Genotypic characterization of *Giardia lamblia* and *Blastocystis* sp. in fecal samples from children in a Community, Florianópolis, SC

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Giardia lamblia and *Blastocystis* sp. are among the most frequently detected protozoa in human fecal samples and are major causes of diarrhea in children—especially those facing water and food insecurity. Recent laboratory and coproparasitological surveys have shown high positivity for *Blastocystis* sp., highlighting the need for molecular characterization to enhance epidemiological understanding. This study aimed to use *nested* PCR to identify and molecularly characterize *G. lamblia* and *Blastocystis* sp. in fecal samples from children in the Serrinha community of Florianópolis, SC. A total of 152 stool samples from children and adolescents aged 2 to 15 years, collected from institutions in the Serrinha community (Bairro Trindade), were preserved in SAF solution and examined by direct microscopy, spontaneous sedimentation, and Faust's method. Samples that were positive for *G. lamblia* and *Blastocystis* sp. by microscopy were then processed for DNA extraction, PCR optimization, sequencing, and classification of subtypes and assemblages. This study was approved by the Ethics Committee of the Federal University of Santa Catarina (CAAE 59641322.1.0000.0121). Among the 152 samples, 64 (42%) were positive for enteroparasites. Detected parasites included *Blastocystis* sp. (34.8%), *Endolimax nana* (21.2%), *Entamoeba coli* (16.7%), *Entamoeba histolytica/E. dispar* (9.1%), *Giardia lamblia* (7.6%), *Ascaris lumbricoides* (3%), *Iodamoeba butschlii* (3%), *Hymenolepis nana* (1.5%), *Enterobius vermicularis* (1.5%), and *Entamoeba hartmanni* (1.5%). Of the *Blastocystis* sp. positive samples, 84.8% were confirmed by nested PCR and classified as subtypes ST1, ST1b, ST2, ST3, and ST3a, which are often linked to symptomatic cases. *G. lamblia* samples were identified as assemblage B, which is common in human and mammalian infections and suggests potential zoonotic transmission. These findings contribute to improved epidemiological insights and help guide future monitoring and control measures.

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