Abstract of “Viral and bacterial components of the human microbiome: profiling in selected gastrointestinal disease states”

Aleksander Szymczak

The advancement of Next-Generation Sequencing has supported the study of the human microbiome. This method allowed for the simultaneous sequencing of multiple samples, which reduced the cost. It enabled researchers to learn about microorganism fractions that could not previously be studied due to cultivation difficulties.

Patients in this study were subjected to gastroscopy by gastroenterologists at the Regional Specialized Hospital in Wroclaw. Over the course of two years, 148 gastric samples were collected from patients at the Endoscopy Department of the Regional Specialist Hospital in Wroclaw. Each patient had two separate specimens taken, and blood samples were collected for further Single Nucleotide Polymorphisms (SNP) analysis. Patients' information was gathered through interviews and the medical database Asseco Medical Management Solutions (AMMS). Following the isolation of DNA from samples, Illumina NextSeq550 and Ion Torrent Personal Genome Machine were used for DNA Next Generation Sequencing. Data from all three types of NGS data analysis were converted into standard formats for further statistical data analysis.

Statistical analysis of bacterial components and ICD-classified diseases revealed fourteen correlations. Statistical analysis of bacteriophage components revealed three correlations with ICD-classified diseases. The analysis revealed 13 SNPs that were associated with significant changes in microbiome diversity. Six different Single Nucleotide Polymorphisms in this gene have been linked to the presence of bacteriophages from the Kayvirus, Punavirus, Lambdavirus, and Teseptimavirus families. Single nucleotide variants found in gastritis-associated pathogens can alter the entire microbiome composition and predispose specific species to grow, resulting in dysbiosis. The presence of specific alleles in genes can promote bacterial growth by impairing the function of the genes in which they occur.

SNPs found in gastritis-associated pathogens can alter the entire microbiome composition and predispose specific species to grow, resulting in dysbiosis and developing disease states.