

# FECAL SHORT CHAIN FATTY ACIDS AND PLASMA TRIMETHYLAMINE, TRIMETHYLAMINE-N-OXIDE LEVELS IN CORONARY ARTERY DISEASE PATIENTS WITH ATRIAL FIBRILLATION

## SCIENTIFIC RESEARCH GROUP:

**Melnychuk Iryna**

PhD, associate professor

*Bogomolets National Medical University, Ukraine*

**Sharayeva Maryna**

PhD, associate professor

*Bogomolets National Medical University, Ukraine*

**Kramarova Viktoriia**

MD, professor

*Bogomolets National Medical University, Ukraine*

**Amrita Gargi**

Medical student 9607M2a

*Bogomolets National Medical University, Ukraine*

**Introduction:** The most known gut microbiota metabolites are plasma trimethylamine-N-oxide (TMAO), trimethylamine (TMA) and fecal short chain fatty acids (SCFA). They characterized the gut microbiota composition, its activity and exchange. By the last data they can be the risk factors of different metabolic and cardiovascular disorders. But their role in arrhythmias development still is not proven yet [1].

**The aim:** To check gut microbiota metabolites (plasma TMA, TMAO levels and fecal SCFA composition) in CAD patients with or without AF.

**Materials and methods:** 300 patients were investigated. They were divided into 3 groups: control group – 28 patients without CAD and arrhythmias; main group – 149 patients with CAD but without arrhythmias; comparable group – 123 patients with CAD and AF paroxysm. Plasma TMAO, TMA, fecal SCFA levels were determined by gas chromatography with mass electron detection.

**Results:** Metabolomic analysis of the gut microbiota metabolites (plasma TMA, TMAO, fecal SCFA) in patients with CAD and AF paroxysm was done in our study. We checked their changes for patients with CAD and AF comparable with CAD patients: increasing of TMA, TMAO plasma levels, fecal valeric acid level (13,88%, 36,52% and 1128,43% respectively,  $p < 0,05$ ) and decreasing total amount of fecal SCFA, USFA, MCFA, butyric, isovaleric, caprylic acids levels (17,09%, 38,16%, 95,54%, 78,75%, 56,29% and 99,21% respectively,  $p < 0,05$ ). Reliable correlations between CAD and AF with TMA, TMAO plasma and fecal SCFA levels were revealed by them and age, BMI, GFR, total cholesterol, TG, LDL, HDL, ApoB levels ( $|r| > 0,3$ ,  $p < 0,05$ ) were revealed that are known risk factors of CAD and AF. Moreover, TMAO, TMA, butyrate, total SCFA, USFA, MCFA levels are closely connected with IL-6 and CRP levels ( $|r| > 0,3$ ,  $p < 0,05$ ).

Conclusions: Gut microbiota metabolites (TMA, TMAO, SCFA, MCFA, USFA, butyric acid) are the new promising therapeutic targets for pathogenetic treatment and prevention AF paroxysm in CAD patients.

Key words: coronary artery disease, atrial fibrillation, gut microbiota composition, trimethylamine-N-oxide, trimethylamine, short chain fatty acids.

### **References:**

1. Lizogub VG, Kramarova VN, Melnychuk IO The role of gut microbiota changes in the pathogenesis of heart disease. Zaporizkiy medical journal. 2019;21 (5-116):672–678. doi: 10.14739/2310-1210.2019.5.179462