Gut microbiota composition in type 2 diabetic patients

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Background: Gut microbiota dysbiosis constitutes a link among gut barrier dysfunction, metabolic endotoxemia and low-grade inflammation. Low-grade inflammation has been suggested as a potential contributing factor for diabetes. In this study, we aimed to compare the gut microbiota composition between type 2 diabetic patients and healthy non-diabetic adults.

Methods: 39 patients diagnosed with type 2 diabetes and 29 normal-weight healthy persons were included in this case-control study. The intestinal microbiota composition was investigated by 16S rRNA amplicon sequencing method. Comparison of alpha diversity indices and relative abundance of taxa between two groups was done using Wilcoxon rank sum test.

Results: The participants’ mean age in the type 2 diabetes and control groups was 60.1 and 34.5 years, respectively. Body mass index was higher in type 2 diabetic patients compared with the healthy controls \( (P <0.05) \). The Simpson alpha diversity index was significantly higher in diabetic patients \( (P =0.02) \). Although, the richness index was not different between two groups. Higher relative abundance of Escherichia, Dorea, Achromobacter, Allisonella and Intestinimonas was observed in type 2 diabetic patients compared with the healthy group \( (P <0.05) \). In contrast, abundance of Romboutsia and Clostridium was higher in healthy control group \( (P <0.05) \).

Conclusions: Gut microbial alterations have been observed in patients suffering from type 2 diabetes mellitus. Evaluating intestinal microbiota changes in various diseases could be helpful in development of strategies for modulating gut microbiota composition.