

Genomic characterization of *Lactobacillus delbrueckii* CIDCA 133: a potential probiotic strain

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Abstract

The probiotic potential of *Lactobacillus delbrueckii* CIDCA 133, isolated from raw cow milk, have been validated by in vitro studies that showed its resistance to high acid and bile concentrations, the ability to inhibit the growth of pathogenic microorganisms such as enterohemorrhagic *Escherichia coli*, resistance to antimicrobial peptides of erythrocyte cells, and anti-inflammatory and immunomodulatory properties. However, despite of these important traits, little is known about the molecular mechanisms involved in these processes. In this study, we performed a comprehensive analysis of its genome to better understand the molecular basis of its in-vitro-tested probiotic characteristics. The genome of *L. delbrueckii* CIDCA 133, herein named CIDCA 133, was sequenced using Illumina HiSeq platform and assembled using Spades. The assembly resulted in 70 contigs and a 6223 bp sized cryptic plasmid. The characterization of its genome confirmed that CIDCA 133 belongs to the subspecies *lactis*, with 98.21% of ANI compared to the type strain *L. delbrueckii* subsp. *lactis* DSM 20072. Comparative genomics analyses were conducted including CIDCA 133 and 64 publicly available *L. delbrueckii* genomes. Despite the expected clustering of the subspecies in the phylogenomic tree, generated by the software PEPR, divergent identifications were found for some *L. delbrueckii* subsp. *bulgaricus* strains, which grouped in the same clade with another *L. delbrueckii* subsp. *lactis*. Given the similarity between the subspecies, our results suggest that some genomes have been misclassified in the GenBank. Hence, greater care should be taken with their characterization, using genomic analysis as part of this process. Preliminary functional analysis shows that CIDCA 133 has 18 exclusive genes, one of these (*nagB*) required for the Amino sugar and nucleotide sugar metabolism pathway. These genes might be related to the metabolic pathway associated with the singular probiotic characteristics described for this strain, and thus, more analyses will be performed in order to characterize them.

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