Worm Profiler: Surveillance and population genetics of Echinococcus in Serbia (WORM_PROFILER)

Principal Investigator: Dr. Aleksandra Uzelac, Institute for Medical Research, University of Belgrade
Participant from IMGGE: Dr. Jelena Karanović

Echinococcus, tapeworms of the Taeniidae family, can infect humans and animals and cause serious, even lethal disease. Global population genetics data suggests that disease presentation, severity, immune response, as well as relative host susceptibility and resistance to infection depend on the species, genotype and haplotype. The species of significant clinical relevance in Europe are *E. granulosus*, the causative agent of cystic echinococcosis (CE) and *E. multilocularis*, which causes the most severe disease, alveolar echinococcosis (AE). Analysis of the population genetics of Echinococcus is an ongoing effort in some parts of Europe, while the Balkans represent a significant knowledge gap. This project aims to comprehensively survey the entire transmission cycle consisting of intermediate and definitive animal hosts and the environment using sample processing and analytical methods which have been standardized, validated and harmonized at the EU level to obtain high quality population genetics data via mitochondrial gene (*cox1* and *nad1*) sequencing and characterization of the EmsB microsatellite from single eggs, worms and protoscolices. As a main novelty, comprehensive *Echinococcus* population genetics data, through a survey of underexplored reservoirs with a high transmission capacity to humans, will be systematized and graphically displayed through an interactive bioinformatics database, WormProfiler, with a user interface tailored to physicians and veterinarians. The impact of the project is the translation of population genetics data to physicians and veterinarians, key stakeholders for transmission prevention to facilitate education of the public and raise awareness of echinococcosis. The project should provide the insight into the genetic diversity of Echinococcus and identification of transmission foci, as well as a software supported framework for systematic surveillance and future development of targeted transmission control actions to reduce echinococcosis case burden.