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Reham Magdy Wasfy, Matthieu Million, Didier Raoult

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Role of Gut Microbiota in Alcohol-related liver disease

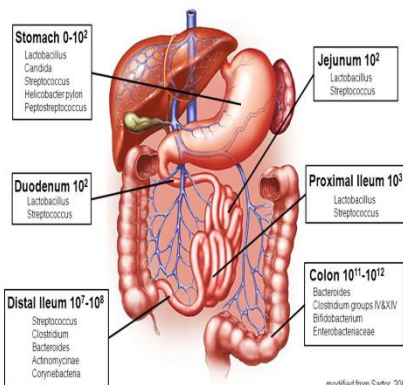
Reham MAGDY WASFY, Matthieu MILLION, Didier RAOULT

Institut Hospitalo-Universitaire (IHU) Méditerranée Infection, 19-21 Boulevard Jean Moulin 13005 Marseille, France.

Background

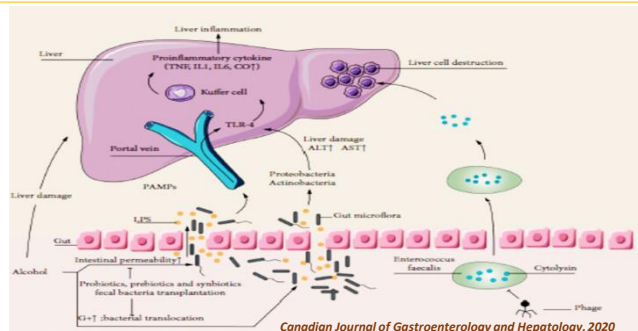
Gut Microbiota is composed of diverse populations of bacteria in addition to protozoa, archaea, fungi and viruses (Tripathi et al., 2018)

It is composed of:
Firmicutes (79.4%)
Bacteroidetes (16.9%)
Actinobacteria (2.5%)
Proteobacteria (1%)
Verrucomicrobia (0.1%)



Alcoholic liver disease (ALD) consists of a broad spectrum from steatosis to cirrhosis and hepatocellular carcinoma (Singal et al., 2018)

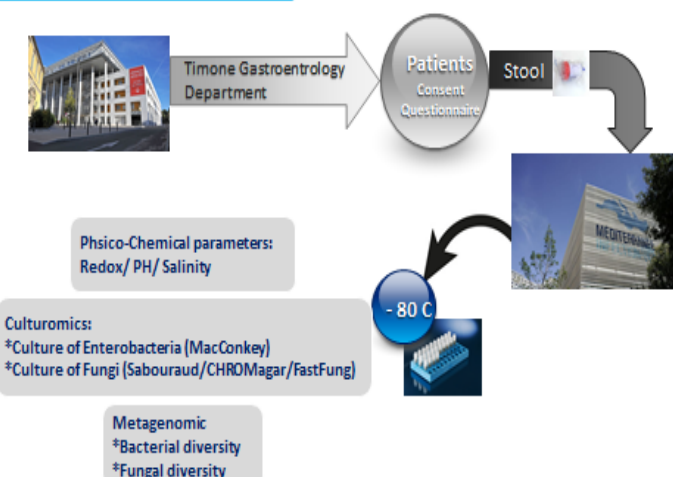
The intestine communicates with the liver through the gut-liver axis which affects pathogenesis of ALD through release of cytokines causing hepatocyte damage (Milosevic et al., 2019)



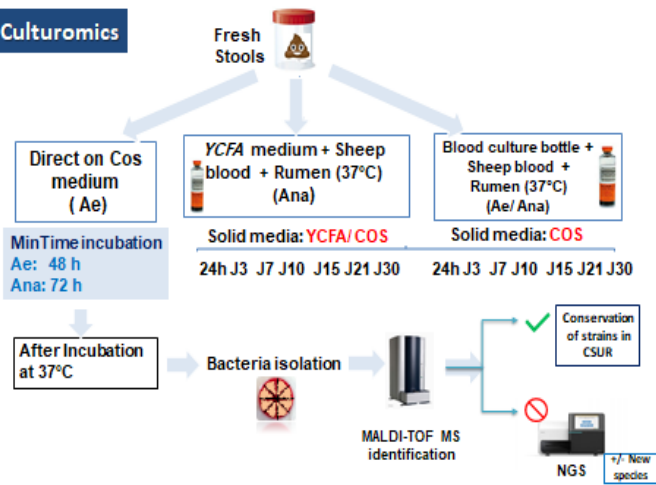
There are distinct changes in fecal microbiome associated with development of but not severity of ALD (Smirnova et al., 2020)

Material & Methods

Study Design: Case-Control study

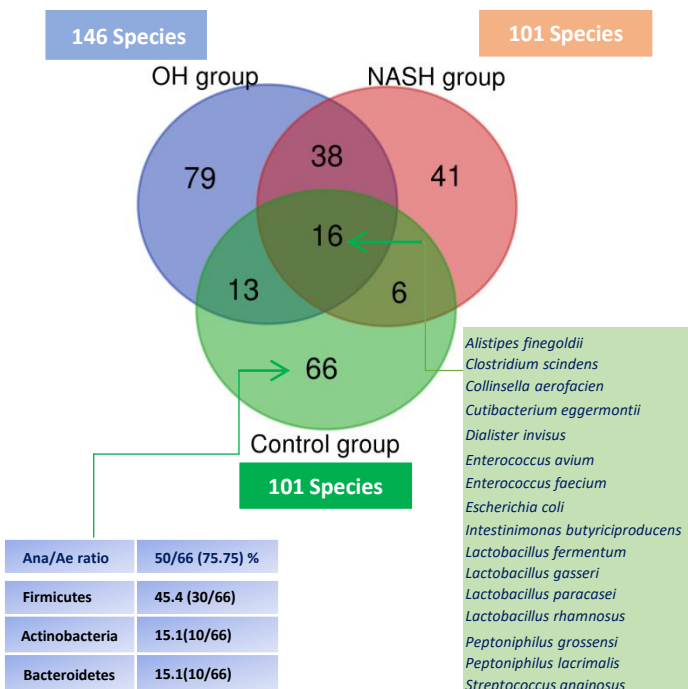


Culturomics

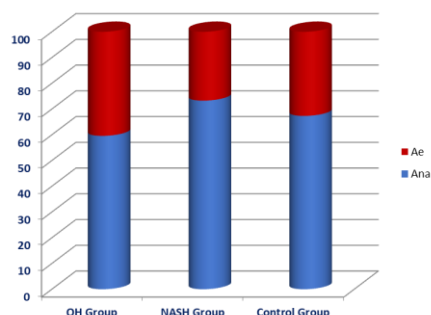


RESULTS

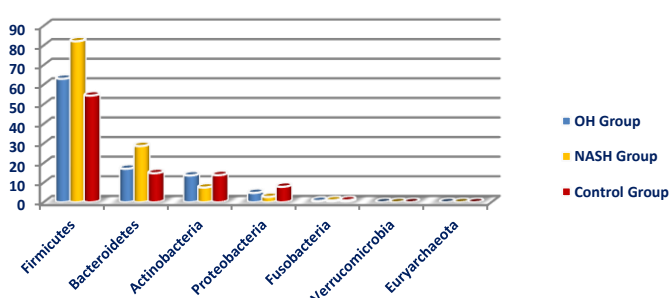
Six stool samples have been collected as follows; 2 for alcoholic hepatitis (OH group), 2 for non-alcoholic steatohepatitis (NASH group) and 2 healthy controls (Control group)



Venn diagram showing comparison between culturomics results of OH, NASH and Control groups



Proportion of Anaerobic and Aerobic species in OH, NASH and Control groups



Proportion of each bacterial phylum in OH, NASH and Control groups

Conclusions

- ALD is associated with gut dysbiosis including a gain and a loss in different bacterial species
- More patients have to be studied with metagenomic analysis to determine specific microbiota pattern in ALD