Microbiota abnormalities in Autism Spectrum Disorders: a pilot comparison in a cohort of adult patients and healthy controls

Alexandru Gaman¹,², Sophie le Fresne³, Alexandra Iamandi², Julien Dubreucq¹, Axelle Martinez Teuilers²,⁻⁴, David Monnet¹,², Nassima Simohammed¹,², Josselin Houenou²,⁻⁵, Julien Dubreucq⁴, Axelle Martinez Teuilers¹,⁵, David Monnet¹,², Nassima Simohammed¹,², Josselin Houenou²,⁻⁵, Muriel Cazaubiel³, Joel Doré⁶, Marion Leboyer¹,²


Background rationale:
Autism Spectrum Disorders is a group of psychiatric conditions with an increasing prevalence in the general population (1 in 68, Center for Disease Control and Prevention, 2010) and presenting with debilitating symptoms in area of social communication, empathy and repetitive behaviours. Recent animal studies unveiled the link between intestinal microbiota abnormalities, intestinal hyper-permeability changes and cerebral modifications that seemed to be associated with ASD symptoms (1). These microbiota changes have also been reproduced in ASD patients where in increased expression of Firmicutes phylum (2) and Bacteoidetes (3) has been observed. With a small number of studies available looking to the structure of microbiota in ASD patients, this domain is still evolving and further clarification is sake by psychiatric world. A previous systematic review (4) reports a positive signal and calling for further data collection.

Aim:
To explore microbiota differences between ASD patients and healthy controls

Methods:
Material and methods: 15 ASD subjects without intellectual deficit diagnosed by a group of experts in the field of autism (“Asperger” Expert Centers Créteil and Grenoble) and 12 adult healthy controls were included for the microbiota analysis. The faecal samples were collected using an auto- collection kit (microbiome-standards.com SOP05) and the microbiota analysed using PCR amplified bacterial 16S ribosomal DNA (V3-V4 region Miseq, Illumina). Mean values of richness (Chao index) and diversity (Shannon index) at genus, phylum and family level were determined to describe the bacterial population.

Results:
Trends of difference were observed at phylum level: Bacteroidetes and Firmicutes were slightly more abundant in ASD subjects while Actinobacteria and Proteobacteria were more abundant in controls. At family level Prevotellaceae is trending more abundant in controls while Bacteroidaceae is more in ASD subjects. The index of richness (Chao) appears to be similar for ASD and for controls, set at around 6500 operational taxonomic units (OTU). The diversity index trends towards being inferior in ASD patients (mean 4.75, range=(4.39-5.24)) versus controls (mean 4.90, range=(4.35-5.65))

Conclusion:
Differences in composition could be associated with different bacterial metabolic products such as short chain fatty acids but also alterations of the intestinal wall permeability (hyper-permeability) and overall inflammatory tone. The fermentation products can pass in increased amounts in the blood and brain, inducing an abnormal cerebral activity, that could contribute to ASD symptoms. As future direction, the findings in this study will be further extended by enlarging significantly the cohort but also correlated with other biomarkers such as metabolomic profiles, inflammation signalling molecules, and cerebral activity.