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GENOME ANNOUNCEMENT

Insights from the Genome Sequence of Quorum-Quenching *Staphylococcus* sp. Strain AL1, Isolated from Traditional Chinese Soy Sauce Brine Fermentation

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We report the draft genome sequence of *Staphylococcus* sp. strain AL1, which degrades quorum-sensing molecules (namely, *N*-acyl homoserine lactones). To the best of our knowledge, this is the first documentation that reports the whole genome sequence and quorum-quenching activity of *Staphylococcus* sp. strain AL1.

Quorum sensing (QS) describes the event of bacterial cell-to-cell communication through production, secretion, and, eventually, binding of the QS signaling molecules to the cognate receptor protein, resulting in mediation of gene expression in response to bacterial cell density (5). Of these QS molecules, *N*-acyl homoserine lactones (AHL) are widely used by many proteobacteria to regulate diverse behaviors, including bioluminescence, antibiotic production, and virulence determinants (4). Quorum-quenching enzymes efficiently degrade QS molecules (1), rendering them not usable for cell-to-cell communication purposes (3, 6, 9). Recently, a quorum-quenching bacterium has been isolated from Chinese soy sauce brine fermentation (11). In our continuous effort to search for enzymes capable of degrading AHL molecules, we have isolated *Staphylococcus* sp. strain AL1, which showed efficient and broad AHL degradation activity from traditional Chinese soy sauce brine fermentation.

The genome sequence of *Staphylococcus* sp. strain AL1 was generated using Illumina Hiseq 2000 and the DNA library was prepared using a TruSeq DNA sample preparation kit (Illumina, Inc., CA). Quality trimming of the raw sequence data followed by assembly was performed using CLC Genomic Workbench version 5.1. During quality trimming, sequence reads with low quality (<Q20), ambiguous nucleotides, and sequence length less than 50 nucleotides were discarded prior to assembly. A total of 4,151,586 paired-end reads amounting to 393,565,942 bases, with an average read length of 92.7 bp, were subjected to assembly. The assembly size of the draft genome was 2,625,406 bases, with an average G+C content of 32.4% and an average sequencing depth of 149.2-fold. The assembly has yielded 94 contigs (>500 bp), with an average contig size of 28.129 kb and the largest contig size at 195.176 kb. Gene prediction was performed using Prodigal (version 2.60) (7), resulting in 2,583 open reading frames being predicted. Subsequently, 1 complete rRNA operon, 1 5S rRNA gene, and 53 tRNA genes were predicted using RNAmmer (8) and tRNAscan-SE (10). Functional annotation of the predicted genes was performed by Blast2GO (2), allowing acquisition of Gene Ontology (GO), Enzyme Code annotation with KEGG maps, and InterPro annotation.

A gene believed to encode AHL lactonase was found by using BLASTX against the quorum-quenching lactonase database acquired from UniProtKB Protein Knowledgebase. AHL lactonases catalyze the hydrolysis of the lactone ring of AHL, resulting in ring opening of the compound (3). Comparative analysis revealed relatively low sequence homology of this putative lactonase gene with other reported AHL lactonase genes, but the sequences of this gene contain a conserved HXHXDH region identical to the zinc binding motif which is also present in these reported AHL lactonases (3). Therefore, acquisition of the gene sequence will allow further characterization of the lactonase enzyme, such as kinetic and substrate specificity.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALOZ00000000. The version described in this paper is the first version, ALOZ01000000.

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