

P0278

Paper Poster Session

Non-culture techniques for challenging situations in diagnostics

Application of the next generation sequencing in the qualitative assessment of the bacterial flora of the duodenal biopsy specimens in patients with obesity and type 2 diabetic

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Background: The scientists suggest the possible impact of bacteria in the etiology of obesity and type 2 diabetes, which are the most prevalent endocrine disease worldwide. The microbiome structure of the human body is relatively stable but most disturbances can lead to serious health consequences such as metabolic syndrome, inflammatory bowel disease including Crohn's disease and ulcerative colitis. Precise assessment and characterization of the microbiota has become a basic research field, which is important to working out new ways of shaping species composition of gut flora, so that its physiological character could be restored.

The main objective of research project was to evaluate the qualitative analysis of the microbiota from the duodenal biopsy specimen in patients with type 2 diabetes, obesity, and in the control group using next-generation sequencing.

Material/methods: The examination materials were biopsy specimen collected from the duodenum of the 38 adult patients, qualified to participate in the project at the Chair of Metabolic Diseases of the Jagiellonian University Medical College and divided into groups with different criteria:

- non diabetic patients with obesity (n = 19), **(I)**
- patients with T2DM and obesity (n = 8), **(II)**
- non diabetic patients with normal weight (n = 11), **(K)**

The samples obtained with the use of a gastroscopy. From biopsy specimen isolated DNA and amplified by PCR. Metagenomic analysis was performed based on the protocol and MiSeq sequencing platform (Illumina).

Results: The dominant in all three groups are bacteria belonging to the phylum: *Firmicutes* (41.6%) and the *Proteobacteria* (40.4%), the other are: *Acinobacteria* (9.5%), *Fusobacteria* (3.8%) and

Bacteroidetes (2, 5%). In the group (II), the percentage of bacteria belonging to the phylum: *Firmicutes* and *Proteobacteria* differs significantly compared to group (K). No such differences were observed when comparing group (I) and (II).

Conclusions: In the presented study it was found statistically significant differences in the percentage distribution of the major phyla of bacteria between the research groups (I), (II), and the control group (K). The different composition of the bacterial flora in obesity and type 2 diabetes can be the result of the course of the disease and the distinct diet.

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COMPARISON RESEARCH GROUPS AT THE PHYLUM LEVEL

