Objective

The aim of this study was to investigate the effects of the probiotic strain Lactobacillus rhamnosus GG (LGG) on the gut microbiota composition, microbial translocation and intestinal inflammation.

Methods

The gut microbiota composition (sequencing of the V3-V4 region of the 16S rRNA gene using the MiSeq platform by Illumina) and level of microbial translocation (circulating lipopolysaccharide, LPS) were determined at baseline and after probiotic intervention. Gut microbial profiles were compared with measurements of intestinal inflammation by %2-fluoro-2-deoxy-2-D-glucose positron emission tomography/magnetic resonance imaging (%2FDG PET/MRI) scans in 15 consecutively selected individuals.

Results

After probiotic intervention, no overall change in microbial alpha diversity (Fig. 1A) or microbial translocation (UPS) (Fig. 1B) could be detected in the study group. However, reduction in the bacterial families Enterobacteriaceae (p=0.018) and Erysipelotrichaceae (p=0.037) were found after probiotic intervention, along with increased abundance of unclassified genus from the Lachnospiraceae family as well as Ruminococcaceae family (Fig. 2). Overall, intestinal inflammation decreased significantly (0.3 mean difference in combined activity score grade from six regions, p=0.006) (Fig. 4 and 5). Comparing individuals with decreased %2FDG uptake on PET/MRI (responders) with individuals with no change in uptake after intervention (non-responders), the relative abundance of Enterobacteriaceae (p=0.048) was significantly reduced in in the gut microbiome of the responders (Fig. 3).

Study Design

The study was a prospective, clinical interventional trial including 45 individuals (15 cART naïve and 30 cART-treated) during the period of January to September 2015 from the outpatient clinic at the Department of Infectious Diseases, Copenhagen University Hospital, Rigshospitalet (see consort diagram and Table 1). Participants ingested LGG twice daily at a dosage of 6 x 10^9 colony-forming units per capsule for a period of eight weeks.

Conclusions

- Reduced abundance of Enterobacteriaceae after probiotic intervention could potentially explain the local anti-inflammatory effect in the gut measured by PET/MRI activity.
- Future studies should focus on the potential effects on mucosal immunity and HIV pathogenesis, with PET/MRI as a non-invasive alternative to regionally explore the distribution of inflammation in the gut.