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Conference Abstract

# Integrating multiple species criteria and species hypotheses in subterranean biology

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## Abstract

Decades of debates around the species problem have resulted in the emergence of a unified species concept with multiple criteria to delimit species taxa. Many biologists now agree to consider species as separately evolving segments of metapopulation lineages (i.e. the species concept), and to consider species taxa (i.e. the elementary units used in biodiversity science) as scientific hypotheses of separately evolving entities. In this framework, sets of species hypotheses are generated using different criteria (i.e. morphological distinguishability, genetic isolation) that mirror the properties expressed by species at different times and sequential orders during the extended and heterogeneous process of speciation. This conceptual and methodological advance in taxonomy has several implications for biodiversity science. First, species taxa represent a heterogeneous set of hypotheses whose properties are contingent on the heterogeneous, continuous and extended nature of speciation. Second, species databases need to integrate information on the diverse properties of species by attributing specimens to multiple species hypotheses generated using different delimitation criteria. Third, biodiversity science at large can provide novel insights into biodiversity processes by incorporating multiple species hypotheses into the analysis of biodiversity patterns. Here, we show how these implications

have been taken into account by subterranean biologists. First, we briefly review the criteria and methods used to delimit species in subterranean biology and the diverse sets of species hypotheses they generated. Second, we present a new generation of species occurrence databases that integrate different species criteria and hypotheses while fully respecting the scientific rigor of taxonomy. Last, we show how incorporating multiple species hypotheses into macroecological analyses of European groundwater fauna bolsters our understanding of the factors shaping large-scale patterns of species richness and geographic range size.

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