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Summary

Blastocystis in Humans and Warm-Blooded Animals in Poland: Genetic Diversity and Zoonotic Potential

Blastocystis cf. *Blastocystis hominis* is one of the most frequently detected protozoa in the large intestines of humans and animals. Infection with *Blastocystis* is generally asymptomatic, but in some cases, blastocystosis is accompanied by diarrhea, abdominal pain, flatulence, constipation, and nausea. The worldwide prevalence of *Blastocystis* spp. in humans ranges from 1.5 to 10% in developed countries, and from 30 to 50% in developing countries. *Blastocystis* cf. *Blastocystis hominis* is a complex of species in which 28 subtypes (ST) have been distinguished so far, including at least nine isolated from humans. It is assumed that the ST1 subtype is the most virulent of the subtypes studied so far. It has also been shown that the subtype structure of human *Blastocystis* isolates may indicate a reservoir and a source of infection.

Material from humans and 73 animal species were tested, including 33 species of mammals belonging to seven orders, and 41 species of birds belonging to six orders: a total of 1,413 samples (784 samples from humans and 629 samples from animals). Microscopic examination of fecal samples and cultures was performed in order to detect *Blastocystis*. PCR was used to amplify a fragment of a gene that encodes the rRNA of a small subunit of the ribosome. The PCR products were sequenced; the obtained sequences were then compared with the sequences deposited in the GenBank database. Phylogenetic analysis using Bayesian inference was performed next. For the first time in Poland, the diversity of alleles of the gene that encodes the rRNA of a small subunit of a small subunit of the ribosome.

Results. The presence of *Blastocystis* was detected in 156 samples (86 positive samples were from humans, 70 from animals).