Microbiome: the human species' evolutionary waltz with bacteria

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I'll present our recent findings from two UK cohorts showing that faecal metabolomics is a powerful tool in nutritional research, enabling in-depth investigation of the complex interplay between habitual diet and the gut microbiome. This approach opens new avenues to uncover mechanistic links, refine our understanding of diet-related disease risk, and identify potential targets for dietary interventions.

Using machine-learning models on metabolomic profiles, we accurately predict habitual intake across major food and beverage groups and capture adherence to healthy and unhealthy dietary patterns. Interestingly, faecal metabolite signatures outperform the DASH dietary score in predicting 10-year atherosclerotic cardiovascular disease risk, suggesting that metabolite readouts can complement - or in some contexts surpass - questionnaire-based assessments.

Diet-linked metabolites capture microbiome diversity and composition, elucidating the mediating pathways between diet and the gut microbiome and revealing how specific foods are converted into bioactive compounds that influence health.

Together, these results position faecal metabolomics as a practical foundation for nutritional research and personalised nutrition, highlighting opportunities to modulate the gut microbiome, including prebiotic strategies based on targeted, diet-derived metabolites.

References

[1] Faecal metabolites as a readout of habitual diet that capture dietary interactions with the gut microbiome. Pope R, Visconti A, Zhang X, Louca P, Baleanu AF, Lin Y, Asnicar F, Bermingham K, Wong KE, Michelotti GA, Wolf J, Segata N, Berry SE, Spector TD, Leeming ER, Gibson R, Menni C, Falchi M, Nature Communications (accepted)

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