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OTH-08

CIRCULATING MICRORNAS LINKED TO IMMUNOMETABOLIC TRAITS ASSOCIATE WITH FAECAL MICROBIOTA TRANSPLANTATION FOR CLOSTRIDIODES DIFFICILE INFECTION

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Introduction The molecular mechanisms underlying successful faecal microbiota transplantation (FMT) for recurrent *C. difficile* infection (rCDI) remain poorly understood. The aim of this study was to characterise alterations in circulating microRNAs and immunometabolic traits following FMT for rCDI.

Methods We analysed a subset of serum samples previously acquired from a prospective multicentre, randomized trial of FMT delivered by capsule vs colonoscopy in the management of rCDI [NCT02254811]. 126 sera from 42 patients at screening, 4 and 12 weeks post FMT [12M, median age 68.5 yrs (2–1); 30 F, 53 yrs (2–1)] were included. MicroRNA panel v3 and the nCounter platform (Nanostring Tech) were used for the analysis of 800 microRNAs. Quantitative PCR and 3'UTR reporter assays were employed to verify microRNA inflammatory protein targets in colonic epithelial and peripheral blood mononuclear cells. Biometal levels were

assessed using inductively coupled plasma mass spectrometry (ICP-MS). Hydrophilic interaction ultra-performance liquid chromatography (HILIC-UPLC) and nano-liquid chromatography coupled with electrospray mass spectrometry (nanoLC-ESI-MS) were utilised to profile the total serum and IgG Fc N-glycome. Pathway analysis was performed using Metacore software. All statistical analyses including non-parametric longitudinal method (nparLD) followed by Wilcoxon signed-rank test for pairwise comparisons and linear mixed modelling were performed in SPSS v.24 and R 3.5.1.

Results MicroRNA profiling revealed an upregulation in the levels of 64 circulating microRNAs 4 and 12 weeks following successful FMT for rCDI compared to screening time point. MicroRNA signatures coincide with a reduction in circulating selenium and copper, and regulate levels of interleukin-12B, (IL-12B), IL-18 and fibroblast growth factor-21 (FGF21) as well as serum protein N-glycosylation traits. MicroRNA alterations reveal commonalities with several types of cancer and multiple sclerosis, and link metabolic traits to immune cell survival and differentiation.

Conclusions These findings contribute to a greater understanding of the molecular mechanisms underlying FMT and identify new potential targets for therapeutic intervention.

OTH-09

FERROUS SULPHATE SUPPLEMENTATION IS ASSOCIATED WITH A CHANGE IN THE FAECAL METABOLOME

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Introduction Oral iron supplementation treats iron deficiency anaemia, but it may cause GI side effects. Iron influences the growth of specific gut bacteria and may lead to dysbiosis, which may contribute to the side effects. Previously, we have shown that oral iron worsens colitis in mice and causes a dysbiosis. Here we report the effect of ferrous sulphate supplementation on the human metabolome by quantifying changes in faecal volatile organic compounds (VOCs), for the first time. VOCs are part of the metabolome and reflect gut

Abstract OTH-09 Figure 1 (A) Pre- and post-iron (Fe) concentrations of 2-pentylfuran. (B) Partial least squares – discriminant analysis (PLS-DA) plot of pre- and post-iron samples.