

Phylogenetic relationships within the subfamily Candoninae: new evidence from combined mtDNA and nDNA data



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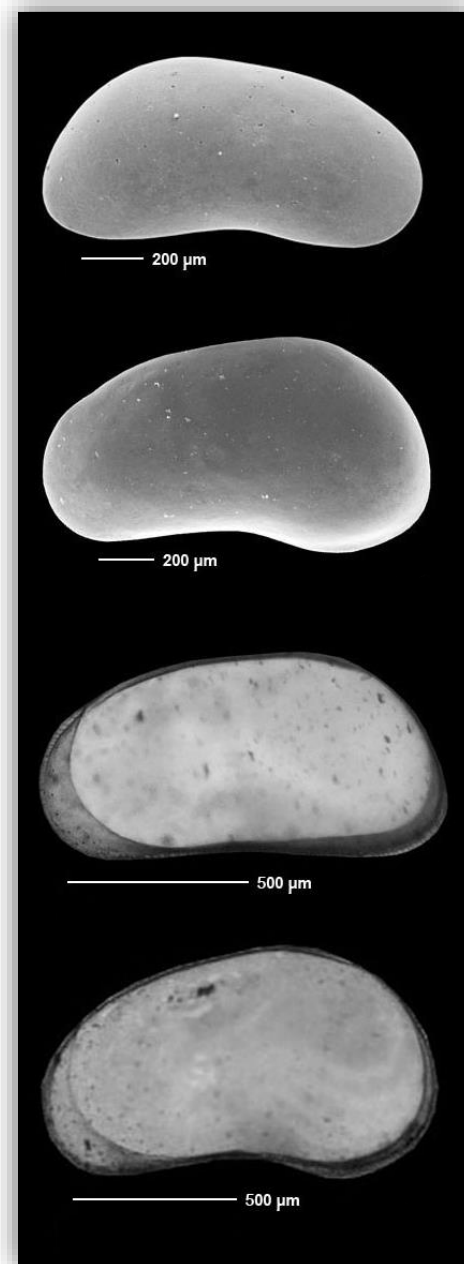


Introduction

The subfamily Candoninae is one of the most taxonomically difficult and species-rich lineage of freshwater ostracods.

Currently this group comprises ca. 50 genera with over 550 species, which are diagnosed almost exclusively by morphological characters. Our knowledge of the above-species systematics on candonines is still very limited and due to several homoplasies, phylogenetic relationships within the subfamily still remain ambiguous.

The present study aims at inferring phylogenetic relationships among Candoninae genera and species occurring in Europe based on two molecular markers.



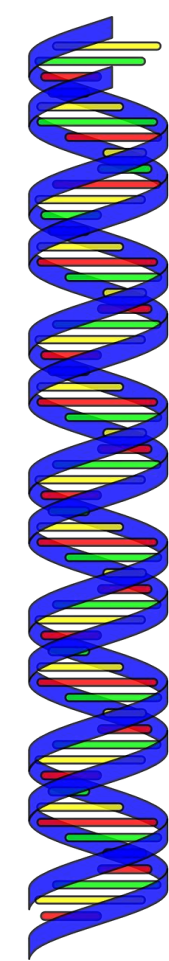
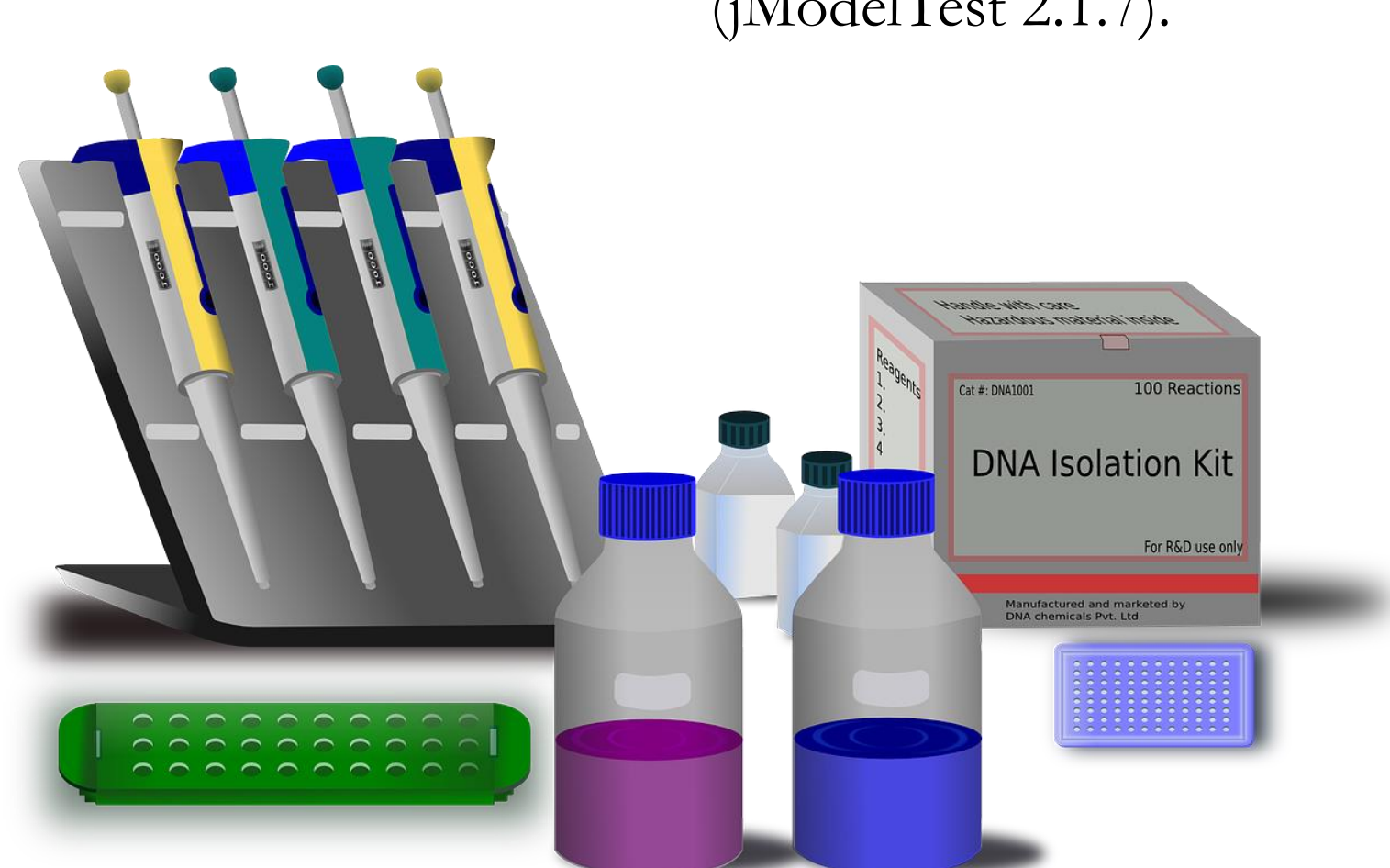
Material and methods

To test the morphology-based taxonomy and monophyly of European morphogenera of Candoninae we used two molecular markers: 1) the cytochrome oxidase subunit I mitochondrial gene (*COI* mtDNA) commonly used as a molecular barcode, and 2) *28S rDNA*, a nuclear region characterized by a lower mutation rate, compared to the former one.

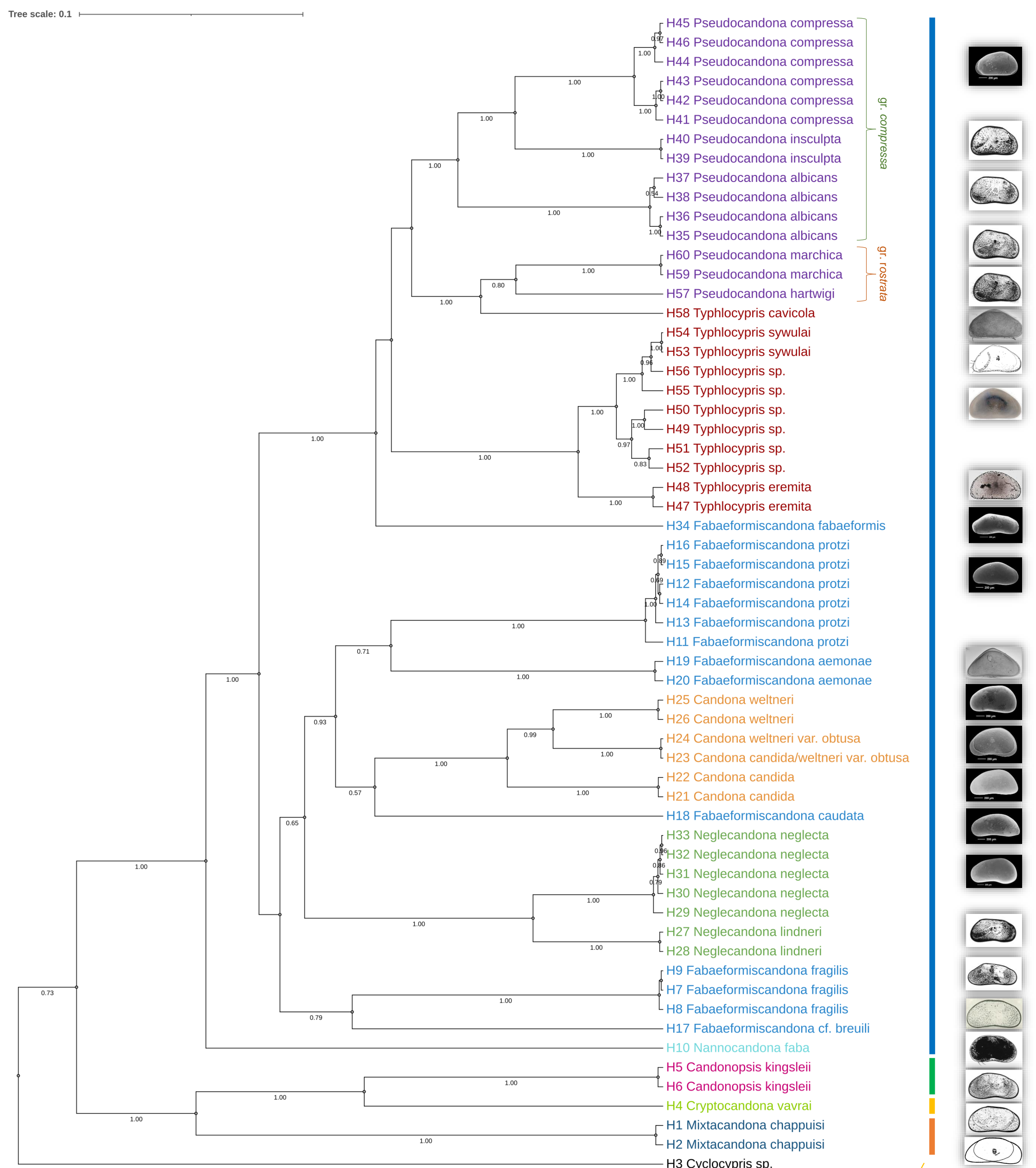
The *COI* gene fragment was amplified using LCO1490/HCO2198 primer pair, while *28S rDNA* amplification was performed using a vv/xx pair of primers.

The data set consisted of 105 combined sequences from representatives of 24 species belonging to nine genera and four tribes of Candoninae. As an outgroup, sequences of *Cycloocypris* sp. were used.

The phylogeny was reconstructed based on partitioned data using Bayesian inference (BEAST v1.10.4) with GTR+G+I model of evolution (jModelTest 2.1.7).

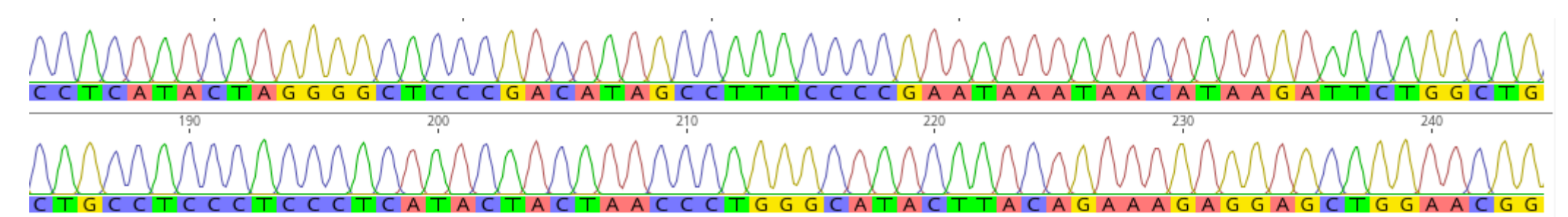


Results



Phylogenetic tree inferred from the combined mitochondrial *COI* gene and *28S rDNA* gene. The results of mtDNA polymorphism analyses and relative frequencies of haplotypes revealed 60 haplotypes found among 106 individuals. Numbers given next to the respective node indicate Bayesian posterior probabilities (>0.50).

— Tribe Candonini
— Tribe Candonopsini
— Tribe Cryptocandonini
— Tribe Trapezicandonini



Conclusions

The genetic results confirm morphological separation of the genus *Typhlocypris* from *Pseudocandona* and also separation of the genus *Neglecandona* from *Candona*, nevertheless maintaining their close relationships. The monophyly of four Candoninae morphogenera belonging to the tribe Candonini seems to be confirmed: *Pseudocandona*, *Neglecandona*, *Candona* and *Typhlocypris* (with exception of *T. cavicola*). Our results also imply that the genus *Pseudocandona* should be divided into two or three clades, which to some extent are consistent with two morphological species groups of the genus (the group *compressa* and *rostrata*). *Fabaeformiscandona*, another morphogenus of Candonini, occurs to be polyphyletic, which has been already documented by several authors based on morphological criteria. It is also worth noting the close relationship between representatives of the genus *Candonopsis* and *Cryptocandona*, which are considered now to belong to two separate tribes, Candonopsini and Cryptocandonini, respectively. *Mixtacandona* (tribe Trapezicandonini) appeared also to form a separate clade with strong support, and although for each of these three genera there was only one species included, these were placed in the basal position as the sister to the genera of the tribe Candonini.

To better understand the evolution and diversification of Candoninae, further studies are needed, including additional nuclear markers and representatives of other European and non-European genera.