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Complete Genome Sequence of *Brevibacterium linens* SMQ-1335

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***Brevibacterium linens* is one of the main bacteria found in the smear of surface-ripened cheeses. The genome of the industrial strain SMQ-1335 was sequenced using PacBio. It has 4,209,935 bp, a 62.6% G+C content, 3,848 open reading frames, and 61 structural RNAs. A new type I restriction-modification system was identified.**

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Brevibacterium linens is a Gram-positive bacterium found on the surface of a variety of washed rind cheeses produced globally (1–3). This non-spore-forming, halotolerant, strictly aerobic chemoorganotroph undergoes a rod-cocci cycle during growth and possesses mesodiaminopimelic acid in its cell wall (1, 2, 4). *B. linens* plays key roles during cheese ripening in the breakdown of lipids and proteins (2), the production of volatile sulfur compounds (5, 6), and the development of color due to carotenoid pigment production (1, 2, 4, 7). Furthermore, the production and accumulation of compatible solutes allows *B. linens* to grow in hyperosmotic environments (4). The genomes of three *B. linens* strains are currently available, of which one is complete (GCA_001606005.1) and two are scaffold and draft sequences (GCA_000167575.1 and GCA_000807915.1, respectively).

The genome of *B. linens* SMQ-1335 was sequenced using one SMRT cell in a PacBio RSII sequencer (Génome Québec Innovation Centre, Montréal, QC, Canada), which generated 76,075 raw subreads of an average length of 9,010 bp that provided an average coverage of 162-fold. The genome was assembled into one contig using HGAP (8). BLASR (9) was used to align and preassemble the sequences using the longest reads as seeds to which all the other subreads were recruited and mapped to correct random errors. The Celera assembler (10) was then used to *de novo* assemble these long and corrected reads into contigs. The sequences were refined using Quiver, wherein the raw reads were aligned on the contigs to generate a consensus sequence containing the complete genome. The single contig had redundant ends of 16,018 bp that were removed from one end for the final assembly. The origin of the genome was set upstream of the gene coding for the replication initiator protein DnaA. Gene prediction and annotation was performed using RAST (11) and BLASTp (12). The *B. linens* SMQ-1335 genome has a high G+C content (62.6%) and is composed of 4,209,935 bp, 3,848 genes, and 61 structural RNAs (49 tRNAs and 12 rRNAs).

In vitro tests revealed that *B. linens* SMQ-1335 is sensitive to vancomycin, daptomycin, gentamicin, tetracycline, and rifampin. However, this strain was insensitive to β-lactam antibiotics (penicillin and ceftriaxone), trimethoprim-sulfamethoxazole (TMP-SMX), and a second-generation fluoroquinolone (ciprofloxacin). A gene likely coding for the lantibiotic linocin was identified using BAGEL3 (13).

No genes coding for known toxins were found in the genome of SMQ-1335 using Virulence Finder (14), Virulence Factor Database (15), and DBETH (16). RAST and PHASTER (17) identified a putative prophage (31,300 bp). Analysis of this prophage sequence revealed many transposases and integrases, suggesting that this may be a nonfunctional prophage.

The methylome (18) of *B. linens* SMQ-1335 was analyzed to identify DNA methyltransferases and restriction endonucleases (19) as well as specificity subunits (20). The new methyltransferase M.Bli1335I, the restriction endonuclease Bli1335IP, and a new type I RM system were assigned, with the recognition site sequence CGGANNNNNTTC. The SMQ-1335 genome may contain additional RM systems (types II, III, and IV). For the type II, a new restriction endonuclease (Bli1335II) was also assigned with DTGAAT as the recognition sequence.

Accession number(s). The complete genome sequence of *B. linens* SMQ-1335 is available in GenBank under the accession number CP017150.

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