

New stygobitic ostracod species of the genus *Candonopsis* (Candonidae) from interstitial waters of Nouvelle-Aquitaine, France

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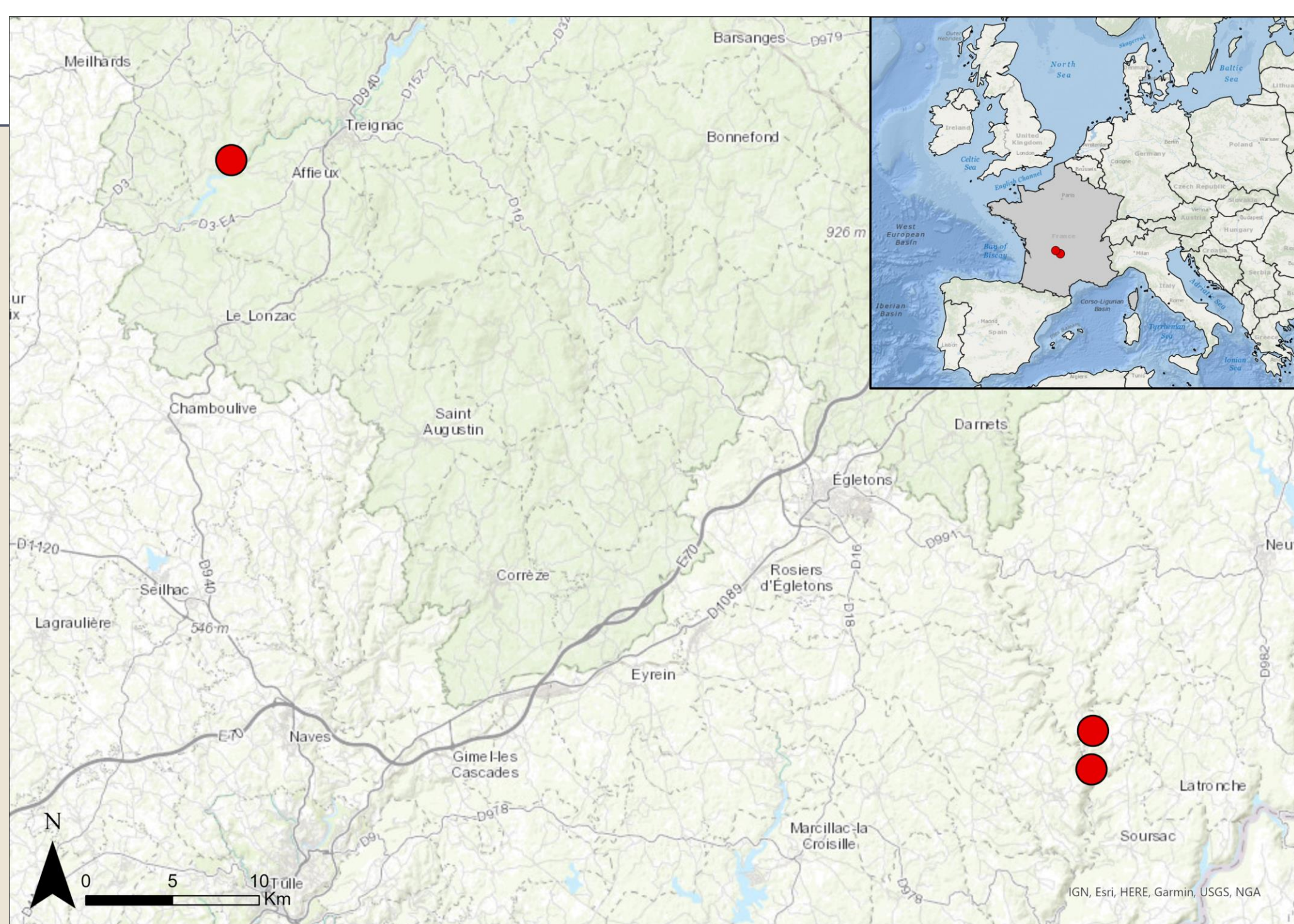
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INTRODUCTION



The tribe Candonopsini (Candonidae) is usually distinguished based on the absence of posterior seta on the caudal ramus. However, due to the frequent reductions of setae and claws in a number of various candonid species, to correctly diagnose Candonopsini this feature must be considered carefully and in concert with other morphological traits, and, if only possible, supplemented with molecular data in integrative taxonomy. In general, the proper assignment of a new candonid species to the tribe and genus remains often challenging due to considerable homoplasy frequently occurring in this group. The genus *Candonopsis* Vávra, 1891 is the type genus of the tribe Candonopsini and comprises 33 recent species classified in two subgenera: *Abcandonopsis* Karanovic, 2004 (7 Australian species) and *Candonopsis* (26 species distributed around the world, including 6 European species).

In this study, we describe a new species of the subgenus *Candonopsis* from male and female individuals collected from hyporheal of three rivers within the catchment of the Dordogne-Garonne Rivers in the Corrèze Department of Nouvelle-Aquitaine in central France.



MATERIAL AND METHODS



The samples were collected following the protocol of the PASCALIS project. Soft parts of dissected ostracods were mounted in glycerin and valves were stored dry on micropalaeontological slides. Carapaces and valves were gold-coated and observed under the scanning electron microscope.

To accurately infer the phylogenetic position of the newly described species, the analyses utilized two molecular markers: mitochondrial cytochrome c oxidase subunit I (*COI* mtDNA) (amplified using LCO1490/HCO2198 primer pair) and more conservative nuclear 28S ribosomal DNA (*28S rDNA*) (amplified using vv/xx primer pair).

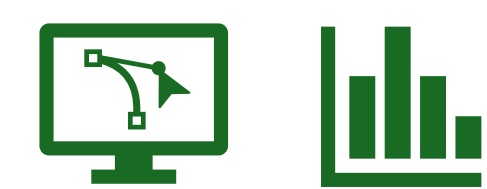
The data set consisted of 25 combined sequences (1038 bp) from representatives of 11 species belonging to six genera of the subfamily Candoninae. As an outgroup, sequences of *Heterocypris salina* were used.

The phylogeny was reconstructed based on partitioned data using Bayesian inference (BEAST 2) with HKY+G+I model of evolution for *COI* partition and TrN+G+I for 28S.

CONCLUSIONS

The present study underscores the significance of employing an integrative approach, which combines the analysis of carapace, morphology of limbs (soft-body) as well as molecular data, to accurately characterize the biodiversity of groundwater ostracods.

RESULTS



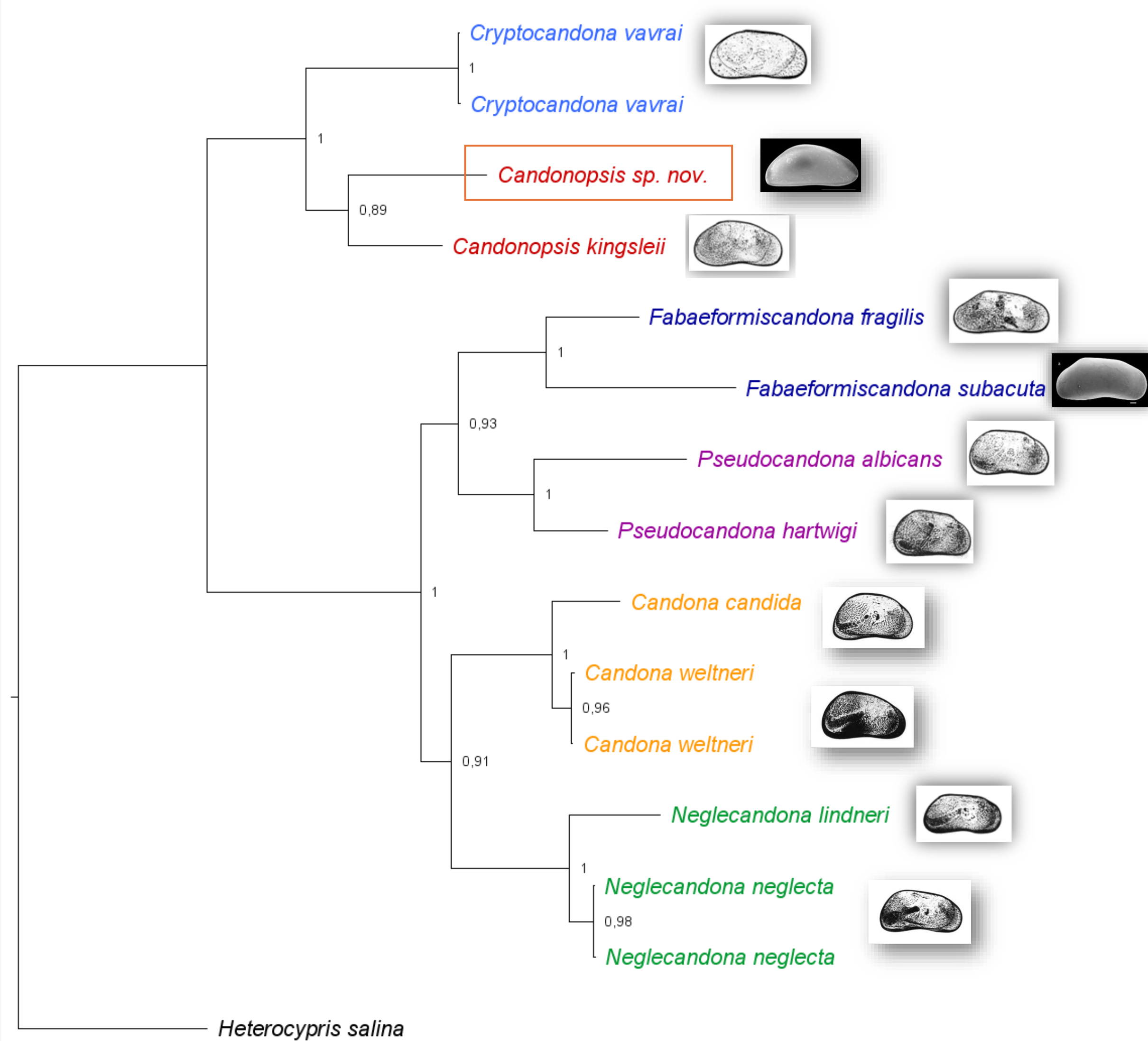
Morphological analyses

The newly identified species based on morphological evidence **differs from other members of the genus by its unique carapace shape** and also by **the structure of the male copulatory organs** (mainly shape of the medial lobe of the hemipenis).

Molecular phylogenetic analyses

Our results showed that *Candonopsis* sp. nov. is **closely related to *Candonopsis kingsleii***, which is the type species of the genus. Both species form well separated common clade, but genetic distance between them is high (0.12).

The results obtained from both morphological and molecular data are congruent, supporting the validity of the description of the new species.



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 14 haplotypes found among 26 individuals. Numbers given next to the respective node indicate Bayesian posterior probabilities.

Candonopsis sp. nov.

