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# Integrated omics approach identified acetate produced by probiotic bifidobacteria to protect host from enteropathogenic infection

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The human gut is colonized with a wide variety of indigenous microorganisms, among which species, the so-called 'probiotics', such as the bacterial genus *Bifidobacterium*, are known to have beneficial effects on human physiology and pathology. Among the most distinctive benefits of probiotic bifidobacteria are a modulation of host defense responses and protection against infectious diseases. Nevertheless, the molecular mechanisms underlying these beneficial effects have barely been elucidated. To address these questions, we have applied an integrated 'omics' approach on a simplified enterohaemorrhagic *Escherichia coli* O157:H7 (O157) lethal infection model using bifidobacteria-monoassociated mice. We found that the genes encoding ATP-binding cassette (ABC)-type transporters for carbohydrates, especially fructose, in certain 'preventive' bifidobacteria largely contribute to the protection of mice from O157-induced death through enhanced production of acetate. This protection is neither associated with the inhibition of O157 growth, Shiga toxin production, mucin production, nor the change of pH, in the intestine; however, the serum concentration of Shiga toxin was kept significantly low in the surviving mice. Comparative genomic, transcriptomic, and metabolomic profilings followed by multivariate analysis revealed that the translocation of Shiga toxin from the gut lumen into the blood was inhibited, most likely by enhancement of intestinal epithelial defense function due to the trophic and/or anti-inflammatory effects of acetate produced by the preventive bifidobacteria in the surviving mice. The abilities of acetate production and fructose consumption were significantly higher in the preventive bifidobacteria than non-preventive bifidobacteria, in accordance with the possession and expression of the corresponding ABC-type carbohydrate transporter genes in the former. Thus, a simplified animal model coupled with 'omics' technologies can provide a unique platform for studying the host–microbial crosstalk and a powerful strategy for dissecting the complex gut ecosystem.