gutflix
GI learning, personalised

Summary

COMPOSITION OF THE GUT MICROBIOME IN INDIVIDUALS WITH CARDIOVASCULAR RISK PROFILES AND PATIENTS WITH ST-ELEVATION MYOCARDIAL INFARCTION

Ranko Gacesa

UEG Week Copenhagen 2023 | Poster

Colorectal

October 15, 2023

A cross-sectional metagenomic study of 411 fecal samples found distinct gut microbiome species and functional pathways in STEMI patients compared to individuals with varying cardiovascular risk levels.

KEY POINTS

- Eight bacterial species and 49 metabolic pathways showed differential abundance across low, intermediate, and high cardiovascular risk groups and STEMI patients, with cardiovascular risk calculated using the Framingham score.
- Collinsella stercoris abundance increased with increasing cardiovascular risk (coefficient 1.75, FDR 0.005), while Bacteroides vulgatus and Bacteroides uniformis were reduced in STEMI patients compared to risk groups.
- Four pathways linked to starch biosynthesis and phenolic compound degradation were upregulated in STEMI patients, whereas pathways associated with nucleotide, fatty acid, lipid, and carbohydrate biosynthesis were decreased.
- No significant trends were found in Shannon diversity or beta diversity measures among the groups.
- The authors state that these species are promising candidates for further investigation and that experimental studies using culturomics and intervention trials are needed to understand causal relationships.

VIEW THIS CONTENT ON GUTFLIX

https://gutflix.eu/search/d/8e4a32f0-743b-11ee-b269-0242ac140004

AI-generated summary

This summary was generated by an AI large language model based on the content transcript. It is for informational purposes only and should not be considered a substitute for clinical judgment. Always rely on your professional expertise and the full clinical context when making clinical decisions.