Dirofilariasis is an expanding disease caused by *Dirofilaria* spp. nematodes vectored by mosquitoes with dogs as main reservoir hosts. The diseases is typical zoonosis (animal-borne infection) and may cause many different symptoms in humans, including subcutaneous nodules, swelling and pain, lung nodules or can affect eye. In many cases, removal of the parasite can be done only surgically.

The geographic distribution of these nematodes (and disease) changes dynamically, also because of climate change, allowing better survival in mosquito vectors. Two main parasite species are *Dirofilaria repens* and *Dirofilaria immitis* (canine heartworm) and their distribution differs, with heartworm being found in warmer regions than *D. repens*. In dogs *D. repens* causes subcutaneous dirofilariasis, and *D. immitis* is much more pathogenic, affecting heart and leading to death.

Humans can be infected by the range of *Dirofilaria* species, however, molecular identification of parasites from human cases is very limited and urgently needed. Despite being cosmopolitan parasites, the knowledge on the genetic diversity of *D. repens* and *D. immitis*, occurrence of subspecies/cryptic species or distinct genetic variants is still insufficient.

The main aim of the current study is to evaluate the genetic diversity of *D. repens* and *D. immitis* from different countries and continents using modern molecular techniques, including metabarcoding and whole genome sequencing. Second main aim is to genotype and identify species and genotypes of nematodes infecting humans for better understanding of transmission routes. The project is planned in international cooperation (Austria and Poland) to enable complementary investigations on *Dirofilaria* genetic diversity: the joined expertise should enable more complex and efficient outcome of the project, with higher effect on global science.

The planned project will enable gathering key knowledge on *Dirofilaria* genetic diversity, epidemiology and evolution in global scale and will help to identify main zoonotic (sub)species/cryptic species involved in human infection.