Our study showed that LSMI and BMI improved following HPN but demonstrated that other anthropometric measurements had poor correlation with LSMI and showed no significant improvement overall after HPN, confirming the known problems of inter-operator and patient variability of these measurements. Whilst we found significant correlation between LSMI and BMI, BMI significantly underestimated the presence and degree of sarcopenia.

We have shown LSMI can provide an objective and reproducible measure of sarcopenia in IF. Future larger studies should be performed to evaluate associations with patient outcomes and utility in clinical decision making.

OWE-021 DESCRIBING THE GUT MICROBIOME AND METABOLIC CHANGES IN BILE ACID DIARRHOEA

¹Nidhi Sagar*, ²Henri Duboc, ¹Gemma Kay, ³Konstantinos Gerasimidis, ³Vaios Svolos, ¹Alfian Wicaksono, ¹Christopher Quince, ¹James Covington, ⁴Nicola O'Connell, ⁴Subiatu Wurie, ^{1,4}Ramesh Arasaradnam. ¹University of Warwick, UK; ²Paris VI University, France; ³University of Glasgow, UK; ⁴University Hospitals Coventry and Warwickshire, UK

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Introduction The diagnosis of bile acid diarrhoea (BAD) is often missed or misdiagnosed for irritable bowel syndrome – diarrhoea predominant (IBS-D) as these conditions have a similar clinical presentation. The principal hindrance to diagnosis of BAD is limited access to the diagnostic SeHCAT scan. Mechanisms of aetiology underlying BAD have not been fully elucidated but it has been accepted that bile acids (BAs) are metabolised by the gut microbiota, therefore their role as signalling molecules in regulating intestinal homeostasis is influenced primarily by the gut commensals.

The aim was to profile the gut microbiome in BAD and investigate the mechanisms of how bacterial metabolic products may influence the development of disease.

Methods 157 patients participated in the study after having a SeHCAT scan to either diagnose BAD or IBS-D (the latter with a negative scan). Exclusion criteria included recent use of antibiotics/probiotics and the diagnoses of coeliac disease, colorectal cancer and active inflammatory bowel disease (unremarkable levels of C-reactive protein and/or faecal calprotectin were required) in type 1 BAD patients. To examine the gut microbiome, 16S ribosomal RNA gene analysis was undertaken. Bacterial metabolites (short chain fatty acids-SCFAs and volatile organic compounds-VOCs) and BAs were measured using gas and liquid chromatography, mass and ion mobility spectrometry.

Results Intestinal dysbiosis with reduced bacterial diversity was observed in patients with BAD compared with IBS-D ($p=0.01$). A greater total concentration of SCFAs ($p=0.17$) with increases in the concentrations of acetate ($p=0.14$) and propionate ($p=0.08$) were observed in BAD compared to IBS-D. An increase in the concentrations of faecal primary BAs ($p=0.05$) and serum CDCA ($p=0.05$) was observed in BAD compared to IBS-D.

Conclusions Intestinal dysbiosis with altered fermentation and resultant BA dysmetabolism were observed in BAD. The metabolic output of the microbiota rather than abundance of specific bacterial taxa appears to be more important in the aetiology of BAD.

OWE-022 GLUTEN FREE DIET ADHERENCE ASSESSMENT USING CDAT AND BIAGI QUESTIONNAIRES IN PATIENTS WITH COELIAC DISEASE

Michelle S Lau*, Peter D Mooney, Michael A Rees, William L White, Lauren J Marks, Marios Hadjivassiliou, David S Sanders. Academic Unit of Gastroenterology, Royal Hallamshire Hospital, Sheffield, UK

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Introduction Non-adherence to a gluten free diet (GFD) could lead to persistent villous atrophy and the development of complications in coeliac disease. However, current adherence assessment methods have their own limitations: dietetic evaluation by a specialist dietitian is usually accurate but resources are often limited; serology has been shown to have poor sensitivities in measuring adherence; and although duodenal biopsies are considered the gold standard, it is invasive and expensive. We aimed to assess the sensitivities of 2 validated questionnaires, which have been suggested as non-invasive markers of adherence.

Methods We prospectively recruited coeliac disease patients who were referred to secondary care for further evaluation of dietary adherence and disease remission. All patients were tested with tissue transglutaminase (IgA-TTG) and endomysial antibodies (IgA-EMA), and completed 2 adherence questionnaires, one devised by Biagi et al.¹ and Coeliac Disease Adherence Test (CDAT) devised by Leffler et al.² The questions were largely related to the patients' attitude and strategy towards gluten avoidance. The Biagi questionnaire consists of 4 questions, and the score ranges from 0–4; score <3 indicates non-adherence. CDAT consists of 7 questions, and the score ranges from 7–35; score >13 indicates non-adherence. Duodenal biopsies were taken from all patients, and the presence/absence of villous atrophy was the reference standard used to determine the sensitivities.

Results A total of 120 patients were recruited, 80 females (67%), median age 54, median duration of GFD 5 years. Forty-five patients (37.5%) had persistent villous atrophy. The median CDAT score was 12, and the median Biagi score was 3. The sensitivities of the surrogate markers for adherence compared to duodenal histology are demonstrated below.

Abstract OWE-022 Table 1

	Sensitivity % (CI)	Specificity % (CI)	Positive predictive value% (CI)	Negative predictive value% (CI)
CDAT	55.4 (40.0–70.4)	57.3 (45.4–68.6)	43.9 (35.0–53.1)	68.3 (59.5–75.9)
Biagi	24.4 (12.9–39.6)	92.0 (83.4–97.0)	64.7 (42.1–82.2)	70.0 (62.9–70.8)
CDAT + Biagi	62.2 (46.5–76.2)	56.0 (44.1–67.5)	45.9 (37.6–54.4)	71.2 (61.8–79.1)
IgA-TTG	40.0 (25.7–55.7)	97.5 (90.7–99.7)	90.0 (68.7–97.4)	73.0 (70.0–77.5)
IgA-EMA	37.8 (23.8–53.5)	97.3 (90.7–99.7)	89.5 (67.3–97.2)	72.3 (67.4–76.7)

Conclusions CDAT alone was not superior compared to IgA-TTG ($p=0.6961$). However, the combination of CDAT and Biagi questionnaires significantly outperformed IgA-TTG ($p=0.0162$) in detecting villous atrophy. These questionnaires