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## Molecular phylogeny of *Niphargus boskovici* (Crustacea: Amphipoda) reveals a new species from epikarst

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### Abstract

We describe a new species of an amphipod *Niphargus zagorae* sp. n. and redescribe its nearest relative and morphologically similar species *N. boskovici* S. Karaman, 1952. We present the geographic distributions of both species, morphological diagnoses and infer their phylogenetic position within the genus based on COI, 28S and H3 markers.

**Key words:** *Niphargus*, taxonomy, cryptic species, epikarst

### Introduction

The amphipod genus *Niphargus* is the most species-rich genus of hypogean amphipods in the world. It consists of over 300 species, which mostly occur in central and southeastern Europe (Väinölä *et al.* 2008). *Niphargus* species have been found in various aquatic habitats related to groundwater, including different types of springs, sinking rivers, cave lakes and interstitial water (Sket 1999). Many species are narrow range endemics—a pattern that reflects the fragmented nature of karstic systems and poor migratory abilities of cave amphipods (Fišer 2012; Trontelj *et al.* 2009).

The highest species diversity of *Niphargus* has been found in the Apennine Peninsula and Dinaric Karst (Zagmajster *et al.* 2014). The Dinaric Karst is a 650 km long limestone massif in the Western Balkans stretching from northwest to southeast along the Adriatic coast (Mihevc *et al.* 2010). Cave fauna of the area has been studied for more than a century and the region itself can be considered as one of the most thoroughly explored areas for subterranean fauna in the world. Despite this, new species from many taxonomic groups are still being discovered (e.g., G. S.Karaman 2014a; Bilandžija *et al.* 2013).

The taxonomy of the genus *Niphargus* is incomplete. Some species are rare, or may live in inaccessible parts of karstic systems; their collection requires additional sampling effort (Fišer & Zagmajster 2009). Some of the species have been simply overlooked, especially if not subject to detailed comparative analyses. Small sample sizes and limited knowledge of intra- and interspecific variation makes taxonomy even more difficult. Moreover, several molecular studies in the past years showed that many nominal species comprise a number of morphologically similar, so called cryptic species (Lefébure *et al.* 2006, 2007; Trontelj *et al.* 2009; Meleg *et al.* 2013; McInnery *et al.* 2014). Species experiencing a similar selective regime may resemble each other to a great extent and may differ only in few minute details (Fišer & Zagmajster 2009). Detection and taxonomic evaluation of such minute differences is demanding and hardly possible without a molecular taxonomic framework, especially if sample sizes are small (see Lim *et al.* 2012 for the problem of sample size in taxonomy). It is becoming more and more obvious that future species discovery within *Niphargus* strongly relies on the use of molecular techniques and that the most accurate morphological diagnosis can be defined *a posteriori*, once species are delineated within a molecular framework (e.g., Schlick-Steiner *et al.* 2010). As taxonomy progresses, new characters are discovered and old descriptions inherently become incomplete. Descriptions of new species therefore often require updated redescriptions of already established species for comparative purposes (Fišer *et al.* 2009).