

## Wild living carnivore species as reservoir hosts of microsporidia and cryptosporidia

Kinga Leśniańska, Joanna Hildebrand, Marcin Popiołek,  
Agnieszka Perec-Matysiak

Department of Parasitology, Institute of Genetics and Microbiology, University of Wrocław, Przybyszewskiego 63, 51-148 Wrocław, Poland

Wild animals living near human settlements, excreting infective forms (oocysts or spores) into the soil and water are considered as the environmental reservoirs for microparasites, including microsporidia—a group related to Fungi and protozoan parasites of the genus *Cryptosporidium*. This group of microparasites—although heterogeneous in terms of taxonomy, morphology and genetically—is characterized by the ability to cause infections, often of zoonotic importance, in a wide range of hosts with diverse immune statuses, including humans. Data on the prevalence and genetic diversity of examined pathogens in wild animals is scarce, with only a few studies having been carried out in Spain, Ireland and in the USA.

We investigated fecal samples from raccoons (*Procyon lotor*), red foxes (*Vulpes vulpes*), raccoon dogs (*Nyctereutes procyonides*), martens (*Martes martes*, *Martes foina*) and badgers (*Meles meles*) obtained from Poland to estimate the prevalence and to identify the species/genotypes of *Cryptosporidium* spp., *Enterocytozoon bieneusi*, and *Encephalitozoon* spp. The detection of the examined microparasites was performed based on the nested-PCR method, using species-specific and/or genus-specific sets of primers. In the case of *Cryptosporidium* spp. a fragment of the 18S rRNA and actin genes were used as molecular markers. To identify microsporidia, *E. bieneusi* and *Encephalitozoon* spp., a fragment of the region of ITS rRNA gene was used. Sequencing of the majority of PCR products obtained was necessary due to the extremely high genetic diversity of identified parasites. Sequence analyses and phylogenetic analyses were then carried out.

As a result of the present study we have positively identified these carnivores as reservoirs of species/genotypes of zoonotic concern for public health, with a high incidence of occurrence observed at some cases. Additionally, this research has expanded the host range of the identified microparasites. These findings are important for the study of cryptosporidia and microsporidia epidemiology and emphasize the fact that invasive and native carnivores, both widely distributed, should be considered more seriously as significant sources of zoonotic pathogens hazardous to domestic animals and humans.