It has long been assumed that differentiation in external appearance is necessary for recognizing distinct species. However, advancements in molecular research over the last decades have shown that a substantial number of species are morphologically indistinguishable (i.e., cryptic). Despite their ubiquity, cryptic species are often not formally described, and, as such, remain unrecognised by nature conservation agencies. This places them under a higher extinction risk than formally recognized species. The reluctance of scientists to describe cryptic species mainly stems from technical and conceptual challenges, since traditional taxonomy is overwhelmingly based on external morphology. This issue is further exacerbated in highly diverse groups that comprise tens to hundreds of cryptic species which are at various stages of species formation. Quantifying the true number of distinct species in such groups remains highly challenging due to the large amount of data needed. A cost-effective molecular method known as DNA barcoding is widely employed nowadays to document undescribed species diversity. Although it has shown great promise in many organisms, its accuracy has still not been tested in challenging groups comprising hundreds of cryptic species. In this project we will focus on hyper-diverse cryptic species of amphipod crustaceans belonging to the genus *Gammarus* from freshwater habitats of the Caucasus region – one of the Earth's major biodiversity hotspots. Our preliminary DNA barcoding analyses revealed that in this region there could be over 100 cryptic *Gammarus* species, although morphologically six main groups have been recognized. Our aim is to integrate multiple lines of evidence (geography, genes, genomes, and external morphology) and analytical approaches to understand the true number of cryptic species, their evolutionary relationships, origin, and time frame of diversification in the Caucasus. These results will help us evaluate the accuracy of DNA barcoding in disentangling challenging groups of organisms, will illuminate our understanding of why some species remain unchanged over time, and will help us uncover the deep historical factors that have shaped the Caucasus biodiversity hotspot. This will contribute significantly to our understanding of the overall pattern of crustacean evolutionary dynamics in freshwaters and mountain ranges at both European and global scales. Finally, the formal recognition of many of these species will ensure their long-term conservation amid the currently unfolding biodiversity crisis.