

## **Phenotype evolution along phylogenetic lineages of Echiniscoidea**

Resolving the riddles of phylogeny, that is the natural history of various organisms which lead to the evolution of the astonishing variety of forms living on the Earth, has always been at the heart of biological sciences. Robust phylogenetic trees, accurately representing evolutionary paths of a given group of organisms, and consequent natural classification (taxonomic system) lie at the base of biodiversity and ecological research. However, still, many groups of plants, animals, or fungi lack reliable phylogenies, which hinders the understanding their biology at different levels – from molecular machinery of cells to behaviour and ecological relationships. Reconstructing phylogenies is particularly difficult for elusive microorganisms, such as tardigrades, tiny animals (typically only half a millimetre long) widely known from their abilities to thrive in harsh environmental conditions. This is so, because of the problems with obtaining high quality DNA sequences and the accurate assessment of morphological variability. This project aims at clarifying morphological evolution and disentangling phylogenetic relationships between members of the tardigrade order Echiniscoidea, fascinating evolutionary lineage inhabiting both tidal (associated with sea shores) and limno-terrestrial (present in freshwater habitats, mosses and lichens) environments.

Research will be focused on exploring the variability of echiniscoideans at distinct levels: molecular diversification of species, morphological characteristics of key genera, and their geographical distribution across the globe in the light of phylogeny. In the face of the sixth mass extinction of organisms (referred to also as “Anthropocene extinction”), the disclosure of the phylogeny and diversity of barely studied groups of animals is particularly important, as it allows for a better apprehension of their biological characteristics and significance. The research program entails comprehensive morphological and molecular multilocus analyses aimed at deciphering relationships between many tardigrade genera. The reconstructed phylogeny will pinpoint likely morphology of the last common ancestor of all echiniscoideans. Consequently, new systematic shifts will be proposed in order to amend and modernise the classification of the group. This will provide sound phylogenetic background for future evolutionary studies on, for example, colonisation of lands by originally marine forms and the origin of cryptobiosis. Last but not least, unravelled affinities within Echiniscoidea will also serve as an exemplary case study for other zoologists working with microscopic invertebrates, demonstrating the “know-how” of dissecting molecular and morphological components of stunningly large and complicated biological variability.