measures (area under curve (AUC)) were anchored around known anatomical landmarks as identified by compartmental pH changes. 60-minute epochs were used to quantify antral, duodenal, ileal, caecal and distal colonic contractility. The maximum and minimum pH was measured either side of the ileo-caecal junction. All data are presented as means ($\pm 95\%$ CI).

Results No differences were seen in any of the motility parameters, compartmental transit times or maximal ileal pH between the two groups. Minimum caecal pH was significantly lower in patients compared to control ($P_x = 5.14 \pm 0.14$ v $C_x = 6.12 \pm 0.16$, $p < 0.0001$). The 95% CI for maximum pH drop across the ICJ in health was 1.65 units. There was a significant correlation between caecal pH and caecal contractility ($r = 0.498$, $p = 0.05$).

Conclusion In this study, we have shown that patients with lower abdominal symptoms typically associated with, but not limited to, conditions such as irritable bowel syndrome (IBS) have a significantly lower caecal pH compared to controls. This low pH environment is maintained by fermentation and subsequent SCFA production. SCFA have been shown to inhibit colonic motility in-vitro and contractility as measured by the WMC was correlated with caecal pH. With the recent success of anti-biotic therapy and low fermentable diets in the treatment of lower bowel symptoms in IBS, measurement of caecal pH using the WMC provides an objective and quantifiable biomarker of fermentation. This may be used to sub-classify patients with a broad spectrum of GI disorders and identify those that may benefit most from antibiotic, probiotic and dietary interventions providing novel insights into the pathophysiological mechanisms of lower GI symptoms.

Disclosure of Interest A. Hobson Paid Instructor for: Given Imaging, S. Mohammed: None Declared, G. Dukes Employee of: GSK, M. Scott: None Declared

PWE-010 BIOFEEDBACK-A SIMPLE AND EFFECTIVE WAY OF MANAGING RECTAL EVACUATORY DYSFUNCTION SECONDARY TO PELVIC FLOOR DYSSYNERGIA AND RECTAL HYPOSENSITIVITY

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Introduction Biofeedback is safe and effective in the management of rectal evacuatory dysfunction (RED), but there is limited data on medium to long-term follow-up. This study evaluated the effectiveness of biofeedback in the medium-term for patients with RED secondary to pelvic floor dyssynergia (PFD) and rectal hypo-sensitivity (RH).

Methods Prospective data was collected from 2010–2013 of 81 consecutive patients who underwent specialist nurse-led verbal biofeedback therapy in the form of rectal sensory re-training or balloon expulsion for PFD or RH. The primary outcome measure was patient satisfaction with their symptom improvement, assessed using a visual analogue scale (Likert scale 0–10). Secondary outcome measures were complete spontaneous bowel movements (CSBMs)/week, time to defecation-assessed using bowel diaries, and KESS/SF-36 quality of life questionnaire scores. All discharged patients received telephone follow-up.

Results 85% patients met the primary outcome measure, with the Likert score improving [mean baseline 3.2 (1–7) vs. post-biofeedback 7.6 (5–9) $p < 0.001$]. Improvements were seen in CSBMs/week [mean baseline: 3.0 (1–14) vs. post-biofeedback: 6.9 (1–13) $P < 0.001$] and time taken to defecate in minutes [mean baseline: 18.7 (5–60) vs. post-biofeedback: 8.7(5–30) $P < 0.001$]. Significant improvements were seen in KESS [mean baseline 13.1 (9–18) vs. post-biofeedback 4.9 (0–16) $p < 0.001$] and SF-36 scores. Mean number of biofeedback treatments received was four (1–6). 89% of patients

discharged still meet the primary endpoint at a mean follow-up of 19 months (range 7–36).

Conclusion Biofeedback has a key role to play in the management of rectal evacuatory dysfunction secondary to pelvic floor dyssynergia and rectal hyposensitivity, with the improvement being maintained in the medium-term.

Disclosure of Interest None Declared.

PWE-011 CHARTING THE VOLATILE ORGANIC METABOLOME (VOM): A COMPARISON OF MURINE AND HUMAN FAECES

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Introduction The metabolome is important in the development of IBD and colorectal cancer. It may be studied using gas chromatography mass spectrometry (GCMS) or electronic noses that sniff the volatile organic compounds, which comprise a large portion of the metabolome. However the healthy volatile organic metabolites (VOMs) of mice remain uncharted, nor have mouse models been validated for use in comparative studies of VOMs with humans.

Methods We collected serial samples from healthy C57 BL/6 mice and a healthy human, as part of our method development for VOM studies in colitis and colorectal cancer. The samples were enclosed in glass vials and the VOMs extracted from the headspace gas. VOMs were analysed using GCMS and the resultant fragmentation patterns compared to the NIST database for compound identification. VOMs from murine and human samples were compared. The consistency of mouse and human samples over time and between individuals was also examined by listing the rank position in quintiles over serial samples.

Results 60 individual VOMs were identified from mice and 87 in the human, with a 22% correlation between the two. Most notable in the murine sample was the high concentration of simple organic molecules such as hexane and short chain aldehydes. Several compounds were found in the murine sample that had not been seen in human samples and probably reflect urine contamination from incontinent mice. The greatest concentration of VOMs in the mouse were: hexanal, 2,2,4,6,6-pentamethyl-heptane and pentanal. By comparison, in the human, complex cycloalkenes and benzene-based compounds, such as 1-methyl-4-(1-methylethylidene)-cyclohexene, were in abundance. Chief compounds in the human were: D Limonene, 2-methyl phenol and indole. Several molecules were prominent in both mouse and human, such as acetone, short chain organic acids including hexanoic, pentanoic and butanoic acids and D-limonene. The more simple compounds likely reflect a combination of the metabolic effluvia of common intestinal microbiota and mammalian physiology. The position of VOMs in each quartile was found to be consistent with 86% recurrence in the first quartile, 71% in the last quartile.

Conclusion This is the first description of the VOC metabolome of C57 BL/6 mice. A comparison with human samples shows there is a low but notable correlation between the two species. Many of the VOCs present are by-products of microbial and cellular metabolism. The difference in number and complexity of the VOCs found in the human, compared with the mouse, may reflect varied diet and a more complex intestinal microbiome. Such data will allow calibration of future studies of colonic disease in humans and through the induction of colonic disease in mice.

Disclosure of Interest None Declared.

PWE-012 ASSESSMENT OF BACTERIAL DIVERSITY IN COLORECTAL ADENOMATOUS POLYPS

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Introduction The human intestinal tract is a complex microbial ecosystem unique to every individual and contributing sufficient metabolic equivalents to be considered an organ in its own right. Dysbiosis is thought to contribute to the chronic inflammation which is involved in colorectal cancer (CRC) development. We have shown that the premalignant adenoma stage of CRC is underpinned by chronic inflammation and hypothesise that the colonic microbiota is an important driver of neoplastic progression. The aim of the study was to compare bacterial diversity in adenomas and paired adjacent normal colonic tissue.

Methods 72 patients undergoing colonoscopy as part of the national bowel cancer screening programme were recruited. All patients underwent polypectomy for large adenomas (> 1cm). Denaturing gradient gel electrophoresis (DGGE on all subjects) and pyrosequencing (18 subjects) were used to compare the bacterial diversity present between the adenoma and adjacent normal paired tissue samples.

Results 46% of patients showed differences in microbial diversity by DGGE analysis between adenoma and adjacent normal tissue. 21% had only limited differences whilst 79% showed dramatically altered diversity profiles. Phylum-level comparisons across the study cohort, based on sequencing, revealed no statistically significant differences for the Bacteroidetes, Firmicutes and Proteobacteria phyla. When samples were split based on DGGE analysis (i.e. similar or different DGGE profiles between paired polyp and normal mucosa), eight of the possible 10 phyla showed statistically significant differences. Collectively samples with similar profiles between polyp and normal tissue (DGGE 'same' group) had higher levels of Bacteroidetes and lower numbers of Actinobacteria, Firmicutes and Proteobacteria than the DGGE 'different' group. However when genus-level comparisons were assessed the DGGE 'different' sample pairs demonstrated a much greater level of dysbiosis. The levels of normal commensal genera were reduced and there was evidence of large numbers of potentially pathogenic bacteria including *Shigella*, *Enterobacter* and *Fusobacteria* spp.

Conclusion Differences in microbial diversity harboured by a significant number of polyps compared to their immediately adjacent normal mucosa point to an important role for these bacteria in CRC progression. We hypothesise that the disturbed microbial homeostasis in these polyps, in genetically predisposed individuals and taking into account multiple environmental factors, underpins the pathogenesis of colorectal neoplasia. The identification of a "harmful" pro-inflammatory microbiota that is associated with precancerous stages (i.e. adenomas) offers the potential for manipulations of this microbiota with probiotic, prebiotic and indeed antibiotic means.

Disclosure of Interest None Declared.

PWE-013 EVALUATION OF FAECAL ASPIRATE AS A PROXY FOR COLONOSCOPY BIOPSY SAMPLING TO ASSESS MICROBIAL DIVERSITY

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Introduction The gut microbiota plays a key role in Inflammatory Bowel Disease (IBD) pathogenesis and is also involved in colorectal neoplastic progression. In particular, the "dysbiosis" theory has evolved from work which has shown IBD sufferers to have different microbiologic profiles to normal controls. There is strong evidence to demonstrate that individuals harbour a unique microbiota with faecal and mucosal ecosystems being distinct. This would indicate that faecal samples are not appropriate surrogate markers for mucosal samples and other alternative sampling options should be considered. The aim of the study was to assess the microbial diversity

of paired biopsies and faecal aspirates to determine whether faecal aspirate can be used as a suitable surrogate for colonic biopsies.

Methods Bacterial DNA was extracted from 21 paired mucosal biopsies and faecal aspirates, and subjected to denaturing gradient gel electrophoresis (DGGE) and q-PCR analysis to quantify the relative abundance of the following major bacterial groups: Bacteroidetes, *Ruminococcaceae*, *Lachnospiraceae* and *Enterobacteriaceae*. The relative abundance of bacterial groups was expressed as a percentage of total bacteria.

Results Increased variation was found across the faecal aspirates compared to biopsies with regards to relative abundance of the four bacterial groups analysed by q-PCR (Table 1). This indicates that microbial diversity of faecal aspirates is more variable than mucosal biopsies. When the mean abundance of each bacterial group across the biopsies and across the faecal aspirates was compared using a Paired t-test, there was a significant difference in levels of *Bacteroides* (62.3% vs 44.4%; $p < 0.05$) but not the other bacterial groups. There was no statistical correlation between paired faecal aspirate and biopsy samples when analysed for the four major bacterial groups by linear regression.

Abstract PWE-013 Table 1

	Biopsy		Faecal aspirate	
	Abundance across samples* (%)	Mean +/- SD	Abundance across samples (%)	Mean +/- SD
Bacteroides	40.5 – 116.3	62.3% ± 20.0%	0.4 – 84.5	44.4% ± 25.8%
Clostridium cluster XIVa	11.8 – 63.7	36.7% ± 16.8%	9.2 – 150.4	39.4% ± 37.5%
Clostridium cluster IV	3.5 – 23.4	11.9% ± 5.9%	1.8 – 36.0	11.9% ± 9.6%
Proteobacteria	0.07 – 34.4	5.6% ± 8.4%	< 0.1 – 59.6	4.0% ± 13.1%

* = calculated based on relative abundance as a percentage of total bacteria

Conclusion Substantial microbial diversity differences exist between faecal aspirate and biopsy samples. Faecal aspirates demonstrate considerably more variation than biopsies, and there would appear to be no correlation between paired samples. These results suggest that faecal aspirate is not a suitable microbiological surrogate for mucosal biopsies.

Disclosure of Interest None Declared.

PWE-014 DEVELOPMENT OF AN OPTIMUM TREATMENT REGIMEN FOR TRANSCUTANEOUS POSTERIOR TIBIAL NERVE STIMULATION FOR FAECAL INCONTINENCE

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Introduction Posterior tibial nerve stimulation (PTNS) is an effective treatment for faecal incontinence (FI). A wide range of PTNS regimens have been reported. The aim of this study was to determine an improved PTNS regimen.

Methods Patients were randomised to either daily or twice weekly unilateral transcutaneous PTNS for six weeks. The investigator was blinded to group allocation. Once completed, further patients were recruited. They received daily bilateral transcutaneous PTNS for six weeks. The primary outcome measure was the change in frequency of FI episodes per week. PTNS was self-administered by each patient from home.

Results Thirty patients received either daily or twice weekly PTNS. The daily unilateral PTNS group achieved a reduction in frequency of incontinent episodes of 5(11.3) to 3.5(4.31), $p = 0.025$. Three achieved complete continence. No change was seen in the twice weekly group. Neither group improved deferral time. A further 20 patients received daily bilateral PTNS. They achieved a