Subtype distribution of Blastocystis isolates from wild animals kept in a zoo and conservation units of São Paulo State

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Blastocystis sp. is a common intestinal parasite infecting humans and a wide range of hosts such as non-human primates and other mammals. Based on molecular analyses of the small subunit rDNA (SSUrDNA) gene, 17 different subtypes (STs) have been proposed among Blastocystis isolates from mammalian and avian hosts. To date, nine different subtypes (ST1-ST9) have been found in human infections. Since several STs are common to humans and animals, it is likely that some human infections may be related to zoonotic transmission. However, the role of animals as potential sources to human infection remains to be clarified. Thus, in this context, we focused our attention here to determine the prevalence and the genetic diversity of Blastocystis isolates related to infection in a cohort of captive wild mammals species kept in one zoo (Bauru Municipal Zoological Garden) and in two units of integral protection and conservation (Conservation Center for Ilha Solteira Wildlife/CCFIS and Anchieta Island State Park/PEIA) in São Paulo State, as well as some employees, including zookeepers/animal handlers, biologists and veterinarians. A total of 83 stool samples (22 from zoo, 32 from CCFIS and 29 from PEIA) from 36 mammalian species and 17 from employees (10 from CCFIS and 07 from PEIA) were submitted to DNA extraction, tested by polymerase chain reaction (PCR) targeting the SSU rDNA gene and the amplicons retrieved were sequenced. Among the animal and human fecal samples screened by PCR, 34.9% (29/83) and 29.4% (5/17) tested positive, respectively. Of these PCR products, 21 (5 from humans, 10 from non-human primates, 2 from artiodactyls, 2 from carnivores and 2 from rodents) were successfully sequenced for STs analysis, revealing infection by ST1 (23.8%), ST2 (14.3), ST3 (23.8%), ST4 (4.8%), ST5 (14.3%) and ST8 (23.8%). Among human samples, only ST1 (3/5), ST2 (1/5) and ST3 (1/5) were identified. However, in addition to ST1, ST2 and ST3, the captive animals carried infection by ST4, ST5 and ST8. Among the mammal groups, the STs distribution was the following: ST2, ST3 and ST5 infecting non-human primates; ST1 and ST5 in carnivores; ST1 and ST8 in rodents and ST4 and ST5. In the present study, the distribution of Blastocystis subtypes was similar to that observed worldwide in which the majority of human infections have been assigned to STs 1, 2 and 3. Considering that some captive animals shared the same STs as those usually seen in humans (ST1, ST2, ST3), the possibility of cross-transmission between these hosts could be suggested. In addition, the finding of ST5 and ST8 in non-human primates and artiodactyls reinforces the fact that these rarer subtypes in humans are more commonly found in other hosts. To the best of our knowledge, this is the first study on subtypes distribution of Blastocystis isolates from wild animals kept in captivity in our country.

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