

## Travelers versus homelovers – global biogeography patterns of deep-sea amphipod crustaceans

The oceans constitute  $\frac{3}{4}$  of the Earth's surface and the seas deeper than 4000 m cover almost 41% of the globe making the abyssal the largest ecosystem in the World. Although large effort is put into the analyses of deep-sea invertebrates diversity our knowledge is still far from being complete.

**Amphipoda are very diverse aquatic crustaceans that belong to the most abundant groups of abyssal zoobenthos.** The more, they are the major component of the deep-sea scavenging assemblages. Different amphipod species present various ecological adaptations and mobility which are associated with different feeding types.

Based on Amphipoda as a model taxon, **the project will address the questions to which extent the ecological niche of deep-sea invertebrate species affect its distribution range and different populations connectivity.**

We want to test the following hypotheses (Figure 1):

1. Amphipoda belonging to scavenger guild, being highly mobile and specialized invertebrates (“travelers”), have large geographic and bathymetric ranges, extending to more than one ocean. Their populations are characterized by constant gene exchange.
2. Non-scavenging but strongly mobile amphipods inhabiting epibenthic realm are characterized by moderately large distributions spanning more than 1000 km with some species present in the whole but single ocean. The gene flow between distant populations of the same species is restricted.
3. Non-scavenging, endobenthic, weakly mobile amphipod species (“homelovers”), exhibit local distribution with ranges restricted to relatively small areas (500 km or less) and the genetic connectivity between individuals is reduced.

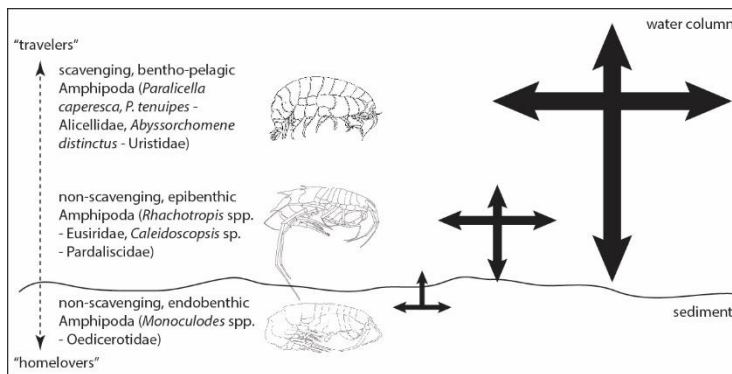


Figure 1. Graphic presentation of the research hypotheses including the summary of the mobility of chosen amphipod ecological groups and families. The thickness of the arrows represent assumed intensity of movement, their length indicate hypothesized extent of horizontal and vertical movement.

**Owing the cooperation of international scientists the extensive collection of deep-sea scavenging and non-scavenging Amphipoda from all three oceans will be studied.** The areas cover North, Central and South Atlantic, central Indian Ocean as well as North, North-West and Central East Pacific. **The present project will combine the molecular and morphological taxonomy methods.**

To assess molecular diversity, the barcoding gene: cytochrome *c* oxidase I gene, will be studied and later supplemented by other genetic markers. On this basis the Molecular Operational Taxonomic Units (putative species) will be designated. Representation of three chosen species from each of the predefined groups will be consecutively analysed using 2<sup>nd</sup> and 3<sup>rd</sup> generation sequencing methods that will allow to infer the extent of gene flow between distant populations of that species. Much effort will be put into morphological identification of the delimited taxa and to the description of the species recognized as new to science.

The results of the present study will shed new light into the deep-sea biodiversity, species distribution and connectivity. As such **it will help in defining deep-sea diversity hotspots, which is crucial for planning of marine protected areas and the zones devoted for deep-sea mining.** The results may be used to recognize indicator species and taxa being the most vulnerable to human induced changes. The preparation of trusted barcode library will be another output that may be later used for faster deep-sea species identification also by non-specialists.