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Summary

The gut microbiome in cardiometabolic disorders

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IBD | Gut Microbiota

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Large-scale shotgun metagenomic analysis of over 35,000 individuals from the PREDICT studies identified and ranked gut microbiome species according to their associations with diet and cardiometabolic health markers, with validation in independent cohorts showing these rankings predict obesity, disease states, and response to dietary interventions.

KEY POINTS

- The speaker reported analyzing more than 35,000 individuals from PREDICT cohorts (UK and US studies), systematically associating over 600 prevalent gut microbiome species with cardiometabolic markers including blood pressure, visceral fat, fasting and postprandial metabolic measurements, and creating a ranked species index from favourable to unfavourable.
- Validation in public datasets showed that healthy-weight individuals had on average 5 more favourably-ranked species and obese individuals had 2 more unfavourably-ranked species; similar association patterns were observed across IBD, colorectal cancer, and type 2 diabetes cohorts.
- In longitudinal intervention studies with personalized diet, species that increased over time showed more favourable rankings while species that decreased showed more unfavourable rankings, consistent with the cardiometabolic index.
- Analysis of more than 56,000 metagenomes showed Blastocystis prevalence was higher in vegetarians and individuals with higher healthy plant-based diet index scores; people with Blastocystis had healthier triglyceride, cholesterol, and glycemic markers and were more likely to have healthy weight.
- Preliminary analysis of more than 229,000 participants identified over 3,000 type 2 diabetes and 14,000 unmedicated prediabetes cases, with close to 600 microbiome species associated with both conditions and detectable even before type 2 diabetes onset.

– The speaker noted in discussion that the team is expanding to over 10 times the current sample size and exploring microbiome-aging relationships, strain-level profiling, and Blastocystis genome reconstruction.

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