

Abstract P324 Figure 1 MNBI is reduced in Barrett's (regardless of PPI use) compared to NERD and FH Median and IQR for the MNBI of: patients with Barrett's off PPIs 406 Ω (368 Ω , 1111.5 Ω); Barrett's on PPIs 453 Ω (261.5 Ω , 1000 Ω); NERD 1160 Ω (964.5 Ω , 2764 Ω) and FH 3355 Ω (2866.5 Ω , 3809.25 Ω)

patients studied off PPI (p=0.97 figure 1). There was no difference in MNBI between the 10 patients with persistent (>3 cm) Barrett's who had attempts at therapy (ablation, mucosal resection) compared to the 27 who had not received therapy (p=0.96).

There was a moderately inverse correlation between Barrett's segment length (median 5 cm (3 cm,9 cm) and MNBI (r = -0.436; p = 0.038).

Conclusion This study suggests that the impact of reflux disease on mucosal permeability (MNBI) may have an influence on symptom perception. Both MNBI and symptom perception were significantly reduced in Barrett's compared to NERD. Furthermore, neither MNBI nor symptom perception are affected by use of acid reducing medication despite the difference in AET. This study provides further validation to the Lyon consensus definition of MNBI as a measure of reflux disease severity.

P325

AN EXPANDED INTESTINAL INTRAEPITHELIAL LYMPHOCYTE COMPARTMENT IS LINKED TO SHIFTS IN COMPOSITION OF MUCOSAL MICROBIOTA

¹JL Alexander*, ^{2,3,4}A Andreasson, ⁵LW Hugerth, ⁵L Engstrand, ^{6,7}MM Walker, ⁷NJ Talley, ¹N Powell. ¹Div. of Digestive Diseases, Imperial College, London, UK; ²Dept. of Psychology, Macquarie University, North Ryde, Australia; ³Stress Research Institute, Stockholm University, Stockholm, Sweden; ⁴Dept. of Medicine Solna, Karolinska Institutet, Solna, Sweden; ⁵Center for Translational Microbiome Research, Karolinska Institutet, Solna, Sweden; ⁶Dept. of Anatomical Pathology, University of Newcastle, Newcastle, Australia; ⁷Faculty of Health and Medicine, University of Newcastle, Newcastle, Australia

10.1136/gutjnl-2020-bsgcampus.399

Introduction The composition of bacteria colonising the gastrointestinal tract shapes mucosal and systemic immune responses and impacts susceptibility to different diseases. However, a consistent microbiome signature of Irritable Bowel Syndrome (IBS) has yet to be established, and the microbiome was not altered in a large, population-based study of IBS¹. Since it has been proposed that immune activation and subtle intestinal inflammation may be present in a subset of IBS², we

hypothesised that alterations in the gut microbiome may underpin changes in gut immune phenotype.

Methods The study population comprised IBS cases and controls (defined by modified Rome III criteria) from the PopCol study¹. All participants had a normal colonoscopy. Biopsies were taken from the terminal ileum (TI), caecum, transverse colon (TC), sigmoid and rectum (Re). Assessment of histology was blinded and dual read, and disagreement was resolved by consensus. Intraepithelial lymphocyte (IEL) counts were dichotomised: high IEL count was defined as >15 per 100 enterocytes in TI and >8 per 100 colonocytes in the colon. Colonic mucosa-associated microbiota (MaM) and faecal microbiota (FM) were characterised by 16S rRNA sequencing on Illumina MiSeq. Data were processed and analysed in R, Graphpad & STAMP, with p value correction for multiple testing.

Results 76 participants (including 30 with IBS) were analysed, in whom IEL and microbiome data were available. The median age was 50 years (range 23–69) and 40 (53%) were women. 55% of TI samples and between 39% (Re) and 51% (TC) of samples from colonic sites had a high IEL count. No difference was observed in alpha diversity of MaM or FM based on IEL count. There were trends towards differences in beta diversity of the MaM according to IEL count in the TI and TC (p=0.079 & 0.072). No difference in FM beta diversity was observed. In the MaM, the genus *Blautia* and *unclassified Clostridiales* were associated with high IEL count in the TI (p=0.024 & 0.036). *Alloprevotella* was associated with low IEL count in the sigmoid (p=0.035).

Conclusions In this nested analysis of participants in the Pop-Col study, modest but discernible differences in the mucosa-associated microbiota were seen according to IEL count.

REFERENCES

- 1. Hugerth LW. Gut (online first) 2019. doi: 10.1136/qutjnl-2019-318717
- 2. Burns G. Am J Gastroenterol 2019 Mar; 114(3):429-436.

P326

IDENTIFICATION OF NOVEL SUBGROUPS IN IRRITABLE BOWEL SYNDROME USING LATENT CLASS ANALYSIS: BEYOND STOOL FORM

¹Christopher J Black*, ²Yan Yiannakou, ³Lesley A Houghton, ⁴Elspeth Guthrie, ⁴Robert West, ^{1,3}Alexander C Ford. ¹Leeds Gastroenterology Institute, Leeds Teaching Hospitals NHS Trust, Leeds, UK; ²County Durham and Darlington NHS Trust, Durham, UK; ³Leeds Institute of Medical Research at St. James's, University of Leeds, Leeds, UK; ⁴Leeds Institute of Health Sciences, University of Leeds, Leeds, UK

10.1136/gutjnl-2020-bsgcampus.400

Introduction Conventionally, patients with irritable bowel syndrome (IBS) are divided into subgroups based on their predominant stool pattern, either diarrhoea, constipation, or mixed stool form. However, factors other than gastrointestinal symptoms, such as psychological co-morbidities, are also highly relevant to IBS symptomatology. We explored alternative approaches to subgrouping people with IBS by incorporating factors beyond stool form alone.

Methods We collected demographic, symptom, mood, and psychological health data from 1375 adult subjects in the UK community who self-identified as having IBS, and identified two cohorts meeting either the Rome III or the Rome IV diagnostic criteria. In each cohort, we performed latent class analysis, a method of cluster modelling, to identify specific subgroups (clusters) within the data. We used the Bayesian information criterion (BIC) to determine the preferred model;

A208 Gut 2021;**70**(Suppl 1):A1–A262