

SEX RELATED DIFFERENCE IN THE PREVALENCE OF *Faecalibacterium prauznitzii* IN THE HUMAN GUT MICROBIOME

Da Silva Santos, A.C. ¹, Romeiro, F.G. ², Sasaki, L.Y ², Rodrigues, J.¹

Intitutions: ¹ Institute of Biosciences (IBB) and ² Botucatu Medical School (BMS) of the State University of São Paulo (UNESP)

Background

A number of studies suggest that the presence of *Faecalibacterium prauznitzii* correlates with a good health condition. Decrease abundance of these bacteria has been associated with a higher risk of post-operative recurrency of ileal Crohn's disease (CD) and its anti-inflammatory properties has been demonstrated in experimental colitis in mice. Also, the reduction in the number of *F. prauznitzii* and other butyrate-production bacteria is a marker of dysbiosis in ulcerative colitis. Although a matter of controversy, apparently in the western countries the incidence of CD in females is higher than that seen in males. Since alteration in the gut microbiome is a feature of CD, we investigated whether there is any difference in bacterial species composition that could be linked to an eventual higher predisposition in women for acquiring CD.

Methods

The species composition of the microbiome was determined by sequencing 16S V6rDNA PCR amplicons by the Ion PGM platform. The templates for the PCR were DNA from 22 gut mucosa biopsies from 11 males (2 biopsies per subject) and from 11 females (2 biopsies per subject). The sequences were compared with previously deposited data in the ribosomal database project and analyzed with MG-RAST tools.

Results and discussion

A number of 2204737 unique 16S V6rDNA sequences were identified among the 44 biopsies analyzed. Eighty and one percent (1789098) of the sequences could be identified at the species level (1041 species belonging to 14 phyla). The dominant phyla were Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, Proteobacteria and Spirochaetes. Comparisons at species level revealed significant differences in 30 of the species detected. Within the species for which at least 100 sequences were identified in at least one of the groups, sex specific significant differences were observed in the following bacteria: *Faecalibacterium prausnitzii*, *Bacteroides fragilis*, *Eubacterium rectale*, *Clostridium scindens*, *Bacteroides stercoris*, butyrate-producing bacteria SS3/4 and *Clostridium hathewayi*. The most abundant species detected (2702±2800 sequences in man), among these was *Faecalibacterium prauznitzii*. In woman, approximately a third of the total of these bacteria found in men were detected (942±681). The results could indicate that the lower prevalence of *Faecalibacterium prauznitzii* among women could represent a predisposing factor for the manifestation of CD.

Key words: Microbiome, *Faecalibacterium*, dysbiosis

Finance support: FAPESP grant 2012/18469-2