ficial taxa relative RNA and DNA abundances are consistent, which can predict hospitalizations similarly.

Disclosures:
Douglas M. Heuman - Consulting: Bayer, Grifols, Genzyme; Grant/Research Support: Exilixis, Novartis, Bayer, Bristol Myers Squibb, Scynexis, Ocera, Mannkind, Salix, Globeimmmune, Roche, SciClone, Wyeth, Otsuka, Ikaria, UCB, Celgene, Centocor, Millenium, Osiris, AbbVie, Gilead; Speaking and Teaching: Otsuka, Astellas; Stock Shareholder: General Electric
Patrick M. Gilleveit - Stock Shareholder: BioSpheres LLC, Metabiotics Corp

The following people have nothing to disclose: Andrew Fagan, Melanie White, Naga Betrapally, Leroy Thacker, Swati Dalmet, Masoumeh Sikaroodi

854 Different intestinal microbiota profile in alcoholic pancreatitis as compared to alcoholic hepatitis

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Objective Chronic excessive alcohol consumption may cause alcoholic liver disease (ALD) or alcoholic pancreatitis (AP) in only a subset of patients. We have shown that individual susceptibility to ALD is substantially driven by intestinal microbiota (IM). However, factors related to tissue predilection, liver or pancreas, to alcoholic controls.

Design 82 alcoholic patients were included into 3 groups according to their complications: AP (N=24), sAH (N=13) and no complication despite a similar amount of alcohol consumption (alcoholic controls, N=45). IM was analyzed using high-throughput sequencing of the 16S ribosomal RNA (16S rRNA) gene. Results Patients with AP had a reduced bacterial diversity (p=0.001) and a different global microbial composition as compared to alcoholic controls (p=0.001). 17 taxa at the genus level were different between the 2 groups, among them, 8 were increased in AP (Klebsiella, Enterococcus, Aquabacterium and Sphingomonas). When compared to sAH there was no difference in bacterial diversity between the 2 groups. However, 16 taxa were increased in sAH and 10 in AP. After adjusting for confounding factors (age, sex, BMI, alcohol intake, diabetes and proton-pump inhibitors) there was a marked increase in Haemophilus in sAH patients. Conclusion Patients with AP have a specific dysbiosis as compared to alcoholic controls. Specific microbiome signatures are associated with AP and sAH.

Disclosures:
Gabriel Perlemuter - Advisory Committees or Review Panels: Biocodex; Board Membership; Servier; Grant/Research Support: Servier; Speaking and Teaching: Gilead, Bayer, Pileje
The following people have nothing to disclose: Dragos M. Ciocan, Vinciane Rebours, Anne-Marie Cassard-Douclier, Cosmin Sebastian Voican, Laura Wrzosek

855 Intestinal Microbiota Transplantation From HFD-fed and Quercetin Treated Donors Results in a Complex Metabolic Phenotype Transfer that Modulates Obesity-Related NAFLD in Germ Free Mice

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Background: Intestinal microbiota imbalance and related gut-liver axis activation have been identified as key mechanisms in nonalcoholic fatty liver disease (NAFLD) development. Modulation of intestinal microbiota, through administration of prebiotics or faecal microbiota transplantation, is a promising therapeutic approach for obesity-associated diseases including NAFLD. The aim of the present study is to evaluate the benefits of gut microbiota transplantation from donors to germ free mice (GfM) following an experimental treatment with the flavonoid quercetin in a high-fat diet (HFD)-based NAFLD model.

Methods: GfM were colonised with gut microbiota from donors and fed with control or HFD for 16 weeks. Gut bacterial communities were identified by pyrosequencing the 16S-rRNA from caecal samples of donors and GfM. Caecal microbiota donors were selected from control (dc), HFD-fed (dHFD- and dHFD+), as non-responder and responder to the HFD, respectively) and control and HFD supplemented with quercetin (dcQ and dHFDQ) groups, according to metabolic parameters. Results: dHFD- and dHFDQ-receiver groups fed with HFD showed reduced body weight gain, NAFLD activity score, HOMA-IR, and endotoxemia, with respect to other receivers. dHFD+ phenotype transfer was associated with increased NAS index and hepatic markers alteration in control diet-fed mice. The microbial composition at phylum level in donor mice showed an increase in Firmicutes and Verrucomicrobia in dHFD- and dHFDQ, respectively, in comparison to the other donors. At the genus level, a higher detection of Helicobacter was observed in dHFD+ vs dHFD-, while Oscillospira, Lactobacillus and Alkaliphilus exhibited an opposite pattern. Interestingly, a dramatically increase of Akkermansia was detected in dHFDQ with respect the other donors. In GfM dc, dcQ, dHFD- and dHFD+ groups fed with HFD a notable increase in Verrucomicrobia was observed, which was detectable in dHFD+ receiver groups independently of the diet. Akkermansia genus was increased in HFD-fed dc, dQ, dHFD- and dHFDQ-receiver and undetected in all dHFD+-receiver groups. Differences in microbiota composition were accompanied by gut-liver axis disturbance and inflammation as activation in dHFD+-receiver mice independently of the diet.

Conclusions: This different microbiota composition could be associated with the transfer of a complex metabolic phenotype with specific functionality in the receivers. Our data sustain the suitability of intestinal microbiota transplantation as a therapeutic approach for obesity-associated NAFLD. Supported by BFU2013-48141-R, LE063U16 (JCyL and FEDER) and GRS 1428/A/16. CIBERehd is funded by ISCIII