

Zoonoses are human diseases transmitted by animals or of animal origin. The best known zoonoses are eg. borreliosis (Lyme disease) or rabies, and recently Covid-19. Models predict that zoonotic outbreaks will intensify in future, and Eastern Europe has been recognized as a hotspot for zoonotic mammal hosts. Among them, bats and rodents, that harbour the highest number of zoonotic pathogens. Many bat and rodent species reach high densities, they live close or within human settlements, often inhabiting cellars, attics, or outbuildings what facilitates transmission. Often, they are also city-dwellers, although the risk of animal-borne diseases in urban areas is poorly understood. The knowledge of the distribution and prevalence (% infected) of the zoonotic diseases in Europe is scattered: we know pretty much about some species, while we do not even expect existence of some others. Thus, in the proposed project we we aim to characterize the zoonotic potential of bats and rodents using metabarcoding approach. This method is based on so-called Next Generation Sequencing (NGS) and is more sensitive compared to others. What is most important, allows to detect *nearly all* pathogens present in a sample, even those that a researcher does not expect to be present in a given area. In the project, we will screen bats and rodents living close or within human settlements for the presence of viruses, bacteria, and protozoa that are potentially infectious for humans. We expect to detect pathogen species that had not been yet reported. We plan to identify ecological factors that are associated with increased zoonotic risk, such as density of the hosts, host community structure, or degree of urbanization. We will also verify the hypothesis if city-dwelling species pose a greater zoonotic risk than their counterparts living in more natural habitats.