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Draft Genome Sequence of *Corynebacterium variabile* Mu292, Isolated from Munster, a French Smear-Ripened Cheese

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Here, we report the draft genome sequence of *Corynebacterium variabile* Mu292, which was originally isolated from the surface of Munster, a French smear-ripened cheese. This genome investigation will improve our knowledge on the molecular determinants potentially involved in the adaptation of this strain during the Munster-type cheese manufacturing process.

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Smear-ripened cheeses harbor complex microbial consortia that are mainly responsible for the production of typical sensory properties (1). Their activities are influenced by the technological processes and manufacturing environment. *Corynebacterium* species are commonly involved in the cheese-ripening process (2–4) and contribute to the flavor and texture of the final product. Three sequenced genomes are currently available for cheese isolates belonging to the *Corynebacterium* genus. Two are affiliated with *Corynebacterium casei* and were isolated from a French (5) and an Irish smear-ripened cheese (6), respectively. The third one is affiliated with *Corynebacterium variabile* and was isolated from Gubbeen (7).

We report here the genome sequence of *Corynebacterium variabile* Mu292, isolated in 1989 from Munster, a soft smear-ripened cheese. Sequencing was performed using Illumina MiSeq technology. After filtering, a total of 1,169,642 paired-ends reads of 250 bp in length were generated and merged using FLASH (8). *De novo* assembly was performed using SPAdes (version 3.1.1, with default parameters) (9), which generated 66 large contigs (≥1,000 bp), with an average sequencing coverage of 100-fold. The unclosed draft genome is 3,185,550 bp in length and has a G+C content of 67.3%. Gene prediction and annotation were performed using the IMG system, as described previously (10). This genome encompasses 3,007 genes, including 2,942 coding DNA sequences, 7 rRNAs, and 58 tRNAs.

Comparative analysis of the genome of *C. variabile* Mu292 with the genome of *C. variabile* strain DSM 44702, isolated from Gubbeen cheese (7), will provide valuable insights into the adaptation of *C. variabile* strains to different cheese technologies. Indeed, Gubbeen and Munster cheeses are differentiated by their technological characters, such as pH of the curd and NaCl and dry-matter contents (11, 12). Interestingly, the presence of a type I restriction-modification system in the genome of *C. variabile* Mu292 might explain why it is devoid of the phage-related chromosomal island of *C. variabile* DSM 44702 (7, 13).

Another feature in the genome of *C. variabile* Mu292 is the presence of a gene coding for a putative arylsulfatase (EC 3.1.6.1), sharing 82% sequence identity (protein level) with the sequence of *Corynebacterium terpenotabidum* Y-11^T (NCBI accession no. WP_020440046), a bacterium isolated from soil and which is phylogenetically close to *C. variabile* (14, 15). This enzyme has been previously described in various soil bacteria and is considered as a key enzyme in sulfur metabolism (16, 17). In the cheese habitat, arylsulfatase may be involved in the release of molecules conjugated with sulfate, such as alkylphenols, which contribute to sheep-like flavors of the cheeses manufactured from sheep's milk (18). Thus, this specificity found in the genome of *C. variabile* Mu292 might be of interest for understanding sulfur metabolism in cheese, which is of great importance for the cheese-making process (19).

This second genome sequence of *Corynebacterium variabile* will allow deeper comparative genomic studies among *Corynebacterium* species and other *Actinobacteria*, provides new elements for understanding the adaptation strategies of cheese bacteria to the cheese habitat, and potentially aids in discovering novel technological properties for the food industry.

Nucleotide sequence accession numbers. The draft genome sequences of *Corynebacterium variabile* Mu292 have been deposited at the EMBL database under accession numbers FAUH01000001 to FAUH01000066.

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