Evolution, transmission, and anti-aging effects of a human gut-derived probiotic

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Video Byte

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Abstract

Genetic and molecular differences in individual bacterial strains of the gut microbiome may affect health outcomes, including aging, in humans. However, the details and effects of host-microbe co-evolution remain unclear. To obtain insights, a recent study investigated *Bifidobacterium longum*, a key long-term member of the human gut microbiome that has also been linked to aging. Population genomics analyses of 418 human gut strains revealed three geographic populations of *B. longum*, with differences in cell wall synthesis genes and carbohydrate metabolism genes. *B. longum* was actively transmitted between individuals, families, and regions, but a single clone tended to colonize each host. *B. longum* relative abundance declined with host age, while certain genotype features, such as a sequence variant in the *B. longum* arginine biosynthesis pathway, were positively related to age. In mice, *B. longum* strains with different arginine biosynthesis gene variants exerted different protective effects against D-galactose-induced aging. Although further mechanistic investigations are needed, the results suggest that probiotic strains with specific genetic features could be useful for promoting host longevity and provide pioneering insights into the evolution and transmission of probiotic species.