Gut Bacteria and Alzheimer's Disease: from dysbiosis to beta-amyloid plaques

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Background

- Alzheimer's disease (AD) is characterized by beta-amyloid $(A\beta)$ deposits, neuro- and peripheral inflammation
- Inflammation could be the cause of AD and AB could act as antimicrobial peptide against bacterial lipopolysaccharide $(LPS)^{1}$
- Gut microbiota (GMB) is one of the possible source of inflammation
- Mice models of AD with no GMB display less A β deposit²
- We previously demonstrated a higher abundance of the genus Escherichia in association with higher peripheral inflammation and A β plaques³
- Escherichia is one of the LPS-producing bacteria

Aims

I) To find a signature in GMB composition in AD patients II) To evaluate the presence of LPS in peripheral circulation

Results

I.a) Metagenomic analyses on stool DNA revealed a higher abundance of the phylum Firmicutes and a lower abundance of the phylum Bacteroidetes in the AD group as compared to HC

I.b) At genus level, 6 genera are significantly more abundant in the AD group as compared to HC

Methods

Sample

- We collected stool and blood samples from:
- 10 amyloid negative controls with no cognitive impairment (HC)

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- 34 cognitively impaired amyloid positive patients (Aβ+)

Stool analyses

- DNA isolation from stool samples
- Bacterial 16S DNA amplification and indexing
- DNA sequencing

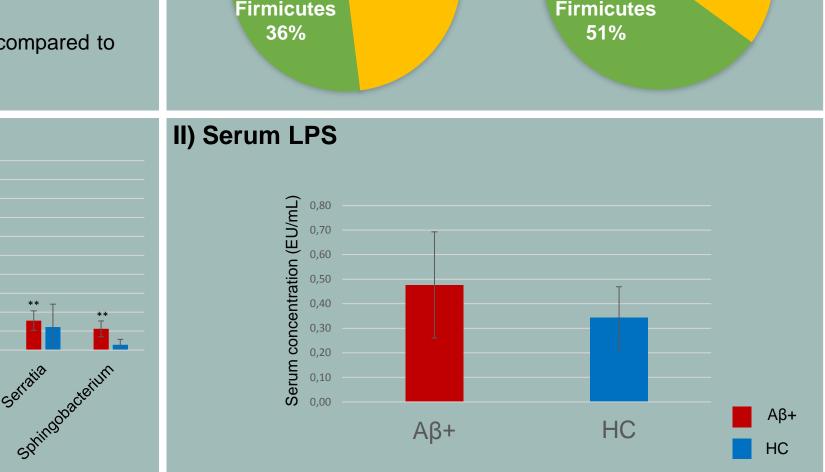
Blood analyses

- Separation of serum from whole blood
- Serum LPS evaluation with a chromogenic assay Statistical analysis
- Mean percentage in stool bacteria at phylum level

- Genera abundance differences among groups were analysed by generalized linear models for zero inflated distributed data. Genera with significant abundance difference between groups were detected by FDR post-hoc correction.

I.a) Bacterial phyla in stool HC Αβ+ Bacteroidetes Bacteroidetes 48% 33%

II) AD group display higher serum LPS level, as compared to HC



Conclusions

Αβ+

HC

*p<0.005 vs HC

**p<0.001 vs HC

I.b) Bacterial genera in stool

0,50 0,45 0,40

(%) 0,35 0,30 0,25 0,20 0,15 0,10 0,10 0,05

0,05

0,00

AKaliphilus

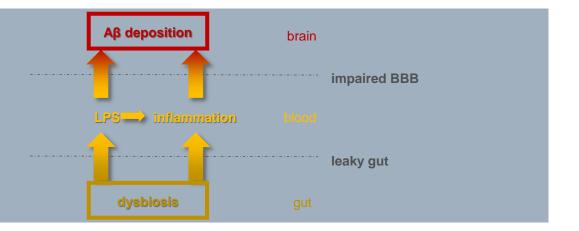
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Our data suggest the presence of a specific GMB composition in association with AD. This signature, maybe as consequence of a more permeable gut barrier, is also associated with higher serum levels of the bacteria component LPS, which may be able to overt inflammation and, once in the brain, to trigger AB deposition and AD pathology.

Escherichia

Heilorestis

Serratia



References: (1) Soscia S.J. et al., The Alzheimer's disease-associated Amyloid β-Protein is an Antimicrobial Peptide. PLoS One. 2010;5:9505; (2) Harach T. et al., Reduction of Abeta amyloid pathology in APPPS1 transgenic mice in the absence of gut microbiota. Sci Rep. 2017 Feb 8;7:41802. doi: 10.1038/srep41802. (3) Cattaneo A. et al., Association of brain amyloidosis with pro-inflammatory gut bacterial taxa and peripheral inflammation markers in cognitively impaired elderly. Neurobiology of aging 49, 60-68, doi: 10.1016/j.neurobiolaging.2016.08.019 (2017)

Acknowledgment: The INDIA-FBP study was funded thanks to a grant by AVID-Radiopharmaceuticals. The project was supported by European Commission (ERANET project, INFLAME-D to A.C.) and by Ricerca Corrente (Ministry of Health) to A.C. We thank all the patients and their families for their participation to the study.