

# Eukaryotic Metataxonomic analysis of faeces for the identification of *Blastocystis* and other intestinal parasites

Cod. 1017

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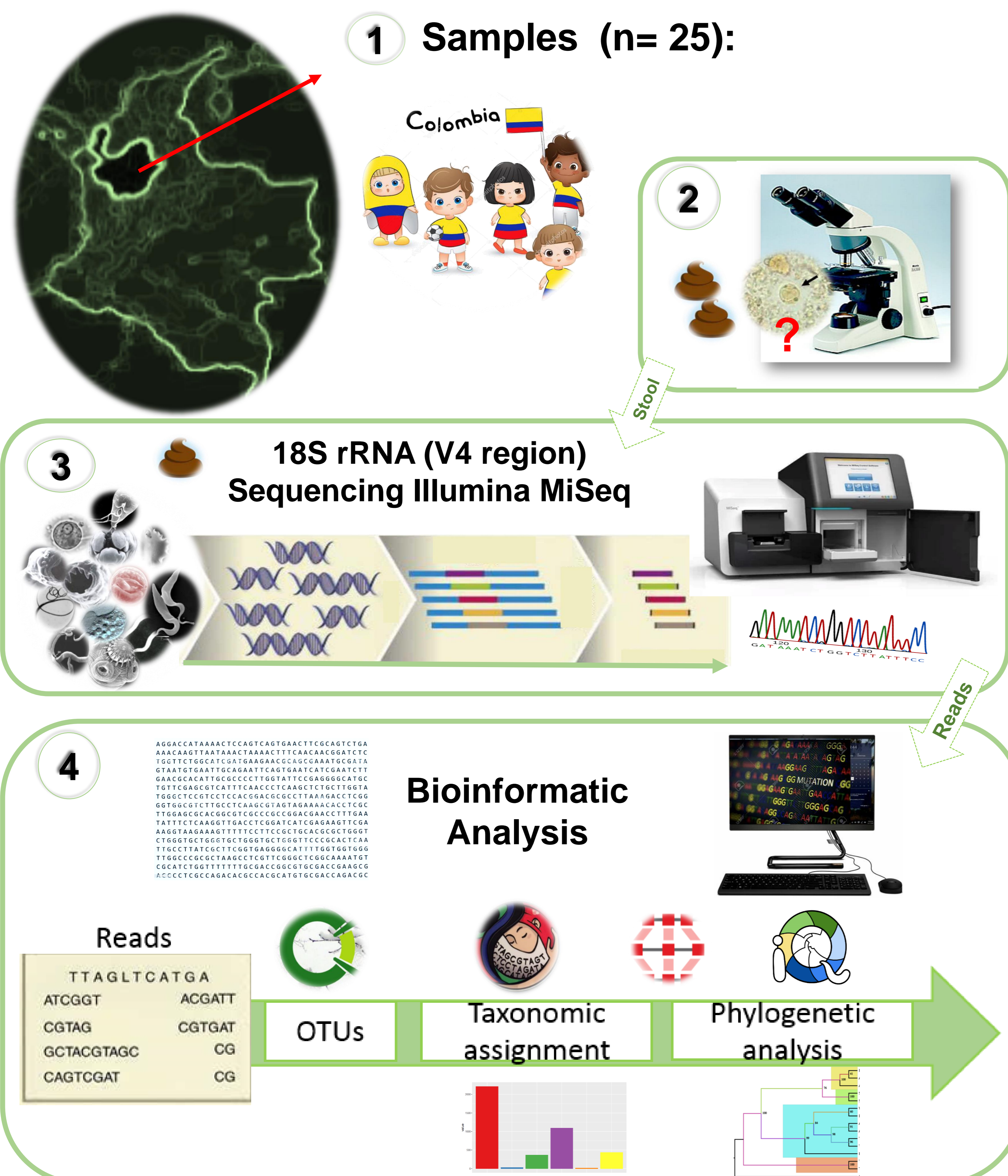
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## BACKGROUND AND AIMS

*Blastocystis* is an intestinal protist with a broad host range and high prevalence in human population worldwide. Next-generation sequencing (NGS) and metataxonomic studies of microorganisms of public health significance has grown considerably in recent years, particularly for prokaryotes. However, a few studies have been reported for eukaryotes like *Blastocystis*. The aim of this study was to confirm the presence of *Blastocystis* and other intestinal parasites in fecal samples from Colombian children through a 18S ribosomal gene metataxonomic approach. In addition, using this methodology, *Blastocystis* genotyping was carried out.

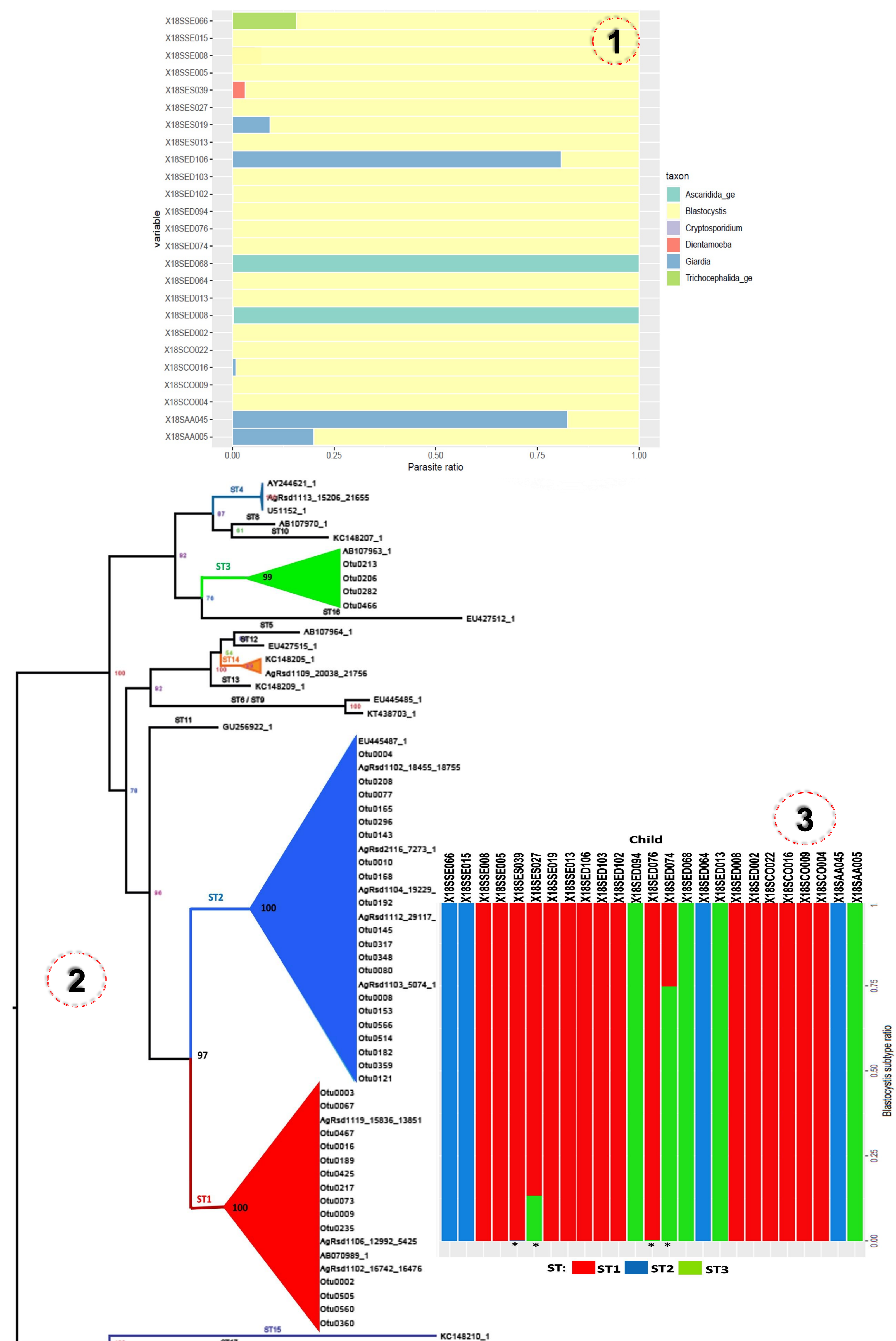
## METHODS

Twenty-five stool samples from children <5 years from daycare centers from Medellín (Colombia), and with a microscopic diagnosis for *Blastocystis* were included in the study. DNA was extracted from fecal samples and the V4 hypervariable region of the 18S rRNA gene was amplified. Sequences were obtained on the Illumina MiSeq platform. Depurated reads were grouped into OTUs and the relative abundance and taxonomic rank for eukaryotes were calculated.



## RESULTS

Metataxonomic experiment confirmed *Blastocystis* in the 25 samples evaluated (Fig 1). ST1, ST2, and ST3 *Blastocystis* subtypes were detected (Fig 2), with four samples being positive for mixed infections (Fig 3). Additionally, a taxonomic coverage for other intestinal parasites was achieved, including *Cryptosporidium* spp., *Giardia* spp, *Dientamoeba fragilis*, Ascaridida and Trichocephalida nematodes (Fig 1).



## CONCLUSION

NGS-based approach enabled intestinal parasites detection and has the potential to evaluate the genetic diversity of eukaryotes in clinical samples. Additionally, metataxonomics proved to be a valuable tool for *Blastocystis* genotyping and identification of mixed infections.

Acknowledgments. This work was supported by CODI (Project 2020-33903); and Escuela de Microbiología (Project 2021-40850). Universidad de Antioquia.

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