

Project objectives

The main aim of this project is to estimate the biodiversity, on morphological and molecular level, and to establish biogeographical affiliations of freshwater gammarids (Amphipoda, Gammaridae) from two Mediterranean islands – Crete and Sicily. The secondary goal of the project is to provide the spatiotemporal framework for the species origin and diversification by reconstructing their time-calibrated phylogeny based on mitochondrial and nuclear molecular dataset its interpretation in the context of the geological history of the islands.

Research

The project will focus on two major, continental Mediterranean Islands: Crete (Greece) and Sicily (Italy). For the geological history of the mentioned islands, analysis of the gammarid fauna from the following reference areas is planned: Peloponnesus for Crete, Apennine Peninsula and Northern Africa (Tunisia) for Sicily. Additionally, some material from Balears, selected Aegean Islands and Cyprus will be analysed to provide a background for interpretation of similarities and differences between the insular fauna from islands of different origin. This will provide more detailed picture of freshwater biodiversity of gammarid fauna of the Mediterranean Islands. DNA needed for molecular analyses will be extracted from at least 12 individuals from each sampling site. Then, the DNA Barcoding with primers for COI (Cytochrome Oxidase subunit 1) will be performed to identify the Molecular Operational Taxonomic Units (MOTU). Then DNA from selected 3 individuals from each MOTU will be amplified for other nuclear and mitochondrial molecular markers. Thanks to using multiple markers, there will be a reliable comparison of the obtained results with other work focused on similar topic and, using the collection already stored in GenBank database, it will be possible to discuss them in broader phylogenetic context. All the sequencing will be performed using Sanger method. It is a method widely used for over 30 years in numerous molecular studies. New species identified during the course of the project will be described using of various types of optical microscopes, scanning electron microscope as well as other tools (digital imaging systems, pen tablet) and software for graphical work. Obtained images will be used as supplementary features (if classic morphological methods fail) for describing new species.

Impact

There are several reasons for choosing this particular research topic. First, islands are considered to be natural laboratories of evolution and places with extremely high level of endemism, and the Mediterranean Region itself is known to be one of the 25 most precious biodiversity hotspots in the world. The proposed project will be also among the first such extensive studies upon the diversity and biogeographical affiliations of epigeic freshwater fauna of the Mediterranean Islands. Second, considering the lack of up-to-date data and the fact, that Gammaridae are known of high cryptic diversity, one may expect presence of new, yet not described species. In case of the species reported from the studied Mediterranean Islands, most of the published descriptions of the species require actualization and taxonomical revision. The results of this study will be helpful in establishing new, up-to-date identification keys based on not only on morphological features, but also on ultrastructural characters and DNA barcodes, making them the most reliable taxonomic tools. Third, still little is known about origin and mechanisms of diversification of freshwater fauna, not only on Mediterranean islands, but on whole continental Europe. With exception of vertebrates, evolutionary mechanisms and historical factors behind formation of freshwater fauna remain poorly known and understood. That is why, due to innovativeness of the research and the research topic, it may be presumed that results of our study will significantly broaden the knowledge of the freshwater fauna in Mediterranean Region. Moreover, the results will help with planning reasonable and effective strategy preventing or at least minimalizing the loss of biodiversity.