Data Article

Whole-genome sequence data and analysis of Lactobacillus delbrueckii subsp. lactis ACA-DC 178 isolated from Greek Kasseri cheese

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A B S T R A C T
Lactobacillus delbrueckii subsp. lactis is employed in the production of various types of cheese. Here, we report the complete genome sequence of L. lactis ACA-DC 178 isolated from Greek Kasseri cheese. The chromosome of ACA-DC 178 contains 2,050,316 bp with a GC content of 49.6%. A total of 2,112 genes were identified in the genome sequence including 1,752 protein-coding genes, 239 putative pseudogenes, 94 tRNA and 27 rRNA genes. According to the COG annotation, about 80% of the protein-coding genes (1,417 proteins) were assigned to at least one functional category. Approximately the 1/3 of these proteins were distributed among three categories, namely replication, recombination and repair (category L: 10.6%), translation, ribosomal structure and biogenesis (category J: 7.5%) and amino acid transport and metabolism (category E: 7.2%). Fourteen integrated GIs with a total of 159 genes were found in ACA-DC 178 genome. Several of these genes encode proteins associated with exopolysaccharide biosynthesis, amino acid transport and subunits of restriction-modification systems. One large CRISPR array of 3,197 bp containing 52 spacers, several of which are identical to phage sequences having hosts in the genus Lactobacillus, was also identified. The annotated genome sequence of L. lactis ACA-DC 178 is deposited at the European...

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In this study, we present the complete genome sequence of *L. lactis* ACA-DC 178 isolated from Greek Kasseri cheese [1,2]. The *L. delbrueckii* species consists of six subspecies, including *Lactobacillus delbrueckii* subsp. *bulgaricus*, *Lactobacillus delbrueckii* subsp. *lactis*, *Lactobacillus delbrueckii* subsp. *delbrueckii*, *Lactobacillus delbrueckii* subsp. *indicis*, *Lactobacillus delbrueckii* subsp. *sunkii* and *Lactobacillus delbrueckii* subsp. *jakobsenii* [3,4]. *L. lactis* is the second subspecies used as a starter in the dairy industry along with *L. bulgaricus* within the *L. delbrueckii* species [3]. The *in silico* assembly of the ACA-DC 178 chromosome was validated against a *Nhe*I whole-genome optical map of the strain (Fig. 1). Our assembly presented 100% matching between the *Nhe*I restriction sites of the optical map and the relevant sites in our genome sequence *in silico* digested with the same enzyme. The genome was found to be 2,050,316 bp with a GC content of 49.6%. We were able to annotate a total of 2,112 genes, including...
1,752 protein-coding genes, 239 putative pseudogenes, 94 tRNA and 27 rRNA genes (Fig. 2). Further analysis revealed that about 80% of the protein-coding genes (1,417 proteins) could be assigned to at least one Cluster of Orthologous Groups (COG) functional category. Most of these proteins (approximately 1/3) were distributed among three categories related to housekeeping processes, namely replication, recombination and repair (category L: 10.6%), translation, ribosomal structure and biogenesis (category J: 7.5%) and amino acid transport and metabolism (category E: 7.2%) (Table 1). Additional features of the ACA-DC 178 included 14 integrated genomic islands (GIs; Fig. 3) and a clustered regularly interspaced short palindromic repeats-CRISPR-associated (CRISPR-Cas) system (Fig. 4). The GIs carry 159 genes some of which could be assigned to functions like exopolysaccharide biosynthesis, amino acid transport and restriction-modification. The CRISPR array was relatively long, consisting of 3,197 bp and 52 spacers. Detailed analysis of the spacers identified several segments of phage sequences, which have hosts belonging to the *Lactobacillus* genus.

Fig. 1. Validation of the *L. lactis* ACA-DC 178 genome assembly. Alignment of the in silico genome assembly of *L. lactis* ACA-DC 178 (bottom) against a *Nhe*I whole-genome optical map of the strain (top).

Fig. 2. Circular map of the *L. lactis* ACA-DC 178 genome. Each ring represents specific genomic features appearing from the periphery to the centre of the map: Forward CDSs (blue); Reverse CDSs (red); Pseudogenes (black); tRNA (green); rRNA (orange); %GC plot; GC skew.
2. Experimental design, materials, and methods

*L. lactis* ACA-DC 178 was grown overnight in MRS broth (Merck, Darmstadt, Germany) at 30 °C. DNA was extracted according to a previously published protocol [5]. The genome was sequenced at the Beijing Genomics Institute (BGI Co., Ltd, Hong Kong) using the Illumina HiSeq 2000 platform (Illumina).

| COG Proteins % Description |
|--------------------------|
| Information storage and processing J 132 7.5 Translation, ribosomal structure and biogenesis |
| K 100 5.7 Transcription |
| L 186 10.6 Replication, recombination and repair |
| Cellular processes and signaling D 19 1.1 Cell cycle control, cell division, chromosome partitioning |
| M 91 5.2 Cell wall/membrane biogenesis |
| N 5 0.3 Cell motility |
| O 47 2.7 Posttranslational modification, protein turnover, chaperones |
| T 52 3.0 Signal transduction mechanisms |
| U 19 1.1 Intracellular trafficking and secretion |
| V 44 2.5 Defense mechanisms |
| Metabolism C 46 2.6 Energy production and conversion |
| E 127 7.2 Amino acid transport and metabolism |
| F 67 3.8 Nucleotide transport and metabolism |
| G 102 5.8 Carbohydrate transport and metabolism |
| H 30 1.7 Coenzyme transport and metabolism |
| I 32 1.8 Lipid transport and metabolism |
| P 73 4.2 Inorganic ion transport and metabolism |
| Q 3 0.2 Secondary metabolites biosynthesis, transport and catabolism |
| Poorly characterized S 262 15.0 Function unknown |
| — 335 19.1 Not in COGs |

Fig. 3. Circular map of the *L. lactis* ACA-DC 178 genome. Highlighted regions correspond to GIs. GIs are colored within the circular map according to the prediction method used: green, orange and blue were predicted by IslandPick, 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 sequence.
employing paired-end libraries of 500 bp, 2,000 bp and 6,000 bp. The assembly of reads with SOAPdenovo v.2.04 [6] resulted in one circular chromosome that was verified against a Nhel whole-genome optical map of the strain [7] produced at Microbion SRL (Verona, Italy). The alignment between the assembly and the optical map was performed with the MapSolver software (OpGen Technologies, Inc., Madison, WI). The ACA-DC 178 genome sequence was analyzed using Prodigal [8], MetaGeneAnnotator [9] and FGENESB [10] gene prediction programs. Genome annotation and prediction of rRNA and tRNA genes was performed with RAST v.2.0 [11] and putative pseudogenes were predicted with the GenePRIMP pipeline [12]. The results of the analysis were optimized with manual curation. COG annotations were computed using eggNOG-mapper based on eggNOG v.4.5 orthology database [13]. Further bioinformatic analysis was performed for the identification of GIs with Island-Viewer 4 [14] and CRISPR with CRISPRFinder [15].

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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