Human impact on ecosystems is enormous and most researchers agree that we are facing a biodiversity crisis. While the conservation efforts are focused on large mammals, birds, and vascular plants, a huge part of biodiversity loss occurs in poorly studied groups, which means that the extent of the true crisis is underestimated. In the proposed project, I will study the effect of human impact on tardigrades, a cosmopolitan phylum of microscopic invertebrates inhabiting moist microhabitats. Tardigrades are known as 'the toughest animals on Earth', due to the ability of some species to enter **cryptobiosis** – an ametabolic state, in which animals can survive extreme conditions. Some studies suggest that anthropogenic changes may influence tardigrade fauna, and indeed it seems that only a subset of species can exist in human-altered environments. However, no study investigated this topic deeply, due to the issues concerning traditional methods (i.e. time-consuming sample processing and challenging species identification), which limit ecological studies of tardigrades. The application of **metabarcoding** (identification of many species in a sample by DNA sequencing) may finally accelerate high-throughput biodiversity inventories.

In the proposed project, I will use metabarcoding to perform a biodiversity survey of tardigrades in areas of three degrees of human impact (i) near-natural forests, (ii) intensively managed forests, and (iii) urban tree stands. As the extinction risk is dependent on species traits, I will also examine the functional traits of the species in relation to their success in colonizing anthropogenic environments. These traits will include body and egg dimensions, pigmentation, reproduction mode, and cryptobiotic potential, all of which can be reasonably expected to differ across a gradient of human influence. I expect to detect tardigrade species differently affected by human impact: **synanthropes** (associated with anthropogenic habitats), '**winners**' (present in natural habitats, successfully colonizing modified habitats), and '**losers**' (found only in natural habitats). By comparing the functional traits of taxa assigned to these groups, I will draw conclusions about their extinction risks and adaptations to modified environments.

The overall results will contribute to the understanding of ecological and evolutionary processes at work in communities of microscopic invertebrates, such as dispersal, habitat specificity, morphological and physiological adaptations of species colonizing anthropogenic environments. By implementing integrative analyses which combine genetic and functional differences on an ecosystem scale, the proposed study will provide a framework for subsequent studies of other groups.