PROKARYOTES

Complete Genome Sequences of Two Strains of the Meat Spoilage Bacterium *Brochothrix thermosphacta* Isolated from Ground Chicken

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ABSTRACT *Brochothrix thermosphacta* is an important meat spoilage bacterium. Here we report the genome sequences of two strains of *B. thermosphacta* isolated from ground chicken. The genome sequences were determined using long-read PacBio single-molecule real-time (SMRT) technology and are the first complete genome sequences reported for *B. thermosphacta*.

Brochothrix thermosphacta, a Gram-positive psychrotrophic bacterium associated with the nonproteolytic spoilage of meat, poultry, and seafood, contributes to spoilage in aerobically packed products and is a dominant microorganism in modified atmosphere- and vacuum-packaged products (1, 2). Despite the significant economic impact of microbial contributors to meat spoilage, detailed understanding of these organisms is lacking. Draft genomes of a few *B. thermosphacta* strains have been published recently (3), but no complete genome is currently available. Here, we report the complete genome sequences of two strains of *B. thermosphacta*.

B. thermosphacta was the bacterial species most frequently isolated from ground chicken samples in our previous study on the nonspecific binding of food-associated microbial flora to immunomagnetic microspheres (4). Two distinct morphotypes were described based on their growth in 96-well microtiter plates; cells of strain BI settled toward the bottom of the wells as an amorphous cellular mass, while strain BII grew as a suspension of large globular aggregates (4, 5).

In conjunction with studies of the unusual growth phenotype exhibited by strain BII, the complete genome sequences of both strains BI and BII were determined. Long fragments of genomic DNA (gDNA) were prepared by using the procedure of Neumann et al. (6) and further purified using the Genomic-tip 500/G (Qiagen). Single-molecule real-time (SMRT) sequencing and *de novo* genome assembly were done at the University of Delaware Sequencing and Genotyping Center using the PacBio RS II SMRT DNA sequencing system (Pacific Biosciences, Menlo Park, CA) and HGAP Assembly.3 software, respectively.

Assembly of the *B. thermospacta* BI and BII genomes resulted in single contigs of 2,647,794 bp (36.4% GC content) and 2,603,084 bp (36.5% GC content), respectively. Sequence coverages were 109× and 108× for strains BI and BII, respectively. The *B. thermosphacta* BI and BII genomes shared high degrees of sequence similarity to each other (OrthoANI [7] value, 99.96%) and to the reference strain DSM 20171 (99.16% and 99.15%, respectively). An automated annotation using Rapid Annotations using Subsystems Technology (RAST) (8) revealed 2,424 protein-coding sequences (CDSs) and

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86 tRNAs in the BI genome and 2,365 CDSs and 85 tRNAs in the BII genome. In addition, both genomes contained 9 copies of the 16S rRNA genes.

Comparative analysis of the two genomes using Mauve (9) and results of analysis for prophage regions using PHAST (10) revealed that the difference in genome sizes (44.7 kb) is primarily due to the presence of mobile genetic elements. Strain BI contains two prophage insertions (33.9 kb and 47.9 kb) that are absent in strain BII, while strain BII carries 10 additional loci encoding intact or partial transposases, as well as a degenerate prophage region (16.4 kb) not present in strain BI. Neither of the two prophages in the BI genome was present in the previously reported *B. thermosphacta* draft genomes (3), nor were these prophages previously described by Kilcher et al. (11) in a study of *Brochothrix* phage genomes.

The complete genome sequences of *B. thermosphacta* strains BI and BII will provide a foundation for a better understanding of the contribution of this species to meat spoilage and serve as reference sequences on studies of the unique growth properties observed in strain BII.

Accession number(s). The genome sequences for *Brochothrix thermosphacta* strains BI and BII were deposited in DDBJ/ENA/GenBank under the accession numbers CP023483 and CP023643, respectively.

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