



Category: Metagenomics

A comparative genomics approach to find out the probiotic effects of *Lactobacillus casei* Lbs2 isolated from healthy gut of Indian population

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Abstract

Lactobacillae are gram positive diverse group of species and have association with nutrient rich niches like humans, animals and plants. *Lactobacillus casei* is considered as one of the most competent probiotic throughout the world. Its microbiological feature historically well-established but genomic analysis including comparative genomics is recent. *Lactobacillus casei* Lbs2 strain was isolated from the gut of a healthy north Indian individual and sequenced. We compared the genomes of *Lactobacillus casei* Lbs2 with 8 other complete genomes of the same species e.g.; LC2W, BL23, BDII, W56, 12A, Zhang, LOCK919, ATCC393 using BRIG (Blast Ring Image Generator), Gene enrichment analysis using Fischer Extract test in R. Lbs2 strain has a number of genes including bile tolerance, stress response re-iterating its probiotic stand. Interestingly, genes coding for transposons, co-enzyme transport and metabolisms are enriched in the Indian Genome. Presence of large number of transposons indicates this genome is undergoing expansion and under adaptive selection pressure. When we compared our genome based on Multilocus Sequence Typing (rMLST), we found this strain is closely similar to *Lactobacillus fermentum* rather than other *L. casei* strains. Comparison of Lbs2 strain with other *L. casei* strains indicates ATCC393 (isolated from daily product) is closer than others.

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