

Molecular systematics and evolution of epiphytic cacti

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Epiphytic cacti have been in the focus of research in Bonn over many decades. According to current knowledge, epiphytism has evolved at least twice in Cactaceae. A great number of morphological characters, including details of pollen morphology, has evolved in parallel in the clearly separate tribes Rhipsalideae and Hylocereeae. This has led to taxonomic confusion during the last century, and is an impressive example of the evolution of convergences in the context of epiphytism. Therefore, Cactaceae will be studied as a promising model group in order to gain insights into fundamental mechanisms of the evolution of epiphytism.

The first aim of this project is to generate highly resolved phylogenetic trees for the epiphytic tribes, based on chloroplast and nuclear data. These phylogenetic hypotheses will allow us to trace morphological characters, especially flower characters and growth forms and to detect changes of character states and putative key innovations during the evolution of epiphytism in Cactaceae/Rhipsalideae. Emphasis will be placed upon characters relevant in the context of pollination biology. In particular, the evolution of pollen characters will be traced and hypotheses on the adaptive value of pollen character complexes will be tested. Finally, the current, morphology-based circumscription of species within Rhipsalideae will be evaluated by means of the generated sequence data. The potential of the DNA regions used will also be tested for their potential as DNA-barcodes for species identification.