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Genetic Diversity and Molecular Epidemiology of *Giardia duodenalis* in Humans and Wildlife from the Brazilian Amazon: A One Health Perspective

Inhalt

Giardia duodenalis infects humans and a wide range of animal hosts; however, information on its genetic diversity in wildlife from the Brazilian Amazon remains scarce. This study investigated the genetic diversity and molecular epidemiology of *G. duodenalis* in humans and wild animals from the Amazon region using multilocus sequence typing (MLST). Assemblages A and B were identified in different host species. Genetic analyses revealed, for the first time, the occurrence of assemblage A in sloths and five bat species from the Amazon region. Assemblage A was also detected in non-human primates, an anteater (*Tamandua tetradactyla*), and humans. Sub-assemblage AII was identified exclusively in humans, whereas AI, a sub-assemblage with recognized zoonotic potential, was detected in sloths, bats, and an anteater. A novel genotype, designated AIV, was identified in non-human primates and formed a distinct lineage in multilocus phylogenetic analyses. Assemblage B exhibited higher genetic diversity than assemblage A and displayed a reticulated phylogenetic pattern. High-resolution MLST schemes based on six loci for assemblage A and three hypervariable loci for assemblage B provided lineage resolution comparable to genome-based analyses. These findings expand current knowledge of *G. duodenalis* diversity in the Brazilian Amazon and provide molecular data for epidemiological investigations at the human–wildlife interface within a One Health perspective.

Keywords

Assemblage; Sub-assemblage; MLST; pós-genômica; genotyping; zoonotic potential

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Yes, I am a Junior Scientist.

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