Microbe-diet interactions influence the effects of fiber on host metabolism

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Abstract

Human microbiomes are diverse and dynamic communities of bacteria, which play a critical role in many aspects of human health, including the breakdown of the food we eat. Research has shown that dietary fermentable fiber generally improves cardiometabolic health. However, past studies have found the response to specific interventions has significant variation between individuals. This variation likely has multiple causes, but the role of gut microbial metabolism has not yet been explored. To test this, researchers colonized germ free (GF) mice with distinct, complex microbial communities and then fed them one of four diets. Each microbiome remained distinct under all diets, but the different diets led to variations in richness and taxon abundance in both microbiomes. Epigenetic, transcriptional, and metabolic analyses showed diet-directed differences between the communities, including changes in metabolic pathways associated with health. While this study utilized only a small number of microbiomes, it highlighted the impact of microbe-diet interactions on host metabolism. It also suggested that the gut microbiome is a differential factor that contributes to individual variation in the health effects obtained from consumption of dietary fiber and that personalized fiber supplementation approaches may be needed for more consistent health outcomes.