DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

(State the objective of the project, describe the research to be carried out, and present reasons for choosing the research topic - max. 1 standard type-written page)

Taxonomy deals with naming and describing species and it is one of the oldest disciplines of science. Taxonomic studies on microscopic invertebrates are often very demanding because many groups of small organisms have very few characteristics that can be used for describing and identifying species. A good example of such a group are water bears (Tardigrada), microscopic animals that can be found in mosses and lichen, known mostly for their remarkable abilities to survive through extremely harsh environmental conditions. The small number of morphological traits that enable the identification of the species and the lack of precise knowledge of the variability in these traits, contributed to notorious and severe underestimation of tardigrade species diversity as difficulties in species identification often translate into erroneous classification of several species as one.

The proposed project is designed to solve ambiguities in the taxonomy and phylogeny (relatedness) of the species which belong to the tardigrade family Macrobiotidae, where we can find many groups neglected by researchers mostly because of the abovementioned difficulties. The solution to this problem will be possible thanks to the use of modern integrative taxonomy methods, which combine data from several disciplines of biology, such as morphology, molecular biology or ecology. During the project, we will obtain detailed morphological data (by using light and scanning electron microscopy) and molecular data (in the form of DNA sequences) on the examined species and their populations. This will allow to redescribe nominal taxa, i.e. species that are "models" for the certain genera or species groups, and for which the original descriptions are outdated and inaccurate. Moreover, thanks to the wide array of data, we will be able to delimit and describe species new for science, what would not be otherwise possible due to their high morphological similarity to scarcely characterised species mentioned above. Furthermore, the DNA sequences obtained during the project will be used to reconstruct the phylogeny, i.e. evolutionary history and relationships between the studied species. Finally, combining morphological data with the reconstructed phylogeny will allow to answer the question how the morphological traits that are used in classical taxonomy evolved within the family.

The project will contribute to a significant broadening of our knowledge on the biology, taxonomy and the relationships between the species, species groups and genera of the family Macrobiotidae. Thus, the results will be a basis for further research related to the diversity and ecology of these organisms. Moreover, the project may become a framework for further research on other high-rank tardigrade groups.