UDC 616.34-008.87
https://doi.org/10.31612/2616-4868.4(26).2023.09

# GUT MICROBIOTA AND CARDIOMETABOLIC RISK FACTORS IN CORONARY ARTERY DISEASE PATIENTS WITH ATRIAL FIBRILLATION

**Iryna O. Melnychuk**

Bogomolets National Medical University, Kyiv, Ukraine

*Summary*

**The aim:** To estimate gut microbiota composition peculiarities in patients with coronary artery disease (CAD) and atrial fibrillation (AF) and to evaluate their connections with known cardiometabolic risk factors (CRF).
**Materials and methods:** 300 patients formed 3 groups: I group – 149 CAD patients without rhythm disorders, II group – 124 patients with CAD and AF paroxysm and control group (CG) – 27 patients without CAD and arrhythmias. 16-S rRNA sequencing checked gut microbiota composition. CRF which was explored are total cholesterol (TC), triglycerides (TG), low density lipoproteins (LDL), high density lipoproteins (HDL), lipoprotein α (Lpα), apolipoprotein A1 (ApoA1), apolipoprotein B (ApoB), C-reactive protein (CRP), interleukin-6 (IL-6), trymetilamine (TMA) and trymetilamine-N-oxide (TMAO).
**Results:** The significant changes of gut microbiota composition were found in CAD patients with AF paroxysm in comparison with CAD patients without arrythmia as increasing Actinomycetota phulum ($P<0.05$); increasing Actinobacter Spp. and decreasing Blautia Spp., Roseburia Inulinivorans, Bacteroides Thetaiotaomicron ($P<0.05$). Moreover, Actinobacter Spp., Akkermansia Muciniphila, Streptococcus Spp., Bacteroides Thetaiotaomicron, Bifidobacterium Spp. have the highest amount of significant correlations with CRF (body mass index, LDL levels; $P<0.05$). By the ROC-analysis we found the acceptable role of Lactobacillus Spp., Bifidobacterium Spp., Bacteroides Thetaiotaomicron, Blautia Spp., Actinobacter Spp. and Eubacterium Rectale in AF paroxysm occurrence in CAD patients (area under ROC-curve (AUC)<0.7). We found gut microbiota combinations with highest AUC for AF paroxysm in CAD patient: all of them include Actinobacter Spp (Actinobacter Spp. + 0.32 * Streptococcus Spp., AUC = 0.9008; 1.56 * Actinobacter Spp. – Blautia Spp., AUC = 0.9008;1.84 * Actinobacter Spp. – Akkermansia Muciniphila, AUC = 0.9008). AF paroxysm duration in CAD patients depends of plasma IL-6, TMAO, fecal Actinobacter Spp. and Akkermansia Muciniphila by the linear multifactorial regression analysis (AF paroxysm duration = 0.68*(Actinobacter Spp., lg/CFU/ml) 0.73*(Akkermansia Muciniphila, lg/CFU/ml) + 0.6*IL6 + 0.34*TMAO 0.98).
**Conclusions:** Gut microbiota condition is closely connected with occurrence AF of paroxysm in CAD patients. To find out the new ways of gut microbiota and CRF correction will be interesting in future investigations.

*Key words:* **gut microbiota, atrial fibrillation, coronary artery disease.**

## INTRODUCTION

Coronary artery disease (CAD) and atrial fibrillation (AF) are the most common cardiovascular diseases and arrhythmia respectively all over the world. Near the half of AF cases associated with CAD. Presence of CAD worsened AF prognosis. CAD and AF have a lot of mutual risk factors as dyslipidemia, diabetes mellitus, inflammatory conditions, etc. But pathogenetic background of AF paroxysm development in CAD patients is still unknown [1, 2, 3].

Gut microbiota composition disturbances are closely connected with CAD and AF risk factors. Widely used «gut-brain» and «gut-heart» axis terms, whish explained the importance of gut microbiota composition role in psychiatric and cardiovascular disorders pathogenesis [4, 5, 6]. Also, gut microbiota composition take part in development in the most metabolic disorders: obesity, dyslipidemia, diabetes mellitus, nonalcoholic fatty liver disease, etc. Chronic inflammation is also linked with gut microbiota disturbances. It can be directly – due to intestinal barrier violations or