

# Microbiota profile in Autism Spectrum Disorder: different metagenomics approaches to analyze 16S and 18S rRNA

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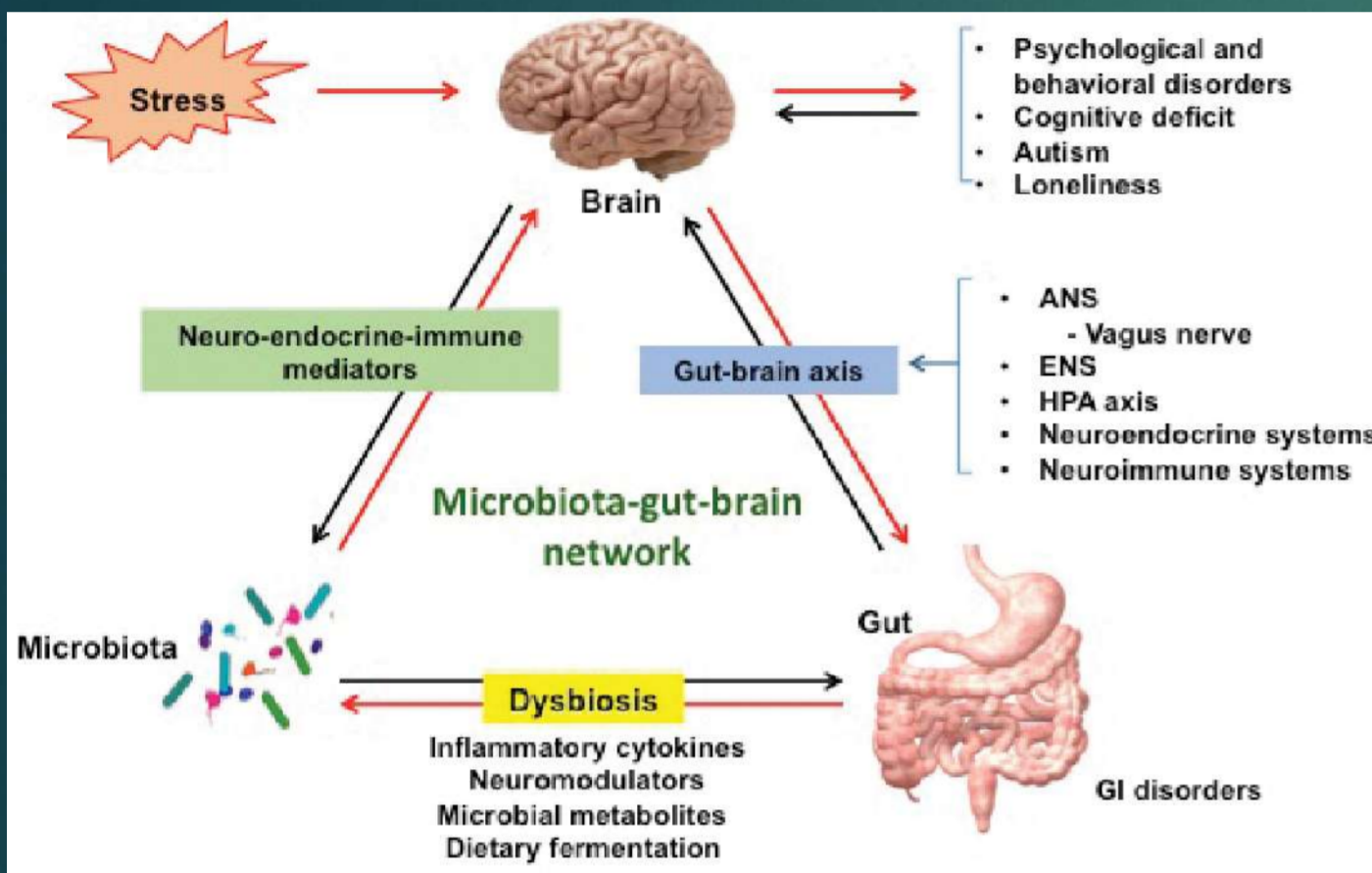
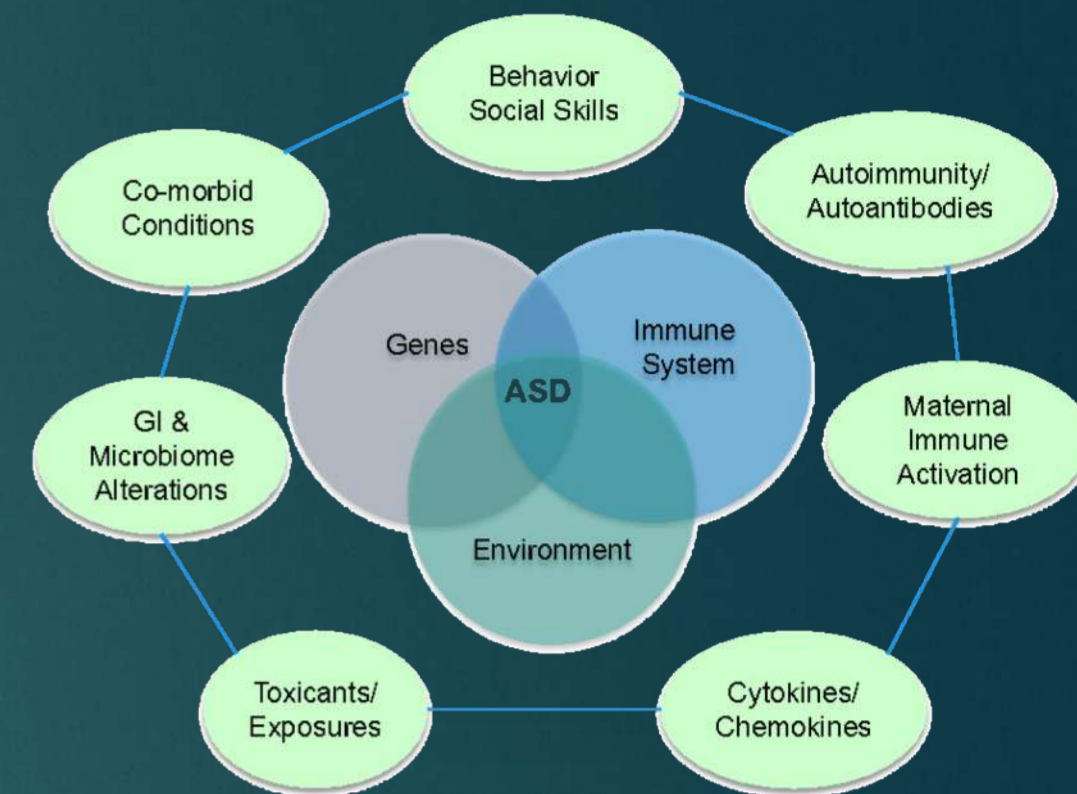
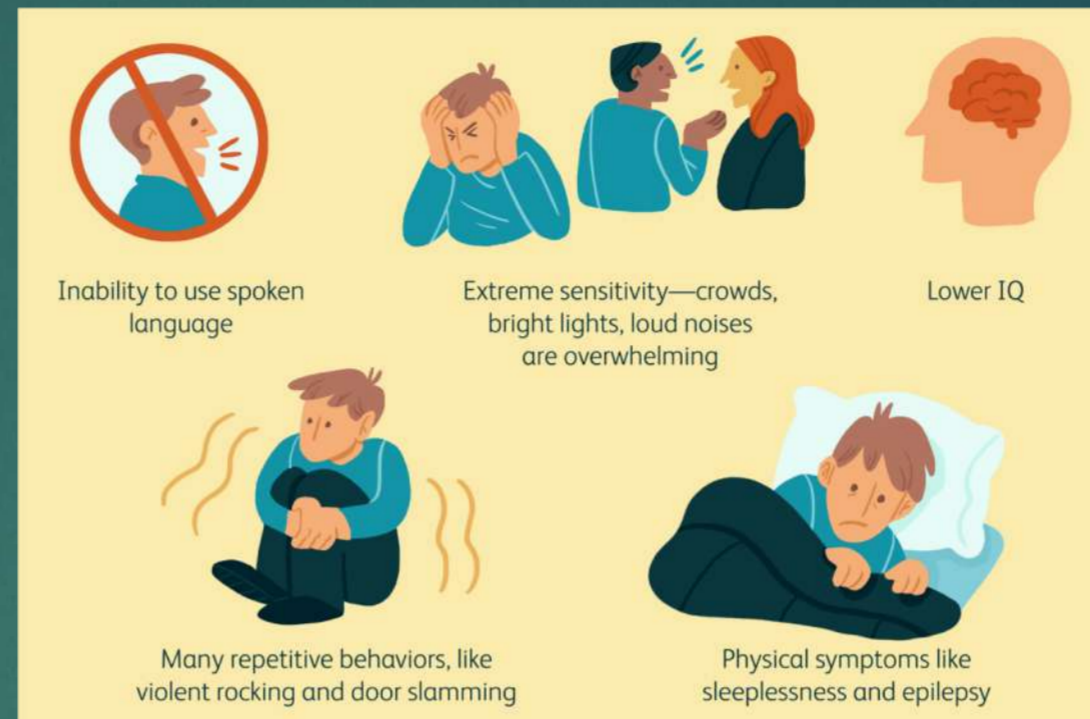
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## Autism

Autism spectrum disorder (ASD)

About **2.24%** of the children population



## Dysbiosis

Metagenomic studies focus especially on the prokaryotic microorganisms

Few literature about eukaryotic colonizer of human intestine and their role in human health

## Aim

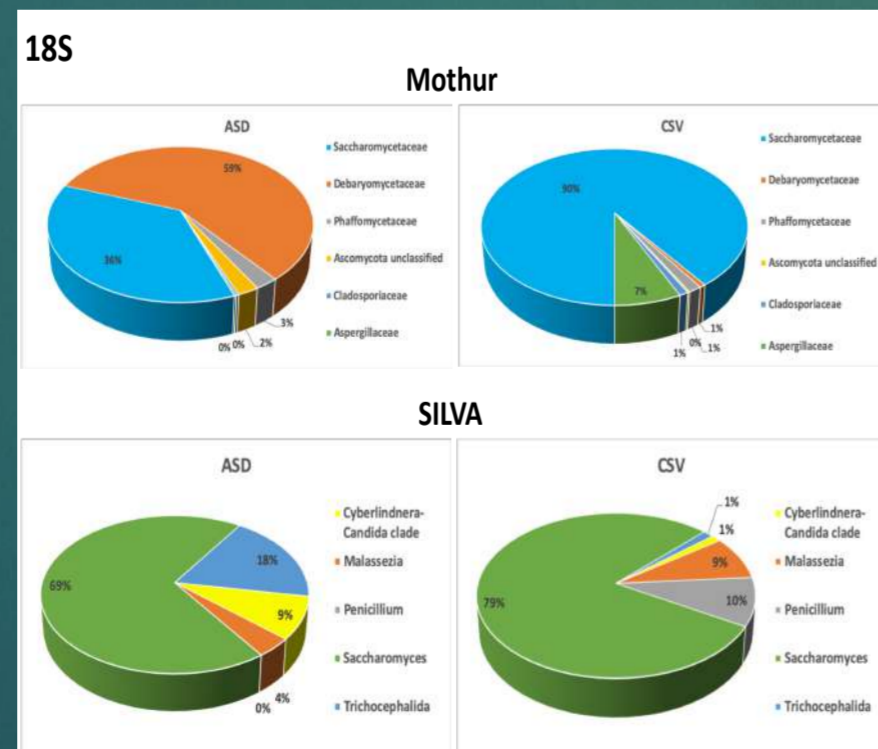
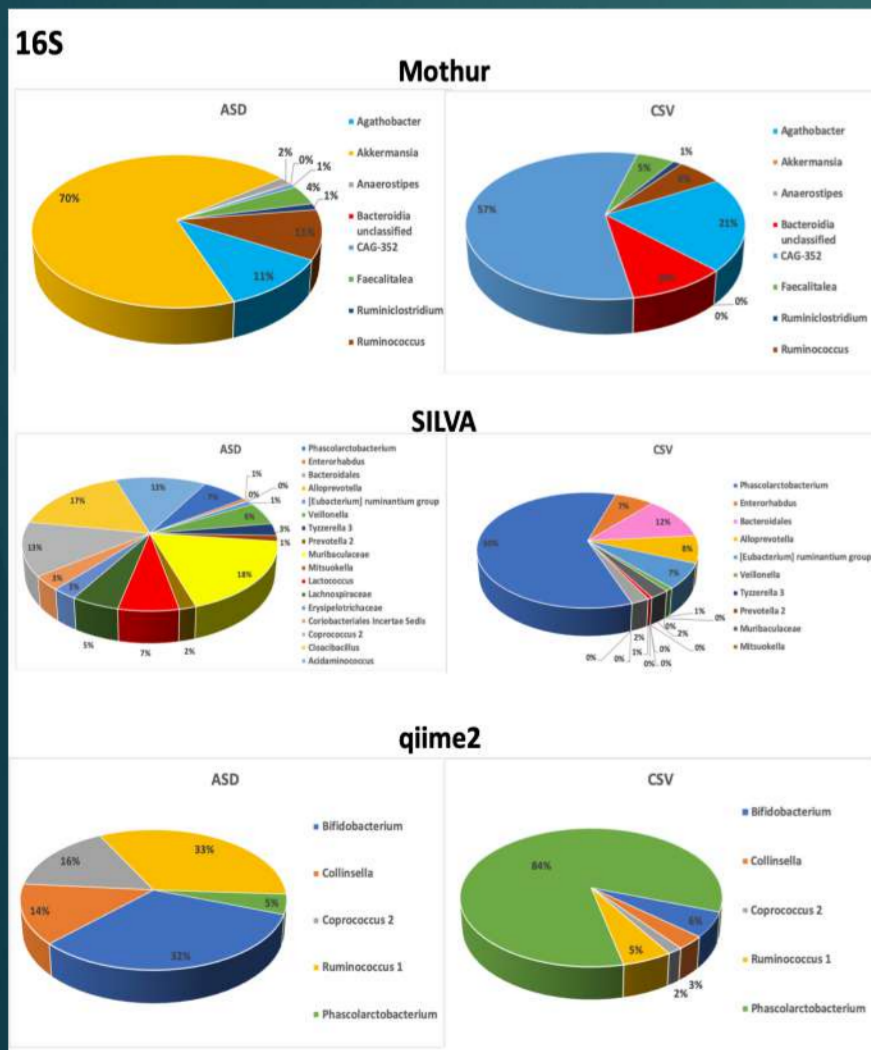
Metagenomics pilot study to define the **prokaryotic** and **eukaryotic** gut microbiota of 6 (5 ♂ + 1 ♀) children with **ASD** and 6 **neurotypical controls** matching for age and sex.

Test different **metagenomics pipelines** + set up bioinformatics conditions

Identify **ASD microbial biomarkers** for patient stratification and personalized treatments

## M&M

- **16S and 18S** illumina (MiSeq platform coupled with Flowcell V3 2X300) libraries; forward and reverse reading -> about 22million of sequences
- Automatic pipeline of **SILVAngs analysis platform**,
- Miseq SOP **Mothur** pipeline,
- **Dada2** and **Deblur** pipelines of **qiime2**.
- **SILVA132** database



Phylum	Class	Order	Family	Mothur	QIIME2	SILVA
Actinobacteria	Coriobacteria	Coriobacteriales	Coriobacteriaceae		↑	↑
Bacteroidetes	Bacteroidia	Bacteroidales		↓		↓
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae		↑	↑
Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	↑	↑	
Firmicutes	Negativicutes	Acidaminococcales	Acidaminococcaceae		↓	↓
Ascomycota	Saccharomycetes	Saccharomycetales	Saccharomycetaceae	↓		↓



**Acknowledgments**  
EU project GEMMA (grant agreement No 825033), EPTRI and CNRBioMics.  
Istituito San Vincenzo Erba and Albese, Italy

