

the missing approach for the Conservation of freshwater Bivalves

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Summary: The decline of freshwater biodiversity has reached alarming proportions. The extinction rate of freshwater biodiversity is predicted to be five times faster than all other groups of species. The Unionidae, being the largest of the freshwater bivalve families, is among the most endangered group in the world. They are important providers of aquatic ecosystem services and are characterized by an unusual pattern of mtDNA inheritance. However, phylogeny, population genetic structure and species-level diversity remains unclear for much of the group.

Aims: With an experienced and well-qualified team, the present project aims to define the most important freshwater mussel taxa and most critical areas for conservation, at European and Global levels, to inform the most relevant policy makers, by integrating a genomics approach with available distribution data, in order to determine and map global species richness, phylogenetic diversity, and weighted endemism.

Methodology: The project is organized in 6 complementary tasks, which rely on the interactive collaboration of team members and that together with the original combination of approaches is expected to overcome the challenge of studying FM at global scale:

Task 1 - Taxon sampling and mtDNA data: Task designed to fill the missing sampling gaps in the existing samples for the development of all the other tasks. Additionally whole F- and M-mitogenomes for all major taxonomic group within Unionida will be obtained, as well as a comprehensive coverage of the main mtDNA lineages of all Western Palearctic taxa.

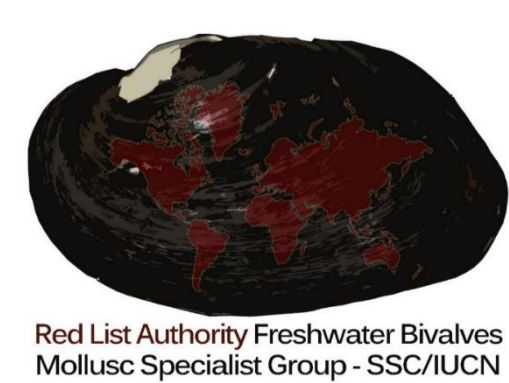
Task 2 - Nuclear loci: This task will allow to obtain, for all Western Palearctic taxa, a nuclear marker and thousands of RAD loci that will be used in Tasks 4-6.

Task 3 - Higher-Order Global Phylogenomics : The goal of this task is to obtain a higher-order global phylogeny. Also, this task will allow the development of a method and a genomic pipeline to be widely applied in studies that use animal mtDNA.

Task 4 - Genetic diversity patterns in the Western Palearctic: This task will retrieve the genetic diversity patterns and phylogeographic structure of the West-Palearctic taxa, and define their Evolutionarily Significant Units.

Task 5 - Species delimitation: The aim of this task is to test different methodologies for species delimitation, to get a robust Integrative Species Delimitation Method, as well as a well-supported checklist of the Western Palearctic freshwater mussel's species.

Task 6 - Priority taxa and areas for conservation: By the integration of all the other tasks, the final outputs of the project are obtained in Task 6. The aims are the definition of the most important FM taxa and areas of critical importance for conservation, both at the European and at a Global level.



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