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Role of Gut Microbiota in Alcohol-related liver disease

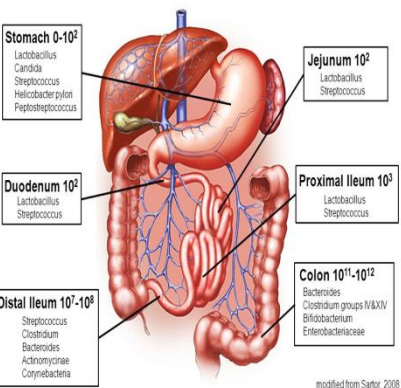
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Background

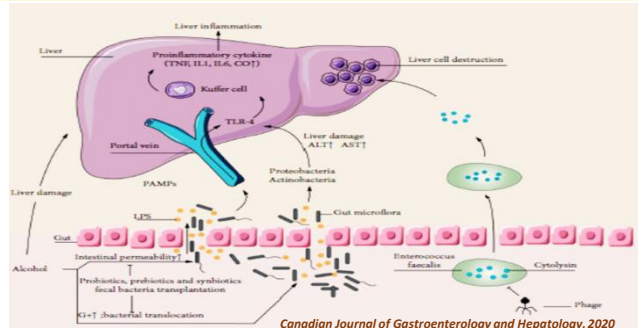
Gut Microbiota is composed of diverse populations of bacteria in addition to protozoa, archaea, fungi and viruses (Tripathi et al., 2018)

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)

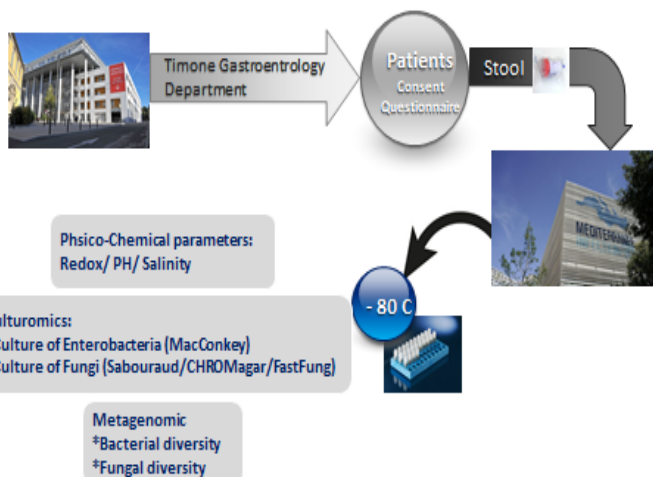
The intestine communicates with the liver through the gut-liver axis which affects pathogenesis of ALD through release of cytokines causing hepatocyte damage (Milosevic et al., 2019)



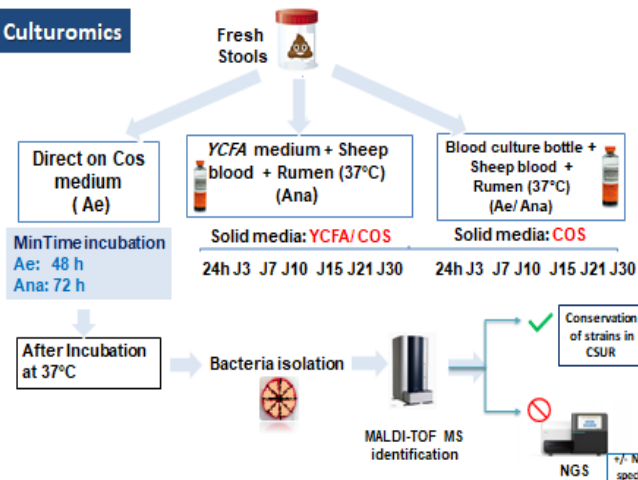
There are distinct changes in fecal microbiome associated with development of but not severity of ALD (Smirnova et al., 2020)

Material & Methods

Study Design: Case-Control study



Culturomics

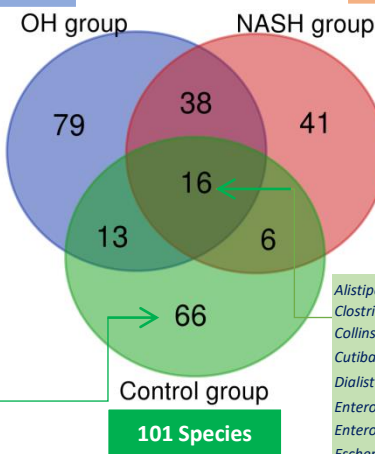


RESULTS

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)

146 Species

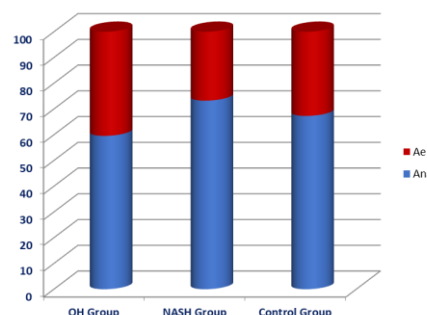
101 Species



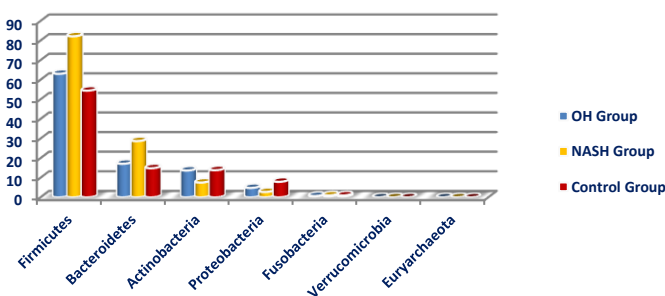
- Alistipes finegoldii*
- Clostridium scindens*
- Collinsella aerofaciens*
- Cutibacterium eggemontii*
- Dialister invisus*
- Enterococcus avium*
- Enterococcus faecium*
- Escherichia coli*
- Intestinimonas butyriciproducens*
- Lactobacillus fermentum*
- Lactobacillus gasseri*
- Lactobacillus paracasei*
- Lactobacillus rhamnosus*
- Peptoniphilus grossensii*
- Peptoniphilus lacrimalis*
- Streptococcus anginosus*

Ana/Ae ratio	50/66 (75.75) %
Firmicutes	45.4 (30/66)
Actinobacteria	15.1(10/66)
Bacteroidetes	15.1(10/66)

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