Long-Term Risk of Heart and Metabolic Disease may Signal by Specific Gut Bacteria

Researchers examined the gut microbiome's role in long-term cardiometabolic health. While a few microbes were linked to increased cardiovascular risk, others appeared protective. Although the microbiota has limited diagnostic value, it shows promise as a potential target for early preventive interventions. Notably, Eubacterium xylanophilum group species remained significantly associated after adjustments. The findings also connect plant-based diets, microbial metabolites, and heart health, highlighting diet and microbiome-focused research as potential preventive strategies.

Study

In this prospective analysis, researchers examined whether gut microbiome composition predicts long-term cardiometabolic outcomes.

The researchers included 4,792 adults from the Healthy Life in an Urban Setting (HELIUS) study (2011, 2015) who had not used antibiotics. They analyzed fecal samples collected from these participants at baseline using 16S ribosomal RNA sequencing to characterize microbial composition. Subsequently, they assessed circulating metabolites using ultra-high-performance liquid chromatography, tandem mass spectrometry (UHPLC-MS/MS) in a subgroup of 105 participants.

The team followed the participants for incident hypertension, diabetes, and dyslipidemia. In addition, they linked hospital and mortality registry data from January 2011 to January 2024 to identify major adverse cardiovascular events (MACE). The team also assessed an expanded cardiovascular outcome (MACE+) that included angina pectoris and other cardiovascular diagnoses recorded in registries. They used the International Classification of Diseases, tenth revision (ICD-10) codes to identify these adverse events.

The team used logistic regression models to estimate the odds ratios (ORs) for associations between microbial features and incident cardiometabolic conditions. In addition, they used Cox proportional hazards models to estimate hazard ratios (HRs) for MACE in cardiovascular disease among free participants at baseline. Study covariates included age, sex, body mass index, alcohol use, and smoking status.

The researchers assessed alpha diversity using the Shannon index and beta diversity using Bray-Curtis distances, stratifying results by ethnic group. They also evaluated potential confounding by dietary factors, including sodium and macronutrient intake. The team analyzed serum data

from a subset of 105 participants to identify metabolites linked to MACE and associated microbes.

The cohort comprised predominantly middle-aged adults (mean age 50 years), with women representing 53%, primarily of Dutch, African Surinamese, and South Asian Surinamese origin. Over 6.2 years of follow-up (maximum 9.5 years), researchers recorded 376 new-onset hypertension cases (21%), 375 new dyslipidemia cases (19%), and 183 new diabetes cases (5.8%).

Cardiovascular outcomes included 129 MACE and 180 expanded MACE+ events (3.8%). These events included cardiovascular diagnoses such as arrhythmia and heart failure, as well as cardiovascular deaths recorded in registries. MACE and MACE+ occurred most frequently among South Asian Surinamese participants. However, the associations between the microbiome and MACE were strongest in Dutch and African Surinamese groups.

The team found associations between several microbes and cardiovascular disease risk. Increased abundance of Akkermansia muciniphila (HR, 0.86) and Lachnospiraceae taxa (HR, 0.84) was linked to a decreased MACE risk. In contrast, Ruminococcus gnavus group species was associated with increased risk in analyses of the expanded cardiovascular endpoint (MACE+) (HR, 1.10). However, these associations generally became non-significant after adjustment for covariates. For MACE+, A. muciniphila (HR, 0.90) and Eubacterium group species (HR 0.81) were protective. Notably, only E. xylanophilum group species remained significant in fully adjusted models (HR, 0.85).

Findings and Conclusion

Participants who developed diabetes, dyslipidemia, or hypertension showed slightly lower microbial diversity, although diversity differences were modest and not strong predictors of disease risk. Microbes associated with higher odds of disease included Flavonifractor plautii (OR, 1.18) and R. gnavus (OR, 1.13) for diabetes. R. gnavus (OR, 1.12) and F. plautii (OR, 1.14) increased odds for dyslipidemia. Streptococcus species (OR, 1.13), F. plautii (OR, 1.17), R. gnavus (OR, 1.07), and Bifidobacterium (OR, 1.06) were associated with increased likelihood of hypertension. In general, Lachnospiraceae taxa, Colidextribacter, and Christensenellaceae species showed protective associations.

Metabolomic analyses linked risk-associated microbes with bile acids and acylcarnitine-related metabolites. Protective taxa correlated with plant-derived microbial compounds, including xenobiotics such as 3-phenylpropionate, cinnamoylglycine, and enterolactone sulfate. These metabolites, likely reflecting microbial metabolism of plant-derived dietary compounds, underscore potential diet-microbiome interactions in cardiovascular protection.

The findings demonstrate that the composition of the gut microbiome is longitudinally linked to cardiometabolic disease and may serve as an early indicator of cardiovascular risk shaped by lifestyle. Protective microbes were associated with plant and diet-derived metabolites, highlighting important diet-microbe interactions. Notably, Eubacterium xylanophilum group species remained significantly protective after full adjustment, making it a candidate organism for further investigation rather than a confirmed therapeutic target.

Future studies should include repeated microbiome sampling, larger metabolomics datasets, external validation cohorts, and experimental work to guide microbiome and dietary strategies

for cardiovascular risk reduction. The authors also note that microbiome profiles were measured at a single baseline time point, which may limit causal interpretation.

Source:
https://www.news-medical.net/news/20260309/Specific-gut-bacteria-may-signal-long-term-risk-of-heart-and-metabolic-disease.aspx