



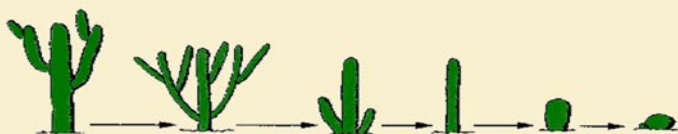
Molecular systematics and growth form evolution in the tribe Trichocereae (Cactaceae)

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Growth form evolution

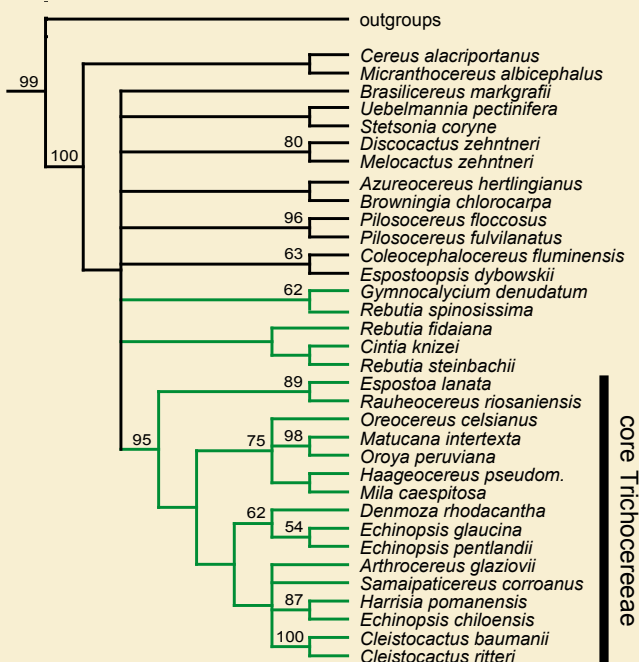
Cacti are very remarkable for their great diversity of specialized growth forms. The evolution of these characteristics, however, is still not understood. The traditional idea formulated by Buxbaum in his „law of the abbreviation of the vegetative phase” is that there is a general „trend” in cactus evolution leading from branched, columnar forms to unbranched, globular types.



Trends usually have been described on the basis of morphoclines in order to establish evolutionary hypotheses, from which phylogenetic diversity is inferred. This is still the prevailing concept in current classification systems in cacti. Instead, a better understanding of a wide range of morphological diversity could be provided from robust phylogenetic analyses, allowing to reconstruct the complex pattern of growth form evolution.

Results from phylogenetics studies

Preliminary results from a molecular systematic analyses indicates that some lineages with exclusively globular growth forms (in particular *Gymnocalycium* and *Rebutia*), which previously have been thought to be “highly derived” within Trichocereae (in green), are not part of the core group of the tribe. Furthermore, the genus *Echinopsis* sensu lato is found to be polyphyletic.

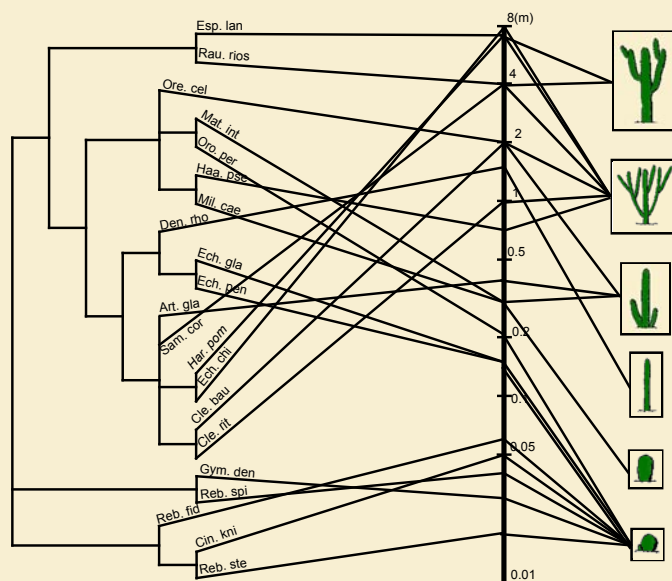


Strict consensus of 46989 most-parsimonious trees of length 1237 derived from an analysis of the combined *trnK/matK*, *rps16* and *trnS-trnG* data set. Bootstrap values are given above the branches.

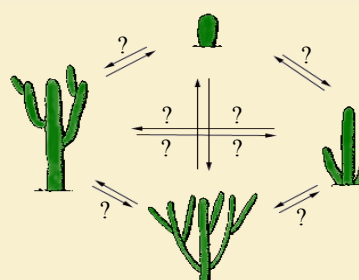


Growth form evolution — first investigations

The preliminary findings illustrate the complex pattern of growth form evolution. Phylogenetic relationships among selected exemplars of Trichocereae mapped onto stem height character space and a classification into six growth-form classes.



The patterns of character transition among the different growth form types in Trichocereae are now going to be investigated with the help of phylogenetic correlation analyses and the estimation of transformation rate differences.



The latter will be done in a likelihood framework using the software program MUL-TISTATE.