

Background

- Bile acids (BA) and gut microbiome-derived BA metabolites (secondary BA [SBA]) modulate immune functions and contribute to intestinal tumorigenesis.
- While diet is known to influence BA production, the effects of dietary fat, carbohydrate, and protein on BA levels remain inconsistent.
- We hypothesize that the impact of diet on BA, particularly SBA levels, may depend on the host's gut microbial features.

Objectives

- We hypothesize that the impact of diet on BA, particularly SBA levels, may depend on the host's gut microbial features.

Methods

- Leveraging the integrated stool metagenomes, stool and plasma metabolome, and long-term habitual dietary data from a subset of the Microbiome Among Nurses study (Micro-N), including Micro-N-diverticulitis substudy (n = 225), Micro-N-polyp substudy (n = 400), and Mind-Body Study (MBS) (n = 220), we explored the interplay between gut microbial species and functions, stool and blood BA metabolites, and diet (41 food groups and 51 nutrients).

Summary

- The methanogenesis pathway encoded primarily by *M. smithii* and the resultant production of methane gas may influence the biotransformation of dehydro-LCA and isoallo-LCA in gut microbial communities and modulate the dietary effect on BA metabolism.

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Key Findings

