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Uncover Unique Microbiota Signatures in Hepatitis B Virus-infected patients: A case-control study

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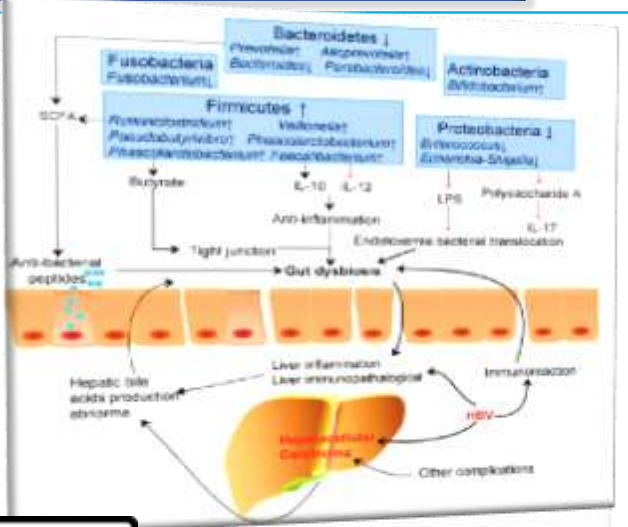
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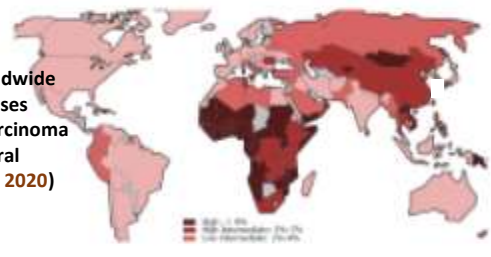
Uncover Unique Microbiota Signatures in Hepatitis B Virus-infected patients: A case-control study

Reham MAGDY WASFY, Babacar MBAYE, Patrick BORENTAIN, Maryam TIDJANI ALOU, Giovanna Mottola, Aurelia CAPUTO, Claudia ANDRIEU, Didier RAOULT, Matthieu MILLION, Rene GEROLAMI
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BACKGROUND AND OBJECTIVES



250 million people worldwide have HBV, which increases risk for cirrhosis and carcinoma despite available antiviral treatments (Zeng et al., 2020)



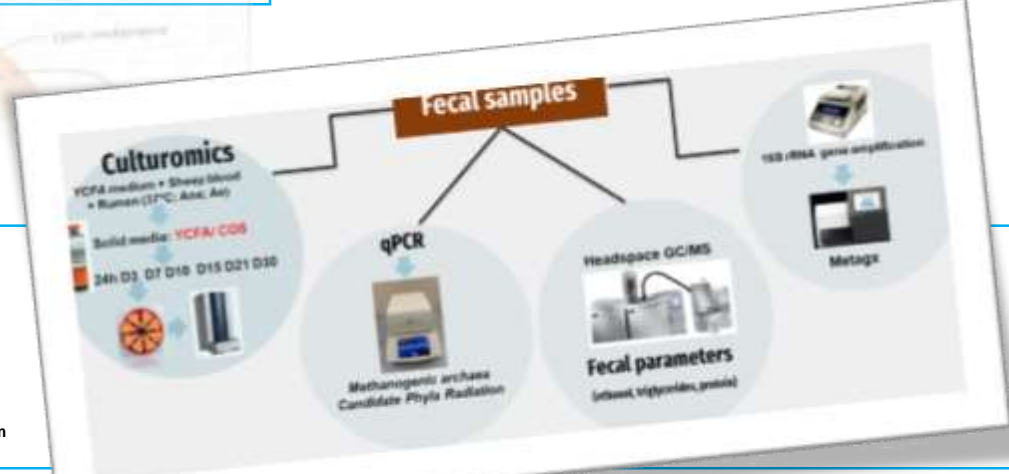
A growing body of evidence suggests a connection between gut microbiota dysbiosis and disease progression in HBV patients (Tranah et al., 2020; Wang et al., 2022). However, the underlying mechanisms are still poorly understood

Our objectives are to define the composition of gut microbiota profile (potential biomarkers) to the species level in HBV infection using different approaches and to investigate microbiota correlation to both fecal and biological biomarkers



VIDEO Abstract is available

SCAN ME

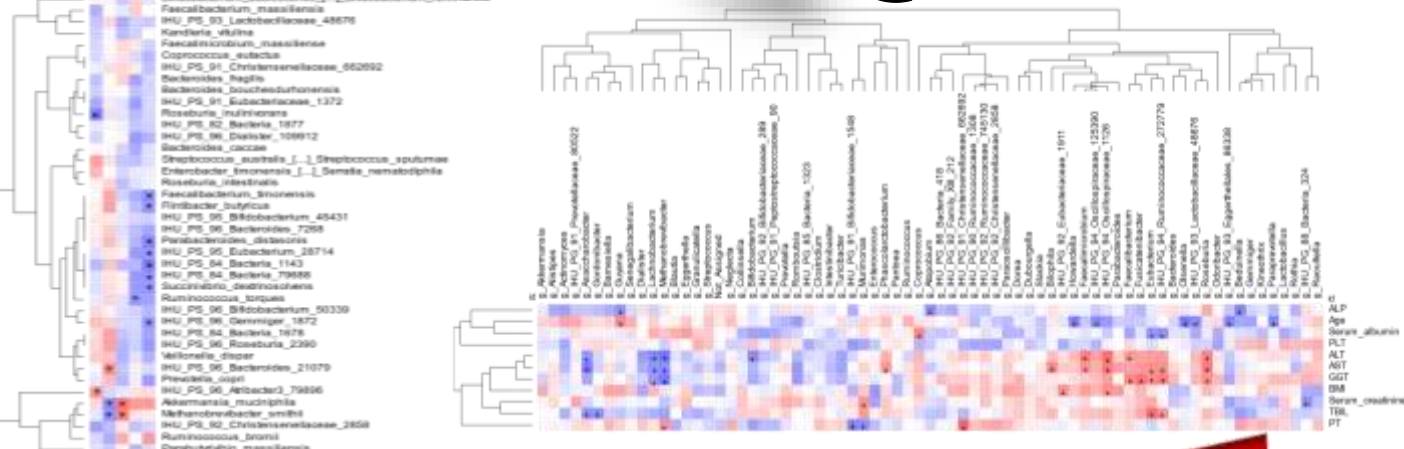
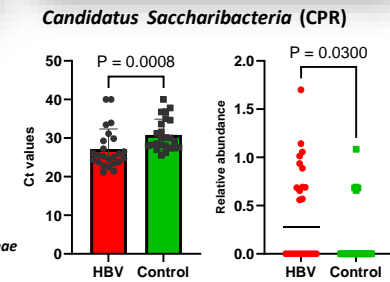
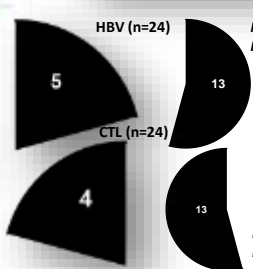
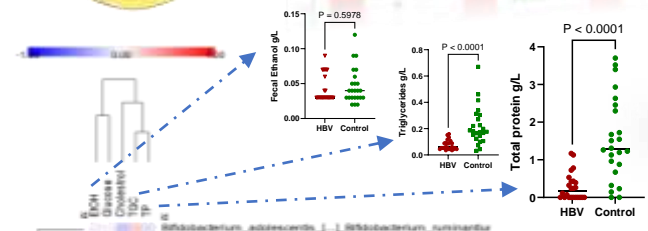
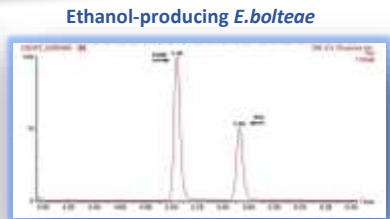
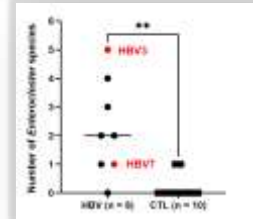
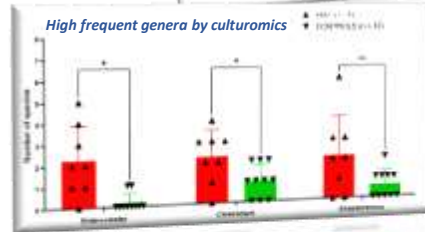
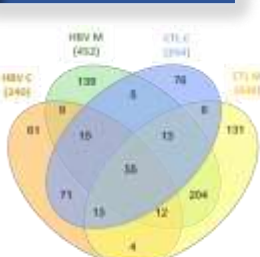


METHODOLOGY

A Case-Control Study
HBV (n=24)
Control (n=24)

YCFA: Yeast extract, casitone and fatty acid medium
 COS: Columbia agar + 5% sheep blood

RESULTS



CONCLUSIONS

- Our study reveals for the first time the identification of EtOH-producing *Enterocloster bolteae*, *Candidatus Saccharibacteria*, and *M. smithii* in HBV-infected patients.
- Those organisms showed significant correlations with elevated liver enzymes, prothrombin index (clotting factor), and other fecal markers suggesting further investigations of their role in hepatic infections

For Data Availability, Contact me

