

Interoperability of whole-genome and metagenomic analyses from patients with ulcerative colitis

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Ulcerative colitis belongs to the group of multifactorial diseases with unexplained etiology. It is assumed that the impaired composition and reduced variety of intestinal microbiota are factors of inflammatory bowel diseases and affect their pathogenesis.

First phase of the study involved 25 patients with ulcerative colitis in whom biopsy was taken from an affected and healthy area of the large intestine. The V3-V4 region of 16S rRNA gene was used for metagenomic analysis of bacterial community. The data was classified using Kraken 2. It was shown that this program is better suited for taxonomic annotations of intestinal microbiota data. Kraken 2, when processing paired reads, processes them separately, checking the information about the paired read; this is an important condition when processing 16S data. The data have been analyzed by Pavian and visualized for comparative analysis in Recentrifuge.

Depending on the database used, a significant increase of Enterobacteriaceae taxa based on greengenes and Escherichia-Shigella taxa based on Silva was found in 2 patients in both areas of the biopsy. The data on taxa values increase, respectively, for 2 patients in the affected area: 6.36 times and 7.21 times higher than mean; 7.27 times and 8.4 times higher than mean.

16S rRNA gene sequencing provides accurate results up to genus level, examination of species diversity depends on the classifier used, however strain diversity is available at whole-genome shotgun sequencing [1].

In inflammatory bowel diseases Escherichia coli variability is an essential microbiological factor [2]. Therefore, in the second stage of the study, microbiological tests for the pathogenic enteric E. coli strains in all patients were conducted. An adherent-invasive pathotype E. coli was found in one patient who was a member of the differentiating group from stage 1. A whole-genome shotgun sequencing of this isolated E.coli was performed, the analysis of which complements the previous results. Genes associated with the adherent-invasive pathotype were found: aap, factor AcfD, fis, aar, aggR, aggA, aggB, aggC, aggD.

References

- 1) Martinez-Medina, M. and Garcia-Gil, L., 2014. Escherichia coli in chronic inflammatory bowel diseases: An update on adherent invasive Escherichia coli pathogenicity. World Journal of Gastrointestinal Pathophysiology, 5(3), p.213.
- 2) Walsh, A., Crispie, F., Daari, K., O'Sullivan, O., Martin, J., Arthur, C., Claesson, M., Scott, K. and Cotter, P., 2017. Strain-Level Metagenomic Analysis of the Fermented Dairy Beverage Nunu Highlights Potential Food Safety Risks. Applied and Environmental Microbiology, 83(16).