

Comparative genomics analysis and classification of the *Lactobacillus casei* species

Rodrigo Bentes Kato, Diego Lucas Neres Rodrigues, Juan Luis Valdez Baez, Roselane Gonçalves dos Santos, Stephane Fraga de Oliveira Tosta, Alessandra Lima da Silva, anne cybelle pinto gomide, Alfonso Gala-Garcia, Francielly Rodrigues da Costa, Vasco Ariston de Carvalho Azevedo

Universidade Federal de Minas Gerais

Abstract

Lactobacillus taxon has been widely studied for its probiotic characteristics, including immunomodulatory and metabolic properties. The World Health Organization (WHO) points out that the genus and species classification of any probiotic is crucial before its use, genomic studies of lactic bacteria are of fundamental importance in the legal, biological and safety aspects. Therefore, gene blocks related to pathogenicity mechanisms should be studied to ensure the use of bacteria in the standards provided by WHO, although the literature indicates that some are symbiosis mechanisms. The aim of the present study was to compare the genome sequence of six strains of *Lactobacillus casei* and to show possible divergence points capable of segregating them from the others in the genus. The six complete *L. casei* genomes were obtained from the platform (NCBI) and standardized for annotation using the PROKKA software. For the comparison was developed a pipeline based on the Average Nucleotide Identity (ANI), performed on the JSpeciesWS platform, and on the construction of a phylogenomic tree of individuals of the genus using the PATRIC platform. Our analysis of genomic plasticity was performed using the visualization tools GIPSY and BRIG. We obtained images showing significant divergent points between the genomes applied to the study, as well as a low nucleotide identity. Islands of pathogenicity totally or partially shared among all genomes were detected. This last result suggests that the use of this bacterium is not safe to use as a probiotic. There is still great difficulty in classifying *L. casei* at the species level. As phylogenetically, *L. casei* is still very confused within the genus as other family members, which negatively influences its taxonomic identification which is crucial as a safety measure for its use in food.

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