Draft Genome Sequences of *Clostridium tyrobutyricum* Strains FAM22552 and FAM22553, Isolated from Swiss Semihard Red-Smear Cheese

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*Clostridium tyrobutyricum* is the main microorganism responsible for late blowing defect in cheeses. Here, we present the draft genome sequences of two *C. tyrobutyricum* strains isolated from a Swiss semihard red-smear cheese. The two draft genomes comprise 3.05 and 3.08 Mbp and contain 3,030 and 3,089 putative coding sequences, respectively.

Assembled genomes were annotated using the RAST server (10). In total, 3,030 putative coding sequences were annotated for FAM22552 and 3,089 for FAM22553. *C. tyrobutyricum* grows in cheese using lactate and acetate as carbon and energy sources (11). A preliminary analysis of the two annotated genomes revealed the presence of putative genes coding for many enzymes needed to convert these two compounds into butyric acid, carbon dioxide, and molecular hydrogen. These include l- and d-lactate dehydrogenases, pyruvate-ferredoxin oxidoreductases, thiolas, hydroxybutyryl-CoA dehydrogenases, crotonases, hydroxybutyryl-CoA dehydrogenases, phosphotransacetylases, and acetate kinases (for a review, see reference 12). Studies are now under way to further clarify the metabolism of *C. tyrobutyricum* in cheese.

Nucleotide sequence accession numbers. The whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers JTER00000000 (for *C. tyrobutyricum* FAM22552) and JTES00000000 (for *C. tyrobutyricum* FAM22553). The versions described in this paper are the versions JTER01000000 and JTES01000000.

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