Meta-analysis of the robustness and universality of gut microbiome-metabolome associations

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Video Byte

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Abstract

Increasing evidence of gut microbe-metabolite-host health interactions has prompted increasing research on the human gut microbiome and metabolome. Statistical and machine learning-based methods have been widely used to identify microbial metabolites that can be modulated to improve gut health, but whether the findings of individual studies are applicable across studies remains unclear. In a recent meta-analysis, researchers searched for metabolites whose levels in the human gut could be reliably predicted from microbiome composition, using a machine learning approach with data processed from 1733 samples in 10 independent studies. While the predictability of many metabolites varied considerably among studies, the search identified 97 robustly well-predicted metabolites that were involved in processes such as bile acid transformation and polyamine metabolism. Some of the robustly well-predicted metabolites were predicted by very different sets of taxa across datasets, suggesting differences in regulating microbes. In addition, models trained on the control groups from individual studies failed to predict the levels of certain metabolites in diseased groups of the same studies, indicating that disease-associated dysbiosis shifted microbial metabolism. Although further research on more metabolites is needed, the results increase understanding of the microbiome-metabolome relationship and will help researchers properly contextualize their findings on microbial metabolites.