

Identifying Novel Biomarkers and Bacterial Strains Relevant in Gut Health for Individuals with Autism

Peñalba, Florencia ¹; Rusiñol, Camila ²; Lamberti, Lucia ²; Garrido, Gabriela²; Florencia Konick ³; Guisande, Andrea ⁴; Iglesias, Claudio ⁴; Mendive, Paula ³; Parada, Andres ^{1,5}; Riera, Nadia ¹.

1 Microbial Genomics Lab, Instituto Pasteur de Montevideo. Montevideo, Uruguay.

2 Academic Unit of Pediatric Psychiatry, Faculty of Medicine, University of the Republic. Montevideo, Uruguay.

3 School of Nutrition, University of the Republic. Montevideo, Uruguay

4 Department of Pediatric Gastroenterology, Hepatology, and Nutrition, Pereira Rossell Hospital Center. Montevideo, Uruguay.

5 Department of Ecology and Evolution, Faculty of Sciences, University of the Republic. Montevideo, Uruguay.

Autism Spectrum Disorder (ASD) is a group of neurodevelopmental disorders frequently associated with various conditions, including gastrointestinal problems. Microorganisms present in the gut can produce and modulate metabolites that can directly influence the host's nervous system, affecting cognitive and social processes. In this study, fecal samples were collected from children diagnosed with autism and their neurotypical siblings, aged between 4 and 10 years. In addition, data on gastrointestinal health, food frequency questionnaires (FFQ), and child's clinical history were gathered. A total of 76 fecal samples were obtained out of which 53 were processed for DNA extraction and purification. From these samples, long-read sequencing of the 16S ribosomal RNA (16S rRNA) gene, using Oxford Nanopore Technology (ONT) was performed. A total of 22 pairs (ASD/Neurotypical) were analyzed, and individually, 4 children with autism and 3 without a diagnosis. Considering the obtained results, the intestinal bacterial community profile of each child was characterized. Using Linear Discriminant Analysis Effect Size (LEfSe), significant differences in the abundance of various bacterial species were identified. In children with autism, a higher abundance of species such as *Faecalitalea cylindroides*, *Lactobacillus* sp., *Mediterraneobacter* sp., *Clostridium colinum*, and *Erysipelatoclostridium ramosum* was observed. In contrast, neurotypical children showed a higher abundance of bacteria such as *Blautia hydrogenotrophica*, *Ruminococcus lactaris*, and *Haemophilus parainfluenzae*. These results suggest that the composition of the gut bacterial community could be associated with autism, which might offer new perspectives for early diagnosis and the design of more precise therapeutic strategies.

Keywords: Autism Spectrum Disorder, microbiota, 16S rRNA.