Predicting heart disease-inducing metabolites from patients' gut microbiomes

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Abstract

The foods we eat, our biological makeup, and the microbes that dwell in our gut share a highly complex relationship. Sometimes, for example, our resident microbes can turn the beneficial nutrients and drugs we take into harmful substances. That's the case for L-carnitine, a nutrient found in red meat and supplements, which certain bacteria metabolize into trimethylamine-N-oxide (TMAO), a compound linked to cardiovascular disease. To understand how different individuals' microbial makeup might predispose them to harmful TMAO production researchers tested 56 individuals who received carnitine supplementation for 1 month. High-TMAO producers showed lower levels of active TMAO, likely because bacteria had already begun to break down a sizeable portion of ingested carnitine. The team also observed that TMAO productivity could be enhanced by carnitine supplementation. Ultimately, high- and low-TMAO producers could be distinguished by their microbial makeup allowing for TMAO production status to be predicted to a certain extent based on gut microbiome features. While a larger sample size is needed to make these predictions more robust the findings could help clinicians identify high-TMAO producers and develop ways of curbing harmful bacterial activity.