

**'Studies on epidemiology of alveococcosis in highly endemic and non-endemic areas in Poland with particular reference to genetic variability *Echinococcus multilocularis* in definitive hosts and humans'.**

*Echinococcus multilocularis* is the most dangerous parasite existing in Northern Hemisphere that causes alveococcosis. The disease is fatal (over 90% mortality rate) if infected individuals are not properly treated, and characterize with long, incubation time up to 15 years and asymptomatic initial phase. Humans become infected by ingestion of eggs excreted by definitive hosts, mainly foxes. Despite of the fact that genetic diversity of the parasite is being discovered together with development of new, better molecular tools, circulation of genotypes of this tapeworm in environment still remains a mystery. Therefore, this project will mainly focus on the variety of genotypes of *E. multilocularis* in chosen regions of Poland taking into consideration their current endemicity status, prevalence in definitive hosts and humans. Pivotal issue will be estimation of link between genetic profiles of parasite and ability to infect humans. Additionally, an attempt will be made to establish a role dogs in epidemiology of *E. multilocularis* infections.

Studies will be performed in endemic Warmia-Masuria Province and nonendemic Pomerania province, Poland. Successively collected samples of intestines from wild definitive hosts, stool samples from dogs, human samples from AE patients after hepatectomy will be examined for presence of *E. multilocularis* with the use of molecular techniques. Next, positive samples will be genotyped with the use of mitochondrial and microsatellite markers and newly developed dynamic representation of DNA.

We expect that results of our study will bring precise and objective information about the prevalence of *E. multilocularis* and its genotypes in wild and domestic definitive hosts, as well as role of dogs in parasite transmission. In consequence, investigations proposed in this study will complement knowledge about epidemiology of *E. multilocularis* infection, which is of high both local and world interest. This project is consistent with worldwide trends in environmental research concerning the threat for human's health and life. Information on the genetic diversity of *E. multilocularis* is necessary to aid epidemiological investigations on the transmission dynamics of this parasite to design new preventive strategies for monitoring and control programs as well as to link pathogenic strains with dominant profiles which would shed light on classifications according to pathogenicity. By implementation of newly developed dynamic representation of DNA assay, we expect to improve and complement data obtained by classical genotyping assays on differences between *E. multilocularis* isolates. Moreover, estimation of prevalence *E. multilocularis* infection in dogs from rural and urban areas will help to understand if, and where dogs may pose a potential threat to owners.