

UNIVERSAL DUODENAL MICROBIOTA WITH IS-PRO IN INDIVIDUALS UNDERGOING ROUTINE GASTROSCOPY

ME Grasman¹, AE Budding², CJ Mulder¹, PHM Savelkoul², AA van Bodegraven¹

1. Department of Gastroenterology and Hepatology

2. Department of Medical Microbiology and Infection control

t.grasman@vumc.nl

Introduction and Aim

The intestinal microbiota received a lot of attention due to its putative role in the pathogenesis of several diseases including inflammatory bowel diseases and obesity. As yet, most research has focused on microbiota residing in colonic mucosal biopsy specimens and faecal samples, which has been shown to be host-specific. Much less is known about the bacterial composition in duodenal mucosal biopsy specimens.

Since most intestinal bacteria are uncultivable, we developed IS-pro; a rapid, highly reproducible method for high-throughput bacterial profiling.

Aim of the present study was to characterise the intestinal microbiota adherent to duodenal mucosal biopsy specimens in individuals undergoing routine gastroscopy.

Material and Methods

Duodenal biopsy specimens were harvested from 21 consecutive individuals undergoing routine gastroscopy. In addition, four accompanying colonic mucosal biopsy specimens and 11 colonic mucosal biopsy specimens from other individuals were harvested during routine colonoscopy. Samples were analysed with IS-pro, which is based on two features of the bacterial genome: species-specific length of the inter spacer (IS) region between the 16S and 23S rDNA and phylum-specific labelled primer sequences. With these specific labelled primers, species can be directly sorted into either Firmicutes/ Actinobacteria or Bacteroidetes phylum. By colour and size sorting of amplified fragments specific bacterial profiles are created. Intra- and inter-individual variation of bacterial profiles was assessed with Pearson's correlation.

Results and Discussion

Duodenal and colonic specimens clustered in two distinct clusters. Colonic specimens were unique per individual with low homology between individuals (6- 59%). In contrast, duodenal specimens showed very high similarity up to 100% identity. Lowest similarity between duodenal specimens (64%) was higher than highest similarity in colonic cluster (59%). Matched duodenal and colonic microbiota were distinct with clustering based upon region of sampling instead of clustering per individual.

Microbiota adherent to duodenal mucosa and to colonic mucosa were distinct. Whereas colonic microbiota was found to be host-specific, duodenal microbiota was extremely homogenous, with inter individual profiles being almost identical. Findings of the present study provide a solid basis for the analysis of potential disease-specific differences in microbiota adherent to duodenal mucosa.

