



Projeto Nº | PTDC/CTA-AMB/3065/2020

Designação do Projeto | EdgeOmics: Bivalves no limite: genómica da adaptação em cenários de alterações climáticas

Entidade Beneficiária | CIIMAR - Centro Interdisciplinar de Investigação Marinha e Ambiental

Copromotores | ICETA - Instituto de Ciências, Tecnologias e Agroambiente da Universidade do Porto; IPBragança - Instituto Politécnico de Bragança; UTAD - Universidade de Trás-os-Montes e Alto Douro; UM - Universidade do Minho

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Data de início | 01/03/2021

Data de conclusão | 29/02/2024

Custo total elegível | 249.389,25€

Valor de financiamento a atribuir no âmbito do Orçamento de Estado | 249.389,25€

Síntese do Projeto: Freshwater mussels (FM) from the Unionidae family, are a group of sessile and often long-lived molluscs extremely interesting from a biological perspective. They play crucial roles in the ecosystems such as water purification, nutrient cycling, as a food resource and habitat provisioning; have a rare life cycle, that requires a host fish species for larval development and upstream dispersal; and are characterized by an unusual pattern of mitochondrial inheritance called Doubly Uniparental Inheritance, in which all individuals have the typical maternally transmitted mtDNA, but the males possess in their germ cells a paternally inherited mtDNA instead. Having all these extraordinary characteristics, FM are particularly vulnerable to habitat degradation, susceptible to anthropogenic and climatic habitat disturbances, and thus, like many other freshwater taxa, FM have suffered huge population losses.

Freshwater ecosystems are indeed at great risk and with unprecedented threats to the biodiversity they support. Climate change is intensifying these trends, with future scenarios predicting an exacerbation of drought conditions in all Mediterranean areas where many watercourses already dry up in summer, challenging the adaptation and survival of freshwater organisms and acting as additional selective stress forces. In southern Europe, despite the lower FM species richness, spatially restricted species make Mediterranean river basins a high conservation priority. On the other hand, there is general warming in Europe, with decadal temperature variations stronger in Scandinavia compared to the global mean, making populations at the Northern edge of their distributions seriously threatened too. FM are especially vulnerable to extreme temperature changes and the few studies to date suggest that some species are already living near their upper thermal limit. Thus, and due to FM's crucial role in the ecosystems and their overall conservation status, identifying and quantifying threats to FM are vital for conserving the biodiversity and ecological integrity of freshwater systems.

During the last ten years, in a series of funded projects, the team has filled the gap of knowledge of FM's evolutionary histories and biological features. Now, the present project will use an innovative multidisciplinary approach to test the adaptive genetic variation related to environmental variation in natural populations of FM. The aims of this proposal are to 1) assess genomic changes and responses associated with climatic adaptations 2) evaluate if adaptation is the factor that can mitigate the impact of

climate regime variation 3) expand our understanding of neutral vs. adaptive genes. As we aim to identify the molecular kernel and functional pathways potentially involved in environmental stress response, three target FM species were selected based on their close evolutionary relationships, similarities in life-history traits, and with both drought (*U. delphinus* and *U. manicus*) and cold (*U. pictorum*) tolerances. They will be sampled (Task1) along a latitudinal and temperature gradient, from the Mediterranean to Scandinavia, allowing the impact of natural selection to be contrasted across areas with very different ecological conditions, where populations will presumably contain functionally important polymorphisms adapted to variation in the environment. We will then sequence each species genome (Task2). This will not only increase dramatically the very limited existing FM genome resources but also allow to identify FM candidate genes and functional pathways potentially involved in environmental stress response. Task 3 is based on the characterization of the main abiotic factors and field observations, designed to reveal which if any populations/species have behavioral strategies that may increase survival (e.g. do FM burrow into cooler, wetter sediments or/and do they move to deeper pools). Later Tasks4 and 5 consist of experimental studies of ecological performance (manipulating the abiotic environment to mimic predicted future climate and behavioral strategies characterization) to tease apart the possible differences in physiological tolerances profiles that might be present due to prior exposure to the stressors. Finally, RNA-sequencing at the population level (Task6) will provide the transcriptome profiles, i.e., differentially gene expression and profiles identification, between exposed (from experimental treatments Task5) and non-exposed (natural environment Task2) specimens, as well as identification of the gene regions that have been affected by selection.

We expect to obtain novel insights into the processes by which freshwater species with broad geographical ranges can/might adapt to local environmental conditions and gain a clearer understanding of the evolutionary history of these imperiled organisms with eventual pay-offs in future management actions devoted to the conservation of these extraordinary organisms.

