ORIGINAL ARTICLE **BIOTECHNOLOGICAL AND PHARMACOLOGICAL DEVELOPMENTS IN THE MODIFICATION OF CHRONIC INFLAMMATION-INDUCED DISEASES**

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Microbial and immune markers of patients with metabolic syndrome and cardiovascular diseases: perspectives for early diagnostics

Tamara MELESHKO [1, 2] ✉, Viktor PETROV [3, 4], Tetyana FALALYEYEVA [5], Nazarii KOBYLIAK [6], Nadiya BOYKO [1, 2, 7]

[1] RDE Center of Molecular Microbiology and Mucosal Immunology, Uzhhorod National University, Uzhhorod, Ukraine; [2] Department of Clinical Diagnostics and Pharmacology, Uzhhorod National University, Uzhhorod, Ukraine; [3] Department of Family Medicine and Outpatient Care, Medical Faculty 2, Uzhhorod National University, Uzhhorod, Ukraine; [4] Prevention LTD, Uzhhorod, Ukraine; [5] Educational and Scientific Center "Institute of Biology and Medicine," Taras Shevchenko National University of Kyiv, Kyiv, Ukraine; [6] Department of Endocrinology, Bogomolets National Medical University, Kyiv, Ukraine; [7] Ediens LLC, Uzhhorod, Ukraine

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BACKGROUND: Intestinal microbiota affects human's metabolic and physiological processes and changes in the microbiome are associated with the progression of metabolic disorders such as obesity, atherosclerosis, and others. Despite the recent emphasis on the importance of the study of intestinal microbiota as a diagnostic and therapeutic target for metabolic syndrome (MS) and cardiovascular disease (CVD), such studies have not been conducted in Ukraine.

METHODS: In this study, three groups of patients were formed: group N. 1 included 30 patients with MS and type 2 diabetes; group N. 2-42 patients with CVDs; group N. 3-15 healthy individuals. Gut microbiota profiles were measured using classical microbiology techniques. Parameters such as C-reactive protein, uric acid, triglycerides, glycosylated hemoglobin, and cholesterol were assayed using Cobas c 311 (F. Hoffmann-La Roche SA, Basel, Switzerland; Hitachi, Tokyo, Japan) Switzerland. Immune parameters such as total antibodies to *Helicobacter pylori*, total immunoglobulin A (IgA) in serum, secretory IgA (SigA) in coprofiltrate, tumor necrosis factor alpha (TNF-α), interleukin - 1β (IL-1β), interleukin - 10 (IL-10), interleukin - 12 (IL-12) were measured using immunosorbent systems.

RESULTS: The most typical pattern of changes in the gut microbiota of patients with MS was a significant decrease in the content of *Bifidobacterium bifidum* and an increase in the number of transient and conditionally pathogenic microbiota. Patients with high levels of glucose and glycosylated hemoglobin (more than 7.4%) demonstrated excess population levels of *Enterococcus faecalis* [(2.5±0.17) × 10^8 CFU/g] and *Clostridium tertium* [(1.0±0.5) × 10^8 CFU/g] and reduced level of *Lactobacillus acidophilus* [(2.2±0.05) × 10^7 CFU/g]. The key changes in the gut microbiota of patients with CVD included: decrease in the total number of normal microbiota representatives: *Lactobacillus* spp., *Escherichia coli* with normal enzymatic properties along with a significant increase in the number of lactose-negative strains of *E. coli, E. faecalis, Staphylococcus aureus, Staphylococcus saprophyticus, Candida albicans*, and *Candida krusei*.

CONCLUSIONS: The identified stable correlations between species and quantitative composition of intestinal microbiota, immune parameters and levels of glycosylated hemoglobin, cholesterol, overweight, and impaired glucose tolerance became the basis for the proposed use of indicators of gut microbiota and immune markers of nonspecific subclinical inflammation for early diagnosis of cardiovascular diseases and metabolic syndrome. The results obtained during the study also can be used for development of targeted microbiota correction approaches for the treatment and prevention of these diseases.