the nuclear markers, the *waxy* locus was the least variable. In contrast, the ITS and ETS regions were relatively rich in phylogenetically informative base substitutions. A strong phylogenetic correlation with geographical distribution was found in *Diplusodon*, where species in basal clades were mainly endemic to Minas Gerais and Bahia states. Another well-supported superclade was present, more distant from the outgroup taxa, containing many species from Goiás state. This clade did, however, contain a secondary lineage restricted to Minas Gerais. Other prominent and well-supported lineages contained species from Goiás state and from Goiás and Tocantins states respectively. The widely-distributed species, *Diplusodon virgatus* was present at the base of the Goiás, and Goiás-Tocantins clades, suggesting a possible pioneer role. The current *Diplusodon* sections, *Penninerves*, *Diplusodon* and *Palmatinerves*, based on leaf venation patterns, were inconsistently represented in the molecular phylogeny and were not monophyletic. This indicates either a need for re-evaluation and reassignment of certain *Diplusodon* species under the current taxonomic framework or the need for a complete revision of the genus.

Financial support: Funarbe