Water mites (Hydrachnidia) are a very diverse and species-rich group. They inhabit nearly all aquatic environments and, being predatory, they have an enormous impact on hydrobiont communities by reducing abundance of many small invertebrates. Given their wide distribution and rather high ecological specialisation at the species level, water mites may be used as bioindicators for assessment of ecological conditions in both, stagnant and running waters. At the same time, the knowledge of the group taxonomy has numerous gaps with many dubious species with imperfect descriptions, and diagnostic features are often weakly defined. Not much is known of the level and extent of the intraspecific phenotypic polymorphism and, so far, nothing is known of the cryptic diversity within water mites. It is commonly assumed that given the high dispersal abilities (parasitic larvae are dispersed by their insect hosts), water mites show extremely low level of endemism. The aim of the current project is an estimation, via DNA barcoding, the factual level of species diversity within two closely related and widely distributed yet ecologically different genera, *Atractides* and *Hygrobates*, and confronting it with conventional systematics based on morphology. Both genera are associated with running waters. However, *Atractides* includes almost exclusively rheobiotic, rheophilic and crenophilic species while *Hygrobates* lives in running waters and springs but also in stagnant waters. The genera differ also in level of species diversity. *Atractides* is one of the richest in species among watermits, while *Hygrobates* includes much less species.

The basic goals of the project are:

1) Estimation of cryptic diversity within both genera with DNA barcoding and molecular species delimitation methods.
2) Comparison of species diversity between the genera based on molecular operational taxonomic units (MOTUs) representing tentative (also cryptic) species. Verification if the observed diversity may be associated to habitat .
3) Defining phenotypic features (morphology) enabling formal descriptions of new species defined via molecular species delimitation methods.
4) Mapping of spatial distribution within both studied genera, delimitation of speciation hotspots.
5) Correlation of the mapped distribution with available environmental descriptors, such as: altitude, water salinity, pH, current speed, habitat typology, in order to defined ecotypes of the studied species/MOTUs.

The study will contribute greatly to building up the knowledge upon water-mite diversity in Europe by: describing new species and assigning publicly available DNA barcodes to the already known species (BOLD), providing insight into speciation and dispersal modes, reliable estimation of endemicity level, better understanding of the role of glacial refugia in shaping diversity of water mites in European inland waters.