

PATTERNS OF GUT MICROBIAL CHANGES LINKED TO OBESITY

WZORCE ZMIAN MIKROBIOTY JELITOWEJ ZWIĄZANE Z OTYŁOŚCIĄ

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Wkład autorów:

- A. Study design/planning
zaplanowanie badań
- B. Data collection/entry
zebranie danych
- C. Data analysis/statistics
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- D. Data interpretation
interpretacja danych
- E. Preparation of manuscript
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- F. Literature analysis/search
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Dear Editor,

We have recently come across an intriguing article written by Chanda et al. [1] that delves into the patterns of gut microbial changes associated with obesity and the consistent factors contributing to functional shifts. We consider this topic to be of significant importance to both individuals with obesity and healthcare professionals, as it illuminates the potential underlying pathophysiological mechanisms.

The worldwide incidence of obesity, affecting roughly 2 billion individuals, is a major health issue attributed to inactive lifestyles and poor eating habits. It is a leading risk factor for metabolic diseases [2].

In healthy adults, the gut microbiome is predominantly made up of Firmicutes and Bacteroidetes, which represent approximately 70% of the entire microbial population. Other groups such as Proteobacteria, Verrucomicrobia, Actinobacteria, Fusobacteria, and Cyanobacteria also exist but in lesser quantities [3]. When comparing the gut flora of obese individuals to those with a lean body type, there's a notable increase in Firmicutes and a decrease in Bacteroidetes among the obese [4].

In the meta-analysis conducted by Chanda D et al. [1] the composition of the gut microbiome in obese individuals was analyzed, revealing a consistent reduction in diversity compared to their lean counterparts. This suggests that the diminished microbial variety in the obese gut contributes to disruptions in the normal functioning of the gut's microbial community.

Furthermore, the identification of 25 species with strong predictive value and 37 pathway associations marked as obesity indicators was accomplished. There was a noticeable reduction in short-chain fatty acid (SCFA) producing species (including various *Alistipes* species and *Odoribacter splanchnicus*), alongside a reduction in

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species that support gut barrier health (such as *Akkermansia muciniphila* and *Bifidobacterium longum*) within the microbiomes of obese individuals. This study highlights the significance of SCFAs and the biosynthesis of purines/pyrimidines, carbohydrate metabolism pathways in individuals with a normal weight, and emphasizes the enrichment of pathways related to amino acid, enzyme cofactor, and peptidoglycan biosynthesis in the microbiomes of obese individuals [1].

The results of the research highlight the microbiome-gut-brain axis as a crucial factor in obesity. The link between changes in gut microbiota and the fundamental mechanisms of obesity implies that focusing on this axis could reveal new approaches to treatment. Continuous investigation is essential to thoroughly understand these interactions and exploit their potential for combating obesity.

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