the complete lack of need for any stricture related surgery are both notable. The apparent efficacy, safety, long term benefit and low re-intervention rate with SEMS therapy in CD, merits further large-scale trial investigation in direct comparison with other modalities.

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ATH-09 METABOLOMICS & MULTI-OMICS ANALYSIS OF CROHN'S DISEASE

¹Alessandra Frau*, ²Rachael Hough, ²Umer Ijaz, ¹Barry Campbell, ¹John Kenny, ³Neil Hall, ⁴Jim Anson, ¹Alistair Darby, ¹Chris Probert. ¹University Of Liverpool, UK; ²University of Glasgow, UK; ³Earlham Institute, Norwich, UK; ⁴Royal Liverpool and Broadgreen University Hospitals, UK

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Background Faecal metabolomic studies show that CD patients have specific volatile organic compounds (VOCs) profiles different from healthy subjects. Integration of metabolomics with bacterial and fungal data is now possible and allows the correlation of metabolites and the microorganisms that are likely involved in their production. We present metabolomics data from a cohort of CD patients and integrate this with microbiome data to assess which microorganisms are likely active in the disease.

Methods Stool samples from 43 donors (23 CD and 20 controls) were analysed. Briefly, gases from 450–500 mg faecal aliquots were analysed by headspace, solid phase micro extraction gas chromatography/mass spectrometry. Data were interpreted using AMDIS with NIST reference library. Statistical analysis was performed in Metaboanalyst. VOCs data were then integrated with bacterial 16S rRNA and fungal 18S rRNA data from the same cohort with DIABLO (MixOmics). This uses supervised analysis to highlight signature features and to identify correlated variables.

Results Analysis of VOCs showed that CD patients formed a separate cluster and several metabolites were increased in CD including VOCs related to fungi: 3,7-dimethyl-1,6-octadien-3-ol and octanal. Branched chained fatty acids were also increased in CD, along with esters, butanoic acid, nonanal and indole. Multi-omics integration analysis comparing CD and controls showed that branched-chain fatty acids (high in CD) were correlated with gut fermenters, mainly Firmicutes. A second comparison saw CD active (n= 11) vs controls (n=20). Correlation of signature variables showed that OTUs assigned to Saccharomycetales yeasts and a mould (*Aspergillus*) were correlated to fungal metabolites (heptanal and 3,7-dimethylocta-1,6-dien-3-ol), supporting a possible role of fungi in active CD. These fungi were also correlated to Clostridiales and Enterobacteriales. This last model gave interesting results, however, the unbalance in number of samples between the two categories contributed to give a balanced error rate (BER) of the model relatively high (≈45%), therefore these data are not definitive.

Conclusion This is the first study to integrate metabolomics, microbiome and mycobiome data in CD: its potential is evident. We were able to pinpoint which microorganisms are likely active in disease and understand which produce metabolites of interest. The metabolomics data are consistent with

earlier literature. The correlation of fungi metabolites with fungal species is also very relevant. The high BER does not allow us to draw definite conclusions and further studies, with larger cohorts, are required. However, we can say that fungi are very likely to be active during relapse.

ATH-10 VEDOLIZUMAB FOR REFRACTORY CROHN'S DISEASE (CD) IN ADOLESCENTS: EXPERIENCE FROM TWO UK IBD CENTRES

¹Rohit Rao*, ¹Radha Gadchok, ²Lisa Whitley, ¹Ana Ibarra, ¹Jonathan Evans, ¹Hee La Lee, ¹Klaartje Kok, ²Sara McCartney. ¹Royal London Hospital, London, UK; ²University College London Hospital, London, UK

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Introduction There is an increasing incidence of CD in adolescents and young persons (AYP). Whilst anti-TNF use in AYP is well established, little is reported on the efficacy and safety of vedolizumab. We describe our multicentre experience.

Methods Data was retrospectively collected on 14–23yr olds starting vedolizumab at University College London Hospital (UCLH) and The Royal London Hospital (RLH) from June 2015–18. Endpoints were: clinical (i) response (reduction in Harvey Bradshaw Index (HBI) of ≥ 3 or sustained HBI ≤ 4 points) (ii) remission (HBI ≤ 4 points), and biological (i) response (50% reduction in CRP) and (ii) remission (CRP < 5 mg/L where baseline CRP > 5 mg/L) at weeks 14, 30 and 54.

Results Table 1 summarises the baseline characteristics of 35 AYP commenced on vedolizumab. 34 patients were included in the analysis at week 54. 28 patients who received induction treatment commenced 8 weekly maintenance infusions at week 14. Overall 28 patients had stopped treatment before week 54 (including 14 for primary non-response and 7 for loss of response). The median time to stopping vedolizumab was 7 months (IQR 4–29, 95%CI 5–10).

Analysing paired data only, mean (sd) HBI showed a downward trend from baseline to week 14, and was significantly decreased from baseline (4.5(4.3)) to week 22 (2.5(2.9), n=20, p=0.03), to week 30 (2.4(2.9), n=16, p=0.02), and week 54 (2.0(3.4), n=9, p=0.02). Mean (s.d.) CRP (mg/L) showed a downward trend from baseline to weeks 14 and 22, and was significantly decreased from baseline (17.8(16.9)) to week 30 (8.3(7.2), n=16, p=0.04). This trend was sustained but did not achieve significance at week 54 (7(6.0), n=9, p=0.2). Mean (sd) weight (kg) showed an upward trend from baseline to weeks 14 and 22 and was significantly increased from baseline (61.5(11.7)) to week 30 (65.6(12.4), n=13, p=0.004), and week 54 (66.3(15.5), n=9, p=0.006).

At weeks 14, 30 and 54, the rates of clinical (i) response and (ii) remission were (i) 56, 37 and 24% respectively and (ii) 47, 37, 24% respectively. At weeks, 14, 30 and 54, the rates of biological (i) response and (ii) remission were (i) 29, 25, and 11% respectively and (ii) 10, 15 and 9% respectively.

Conclusions We report on the use of vedolizumab in AYP at 2 tertiary IBD centres. Our experience suggests that whilst medium term (6 month) effectiveness in an anti-TNF experienced cohort is comparable with outcomes from adult and trial data, this is not sustained to a year. This may be reflective of a cohort of patients with early onset CD with a more aggressive phenotype and coexisting perianal disease. Further studies may help identify which adolescents would most benefit from vedolizumab. This is of growing importance in the face of an expanding therapeutic armamentarium in CD.