

***Niphargus* diversity from South-West France through the lens of the barcoding fragment of cytochrome-oxidase I (Crustacea, Amphipoda)**

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Niphargus is the most speciose amphipod genus inhabiting groundwater of the Western Palearctic, counting over 450 described species. The genus is known for its problematic taxonomy, including large within-, yet sometimes negligible between-species variation, often associated with cryptic diversity. With the onset of the molecular methods, it became clear that morphological variation captures between one half to one third of genus's genetic species diversity, raising the need to revise past taxonomic and faunistic efforts using molecular markers. Research efforts of several laboratories in Europe have been dedicated to this task during the past two decades. Hence, *Niphargus* was a subject of intense exploration in parts of Great Britain and of Pyrenees, Alpine and Carpathian arch, Dinaric region and Caucasus. Surprisingly, France remained relatively understudied, despite the long tradition in *Niphargus* research and the fact that the very first molecular studies on *Niphargus* originated from this country. Here, we fill this gap and revise diversity of *Niphargus* in France using molecular markers. We accumulated a large number of samples originating from dedicated sampling campaigns of stygofauna in the south-western parts of the country, samples collected during exploration of isopods and other occasional sampling events. The samples covered altogether over 260 locations. Of these, we selected 434 individuals, whose morphology corresponded to 26 nominal species. We isolated DNA and amplified the Folmer's fragment of the mitochondrial COI marker. To test for species diversity, we employed unilocus species delimitation Assemble Species by Automated Partitioning (ASAP) and identified 136 Molecular Operational Taxonomic Units (MOTUs). Notwithstanding the limits of ASAP and similar statistical species delimitation techniques, more than 80 MOTUs need to be investigated as putative new species, indicating that *Niphargus* diversity in France is probably as underestimated as in the rest of this genus range. We detected up to 6 MOTUs within the morphological species identified as *N. ciliatus*. Moreover, we assessed phylogenetic origin of *Niphargus* collected in France. We selected one individual per MOTU and amplified three additional nuclear markers (two 28S fragments and Histone 3, subunit 2). The phylogenetic hypothesis unveiled that *Niphargus* from France comprise lineages derived from deep splits within the genus and recent speciation events. The study closed an important knowledge gap in molecular-spatial coverage of *Niphargus* and the available barcodes will contribute to future integration of *Niphargus* into biodiversity studies.

