

The deep sea remains one of the least explored ecosystems on Earth. These are extreme environments – devoid of light, characterized by low temperatures, high hydrostatic pressure, and limited food availability. As recently as the early 20th century, these regions were believed to be entirely devoid of life. Today, thanks to technological advances – particularly in deep-sea exploration methods and equipment – it is well established that these habitats not only support life, but also exhibit remarkable biodiversity and highly specialized adaptive strategies. Although our understanding of the molecular basis of deep-sea adaptation has been steadily expanding, many taxonomic groups remain outside the scope of such research. One such group is the order Tanaidacea – small benthic crustaceans inhabiting both shallow coastal zones and the deepest parts of the ocean.

The **HADDeS** project aims to determine when and how deep-sea adaptations have evolved in this group, and how these traits function at the molecular level. While depth-related morphological changes in Tanaidacea have already been described, the genetic mechanisms underlying them remain unknown. **HADDeS** involves a comparative approach using closely related shallow- and deep-water species from four different tanaidacean families. The project will apply modern molecular techniques to identify genes involved in, among others, protein stabilization under high pressure, osmotic regulation, membrane fluidity maintenance, calcium homeostasis (related to the carbonate compensation depth), development of sensory organs, and morphological traits. DNA and RNA sequencing will provide data for comparative, phylogenetic, and gene expression analyses. Optionally, selected genes may also be expressed in a bacterial system to investigate the functional consequences of the observed molecular changes.

The project is innovative in both its choice of study system and the methodologies applied. **HADDeS** will develop the first sets of primers and molecular probes specifically tailored to this group, designed to target genes potentially involved in bathymetric adaptation. The combined use of two complementary library enrichment strategies will enhance both the completeness and reliability of the sequencing data. Importantly, the project also includes an experimental stage of functional validation – bacterial expression of selected genes – which will allow for linking sequence variation to potential biological effects.

The expected results will contribute not only to a better understanding of adaptive mechanisms in deep-sea environments but may also uncover novel genes with biotechnological potential, particularly relevant in the context of increasing industrial exploitation of deep-ocean ecosystems.