Intestinal dysbiosis occurs in iron deficiency as well as active IBD

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Introduction: We have previously shown that decreases or increases in dietary iron exacerbate murine models of inflammatory bowel disease (IBD). Active IBD is associated with a dysbiosis typified by a reduction in Bacteroidetes and an increase in Firmicutes. We have investigated the human intestinal microbiome in relation to luminal iron, by studying patients with iron deficiency anaemia (IDA) and inactive/active IBD. We report results of changes at the phylum level.

Methods: Bacterial gDNA was extracted from faeces of patients with IDA (10), Crohn’s disease (CD 6 active, 24 inactive), ulcerative colitis (UC 7 active, 13 inactive) and healthy controls (24). Faecal iron and calprotectin were assayed by ELISA. Microbiota composition was determined from the sequence of V4 region of 16S rDNA on the Illumina MiSeq platform. Statistical inferences were made using Welch’s t-test with post-hoc analysis (Bioinformatics 2010; 26:715-21). Shannon Diversity Index (SDI) and Principal Component Analysis (PCA) were employed to compare population and phylum-level changes among study groups.

The results: Faecal iron concentrations were least in IDA (ANOVA, p=0.001) and significantly lower in IDA than each other group (post hoc p<0.05 for all comparisons). Calprotectin concentrations were increased in association with IBD disease activity.

Faecal phyla changes were seen in IDA as well as in IBD: Proteobacteria were markedly reduced in IDA (1.4%) compared to active IBD (15.5%); IBD and IDA were associated with increased proportions of Firmicutes (P=0.01 and P=0.05 respectively).

Conclusion: Dysbiosis occurred in IDA as well as in active IBD. Proteobacteria are clearly iron-responsive: the increase in luminal iron associated with active IBD appears to promote their growth and might contribute to the excess of this phylum during relapse. The changes in Bacteroidetes appear independent of luminal iron, unlike Firmicutes. The influence of iron deficiency and supplementation upon the colonic microbiome warrants further investigation.

Keywords: Microbiota, iron, IBD