Butyric clostridia are spore-forming anaerobic bacteria affecting the dairy industry by causing late-blowing defect, a particular kind of food spoilage in hard and semihard cheeses, such as Grana Padano, Parmigiano Reggiano, Emmental, and Gouda (1–6). Among them, _Clostridium tyrobutyricum_ is considered the main organism that is responsible for this problem (3, 4). Its spores, which contaminate milk and are resistant to whole-cheese manufacturing, germinate during ripening, and the butyric fermentation of the vegetative cells causes the production of butyric acid, acetic acid, hydrogen, and CO₂, bursting of cheese paste, and fermentation of the vegetative cells causes the production of butyric acid, acetic acid, hydrogen, and CO₂, resulting in undesirable taste. Recently, _C. tyrobutyricum_ obtained great attention for biofuel, acetic acid, and butanol production (7, 8). A deeper investigation of its metabolic pathways and adaptation mechanisms can help to understand its negative and positive effects in food production and industrial applications.

In this work, a *de novo* shotgun sequencing of _C. tyrobutyricum_ strain UC7086, isolated from Grana Padano cheese with blowing defect, and of _C. tyrobutyricum_ DSM 2637 type strain has been performed. The genomes were sequenced using an Illumina HiSeq 1000 platform from the Functional Genomics Centre, Scientific and Technological Department of the University of Verona. Quality-filtered reads were assembled using the Velvet software (version 1.1.04) (9), and contig sequences were annotated in the RAST server (10). A 3,064,215-bp assembly was obtained for _C. tyrobutyricum_ UC7086, consisting of a total of 110 contigs and with a mean G+C content of 31%. The type strain _C. tyrobutyricum_ DSM 2637 has 3,007,342 bases and was assembled in 175 contigs with a mean G+C content of 30.6%. The annotated contigs contain 3,038 putative coding sequences (CDSs) and 51 predicted RNAs for _C. tyrobutyricum_ UC7086 and 3,066 CDSs and 41 predicted RNAs for _C. tyrobutyricum_ DSM 2637. Loaded in the RAST server, the reported genomes of UC7086 and DSM 2637 contain 350 and 365 subsystems, respectively, which constitute the basis for creating the _C. tyrobutyricum_ metabolic network.

A comparative genome analysis between both _C. tyrobutyricum_ deep-sequenced genomes revealed an overall high protein sequence identity. A total of 29 protein-coding genes were unique in _C. tyrobutyricum_ UC7086 and 35 in DSM 2637. Strain UC7086 has genes for proteins that are involved in amino acid metabolism, which reveal a possible adaptation to the cheese environment during ripening (lysine and proline uptake and degradation and arginine and ornithine degradation), DNA metabolism (CRISPR-associated proteins and restriction-modification systems), and carbohydrate metabolism (mannose and xylose utilization), phage packaging machinery, replication and introns (helicase, terminase), spore germination (gerKB), and motility (filH).

Further analyses are in progress to better understand the annotated genome sequence data, as well as the gap closure to complete the present draft genome. This information will be useful to compare the genomes of different _C. tyrobutyricum_ strains to one another and to those of other _Clostridium_ species.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ANOE00000000 for _C. tyrobutyricum_ UC7086 and ARYO00000000 for _C. tyrobutyricum_ DSM 2637. The versions described in this paper are the first versions, with accession no. ANOE01000000 and ARYO01000000.

**ACKNOWLEDGMENTS**

The research was supported by grants from the Consorzio per la Tutela del Formaggio Grana Padano, Italy, the Ministero delle Politiche Agricole, Alimentari e Forestali (MIPAAF) national project “Filigrana” DM 25741/7303/11, and Regione Lombardia founding scheme “GENOBACT” project G4110000400002.

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Machine translation from Italian to English.