Comparative genomic analysis between Lactobacillus delbrueckii subsp. lactis and Lactobacillus delbrueckii subsp. bulgaricus of dairy origin

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Abstract

Lactobacillus delbrueckii subsp. lactis and Lactobacillus delbrueckii subsp. bulgaricus are lactic acid bacteria commonly exploited by the dairy industry as starter cultures, mainly for the production of cheese and yogurt. In this work, we present the comparative genomic analysis between the recently sequenced genomes of L. lactis ACA-DC 178 and L. bulgaricus ACA-DC 87, isolated from Kasseri cheese and yogurt, respectively. The genome of L. lactis ACA-DC 178 is larger than that of L. bulgaricus ACA-DC 87, containing 2,048 and 1,928 protein coding genes, respectively. Full chromosome alignments revealed strain specific differences, although a high degree of synteny between the two strains was also observed. The core genome of the two strains contained about 1,200 genes while the unique genes of the two strains were also identified. The two genomes contained several genomic islands, indicating that a number of genes have been acquired through horizontal gene transfer. We also predicted one confirmed CRISPR system in each genome, three potential antimicrobial peptides in total and also prophage sequences integrated into the genomes of the two strains. Overall, our analysis provides useful insights into the technological potential of the ACA-DC 178 and ACA-DC 87 strains.

Results

Figure 1 - Circular maps of the genome of L. lactis ACA-DC 178 (A) and L. bulgaricus ACA-DC 87 (B). Genomic features appearing from the periphery to the center of the map: 1. Forward CDSs (cyan); 2. Reversed CDSs (red); 3. tRNA genes (blue); 4. rRNA genes (green); 5. GC-plot; 6. GC skew.

Figure 2 – Chromosome alignments of the strains as calculated by progressiveMauve. The L. bulgaricus ATCC BAA-365 and the L. bulgaricus NDO1 strains were used as the reference genomes for the L. bulgaricus ACA-DC 87 and the L. lactis ACA-DC 178 strains, respectively. Although the NDO2 strain is deposited in NCBI as Lactobacillus delbrueckii subsp. bulgaricus, Kalb et al. 2014 suggested that the NDO2 is a Lactobacillus delbrueckii subsp. lactis strain. Local collinear blocks (LCBs) of conserved sequences among the strains are represented by rectangles of the same colour. Connecting lines can be used to visualize synteny or rearrangement. LCBs positioned above or under the chromosome (black line) correspond to the forward and reverse orientation, respectively. The level of conservation is equivalent to the level of vertical colour filling within the LCBs (e.g. white regions are strain specific). Sequences not placed within an LCB are unique for the particular strain.

Figure 3 – The pangenome, the core genome, the accessory and the unique genes as obtained through the analysis of each set of genomes sequences with progressiveMauve. Genome sequences of L. bulgaricus strains (A). Genome sequences of L. lactis strains (B). Genome sequences of L. bulgaricus ACA-DC 87 and L. lactis ACA-DC 178 (C).

Figure 4 – CRISPR systems in the genome sequences of L. lactis ACA-DC 178 (A) and L. bulgaricus ACA-DC 87 (B) as predicted by CRISPRfinder.

Figure 5 – Circular maps of L. lactis ACA-DC 178 (A) and L. bulgaricus ACA-DC 87 (B) genomes. Highlighted regions correspond to genomic islands (GIs). GIs are colored within the circular maps according to the tool that predicted each one: orange and blue were predicted with SIGI-HMM and IslandPath-DIMOB, respectively. The integrated GIs are presented on the periphery in red. The black line plot represents the GC content (%) of the genomic sequences. Numbering of the GIs for each genome starts from the first GI found after position 0 of the genome and going clockwise.

Figure 6 – Genes encoding for antimicrobial peptides in the genome sequences of L. lactis ACA-DC 178 (AB) and L. bulgaricus ACA-DC 87 (C), as predicted by BAGEL3.

Figure 7 – Prophage sequences of L. lactis ACA-DC 178 (A) and L. bulgaricus ACA-DC 87 (B) as predicted by PHAST.

Bibliography

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