

DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

In the present proposal, using midges (Diptera Chironomidae) as flagship taxa of freshwater ecology, I am focusing on the interesting model represented by the Skadar Lake system, a well-known hotspot of freshwater biodiversity composed by the young lake Skadar (originated 1200 BP) and by its old system of springs (originated during Pliocene).

The main goal of following project is to explain two relevant evolutionary questions different scales:

Q1) Where the midges community of Skadar Lake system came from? Basically, I would like to compare the midges community of Skadar Lake system, in term of species composition, with those of other, investigated lakes belonging to a similar mediterranean ecoregion and placed at different distances from it;

Q2) Have the old springs system represented the source of organisms for the colonization of Skadar lake after its appearance? Skadar Lake is probably the remnant of previous, much broader interlinked lacustrine system, first brackish and then freshwater, which has gradually fragmented and finally disappeared.

In this project I intend to develop a multifaceted approach, using state-of-the-art massive data generation technologies such as the **DNA metabarcoding** and the **RADsequencing** based on *cytochrome oxidase* subunit 1 (*cox1*, *COI*) gene, to address the two proposed main hypotheses. Proposed **Next Generation Sequencing Techniques (NGS)** allows to reduce the cost and time of analysis of each individual while increasing the amount of information obtained after sequencing. This increases both the range (extension) and accuracy of research. These techniques combined with traditional taxonomy based on morphological characteristics and numerical methods applied in ecology will give an unequivocal answer to main questions.

The pioneering nature of the project is to achieve two basic tasks. First, to **assess the species composition of the unique habitat almost unexplored basin, which is the Skadar Lake**. Secondly, to **develop the knowledge on fundamental processes shaping the distribution of species Chironomidae**. This task, based on the hypothesis that the old springs system might, or not, have represented the source of chironomid species for the colonization of Skadar Lake after its appearance. These objectives can be achieved using as model the flagship taxa (=taxocenosis) of freshwater ecology represented by Diptera Chironomidae and benefiting of high-throughput sequencing technologies, as the DNA barcoding and the RAD sequencing.

Beside the improvement in the knowledge of chironomids fauna inhabiting the analysed Skadar Lake water system, (i.e., understanding pattern and processes that lead to the present Skadar system fauna) the results achieved during this study will have major implications in the development of farsighted strategies of freshwater biodiversity conservation, especially within a scenario of global warming, as that observed in the last decades. Midge larvae are very important for water quality assessment and they remain underutilized since the current sorting techniques cannot deliver species-level resolution at a reasonable cost. In addition, only the adult male stage is described for most non-European species, leaving out larvae that would be most useful in bio-assessment. Beside the previously highlighted impact, the **development of an accurate database of cytochrome oxidase subunit 1 (*cox1*) gene sequences for midges inhabiting the Skadar Lake system, will be of extreme interest for existing databases (e.g., BOLD, GenBank) and ongoing projects (e.g., DNAqua-Net COST Action CA 15219).**