Intestinal microbes feed on dietary protein sources resilient to host digestion

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Abstract:

Diet impacts the gut microbiota's composition and function, influencing host health. Gut microbiota can transform resilient dietary proteins to produce metabolites that affect host health, such as beneficial fatty acids or proinflammatory indoles. However, it remains unknown which components of dietary proteins evade host digestion and undergo gut microbial metabolism. Current methods that indirectly measure digestive efficiency and the fate of dietary proteins by quantifying amino acids are inadequate to address these questions, necessitating more efficient techniques to detect and quantify dietary proteins in fecal samples. To address these knowledge gaps, we used metaproteomics to investigate the fate of purified dietary proteins from 6 plant and animal sources, including casein, soy, egg, yeast, pea, and rice, in male and female, germ-free and conventional mice. We also tracked soy and casein dietary proteins throughout the intestinal tract. Results revealed that purified dietary proteins contain hundreds to thousands of distinct proteins, ranging from 44 proteins in egg white to 1476 proteins in torula yeast. Notably, microbial proteins constituted a substantial portion of the purified casein diet. The digestive efficiency of these dietary proteins differed significantly with and without gut microbiota. Brown rice protein yielded the highest recovery of dietary proteins in fecal samples, followed by egg white and casein. We identified tens to hundreds of proteins in each diet that were resilient to host digestion but consumed by the gut microbiota. These proteins, including Ovomucin in egg and the Kunitz trypsin inhibitor in soy, were enriched in germ-free samples but depleted in conventional samples. We also identified proteins resistant to both host and microbial conversion. Moreover, higher protein content in the diet correlated with a greater proportion of undigested protein in feces. Our study challenges assumptions, highlighting substantial differences in dietary protein degradation by the host and gut microbiota. These findings further our understanding of microbial nutrition and metabolism in the gut. This knowledge can also aid in customizing protein aspects of gut-healthy diets, considering their accessibility to the gut microbiota and their nutritional efficacy for the host.