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Topic: AS02.3 Intestinal parasitic diseases

## EUKARYOTIC METATAXONOMIC ANALYSIS OF FAECES FOR THE IDENTIFICATION OF BLASTOCYSTIS AND OTHER INTESTINAL PARASITES

Ana Luz Galván-Díaz<sup>1</sup>, Gisela Maria García-Montoya<sup>2</sup>, Juan F. Alzate<sup>2</sup>

<sup>1</sup>Universidad de Antioquia, Grupo De Microbiología Ambiental. Escuela De Microbiología, Medellín, Colombia, <sup>2</sup>Universidad de Antioquia, Centro Nacional De Secuenciación Genómica Cnsg. Departamento De Microbiología Y Parasitología. Grupo Pediaciencias. Facultad De Medicina., Medellín, Colombia

**Introduction:** Blastocystis is an intestinal protist with a broad host range and high prevalence in human population worldwide. Next-generation sequencing (NGS) and metataxonomic based 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 evaluate the presence of Blastocystis in fecal samples from Colombian children through a 18S ribosomal gene metataxonomic approach.

**Methods:** Twenty-eight 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 V3-V4 hypervariable regions of the 18S rRNA gene was amplified. Sequences were obtained on the Illumina MiSeq platform. Depleted reads were grouped into OTUs and the relative abundance and taxonomic rank for eukaryotes were calculated.

**Results:** Metataxonomic experiment detected Blastocystis in the 28 samples evaluated. Additionally, a taxonomic coverage for other intestinal parasites was achieved, including Cryptosporidium, Giardia, Dientamoeba fragilis, and ascaridida nematodes.

**Conclusions:** NGS-based approach enabled intestinal parasites detection and has the potential to evaluate the genetic diversity of eukaryotes in clinical samples. Acknowledgements. This work was supported by Convocatoria Programática 2019-2020: Área de Ciencias de la Salud, CODI (Project 2020-33903); and Convocatoria interna para financiar proyectos de investigación en la Escuela de Microbiología-sede central (Project 2021-40850). Universidad de Antioquia.

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