Long-term effect of *Helicobacter pylori* eradication therapy on gastrointestinal microbiome in a Latvian population

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Introduction: *H. pylori* infections are present in 80% of Latvian population thus increasing the susceptibility of numerous of the gastric tract diseases, including gastric adenocarcinoma.[1] The 1st line *H. pylori* eradication therapy includes treatment with clarithromycin in combination with amoxicillin or metronidazole and a proton pump inhibitor. However, potential adverse events caused by such therapies to microbiome are insufficiently studied. Therefore, the aim of this study was to evaluate the long-term effects of *H. pylori* eradication on gastrointestinal (GIT) microbiome.

Methodology & Theoretical Orientation: The assessment of *H. pylori* eradication therapy on GIT microbiome was performed on 120 faecal samples that were acquired from 60 adults: samples from each individual were collected before starting the eradication therapy, and one year after the final treatment. Samples were collected in OC-Sensor (Eiken Chemical Co., Tokyo, Japan) sample collection containers and stored at -86℃. Total DNA was extracted using FastDNA Spin Kit for Soil (MP Biomedicals, USA) and was followed by 16S rRNA V3 gene sequencing employing Ion Torrent Personal Genome Machine (Life Technologies, USA). The obtained raw 16S reads were analyzed using QIIME v.1.9.0 and UPARSE v.7.0.1001.

Conclusion & Significance: Overall microbiome community composition remained stable between pre- and post-eradication microbiome samples, however, shifts between predominant enterotypes as well as positive correlation for certain bacteria between the two categories was found in relation to age, individual, experience respiratory and/or allergic diseases and if the eradication therapy was used as prescribed. Modest global differences at the community level exist between individuals before and after the eradication therapy when considering the long-term impact; however, the microbiome structure is more related with the patient-specific parameters, such as age or experienced diseases, rather than by the eradication therapy itself.

Biography

Darta Pupola has finished University of Latvia as a biologist. She has experience in genomics, cell culturing and signaling pathway analysis in a field of oncology and GIT microbiome, where combining all knowledge from different kind of fields it becomes possible to look at disease and health conditions as a complex interaction network.

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