

Nematodes of the genus *Trichinella* are widespread parasite throughout the world. They can occur in many species of land and marine animals and even in birds. The life cycle of *Trichinella* consists of two phases: the intestinal and muscle, and infecting occurs after eating raw or undercooked meat containing larvae of *Trichinella* spp. *Trichinella* infections are also observed in humans on all continents excluding Antarctica. Trichinosis in humans is known to acute diseases and its clinical symptoms are non-specific (eyelid edema, fever, muscle aches and headache). Annually, worldwide observed more than 10 000 *Trichinella* infections, and death rate is 0.2%. However, non-specific symptoms indicate that the number of cases of trichinosis in humans could be significantly more.

A special place in the life cycle of *Trichinella* take carnivores and omnivores because they are the main reservoir of trichinosis in the environment. Preliminary studies of our team showed that infecting forest animals by *Trichinella* spp. is 20%. In addition, these animals can migrate and transmit new *Trichinella* species over long distances and create new outbreaks of trichinosis. Therefore, the monitoring free-living animals for the occurrence of *Trichinella* is really important. In Poland, the dominant species is *T. spiralis* and *T. britovi*. Also, it is important to know the source of the invasion in the environment, because this will allow assessment of parasite migration pathways. This is necessary because in Poland in 2013 have been found two new species of *Trichinella*: *T. nativa* – resistant for long periods freezing, and *T. pseudospiralis* – non-encapsulating nematode. This creates a new risk for human health because different species of *Trichinella* cause various clinical symptoms and require different treatments.

The aim of the project is to investigate of occurrence of *Trichinella* in free-living animals and analysis of genetic diversity within the genus *Trichinella*, which will know the transmission pathways of the parasite in the environment and assess the real risks to human health and domestic animals.

The research will be carried out using the methods of classical parasitology, molecular biology and bioinformatic analysis. The study material will be muscles collected from free-living animals. Then muscles will be digested in artificial gastric juice for isolation *Trichinella* larvae. Obtained larvae will be counted to determine the intensity of the invasion. DNA will be isolated from single larvae and will be used in a series of molecular tests to determine *Trichinella* species, and will help to define genetic diversity and relationship of *Trichinella* spp. larvae, for example: Multiplex-PCR, or amplification using primers specific for 5S rDNA and CO1 gene. Phylogenetic analysis of *Trichinella* isolates will determine the way of transmission of new *Trichinella* species in Poland.