PWE-107 **OSTEOPOROSIS IN CROHN'S DISEASE PATIENTS EXPRESSING AN AUTOPHAGY-RELATED ATG16L1 GENE VARIANT**

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Introduction Osteoporosis is common in Crohn's disease patients.¹ Autophagy genes have so far never being studied as potential risk factors for osteoporosis in Crohn's disease.

Methods We have analysed the risk for osteoporosis among Crohn's disease patients expressing the rs2241880 polymorphism of the ATG16L1 gene. Patients diagnosed with Crohn's disease through histological, radiological and endoscopic findings were recruited. A blood sample for genotyping was taken and a DEXA Bone Density scan was performed in each patient. Genotyping for this variant involved:

- DNA extraction
- Gradient Polymerase Chain Reaction (PCR)
- Quantitative PCR and High Resolution Melt (HRM)
- Restriction Fragment Length Polymorphism (RFLP) of PCR product

Results 83 Crohn's patients were included in the study. Following genotyping, 33 patients were found to have no mutation (wild type), 44 were heterozygous and 6 were homozygous for the rs2241880 variant of the ATG16L1 gene. The table below shows the mean T and Z scores at the hip and spine of patients with the wild type, heterozygous and homozygous variants.

Patients Homozygous for the rs2241880 variant had lower mean T and Z scores at the hip than those Heterozygous or Wild Type. Using t-test, there was no statistical difference between the Homozygous, Heterozygous and Wild Type patients' hip T scores ($p:0.314$), Z scores ($p:0.441$), and spine T scores ($p:0.751$) and Z scores ($p:0.822$). Using χ^2 test, the relationship between the 3 different variants (homozygous, heterozygous and wild type) and the risk of osteoporosis (T score < -2.5), osteopenia (T score: -1.0 to -2.5) and normal (T score > -1.0) was not statistically significant ($p:0.978$).

Conclusion We found no significant difference between the T and Z scores of patients with ATG16L1 Homozygous, Heterozygous and Wild Type alleles. However, there is a trend in the mean T and Z scores at the hip with lower scores in patients with Heterozygous/Homozygous alleles. Such a trend is not present in the spine. While the authors can offer no explanation for this difference, studies on larger populations are needed to better investigate the relationship between ATG16L1 mutations and the risk of osteoporosis.

Disclosure of Interest None Declared.

REFERENCE

1. Lewis NR, Scott BB. British Society Guidelines for osteoporosis in inflammatory bowel disease and celiac disease. BSG guidelines in Gastroenterology. June 2007; 1–12.

PWE-108 **ASSESSMENT OF THE MUCOSAL MICROBIOTA IN INFLAMMATORY BOWEL DISEASE**

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Introduction Great progress has been made in understanding the pathophysiology of Crohn's disease (CD) and ulcerative colitis (UC), and it is now widely believed that dysregulation of the relationship between the gut microbiota and the host immune system is central to both diseases. Most published studies to date have focused on assessing the microbiota found in faecal samples, but it is increasingly recognised that this may not be an accurate reflection of what is happening at the mucosal level.

The Aims of this study were to establish a bioresource of IBD patients and controls, and to use this to assess differences in gut microbiota between cases and controls and between different IBD subphenotypes.

Methods Patients undergoing colonoscopy and flexible sigmoidoscopy were recruited to the South East Scotland IBD bioresource. Mucosal biopsies were obtained and snap-frozen using dry ice. DNA was then extracted using a QIAGEN spin column-based method. Blood and serum samples were also biobanked for genetic, epigenetic and metabolomics analysis. Quantitative PCR was used to measure the relative abundance of different bacterial classes compared to the total measured with universal primers. Statistical analysis was done using Mann Whitney U, chi squared and Fisher's exact tests using R 2.15.2.

Results After quality control, results were available from 147 biopsies taken from 84 patients. There were 20 patients with CD, 26 with UC, 2 IBD-U, 20 healthy controls (HC) and 16 with other diagnoses. Median age was 45 years (interquartile range [IQR] 28–50) in the CD group, 51 y (38–63) in the UC group and 39 (30–49) in the HC group. There were no significant differences in age or sex distribution between the CD, UC and HC groups.

There was a statistically significant reduction in CD compared with HC in Ruminococcaceae ($p = 0.002$, figure 1), Lachnospiraceae ($p = 0.046$) and Bacteroides (0.024) and an increase in Enterobacteriaceae ($p = 0.046$). Comparing UC with HC, there was a significant increase in Enterobacteriaceae ($p = 0.025$), but no difference in the other classes. There were no significant differences in any bacterial class between biopsies taken from inflamed and non-inflamed sites in IBD patients.

Conclusion This study confirms reductions in Ruminococcaceae described previously in CD, and increased Enterobacteriaceae in both CD and UC. The presence of paired DNA and serum samples offers the exciting potential to explore the relationship between the gut microbiota, epigenetic and metabolomics changes.

Disclosure of Interest None Declared.

Abstract PWE-107 Table

rs2241880 variant of ATG16L1 (95% Confidence Interval)	T Score, Hip	T Score, Spine	Z Score, Hip	Z Score, Spine
Wild Type (n = 33)	-1.48 (-1.91 - -1.05)	-0.96 (-1.41 - -0.51)	-0.75 (-1.20 - -0.31)	-0.45 (-0.91 - +0.01)
Heterozygous (n = 44)	-1.68 (-2.32 - -1.22)	-0.94 (-1.41 - -0.47)	-0.92 (-1.38 - -0.46)	-0.34 (-0.82 - +0.14)
Homozygous (n = 6)	-1.84 (-2.71 - -0.97)	-0.14 (-1.10 - 0.82)	-0.99 (-1.86 - -0.14)	-0.34 (-0.62 - +1.33)