



#2
2022

Proceedings of the Shevchenko Scientific Society. Medical Sciences 2022, 2 (69). <https://doi.org/10.25040/ntsh>

www.msps.org.ua

DOI: 10.25040/ntsh2022.02.12

Original research: Clinical Sciences

For correspondence: Shupyk
National Healthcare University of
Ukraine, 9 Dorohozhytska Street,
Kyiv, Ukraine, 04112
Twitter: @CheverdaTetiana
E-mail: cheverda.doc@gmail.com

State of the gut microbiota in patients with metabolic-associated fatty liver disease with type 2 diabetes mellitus

Andriy Dorofeyev¹, Mykola Rudenko², Tetiana Cheverda¹

Received: 10 Oct, 2022
Accepted: 12 Dec, 2022
Published: 30 Dec, 2022

¹ Shupyk National Healthcare University of Ukraine, Kyiv, Ukraine

² Bogomolets National Medical University, Kyiv, Ukraine

ORCID IDs

Andriy Dorofeyev:
<https://orcid.org/0000-0002-2631-8733>

Mykola Rudenko:
<https://orcid.org/0000-0003-3536-0455>

Tetiana Cheverda:
<https://orcid.org/0000-0003-2081-1874>

Disclosures: The authors declared no conflict of interest.

Author Contributions:

Conceptualization: Andriy Dorofeyev, Mykola Rudenko, Tetiana Cheverda;

Results of study: Andriy Dorofeyev, Mykola Rudenko, Tetiana Cheverda;

Writing: Andriy Dorofeyev, Mykola Rudenko, Tetiana Cheverda;

Review & editing: Andriy Dorofeyev, Mykola Rudenko, Tetiana Cheverda.

Ethical approval: The Bioethics Committee of Shupyk National Healthcare University of Ukraine, protocol No. 5, March 2, 2020. All patients signed informed consent.

Funding: The authors received no financial support for their study.

Introduction. One of the frequent complications of the type 2 diabetes mellitus (T2DM) is a metabolic-associated fatty liver disease (MAFLD). Aim. To study the composition of gut microbiota in patients with a combination of T2DM and MAFLD and to compare it with the microbiota in isolated T2DM and MAFLD.

Methods. 111 patients were studied. The main group consisted of 56 patients with a combination of MAFLD and T2DM; the 1st group included 28 patients with MAFLD and the 2nd - 27 patients with T2DM. The control group consisted of 30 practically healthy people. Diagnosis was made by steatometry, shear wave elastography, lactulose H₂ breath test, qPCR of feces using primers targeting the 16S rRNA gene, and stool culture.

Results. In the the main group SIBO was found in 48.2%, in 1st - 35.7%, in 2nd - 33.3%, compared to 10% in the control group. When compared with healthy people, the number of "other" microorganisms significantly increased in the group with isolated T2DM and *Clostridium*, *Proteus* and *Candida* were cultured; in the case of isolated MAFLD, a decrease in *Bacteroidetes* and an increase in the *Firmicutes/Bacteroidetes* ratio, as well as an increase in *Klebsiella* and *Clostridium*. In the main group, an increase in *Actinobacteria*, "other" microorganisms, a ratio of *Firmicutes/Bacteroidetes* and a decrease in *Bacteroidetes* were found, when cultured - an increase in *Clostridium*, *Klebsiella* and *Candida*.

Conclusions. Only the group of MAFLD with T2DM was characterized by increased *Actinobacteria*; decreased absolute number of *Bifidobacterium* and *Lactobacillus* and increased *Escherichia*, including with altered enzymatic properties in the stool culture.

Keywords: Metabolic-associated fatty liver disease, type 2 diabetes mellitus, bacterial overgrowth syndrome, gut microbiota.

