GGT (OR = 2.24; p = 0.007)). The same GGT haplotype but in Belgian cohort was further associated with severe disease course (need of biologics in the first 2 years after diagnosis—OR = 2.11; p = 0.037; SNP2–G carrier (OR = 2.21; p = 0.027) and SNP3–T carrier (OR = 2.51; p = 0.012)), as well as with disease extension (OR = 7.75; p = 0.007; G (SNP2) and T (SNP3) carriers—OR = 2.17; p = 0.041 and OR = 2.81; p = 0.007, respectively). In addition, the haplotype ACA appeared to be associated with family history (OR = 2.39; p = 0.021; SNP1 AA genotype—OR =3.59; p = 0.021) in Belgian cohort. Interestingly, HIGH-risk MGAT5 genotypes were associated with low levels of MGAT5 gene expression on blood T cells.

**Conclusions:** Altogether, we show that genetic variants in the MGAT5 glycosyn can be used to stratify HIGH vs. LOW risk UC patients serving as a potential biomarker that may help the process of therapy decision-making.

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**Microbiology**

**P851**

**Oral delivery of Human β-defensin 2 is reversibly increasing microbiome diversity and is effective in the treatment of experimental colitis**

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**Background:** Inflammatory bowel diseases (IBD), Crohn’s disease and ulcerative colitis, are characterised by complex deficiencies of the mucosal antimicrobial barrier. Different epithelial secreted antimicrobial peptides protect the surface and regulate the gut luminal microbial community while ensuring a beneficial homeostasis. Disrupting this balance by an excessive or dysregulated immune response also results in a so-called “dysbiosis” but cause and consequence is still unclear. Independent of this causality debate, a decreased complexity and diversity of the gut microbiota are common features of chronic inflammation in IBD. The aim of this study was to translate these changes in disease understanding into a clear therapeutic approach. In detail, we tested the human host defence endogenous antimicrobial defensin in terms of (A) microbiome modulation and (B) therapeutic efficacy in experimental colitis.

**Methods:** Mice were treated orally with a dose of 1.2 mg/kg per day for one week. Alterations in bacterial composition were analysed by next-generation sequencing on day 0, day 7 and day 14. Based on these results we tested the bacteriocidal and static effect of hBD2 on different commensal species using MIC in vitro. In a second approach, we tested oral administration of hBD2 in an experimental induced DSS colitis mouse model, compared with the standard therapy with prednisolone.

**Results:** Analysing the gut microbiome, a significant increase of diversity was observed during hBD2 treatment. Of note, these changes shift backwards after stopping the application. Hypothesis-driven MIC experiments were consistent with deep sequencing results of overall analysis. Testing the same dose in an experimental colitis model, the treatment resulted in a significantly lower weight loss (p < 0.05) and a strongly improved disease activity index (p < 0.001). Furthermore hBD2 reduced mucosal damage (p < 0.001). In this setting, the oral administration of hBD2 significantly improved the health in DSS colitis model.

**Conclusions:** It seems that this effect is dependent on the ability of hBD2 to modulate the microbiome towards homeostasis. HBD2 shows promising effect in experimental DSS colitis model. The results and the better effect than prednisolone support a therapeutic application as a drug for IBD. These findings suggest the possibility of hBD2 be used alone or in combination with anti-inflammatory substances in microbiome associated diseases.

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**P852**

**A metabolomics approach to discover biomarkers of chronic intestinal inflammation associated with gut microbiota dysbiosis in ulcerative colitis and Celiac Disease**

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**Background:** The effect of gut microbiota dysbiosis on human metabolome and the potential of microbial and endogenous metabolites as biomarkers of chronic intestinal inflammation (CII) are not clear.

**Methods:** Forty ulcerative colitis (UC) patients, 43 celiac disease (CD) patients and 42 healthy volunteers (HV) were enrolled. The qRT-PCR was used for fecal microbiota assessment. Serum metabolic assays were conducted using the GC-MS. UC patients were randomised into A1 and A2 groups and CD patients were randomised into B1 and B2 groups. A1 and B1 groups received oral calcium butyrate plus insulin for 28 days as supplement to oral mesalazine in UC or gluten-free diet (GFD) in CD. A2 and B2 groups received standard treatment or GFD.

**Results:** Butyrate-producing bacteria (BPB) were depleted in UC compared with HV. CD patients had lower Bifidobacterium spp. counts than HV or UC. Taxonomic dysbiosis in both UC and CD was characterised by a higher Bacteroides fragilis/Faecalibacterium prausnitzii ratio compared with HV. Significant changes in gut microbiota in both UC and CD were accompanied by changes in serum microbial metabolites levels. In UC serum lactic acid, 2-hydroxybutyric acid (2-HBA), 3-hydroxyisobutyric acid (3-HIBA), 2-hydroxyisovaleric acid (2-HIVA), 3-hydroxyisocynamic acid, succinic acid (SA), benzoic acid (BA) and 4-hydroxyphenylacetic acid (4-HPAA) levels were significantly increased compared with HV. Serum levels of caproic acid, linoleic acid (LA) and eicosadienoic acid (EDA) in UC were significantly lower than in HV. Serum of CD patients showed significant increases in stearic acid (StA), 2-HIVA, fumaric acid and...