METATRANSCRIPTOME AND TRANSCRIPTOME ANALYSIS IN HEALTHY HUMANS AND IRRITABLE BOWEL SYNDROME PATIENTS

Lauma Jagare[1], Maija Rozenberga[1], Ivars Silamikelis[1], Laura Ansone[1], Ilze Elbere[1], Monta Briviba[1], Kaspars Megnis[1], Ilze Konrade[2], Ilze Birka[3], Zane Straume[3], Janis Klovins[1]

[1]Latvian Biomedical Research and Study Centre, Human genetics and disease mechanisms group, Rātsupītes 1, Riga, Latvia, LV-1067

[2]Riga Stradins University, Dzirciema 16, Riga, Latvia, LV-1007

[3]Pauls Stradins Clinical University Hospital, Pilsonu 13, Riga, LV-1002

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Objectives

There is a growing body of evidence on the existence of a blood microbiome in healthy humans, but questions remain regarding its origin and role in host physiology. The objective was to investigate association of blood microbiome with increased gut permeability by comparing its taxonomic composition between healthy individuals and irritable bowel syndrome (IBS) patients, as well as to analyse host gene expression in both groups.

Methods

Blood samples were collected from IBS patients and healthy volunteers, RNA was isolated, RNAseq performed, and reads corresponding to microbial genomes were identified with kraken2's standard plus protozoa and fungi database, and re-estimated at genus level with bracken 2.7. Taxonomic composition was compared between the IBS and control groups and against other factors. Host transcriptome was analysed to reveal differential gene expression.

Results

Dominating genera found in the blood were *Cutibacterium*, *Bradyrhizobium*, *Escherichia*, *Pseudomonas*, *Micrococcus*, *Delftia*, *Mediterraneibacter*, *Staphylococcus*, *Stutzerimonas*, and *Ralstonia*. Some of these are typical environmental bacteria and could partially represent contamination. Results of negative controls however suggested that the genetic material of those microorganisms which are characteristic to the gut microbiome (*Escherichia*, *Mediterraneibacter*, *Blautia*, *Collinsella*, *Klebsiella*, *Coprococcus*, *Dysosmobacter*, *Anaerostipes*, etc.) is less likely to be contamination but is genuinely found in the blood. Moreover, differential analysis showed that some genera typically associated with gut microbiome are more prevalent in IBS patients. No significant correlations with other factors were identified.

Host transcriptome analysis revealed that the most upregulated gene in some IBS patients was *NOS1AP* which plays an important role in depression and anxiety, and might be important for diabetes mellitus progression. Among the other most upregulated genes in the IBS group were *CD81-AS1*, *ENSG00000226252*, and *NAV3*.

Conclusion

Findings support the existence of blood microbiome and suggest the gut and possibly oral microbiome as its main origin. Blood microbiome is likely influenced by states of increased gut permeability such as the IBS.