On Gut Microbiota Scientists Uncover Coffee's Surprising Effect

Scientists identify a metabolic link between coffee consumption and the abundance of specific gut microorganisms across different human populations.

Study

The study analyzed more than 35,000 metagenomic samples from three study cohorts, including the ZOE Personalized Responses to Dietary Composition Trial (PREDICT) metagenomics study, the Mind–Body Study (MBS), and the Men's Lifestyle Validation Study (MLVS).

The study analysis also included more than 54,000 metagenomic samples from public sources, including healthy individuals, non-Westernized individuals, newborns and infants, ancient microbiome samples, non-human primates, and individuals with a specific disease.

Study Findings

The study investigated the association between coffee intake and gut microbiota composition by categorizing the participants into three coffee-drinking levels: never-drinking, moderate-drinking, and high-drinking.

The findings revealed a strong correlation between coffee intake and gut microbiota composition across different study populations. The gut microbiota exhibited distinct compositions in coffee drinkers compared to non-drinkers, with a modest effect on differentiating the level of coffee drinking.

In general, coffee showed stimulatory rather than inhibitory effects on the abundance of gut microbial species. The strongest association of coffee intake was observed with the abundance of the Gram-positive bacterium Lawsonibacter asaccharolyticus. This association remained the same for both decaffeinated and caffeinated coffee.

The abundance of *Lawsonibacter asaccharolyticus* was 4- to 8-fold higher among high coffee drinkers compared to that among non-drinkers. Among moderate drinkers, the abundance was 3- to 4-fold higher than non-drinkers.

The study conducted a set of in vitro experiments to confirm the observed association further. In these experiments, coffee was added to the culture media of *Lawsonibacter asaccharolyticus*.

The findings revealed that coffee significantly increased the growth of *Lawsonibacter asaccharolyticus* by 3.5-fold, irrespective of the types (moka brewed and instant coffee) and the presence of caffeine.

The study also identified a panel of 115 gut microbial species positively associated with coffee consumption, highlighting coffee's broader influence on the microbiota.

Besides the coffee-mediated increased abundance of *Lawsonibacter asaccharolyticus* at the individual level, the study found that the overall prevalence of the bacterium in a population can be driven by the population-level consumption of coffee.

The analysis of 438 plasma metabolomes identified several metabolites enriched among coffee drinkers, with quinic acid and its potential derivatives associated with coffee and *Lawsonibacter asaccharolyticus*. Unannotated metabolites potentially derived from quinic acid were also highlighted, emphasizing the need for future biochemical investigations.

Conclusion

The study finds a strong correlation between coffee intake and gut microbiota composition across five US and UK populations.

A positive association has been observed between coffee intake and a set of 115 gut microbial species. Among these microorganisms, the strongest association has been observed for *Lawsonibacter asaccharolyticus*.

The observed stimulatory effect of coffee on the growth of *Lawsonibacter asaccharolyticus* provides a background for future studies aiming to decipher the extent of this stimulatory effect. Such studies should investigate the effect of different concentrations of coffee on the growth rates of a panel of coffee-associated gut microorganisms.

The study also identified variations in the prevalence of *Lawsonibacter asaccharolyticus* between Western and non-Western populations, potentially linked to differences in coffee availability and consumption habits.

The metabolomic analysis carried out in this study reveals that quinic acid, trigonelline, and other potential metabolites are significantly enriched in coffee drinkers carrying *Lawsonibacter asaccharolyticus*.

Chlorogenic acid is one of the main polyphenols in coffee. Gut microorganisms metabolize it to caffeic acid, quinic acid, and several other metabolites. Gut microorganisms responsible for this biotransformation include *Bifidobacterium animalis, Bifidobacterium lactis, Escherichia coli*, and *Lactobacillus gasseri*.

The caffeine-independent strong association between *Lawsonibacter asaccharolyticus* abundance and coffee intake indicates that it may also respond to activities within these polyphenol metabolism pathways.

Caffeine and its derivatives were prioritized in the study because of their association with *Lawsonibacter asaccharolyticus*. However, the enrichment of microorganisms in decaffeinated coffee drinkers indicates that caffeine does not occupy the central position in this complex crosstalk. Instead, quinic acid and its derivatives may play a pivotal role.

Overall, the study provides a framework for understanding microbial dietary responses at the biochemical level.

Source:
https://www.news-medical.net/news/20241203/Scientists-uncover-coffees-surprising-effect-on-gut-microbiota.aspx