Molecular characterization of *Blastocystis* subtypes isolated from various mammalian groups living in Wrocław ZOO, Poland

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Blastocystis sp. is a common enteric protistan parasite infecting humans and a variety of animals. Blastocystis infection is accompanied by symptoms such as abdominal pain, diarrhea, nausea and vomiting. It exhibits an extensive worldwide genetic diversity and 26 subtypes (ST1–ST26) have been described. Nine subtypes (ST1 to ST8 and ST12) have been reported in both humans and animals.

The purpose of this study was to determine the prevalence of *Blastocystis* infection in mammals bred in Zoological Garden in Wrocław and to extend the knowledge about the transmission and epidemiology of this parasite.

A total of 110 stool samples from 57 mammalian species belonging to 10 orders were analyzed using in vitro cultivation as well as molecular methods (PCR). Primates (44 individuals) and Artiodactyla (36 individuals) were the most studied.

Genomic DNA was extracted from positive cultures using QIAamp DNA Mini Kit according to manufacturer's recommendations and stored at $-20~^{\circ}$ C until analysed. Gene fragment of SSU-rRNA was amplified with forward primer RD5 (5'-ATCTGGTTGATCCTGCCAGT-3') and reverse primer BhRDr (5'-GAGCTTTTTAACTGCAACAACG-3'). All PCR products were sequenced to determine subtypes.

Preliminary molecular study on the Zoo animal samples revealed four STs: ST1, ST2, ST5 and ST8. The most common was ST2.

Our results showed that animals housed in a zoological garden can be a reservoir of *Blastocystis* and play a role in transmission of this parasite. All subtypes detected in animals bred in Zoological Garden in Wrocław can also infect people what suggests a likelihood of zoonotic transmission. Animals bred in a zoo have limited contact with visitors, therefore the greatest risk of infection is for animal-keepers.