

**UNIVERSITÀ DEGLI STUDI DI MILANO-BICOCCA**  
***DOTTORATO DI RICERCA IN Tecnologie Convergenti per i Sistemi***  
***Biomolecolari – XL CICLO***

**Research Topic ID: XL – 1.15**

**Proponent:** Dr. Davide Maggioni

**Project Title:** The effects of environmental and anthropogenic stressors at the genomic and transcriptomic level in non-model animal species

**Scientific background and ‘open issues’**

The loss of biological diversity is a global phenomenon leading to the decline of species, communities, ecosystems and ecological functions. Recent syntheses highlighted that the main anthropogenic driver of biodiversity loss is land/sea use, followed by exploitation of resources, pollution, climate change, and invasive species [1]. These stressors affect the diversity of genes, organisms, and functions, therefore also resulting in the decline of the goods and services that biodiversity offers to humanity [2].

Environmental and anthropogenic stressors have been demonstrated to directly interfere with the phenotypes, population dynamics, interactions, and evolution of different species. However, the genetic changes and the genomic architecture of the adaptations associated with these stressors are still poorly understood [3]. This is likely about to change soon due to the rapid advances in genomics and transcriptomics, and because of both the steadily increasing stressors and the growing interest in preserving and enhancing the biodiversity. Indeed, the characterization of the fine-scale effects of stressors at the genomic level is fundamental for the understanding of the short- and long-term consequences on biodiversity, the definition of conservation units, and the identification of the most effective conservation measures.

**Objectives**

The project aims at defining the effect of environmental and anthropogenic factors on selected functionally important non-model animal species (e.g. pollinators, bioindicator species). The overall objective is the characterization of the effect of these factors at the genomic and transcriptomic scale, with the final aim of helping guide conservation and sustainability efforts.

Specifically, the candidate will work to address biological questions including:

1. Assessment of the effect of natural environmental parameters, habitat fragmentation, land use and urbanization on genetic variation, population genetics parameters, demography, gene flow and connectivity of the studied populations.
2. Identification of putative regions of the genome under selection, to assess the local adaptation of the populations to the above-mentioned environmental and anthropogenic factors.

3. Assessment of the differential gene expression among the populations sampled in different conditions and identification of putative stress biomarkers that will be further explored and implemented.

### Methodologies

Analyses will be performed on already obtained and newly collected specimens, therefore requiring field activities during the course of the project. Sampling sites will be selected according to the variables of interest. Environmental data will be collected directly and through publicly available databases to characterize the sampling localities in terms of environmental and anthropogenic stressors.

Samples will be then sequenced mostly using whole genome sequencing and mRNA sequencing, and the obtained data will be analysed using different bioinformatic approaches.

Neutral DNA markers will be investigated to obtain information on population genetics parameters, genetic variation within and among populations, gene flow and connectivity. These data will be analysed in a landscape genetics framework, to assess the influence of different environmental variables on the genetic diversity and structure of the organisms.

The adaptive DNA variation will be analysed to identify genomic regions under selection and to assess local adaptation to specific environmental variables, using a comparative genomics approach and association studies. The panel of identified loci will be further tested for their role in local adaptation, allowing the characterization of the genomic architecture of the adaptation to different stressors.

Finally, RNA data will be used to assess the fine-scale differential gene expression profiles under different conditions and the obtained results will be compared with genomic data to understand the responses of the species at different evolutionary scales. These data will be also used to identify putative stress biomarkers to be further tested and implemented.

### Project's Sustainability & Mobility

The research group has a consolidated experience in molecular biodiversity analyses on non-model organisms, including for instance population genetics and phylogenetics using both first- and second-generation sequencing techniques [4-7]. The group is currently working on projects dealing with the effect of environmental stressors on genomes and transcriptomes of functionally important invertebrates.

The research group collaborate with several Italian and foreign institutions, and the candidate will have the chance to spend a period of approximately six months in other laboratories, in order to acquire further multidisciplinary skills. Possible foreign destinations could be the National University of Singapore (Singapore) and Naturalis Biodiversity Center (The Netherlands).

### References

- [1] Jaureguiberry et al. (2022). *Sci Adv*, 8, eabm9982.
- [2] Cardinale et al. (2012). *Nature* 486, 59-67
- [3] Rivkin et al. (2019). *Evol Appl* 12, 384-398
- [4] Maggioni et al. (2020). *Mol Phylogenet Evol* 151, 106893
- [5] Galimberti et al. (2020). *Mol Ecol Res* 21, 183-200
- [6] Maggioni et al. (2024). *Cladistics* 40, 107-134

[7] Taninaka et al. (2021). *Front Mar Sci* 8, 714662.