

## Gut microbiota composition in type 2 diabetic patients

Seyed Davar Siadat<sup>1\*</sup>, Sara Ahmadi Badi<sup>1</sup>, Samira Tarashi<sup>1</sup>, Hanieh-Sadat Ejtahed<sup>2</sup>, Atiyyeh Motahhary<sup>1</sup>, Saeed Bouzari<sup>1</sup>, Arfa Moshiri<sup>3,4</sup>, Ayoub Rahimi<sup>1</sup>, Mehrangiz Zanganeh<sup>5</sup>, Farzam Vaziri<sup>1</sup>, Abolfazl Fateh<sup>1</sup>, Shirin Hassani Ranjbar<sup>6</sup> and Bagher Larijani<sup>7</sup>

\*( Seyed Davar Siadat) [d.siadat@gmail.com](mailto:d.siadat@gmail.com)

<sup>1</sup> Microbiology Research Center, Pasteur Institute of Iran

<sup>2</sup> Obesity and Eating Habits Research Center, Endocrinology and Metabolism Clinical Sciences Institute, Tehran University of Medical Sciences, Tehran, Iran

<sup>3</sup> Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences

<sup>4</sup> Laboratory of Experimental Therapies in Oncology, IRCCS Istituto Giannina Gaslini

<sup>5</sup> Tehran Medical Branch, Islamic Azad University, Tehran, Iran

<sup>6</sup> Tehran University of Medical Sciences, Tehran, Iran

<sup>7</sup> Endocrinology and Metabolism Research Center, Endocrinology and Metabolism Clinical Sciences Institute, Tehran University of Medical Sciences, Tehran, Iran

**Keywords:** Gut microbiota, diabetes mellitus, gut dysbiosis

**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.