O45   INVESTIGATING CHRONIC DIARRHOEA WITH SEHCAT – WHO DO WE SCAN? WHAT DOES IT SHOW?

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Introduction Bile acid diarrhoea (BAD) remains an underdiagnosed cause of chronic diarrhoea. Recent guidelines[1] have advocated the use of SeHCAT scans when investigating chronic diarrhoea. We performed a 7-year retrospective analysis of all patients in Swansea Bay University Health Board (SBUHB) who underwent SeHCAT scans from 2013 to 2020. We have assessed their demographics in relation to results and reviewed how our diagnostic yield has changed over time.

Method We used 'SYNAPSE' imaging system to review all scans requested by gastroenterologists in SBUHB. We classified positive scans as SeHCAT retention <15%, and negative as ≥15% (in SBUHB patients with a SeHCAT retention of <15% are offered treatment). We then analysed the number of tests performed and the diagnostic yield.

Results 212 scans were performed. The majority of tests were performed in the last 2 years (2018–2019, n = 123). See table 1 below.

There was an overall diagnostic yield of 126 (59.4%) positive results, with 86 (40.6%) negative results. From 2014 to 2020 there was similar percentage of positive tests (56.8% to 64.7%). In 2013 there were only two scans (both positive).

72.6% of patients were female (n=154) and 27.4% male (n=58). The positive test rate was 59.7% and 58.6% respectively.

The median 10-year age range was 50–59 making up 22.6% of the data set. All age groups had >50% positive test rate. The largest positive rate was found in the 70–79 years group (n=21) with 76% of patients having a positive test. The lowest was the 19–29 years age group (n=10) with 50% positive tests.

Conclusions Our data shows that our use of SeHCAT has increased significantly since the publication of new BSG guidelines, but our diagnostic yield remains high, despite these increased numbers. If we were scanning too many people, we would expect proportionally more negative tests. This is not the case. This suggests, despite SeHCAT becoming more widely available and awareness of BAD increasing we are still not over investigating our population.

Most of our patients were female, however the positive test rate remained similar between males and females. The factors effecting the disproportionate numbers of females to males is not possible to assess from this data set.

We observed a high rate of positive tests in all age ranges giving us no significant evidence to limit scanning based on age. This is important moving forward as the question of which patients with chronic diarrhoea to perform SeHCAT scanning on in a resource limited NHS remains unanswered.

REFERENCE

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O46   FLOW CYTOMETRY- THE NEW 'GOLD STANDARD' FOR COELIAC DISEASE DIAGNOSIS?

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Introduction The diagnosis of coeliac Disease is not always easy. Up to 20% of cases of Coeliac Disease identified through serological tests have normal mucosal biopsies ('potential' Coeliac disease) and a small proportion are diagnosed on the basis of mucosal biopsies in the absence of confirmatory serology. Furthermore, over 25 different commercial kits are used for IgA anti tissue transglutaminase (TTG) antibody measurement in the UK all of which behave differently, and mucosal biopsy interpretation is variable depending on biopsy orientation and quality. Both serological and histological changes are dependent on the patient continuing to eat gluten.

Methods IEL flow cytometry was established in our centre as a diagnostic tool for refractory Coeliac disease in 2015. 8- 10 additional biopsies are taken from the duodenum at endoscopy at the time of diagnostic biopsies that are sent for histopathology. Epithelium is separated from the biopsies using ethylenediaminetetraacetic acid (EDTA) and dithiothreitol (DTT) and vortexed to separate cells. Cell suspensions are divided into aliquots and incubated with fluorochrome labelled antibodies against cell surface markers. A cell permeabilisation step is undertaken with dual fluorochrome staining for CD3 to identify cytoplasmic and surface CD3 expression before identifying tagged lymphocyte subpopulations through a flow cytometer.

Results Biopsies were analysed by flow cytometry from patients *without* Coeliac Disease (CON, n=37); patients with villous atrophy and positive anti TTG antibodies (CD, n=54); patients with unusual enteropathies (ENT; n=17); patients with normal biopsies on long term follow up for Coeliac Disease (FU; n=18) and patients with positive TTG antibodies but normal biopsies (POT; n=15).

The proportion of IELS expressing surface and cytoplasmic CD3 was charted against the proportion of CD3+ IELS expressing the γδ receptor. A striking separation was noted between CON and CD groups, with a function of %(CD3+) =2x% (γδ+) ≥ 100 being diagnostic for Coeliac Disease. Initial analysis revealed a sensitivity of 92% and a specificity of 94.5% for this test. However closer analysis of cases revealed that some individuals diagnosed with coeliac disease may not have had the condition (based on diagnosis made in the 1950's in 2 cases prior to the availability of diagnostic tests) or may have been excluding gluten and undergone inadequate

Abstract O45 Table 1

Year	Total No. scans	No. positive scans	% Positive scans
2013	2	2	100.0%
2014	10	6	60.0%
2015	17	11	64.7%
2016	25	16	64.0%
2017	28	17	60.7%
2018	42	24	57.1%
2019	81	46	56.8%
2020	7	4	57.1%

gluten challenge. Adjusting for these cases led to a sensitivity of 98% and a specificity of 97%.

Conclusions Appropriate use of IEL flow cytometry yields surprising results and is the only existing test capable of reliably diagnosing Coeliac Disease in the presence of gluten withdrawal, normal biopsies and negative serology. Whilst expensive and time consuming, it now represents the 'gold standard' of diagnosis in Coeliac Disease.

Nutrition

| O047 | THE DOSE-DEPENDENT EFFECT OF ENTERAL NUTRITION ON FAECAL MICROBIAL METABOLITES OF HEALTHY VOLUNTEERS |

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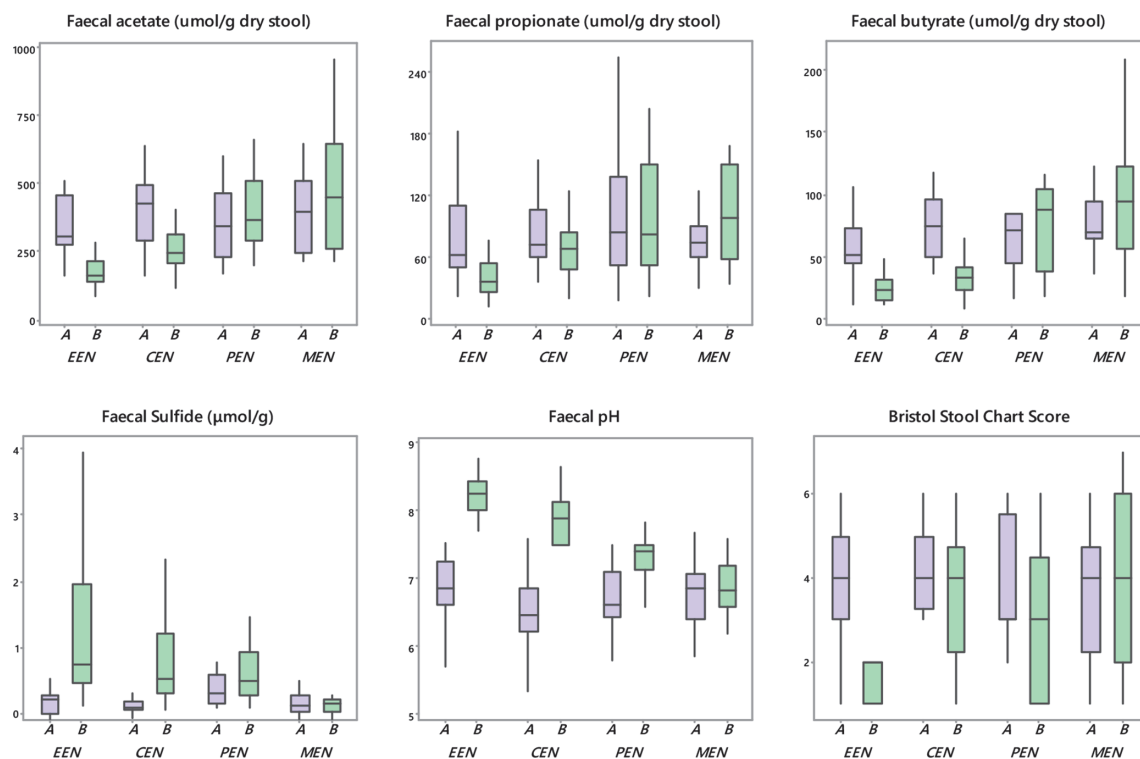
Introduction Treatment with exclusive enteral nutrition (EEN) offers a nutritional therapy paradigm in Crohn's disease, with the extensive modulation of gut microbiome being its proposed mechanism of action(1). Recent studies propose variable clinical efficacy for 85% EN (Cheat EN/CEN), 50% EN (Partial EN/PEN) and 20% EN (maintenance EN/MEN), and a dose-dependent effect of EN use in CD(2–4). Therefore, this study aims to investigate the dose-dependent effect of 100%, 85%, 50%, and 20% EN on faecal microbial metabolites; and to investigate if this effect can be used as a compliance marker for EEN.

Methods Healthy adults followed EEN, CEN, PEN or MEN diet for 7 days. Fresh faecal samples were collected before and after each dietary intervention. Dietary assessment was performed throughout the intervention using estimated weight food diaries. Faecal pH, Bristol Stool Chart Score (BSCS), short chain fatty acids and hydrogen sulphide were measured.

Results 122 faecal samples were collected from 61 subjects. The Mean(SEM) EN intake for the 4 groups was EEN:100(0), CEN:86(0.5), PEN:50(0.4), MEN:20(0.2)% of total energy intake. The baseline levels of all faecal sample measures were no different between the 4 groups. Faecal propionate and BSCS significantly decreased only during EEN (all $p \leq 0.03$). Faecal pH significantly increased during EEN, CEN and PEN (all $p < 0.001$), but not during MEN ($p = 0.728$). Faecal pH post intervention was highest for EEN, followed by CEN and PEN [Mean(SEM), EEN:8.2(0.1); CEN:7.8(0.2); PEN: 7.3 (0.1), all pairwise $p \leq 0.002$]. Faecal concentration of hydrogen sulphide, acetic and butyrate significantly changed following both EEN and CEN groups (all $p \leq 0.009$). The concentration of acetate post EEN was significantly lower than the concentration post CEN [Mean(SEM), EEN: 173(10); CEN: 261(24) umol/g, $p = 0.001$]. Hydrogen sulphide and butyric acid concentrations post EEN and post CEN were non-different ($p = 0.337$, $p = 0.141$).

Conclusions EEN and CEN extensively modulate faecal microbial metabolites. PEN induces variable effects and further analysis should investigate if this variation reflects differences in the non-EN food intake of the participants (50%). MEN had no effect on faecal microbial metabolites. Further analysis including high-throughput deep sequencing techniques will provide additional information about the dose-dependent effect

Abstract O047 Figure 1