

Complete Chromosome Sequence of *Carnobacterium maltaromaticum* LMA 28

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Within the lactic acid bacterium genus *Carnobacterium*, *Carnobacterium maltaromaticum* is one of the most frequently isolated species from natural environments and food. It potentially plays a major role in food product biopreservation. We report here on the 3.649-Mb chromosome sequence of *C. maltaromaticum* LMA 28, which was isolated from ripened soft cheese.

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The genus *Carnobacterium* belongs to the lactic acid bacteria, and currently consists of 11 species. *Carnobacterium maltaromaticum* strains are widely found in foods, including dairy products (1). This species has potential for application as a protective culture in foods. Most research has focused on the production of bacteriocins, on their roles in the inhibition of *Listeria monocytogenes*, and on the regulation of metabolic pathways of sensory importance (2). *C. maltaromaticum* LMA 28 was isolated from a soft ripened cheese (3).

The genome sequence of *C. maltaromaticum* LMA 28 was determined using 454 pyrosequencing GS-FLX system (Roche 454 Life Sciences, Mannheim, Germany) and Illumina sequencing. Pyrosequencing runs, including shotgun and paired-end runs, resulted in 15 scaffolds containing 123 contigs and 55-fold coverage. A subsequent Illumina sequencing run performed with a paired-end library corrected 923 indels. PCR-base techniques and Sanger sequencing of the products were used to close the remaining gaps. The manually curated sequence of LMA 28 comprises one chromosome of 3,649,737 bp with an overall G+C content of 34.5%. Coding sequence (CDS) predictions and annotations were performed with Integrative Services for Genomics Analysis (ISGA) (4) and provided 3,933 predicted CDSs, 59 tRNA genes, 6 rRNA operons, and a single 5S rRNA gene.

So far, three genomic sequences of *Carnobacterium* have been published: the complete genome sequence of *Carnobacterium* sp. 17-4 (5) isolated from permanent cold seawater; the draft genome sequences of *C. maltaromaticum* ATCC 35586, isolated from a diseased salmon (6); and the draft genome of *Carnobacterium* sp. AT7, a piezophilic strain isolated from the Aleutian trench (7). The genome size of the strain ATCC 35586 (3.5 Mbp) is similar to that of LMA 28, and both are approximately 1 Mbp larger than the genomes of *Carnobacterium* sp. 17-4 and AT7 (2.6 Mbp and 2.4 Mbp, respectively). The larger chromosomal size of *C. mal-*

taromaticum might explain the ability of this species to adapt to multiple and diverse environments compared to the other carnobacterial species. This genomic trait is illustrated by the presence of genes involved in the metabolism of branched-chain amino acids.

Indeed, the species *C. maltaromaticum* is well known for its ability to produce the flavor compound 3-methylbutanal, which is the result of leucine catabolism. In lactic acid bacteria, the more prevalent pathway is the α -keto acid dehydrogenase (K₂ADH) pathway (8). A less common alternative pathway is the α -keto acid decarboxylase pathway, encoded by gene *kdcA*. This gene is only described for two strains of *L. lactis* (8). In the genome sequences of *C. maltaromaticum* LMA 28 and ATCC 35586, an orthologous gene of *kdcA* was found (2) that is absent from the genomes of the other *Carnobacterium* strains.

Nucleotide sequence accession number. The complete chromosome sequence of *Carnobacterium maltaromaticum* LMA 28 has been deposited at EMBL/GenBank under the accession number no. [HE999757](http://www.ncbi.nlm.nih.gov/nuccore/HE999757).

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