and *ASV 313 (Faecalibacteria)* was present. In the microbiome of healthy controls, 20 ASVs were abundant, including*: ASV-14 G-Alistipes uncl., ASV 20-(Akkermansia muciniphila),*(bacterium belonging to the phylum *Verrucomicrobia), ASV 321* (*Clostridia uncl.),* ASV 96 *(Rumminococcaceae uncl.), Alistepes uncl. (ASV 61), Subdoligranulum uncl. (ASV 453)* and the *unclassifiable bacteria*. A higher amount of *Verrucomicrobia* was present in the healthy group as opposed to the IBD.

Conclusion: *ASV 249- Parasutterella unlc.,* was indicative of CD associated microbiome through the indicator species analysis. Typical microbiome changes in IBD patients include increased abundance of the pro-inflammatory species with a reduction in anti-inflammatory bacterial species, with a noticeable reduction in alpha and beta diversity. In the local cohort, a particular change in the local α- and β diversity was noted to be present between healthy controls and IBD cohort. This could be a potential way in which targeted therapeutic approaches using specific dosage and durations of probiotic or faecal transplant can be used to alter faecal microbiome using specific bacteria present in healthy controls and with elimination of potentially harmful bacteria in IBD patients.

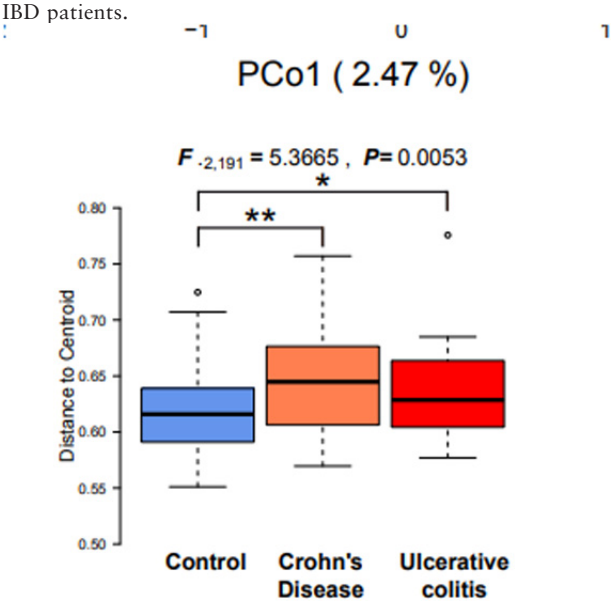

Figure 2: Beta diversity between different groups using Bray-Curtis dissimilarity, Jaccard distance.

Microbiology

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Definition of a microbial signature as a predictor of anti-TNFα treatment response

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Background: Crohn's disease (CD) and ulcerative colitis (UC) evolve with alternate outbreaks and remissions of variable duration. Tumour necrosis factor α antagonists (anti-TNFα) have enhanced the treatment of patients with inflammatory bowel disease (IBD), improving the patient's quality of life by reducing the number of surgeries and hospitalizations. Despite these advances, about 10–30% of patients do not respond to the treatment after the induction period.

Recent studies have pointed, on one hand, gut microbiota can play a role in the anti-TNFα treatment response as gram-positive bacteria can modulate the response of NOD proteins and, on the other hand, gram-negative bacteria can stimulate TLR4 receptors causing activation of NFkß.

This study aimed to define a microbial signature that could be used to predict the response of patients with CD and UC to anti-TNFα treatment.

Methods: This observational study consisted of obtaining a stool sample from 38 IBD patients before starting an anti-TNFα treatment. Patients were recruited at Hospital Universitari Dr. Josep Trueta (Girona) and Hospital Universitari de Bellvitge (l'Hospitalet de Llobregat).

During the one-year follow-up period, disease activity levels, faecal calprotectin evolution, and anti-TNFα antibody levels were analysed to assess response to treatment, differentiating 2 groups: responders and non-responders.

From each sample, DNA was purified and used in a qPCR for the quantification of the following markers: *F. prausnitzii* (Fpra) and its phylogroups (PHG-I and PHG-II), *E. coli* (Eco), *A. muciniphila* (Akk), *Ruminococcus* sp. (Rum), Bacteroidetes (Bac), *M. smithii* (Msm), and the total bacterial load (Eub).

Results: In this proof of concept, the predictive ability to identify anti-TNFα treatment responders was analysed. Individually, none of biomarkers demonstrated the ability to differentiate between groups with high sensitivity and specificity. However, an algorithm consisting of the combination of 5 microbial markers (Msm, Fpra, PHGII, Rum, and Eub) showed a high capacity to discriminate between responders and non-responders. The algorithm proved high sensitivity and specificity reporting values of 93.33% and 100%, respectively, with a positive predictive value of 100% and a negative predictive value of 75% for predicting response to biologic treatment.

Conclusion: A specific microbial signature could beneficiate patients with IBD by predicting the therapeutic effectiveness of an anti-TNFα treatment, which could lead to a personalized therapy, improving the patients' quality of life, saving costs, and gaining time in patient recovery.A larger prospective study will be needed to validate these results.

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Flavonoid-degrading bacteria have central positions in correlation network analysis in patients with Inflammatory Bowel Disease

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