SIBLINGS OF CROHN

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]

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 community similarity (Bray-Curtis) between whole metacommunities. Similarity of Percentages analysis of bacterial community similarity (Bray-Curtis) between whole metacommunities.

<table>
<thead>
<tr>
<th>Species</th>
<th>Bacteria mean abundance (%)</th>
<th>Healthy mean abundance (%)</th>
<th>Average dissimilarity (%)</th>
<th>Contribution to dissimilarity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Faecalibacterium prausnitzii</td>
<td>23.4</td>
<td>30.0</td>
<td>10.4</td>
<td>18.9</td>
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<tr>
<td>Escherichia fergusonii</td>
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<td>3.9</td>
<td>5.8</td>
<td>10.6</td>
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<tr>
<td>Sutterella wadsworthensis</td>
<td>5.8</td>
<td>8.6</td>
<td>5.2</td>
<td>9.4</td>
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<tr>
<td>Shigella flexneri</td>
<td>6.9</td>
<td>3.5</td>
<td>4.6</td>
<td>8.4</td>
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<tr>
<td>Bacteroides vulgatus</td>
<td>7.3</td>
<td>7.9</td>
<td>4.6</td>
<td>8.4</td>
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<tr>
<td>Eubacterium rectale</td>
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<td>9.5</td>
<td>3.9</td>
<td>7.0</td>
</tr>
<tr>
<td>Oscillospira guillermondii</td>
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<td>8.1</td>
<td>3.9</td>
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<tr>
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<td>3.0</td>
<td>5.4</td>
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<tr>
<td>Ruminococcus granus</td>
<td>4.7</td>
<td>4.0</td>
<td>2.2</td>
<td>4.1</td>
</tr>
</tbody>
</table>

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. [2]

Disclosure of Interest
None Declared.

REFERENCES
2. van der Gast CJ et al. ISME J 5:780–791

Liver section symposium “Organ dysfunction in the cirrhotic”

Disclosure of Interest
None Declared.

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 efficacy 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 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 (SBC)) index of similarity with unweighted pair group averages showed core microbial metacommunity of SIBS to be more similar to CD (SBC=0.70) than to HC, whereas the rare microbial metacommunity of SIBS was more similar to HC (SBC=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. Dysbiosis in otherwise healthy, but at-risk people implicates microbiological processes in CD pathogenesis and risk.
admissions in a large acute hospital serving a catchment of 650,000.

Methods From July 2011 to December 2012, all admissions via the Acute Medical Unit (AMU) were screened using the VitalPAC clinical observation system with a VitalPAC Alcohol Assessment Score (VPAAS) based on the Paddington Alcohol Test. At-risk patients (VPAAS of 6 or more) were referred to the ASNS and an Alcohol Use Disorders Identification Test (AUDIT) performed. Data analysis was performed on patient demographics, unit consumption, diagnosis, mortality and previous ED attendances and admissions.

Results There were 29,361 admissions of whom 28,098 (96%) completed VPAAS alcohol screening. Mean AMU population age was 67.4 years, 52.3% female. Of 1,123 high risk cases, 770 were seen by the ASNS and 636 defined as dependent (AUDIT >20). Compared to the general AMU cohort, the at-risk group had more ED attendances (7.8 vs. 2.9) and hospital admissions (4.8 vs. 3.1) in the previous 3 years and a lower age of death (58.3 vs. 81.5). Dependent women had fewer recurrent attendances and admissions than men but had a higher mortality rate and lower age of death (52.2 vs. 62.4). The maximum AUDIT score of 40 was recorded in 41% of cases seen by the ASNS and this subgroup had a mean age of death of 52.7 with 6.2 admissions recorded in 41% of cases seen by the ASNS and this subgroup had a mean age of death of 52.7 with 6.2 admissions and 10.8 ED attendances previously. The most frequent primary diagnoses in those with a VPAAS of 6+ were liver disease, mental health disorders and GI bleeding.

Conclusion Our analysis of over 28,000 admissions demonstrates that screening of all medical patients for alcohol misuse is achievable. We successfully identified a cohort of high risk patients with recurrent admissions and ED attendances, high unit consumption and an elevated risk of liver disease and early death. This cohort can be targeted with interventions to reduce the burden of alcohol related harm.

Disclosure of Interest P. Meredith: None Declared, P. Schmidt Conflict with: Unpaid research advisor to The Learning Clinic Ltd that created and licences use of VitalPAC, S. Atkins: None Declared, P. Greengross Conflict with: Part-time Medical Director of The Learning Clinic Ltd that created and licences the use of VitalPAC, G. Westwood: None Declared, R. Aspinall: None Declared.

Disclosure of Interest None Declared.