



COMPARING TRADITIONAL AND INNOVATIVE TOOLS FOR ANALYSING THE BIODIVERSITY OF AQUATIC ECOSYSTEMS IN ALBANIA

PhD Student: Dr Mariola Ismailaj; *Scientific Tutor:* Prof. Maurizio Pinna; *Academic supervisor:*
Prof. Luciana Migliore

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Aquatic biodiversity includes all unique species, their habitats, their interaction, and ecosystem functions. In Albania, 3,200 taxa of higher plants, 800 fungi, 1,200 diatoms, as well as 313 taxa of fish, 323 birds, 36 reptiles, 70 mammals, and 520 mollusks, have been identified, both in terrestrial and aquatic ecosystems. A total of 27 plant species, with 150 sub-species, are endemic to the country. There are several threatened species (73 vertebrates and 18 invertebrates) and almost 79 alien species. Albania is also well known for its rich and complex hydrographic network composed of rivers, lakes, wetlands, groundwater, and sea, but the whole biodiversity is not completely known, yet as well as its responses to natural and anthropogenic pressures. So, monitoring biodiversity and conservation strategies to protect and conserve aquatic life is necessary to maintain the balance of nature and resources for future generations.

The current status of aquatic biodiversity monitoring in Albania is rather incomplete and fragmented. The bioassessment of aquatic ecosystems is currently based on various biotic indices that use selected taxonomic groups' occurrence and or abundance to define ecological status. These conventional indices have some limitations, often related to difficulties in morphological identification of bioindicator taxa. However, the recent development of DNA barcoding and metabarcoding could potentially alleviate some of these limitations, by using DNA sequences instead of morphology to identify organisms and to characterize a given ecosystem.

This project aims to compare the actual data based on the traditional methods of morphological with the gained data that we can have with the new DNA-based methods of analyzing aquatic biodiversity. The proceeding of the project will be with the review of the existing data on the biodiversity of aquatic ecosystems in Albania, a gap analysis of available DNA species sequences, to identify target aquatic ecosystems for new experiments, to define the experimental design, sampling collection, and analysis, and finally to compare the traditional and innovative methods. The methodology will include isolation of DNA, amplification with PCR, reduction of replication sequences, and taxa identification. We will compare the main advantages and disadvantages of metabarcoding approaches to assess parameters such as richness, abundance, taxonomic composition, to be used for the calculation of biotic indices. We will also propose some recommendations for the future integration of DNA metabarcoding into routine biomonitoring programs.

It is expected that this study will contribute to subsequent collaborations in the context of environmental management of aquatic ecosystems of Albania.