

A candidate probiotic evolves rapidly and convergently but affects microbiomes differently

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Abstract

Interactions among probiotics, resident gut microbes and host factors affect probiotic engraftment and the resulting therapeutic effects. These interactions depend on gut-adaptive evolution of the probiotic strains, but the underlying processes—and their differences among host species—are unclear. In addition, the evolutionary effects of probiotics on native gut microbes are not well characterized. A recent genomics study examined the evolution and effects of the probiotic *Lactiplantibacillus plantarum* HNU082 (Lp082) in the human, mouse, and zebrafish gut. In all three species, Lp082 acquired single-nucleotide mutations. *In vitro*, the gut-adapted strains exhibited improved fitness related to carbohydrate utilization and acid tolerance and remained genetically stable for three months. In the human and mouse gut, Lp082 engraftment increased the numbers of mutations of the resident gut microbiota (GM) by 10- to 70-fold. Strains that competed with Lp082, such as *Bacteroides* and *Bifidobacterium* strains, were especially affected. However, the gut microbiome was more ecologically and genetically stable in humans than in mice. Although the long-term effects of probiotic-induced microbiota evolution are unclear, the results suggest that Lp082 adapts similarly to the gut environment regardless of host but induces host-specific changes in resident gut microbes, providing important insights for the use of animal models in probiotic engineering.