

Parasites are found in almost all living organisms and they are extremely diverse. Genetic studies of marine parasites lag far behind those on free-living organisms and terrestrial systems, despite their relevance for conservation of wild populations. The main aim of my project is to fill this gap by implementing state-of-the-art population genomic tools to examine processes that shape genetic diversity of parasites of marine mammals. As a model, I will use seal lice and intestinal worms in northern hemisphere seal species. I will firstly test if parallel loss of genetic diversity in hosts and their parasites can be observed in small, isolated seal populations. Further, I will investigate how the mode of parasite transmission, the number of potential host species and genetic structure of host population influence genetic diversity of parasite populations. Finally, I will test if we can get insight into the evolutionary history of enigmatic species of seals from the Lake Baikal and Caspian Sea by studying the genomes of their parasites. Unique species of parasites can be threatened by extinction along their host. My project will not only describe the processes shaping genetic diversity of marine parasites, but will also help to understand the co-extinction process - probably one of the most common forms of biodiversity loss.