Closed Genome Sequence of *Clostridium pasteurianum* ATCC 6013

Carlo Rotta,a,c Anja Poehlein,b Katrin Schwarz,a Peter McClure,c Rolf Daniel,b Nigel P. Mintona

The Clostridia Research Group, BBSRC/EPSCF Synthetic Biology Research Centre, School of Life Sciences, Centre for Biomolecular Sciences, University of Nottingham, Nottingham, United Kingdom; Genomic and Applied Microbiology & Göttingen Genomics Laboratory, Georg-August-University Göttingen, Göttingen, Germany; Unilever, Research and Development, Bedford, United Kingdom

We report here the closed genome of *Clostridium pasteurianum* ATCC 6013, a saccharolytic, nitrogen-fixing, and spore-forming Gram-positive obligate anaerobe. The organism is of biotechnological interest due to the production of solvents (butanol and 1,3-propanediol) but can be associated with food spoilage. The genome comprises a total of 4,351,223 bp.

The genome harbors 10 rRNA operons, 81 tRNA genes, 3,220 predicted protein-encoding genes with function prediction, and 768 putative genes coding for hypothetical proteins. Present are eight GerK spore germination receptors, with 3 orphan gerK genes and a gerKA-gerKC and a gerKA-gerKC-gerKB cluster, and two copies of a spore cortex-lytic SleB enzyme (18). The Spo0A master regulator of sporulation is atypical. It carries a lysine residue at position 255 as opposed to the glutamine present in other clostridial Spo0A proteins (19), including that of *C. pasteurianum* DSM525. Strain ATCC 6013 produces higher spore titers than DSM 525 (20).

**Nucleotide sequence accession number.** The genome sequence has been deposited in GenBank under the accession number CP009267.

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