

Assessment of the PhD thesis of Eliška Záveská

The thesis „Phylogenetic studies in the polyploid genus *Curcuma* L.“ focuses on the phylogeny of the genus *Curcuma*, its taxonomic revision and reticulate evolution from various thematical perspectives and with a wide spectrum of appropriate lab methodology and analytical approaches. It is cohesive and the chapters/publications build on one another thematically: The first publication deals with the phylogenetic relationships within *Curcuma* subg. *Curcuma* utilizing amplified fragment length polymorphisms. The second paper issues the phylogeny of the entire genus with special emphasis on the *Curcuma*-like taxa, based on classical molecular markers (nuclear internal transcribed spacer and three plastid markers), and a third subgenus, *Ecomata*, is proposed. Results from this study are taxonomically summarized in a submitted manuscript, which was mainly done by other members of the Zingiberaceae research team. In the fourth part of the thesis low-copy nuclear markers are used to study hybridization between distantly related *Curcuma* species, and an analytical pipeline was developed to test if hybridization played the crucial role in speciation of certain taxa. This pipeline includes gene-tree/-network as well as species-tree/-network reconstructions and tests for incongruencies amongst gene-trees as well as between gene-trees and species-trees.

Lab work was mainly conducted by the PhD candidate, assisted by two technicians, data analysis performed by the candidate alone, incorporating knowledge from attended PhD courses. Collection of the material as well as its determination was done by the consultant Jana Leong-Škorničková. For me it is difficult to say if a significant amount of data for larger parts of publications 1 and 2 were already collected during the MSc thesis of the candidate (see first sentence on page 46), which would then slightly weaken the impression of this striking piece of work. In summary, the thesis demonstrates that the PhD candidate is strong in wet lab and data analysis, following newest trends in the research field, and is capable of interpreting results in a broad context (including morphology, karyology, mating system, biogeography). The candidate has hereby shown that she is able to perform independent research as a systematic botanist and evolutionary biologist with a focus on molecular techniques.

Questions to the defendant

Based on your data, are you more in favor of a WGD event preceding *Curcuma* diversification or occurring within the genus *Curcuma* after its diversification? (Introduction)

Where do you see your evidence for polyploidization following hybridization as the most important evolutionary process in *Curcuma*? (Paper IV)

Do chromosome counts and/or ploidy measurements support the subgeneric phylogenetic assignment of the *Curcuma*-like taxa in the ITS and plastid trees? (Paper II)

You aimed at a new infrageneric classification covering genetic and morphological variation within the genus. However, taxonomic treatment in Paper III is mainly based on your genetic results. Has the mentioned congruence between the degree of genetic and morphological variation ever been analytically addressed (in the text it's only described but no data are shown) and how would you translate this into a taxonomic concept? (Paper III)

Further comments

In my opinion the band-sharing approach as you applied it leads to an overestimation of allopolyploids. Guo et al. (2005) used exclusive AFLP bands that were stabilized „in all the individuals of a species or at least in one large population of a species“. Regarding the low number of populations per species and individuals per populations in the *Curcuma* subgenus *Curcuma* study this is critical. (Paper I)

Have you tried HybTree (Gerard et al., 2011) which is able to detect hybridization in the presence of incomplete lineage sorting? (Paper IV)