

# ITS EVOLUTION IN PLATANUS: HOMOEOLOGUES, PSEUDOGENES, AND ANCIENT HYBRIDISATION

Guido W. Grimm<sup>1</sup>, Thomas Denk<sup>2</sup>

<sup>1</sup> University of Tübingen, Institute of Geosciences, Biogeology, Sigwartstrasse 10, 72076, Tübingen, Germany

<sup>2</sup> Natural History Museum, Palaeobotany, Box 50007, 10405, Stockholm, Sweden

guido.grimm@uni-tuebingen.de

Platanaceae is an old family of angiosperms extending back to the Early Cretaceous but consisting of a single extant genus *Platanus*. Species of *Platanus* have long been known to hybridize, and the ‘London Plane’ *Platanus x hispanica* is a well-known example for a hybrid species that formed in historical times. Morphological studies suggested past interspecific or interlineage hybridisation (reticulation) as possible important factors in the evolution of the genus. The internal transcribed spacers (ITS) of the 35S nuclear ribosomal DNA cistron are a biparentally inherited, multi-copy marker with a high potential for resolving intrageneric relationships especially when ancient hybridisation (reticulation) is involved. In addition to phylogenetic trees, splits graphs and motif analysis can be used to extract phylogenetic information from 223 cloned ITS sequences. Non-pseudogenous and pseudogenous sequence motives are assessed to explain how different evolutionary modes contribute to possibly conflicting character state patterns in the ITS. Putative non-functional ITS copies (‘pseudogenes’) form independent groups in phylograms and splits graphs; distinct pseudogenous lineages reflect ancient (Palaeogene, Cretaceous) hybridisation events conserved in the ITS. Specifically, pseudogenous clones of an ‘Atlantic’ North American clade appear closest related to non-pseudogenous clones of the western (‘Pacific’) North American *P. racemosa* species aggregate. Recent lateral gene flow is evidenced as an important factor in the evolution of the Central Mexican *P. rzedowskii* including additional nuclear sequence data (2nd LEAFY intron, 5S rDNA intergenic spacer). We promote the use of broad (cloned) ITS data sets covering intra- and interindividual variability to analyse primary mechanisms of evolution: the ‘feared’ incompatible signals in cloned ITS sequences contain information about complex patterns and reticulate evolutionary pathways, which can be visualized with splits graphs but not with bifurcating trees.