

Vondrák J., Svoboda S., Košnar J., Malíček J., Šoun J., Frolov I., Svensson M., Novotný P. & Palice Z. (2023) **Martin7: a reference database of DNA barcodes for European epiphytic lichens and its taxonomic implications.** – *Preslia* 95: 311–345.

**Supplementary data S2.** Phylogenetic analysis, *Cheiromycina*.

The alignments for mtSSU and LSU from the *Malmideaceae*-analysis of Kantvilas et al. (2021) were used (see their Table 1 for sequence-ID:s). In the mrSSU-alignment, *Cheiromycina* sequences from the Martin7 database were added. One terminal named *Cheiromycina flabelliformis* in Kantvilas et al. (2021) and Muggia et al. (2017) has been revised to *C. petri* in Martin7.

Name in Kantvilas et al. (2021)	Name in this analysis	GenBank-ID:s for markers used here
<i>Cheiromycina flabelliformis</i>	<i>C. petri</i> (A)	MF431799 + MF431804
<i>Cheiromycina petri</i>	<i>C. petri</i> (B)	MF431800 + MF431805
<i>Cheiromycina reimeri</i>	<i>C. reimeri</i> (C)	MF431802 + MF431806

The matrices for mtSSU and LSU were aligned separately using PASTA (Mirabab et al. 2015). After trimming of the ends of the aligned matrices, they were concatenated into one alignment and analysed using maximum likelihood as implemented in IQTree2 (Minh et al. 2020). The mtSSU and LSU alignments were submitted to the analysis as two partitions, but allowing merging if this improved model fit. The best model fit was achieved with the models TVM+F+G4 (mrSSU) and TIM3+F+ I+G4 (LSU), without merging of partitions. The assessment of branch support was calculated using ultrafast bootstrap, implying that only support values of 95% or over should be viewed as significant (Hoang et al. 2018). Only UBOT values above 95% were included in the figure below.

## References

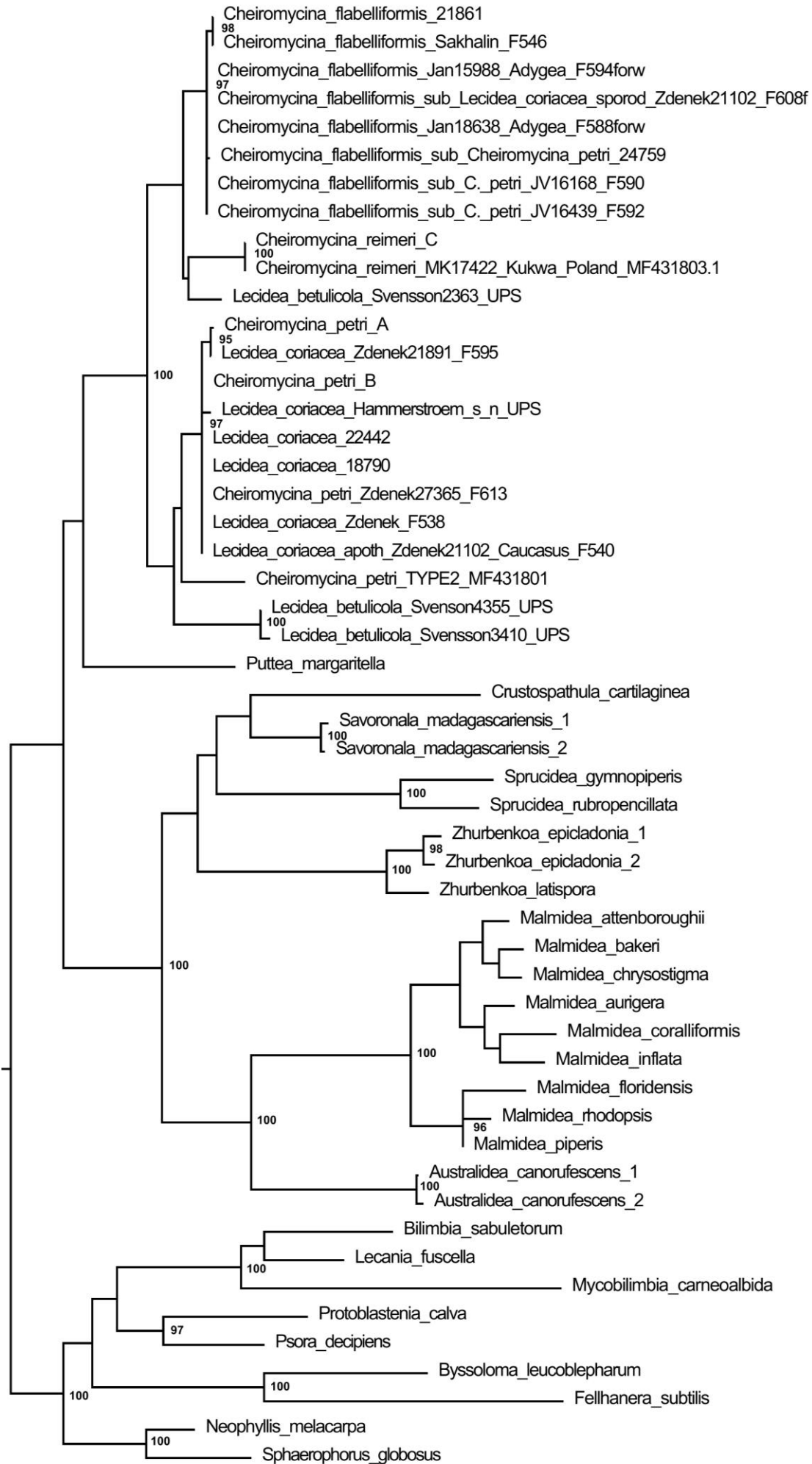
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