standards and concrete formulation of action plans. All found UGIB-DOPS feasible to use and the rating scale more transparent than currently used DOPS.
Conclusion Creation of the UGIB-DOPS has for the first time introduced defined assessment standards in UK UGIB management facilitating formative assessment leading to a feasible improvement in workplace training. A larger pilot is now required to determine the reliability of UGIB-DOPS prior to considering its use as part of the summative assessment of endoscopist's competence.
Disclosure of Interest None Declared.

Inflammatory bowel disease section symposium "Treatment and care – where we're at"

OC-051 SIBLINGS OF CROHN'S DISEASE PATIENTS EXHIBIT A BIOLOGICALLY RELEVANT DYSBIOSIS IN THE MUCOSAL MICROBIAL COMMUNITY: A 16S RRNA GENE PYROSEQUENCING STUDY

[1]C Hedin*, [2]C van der Gast, [3]GB Rogers, [4]S McCartney, [5]AJ Stagg, [6]JO Lindsay, [1]K Whelan. *[1]School of Medicine, King's College London, London, UK; [2]NERC, Centre for Ecology and Hydrology, Oxfordshire, UK; [3]Immunity Infection and Inflammation Program, Mater Research Institute, University of Queensland, Woolloongabba, Australia; [4]Centre for Gastroenterology and Nutrition, University College London, London, UK; [5]Blizard Institute, Queen Mary University of London, London, UK; [6]Gastroenterology Division, Barts and the London NHS Trust, London, UK*

10.1136/gutjnl-2014-307263.51

Introduction Reduced mucosal *Faecalibacterium prausnitzii* predicts disease recurrence in Crohn's disease (CD) patients. Siblings (SIBS) of CD patients have elevated risk of developing CD and share aspects of CD phenotype including faecal dysbiosis. [1] No study has compared mucosal microbiota in CD SIBS to unrelated healthy controls (HC).
Methods Phenol/chloroform DNA extraction from rectal biopsies of 21 patients with quiescent CD, 17 of their healthy SIBS and 19 unrelated HC, and PCR amplification of the V1-V3 region of the bacterial 16S ribosomal RNA gene were performed. Microbiota composition was resolved by 454 pyrosequencing.
Results For each group, mucosal microbiota were classified into common/abundant (core) vs. infrequent/rare.[2] In terms of both microbial diversity (Shannon-Wiener and Simpson's indexes of diversity) and species richness, core microbiota of both SIBS and CD patients were significantly less diverse than HC. The rare microbiota diversity was lower in CD compared with HC, but was not different between SIBS and HC. Metacommunity profiling (Bray-Curtis (S_{BC}) index of similarity with unweighted pair group averages) showed core microbial metacommunity of SIBS to be more similar to CD (S_{BC}=0.70) than to HC, whereas the rare microbial metacommunity of SIBS was more similar to HC (S_{BC}=0.42). As in CD patients, the species that contributed most to the dissimilarity of healthy SIBS vs. HC was *F. prausnitzii*, Table 1.
Conclusion This is the first in depth case-control study of the mucosal microbiota of SIBS of CD patients. Dysbiosis in SIBS was characterised by reduced diversity of core microbiota and lower abundance of *F. prausnitzii*. This dysbiosis in otherwise healthy, but at-risk people implicates microbiological processes in CD pathogenesis and risk.

REFERENCES

1 Hedin C *et al*. *Gut* 2014 doi:10.1136/gutjnl-2013–306226
2 van der Gast CJ *et al*. *ISME J* 5:780–791

Disclosure of Interest None Declared.

Liver section symposium "Organ dysfunction in the cirrhotic"

OC-052 UNIVERSAL SCREENING FOR ALCOHOL MISUSE IN ACUTE MEDICAL ADMISSIONS IS FEASIBLE AND IDENTIFIES PATIENTS AT HIGH RISK OF LIVER DISEASE

[1]P Meredith, [2]P Schmidt, [2]S Atkins, [3]P Greengross, [4]G Westwood, [5]R Aspinall*. *[1]TEAMS Centre, Portsmouth Hospitals NHS Trust, Portsmouth, UK; [2]Medicine, Portsmouth Hospitals NHS Trust, Portsmouth, UK; [3]Primary Care and Public Health, Imperial College Healthcare NHS Trust, London, UK; [4]Clinical Academic Facility, Portsmouth Hospitals NHS Trust, Portsmouth, UK; [5]Gastroenterology and Hepatology, Portsmouth Hospitals NHS Trust, Portsmouth, UK*

10.1136/gutjnl-2014-307263.52

Introduction The 2013 NCEPOD report into deaths from Alcohol Related Liver Disease (ARLD) highlighted missed opportunities for detecting alcohol misuse in recurrent hospital admissions. Universal screening of medical patients was advised but little is known of the achievability of this or its efficiency at detecting high risk cases. In 2011, Portsmouth Hospitals NHS Trust introduced a 7-day Alcohol Specialist Nursing Service (ASNS) coupled with universal screening of medical patients using a novel electronic data capture system. We present data on the feasibility of unselected screening and the resulting alcohol profiles of over 28,000 medical

Abstract OC-051 Table 1 Similarity of Percentages analysis of bacterial community similarity (Bray-Curtis) between whole metacommunities. The 9 species with the greatest contribution to dissimilarity are shown

	Siblings mean abundance (%)	Healthy mean abundance (%)	Average dissimilarity (%)	Contribution to dissimilarity (%)
Faecalibacterium prausnitzii	23.4	30.0	10.4	18.9
Escherichia fergusonii	9.6	3.9	5.8	10.6
Sutterella wadsworthensis	5.8	8.6	5.2	9.4
Shigella flexneri	6.9	3.5	4.6	8.4
Bacteroides vulgatus	7.3	7.9	4.6	8.4
Eubacterium rectale	6.1	9.5	3.9	7.0
Oscillospira guilliermondii	7.6	8.1	3.9	7.0
Bacteroides dorei	5.5	0.0	3.0	5.4
Ruminococcus gnavus	4.7	4.0	2.2	4.1