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Christophe C. Monnet, Valentin Loux, Pascal P. Bento, Jean-Francois J.-F. Gibrat, Cecile C. Straub, et al.. Genome sequence of *Corynebacterium casei* UCMA 3821, isolated from a smear-ripened cheese. *Journal of Bacteriology*, 2012, 194 (3), pp.738-739. 10.1128/JB.06496-11 . hal-01000221

**HAL Id: hal-01000221**

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Submitted on 28 May 2020

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# Genome Sequence of *Corynebacterium casei* UCMA 3821, Isolated from a Smear-Ripened Cheese

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*Corynebacterium casei* is one of the most prevalent species present on the surfaces of smear-ripened cheeses, where it contributes to the production of the desired organoleptic properties. Here, we report the draft genome sequence of *Corynebacterium casei* UCMA 3821 to provide insights into its physiology.

Smear-ripened cheeses, such as Livarot, Maroilles, Munster, Limburger, and Tilsit, are characterized by a complex surface microflora, composed of various species of yeasts and bacteria. These microorganisms have a strong effect on the flavor, texture, and appearance of the cheeses. Their rapid growth also reduces the risk of contamination with spoilage microorganisms and pathogens, such as *Listeria monocytogenes*. In many cases, the dominant bacteria of smear-ripened cheeses, whose concentration may exceed  $10^{10}$  cells per  $\text{cm}^2$  of the cheese surface area, belong to the genera *Corynebacterium*, *Arthrobacter*, *Brevibacterium*, *Staphylococcus*, and *Micrococcus* (1, 2, 5, 7, 8, 15, 17, 20). *Corynebacterium casei* (4) is one of the typical species from the surfaces of smear-ripened cheeses (5, 15, 18, 20, 22), and it is sometimes used as a component of ripening cultures (3, 10, 19).

The genome sequence of *Corynebacterium casei* UCMA 3821, isolated in 2002 from a French smear-ripened cheese, was determined by Roche/454 pyrosequencing and assembled with CABOG 6.1 software (9), which generated 106 contigs larger than 1,000 bases, with an average sequencing coverage of 24-fold. Genome annotation was performed with AGMIAL (6), an integrated bacterial genome annotation system. Prediction of coding sequences used the self-training gene detection software SHOW based on hidden Markov models (<http://genome.jouy.inra.fr/ssb/SHOW/>). tRNA and rRNA were detected using tRNAscan-SE (13) and RNAmmer (12) software, respectively. Web-based software and databases were used to manually curate predicted genes after comparing data to those in public databases (COGs [21], Conserved Domains Database [14], and InterPro [11]). The unclosed draft genome is 3,112,736 bp in length, has a G+C content of 55.3%, and is composed of 2,700 predicted coding sequences (CDSs). Biological functions could be defined for 1,653 (61.2%) of the predicted proteins.

One of the most significant features of *Corynebacterium casei* UCMA 3821, like *Arthrobacter arilaitensis* Re117, another bacterium isolated from the surface of a smear-ripened cheese (16), is the presence of a large number of genes assigned to  $\text{Fe}^{3+}$ /siderophore transport components (33 CDSs, including 13 substrate-binding components). Furthermore, the *C. casei* genome encodes eight putative proteins required for iron release from the  $\text{Fe}^{3+}$ /siderophore complexes. The availability of the genome sequence of *C. casei* UCMA 3821 will allow deeper comparative genomic studies for the analysis of genetic determinants involved in the ability of bacteria to grow at the surface of cheeses and provide

data for investigating the generation of functional properties, such as aroma compound production.

**Nucleotide sequence accession numbers.** The genome sequence and annotation of *Corynebacterium casei* UCMA 3821 have been deposited in the EMBL database under accession numbers [CAFW01000001](http://www.ebi.ac.uk/EMBL/seqdata/accession/CAFW01000001) to [CAFW01000106](http://www.ebi.ac.uk/EMBL/seqdata/accession/CAFW01000106).

## ACKNOWLEDGMENTS

This work was supported by the ExEco (a joint meta-transcriptomic and biochemical approach of the cheese ecosystem: for an improved monitoring of the EXpression of a complex food ECOSystem) program (ANR-09-ALIA-012-01) funded by the French National Research Agency (ANR). C.S. is grateful to the ANR for a postdoctoral fellowship.

We are grateful to N. Desmasures for the gift of strain UCMA 3821 and to the INRA MIGALE bioinformatics platform (<http://migale.jouy.inra.fr>) for providing computational resources.

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Received 10 November 2011 Accepted 11 November 2011

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doi:10.1128/JB.06496-11

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