

Cryptosporidiosis in humans and animals from Poland: molecular diagnostics and epidemiological implications

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Cryptosporidium parasites cause severe diarrhoea in immunocompromised humans all over the world. The parasites have been found in more than 150 vertebrate species, and the prevalence is particularly high in livestock animals, which are considered reservoirs for human infection. In Poland little is known on the epidemiology of cryptosporidiosis due to the limited number of studies. Our aim was to determine *Cryptosporidium* species/genotypes in isolates of human and animal origin collected in Poland and to compare species/genotypes between human cases and potential animal reservoirs.

One hundred and three faecal samples were collected from 35 hospitalized patients (both children and adults) of The Children's Memorial Health Institute, Cancer Centre in Warsaw, and Children's Hospital in Otwock. Samples were also collected from 22 European beaver (*Castor fiber*), 55 European bison (*Bison bonasus*), 5 Polish horse (*Equus gmelini*), 14 European wolf (*Canis lupus*), 52 red deer (*Cervus elaphus*), 23 roe deer (*Capreolus capreolus*) and 5 boar (*Sus scrofa*).

Cryptosporidium infections were diagnosed in 12 (34.3%) patients by nested PCR assays. Genotyping of parasite isolates performed by PCR-RFLP or sequencing of COWP and beta-tubulin gene fragments revealed infections with 3 different *Cryptosporidium* species, namely *C. parvum* (9 cases), *C. hominis* (1 case) and *C. meleagridis* (1 case).

Cryptosporidium positive samples were identified microscopically in 5 of 7 studied animal species (the prevalence ranged from 9% in roe deer to 36% in wolves). *C. parvum* was identified using molecular techniques in 5 isolates from wolves. These results suggest multiple routes of transmission of *Cryptosporidium* in humans in Poland, and indicate a possible contribution of zoonotic transmission.

The study was partially supported by State Committee for Scientific Research, KBN, through grant no. 2PO4C09827.