# ANALYSIS OF FAECAL MICROBIOME AND SMALL ncRNAS WITH POSSIBLE IMPLICATIONS IN HOST-GUT MICROBIOTA CROSS-TALK: A PILOT STUDY IN AUTISM

Federica Chiappori[1], Francesca Anna Cupaioli[1], Arianna Consiglio[2], Noemi Di Nanni[1], Ettore Mosca[1], Vito Flavio Licciulli[2], Alessandra Mezzelani[1]

[1]Institute for Biomedical Technologies, National Research Council of Italy, 20054 Segrate, Italy.

[2]Institute for Biomedical Technologies, National Research Council of Italy, 70126 Bari, Italy.

## Background:

Gut dysbiosis, characterized by reduced bacterial variability and diminished beneficial commensals, correlates with symptoms severity in autism. Microbiota can influence the expression of host microRNAs and in turn this regulate the growth of intestinal bacteria. Therefore, we investigated possible bidirectional host-gut microbiota cross-talk between gut microbes and host transcriptional modulators.

## Methods and Results:

We analysed, by "omics" technologies, faecal microbiome, mycobiome, and small-non-coding-RNAs of children with autism and neurotypic.
We confirmed gut dysbiosis with reduction of healthy microbiota in autistic children, and identified novel fungi genera in faecal samples of patients. Microbial families, involved in essential metabolites production, are underrepresented in patients with consequent negative effect on health. Moreover, we identified up-regulated transcriptional modulators, in particular miRNAs and piRNAs: for the first time, we described faecal miRNAs in autism and detected piRNAs in stool. The targets of dysregulated small-non-coding-RNAs are involved in intestinal permeability, inflammation, and autism.

## Conclusions and Significance:

Faeces represent a source of information that should be studied as a whole (bacteria, fungi and RNAs) to understand microbiome composition and host-microbiome interaction. Omics and multi-omics approaches fit this purpose and, here, detected dysbiosis and dysregulated small-non-codingRNAs as possible biomarkers and therapeutic targets.
Interomics (PB05); H2020 GEMMA-project ID:82503 www.gemma-project.eu

## Keywords:

Autism; microbiome dysbiosis; host-microbiota cross-talk; omics; non codingRNAs.

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**Thematic Area**:

- Microbiome: from Research to Clinics

**Infrastructures:**

N.A.