Dietary plant metabolites as modulators of gut microbial dynamics

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Plant specialized metabolites (PSMs) are increasingly consumed with plant-rich diets, yet quantitative dietary exposure and microbiome-relevant mechanisms remain poorly resolved. Here, we quantified the dietary occurrence of *Plant Metabolite a* (PMa) across ~300 plant-based foods and beverages using Liquid-Chromatography coupled to Mass-Spectrometry (LC-MS) and observed strong variability across product categories, consistent with highly heterogeneous dietary exposure. *In vivo* PMa ingestion in mice was associated with microbiome shifts in both the colon and feces, including a decrease in the relative abundance of *Lactobacillus reuteri* and *Enterococcus faecalis*. To mechanistically link these observations to direct bacterial responses, we profiled PMa effects on *E. faecalis* and *L. reuteri* in monoculture. While PMa did not alter *L. reuteri* growth under the tested conditions, it triggered a time-dependent response in *E. faecalis*, with early growth inhibition (~6 h) followed by a rebound (~18 h) and no detectable effect at stationary phase (~28 h). Untargeted metabolomics of culture supernatants further indicated that both strains depleted PMa from the medium, suggesting microbial processing that may reflect utilization as a carbon source, unspecific metabolization, and/or detoxification, possibly explaining the time-dependent response of *E. faecalis*. Together, these results suggest that the *in vivo* decrease of *E. faecalis* and *L. reuteri* may arise from both direct and indirect PMa-mediated mechanisms in the gut environment. Ongoing work therefore aims to bridge *in vitro* and *in vivo* outcomes by testing (i) PMa-driven changes in gut physicochemical conditions, and (ii) microbiome-mediated conversion of PMa into secondary products. Because *E. faecalis* is an opportunistic pathobiont whose abundance is tightly linked to gut ecosystem stability, the observed PMa-dependent responses suggest that dietary plant metabolites may play a role in constraining taxa with high inflammatory potential.