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Complete genome sequence of *Alkalitalea saponilacus*, an anaerobic haloalkaliphilic bacterium capable of secreting halostable xylanase

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The anaerobic haloalkaliphile *Alkalitalea saponilacus* SC/BZ-SP2T could utilize xylan as sole carbon source and produce propionate as the main fermentation product. The xylanase activity from A. using the combined substrates of 0.4% (w/v) sucrose + 0.1% (w/v) birch xylan was 3.2-fold than that of 0.5% (w/v) sucrose or 0.5% (w/v) birch xylan. The xylanse is halo-stable as it exhibited optimal activity at a broad range of 2-6% NaCl. Its activity was inhibited by Cu^{2+}, Fe^{3+}, Ni^{2+}, Al^{3+}, Mn^{2+}, Co^{2+}, Zn^{2+} and Ca^{2+} while increased 1.16-fold with the addition of Tween 20. In order to get a deep understanding of the potential genetic mechanisms of xylanase secretion and adaptive saline-alkali tolerance, the complete genome sequence of strain SC/BZ-SP2T was performed with the Pacbio SMRT and Illumina Misseq platforms. The genome contained one chromosome, with the total size of 4,775,573 bps, and the G+C content of this strain was 39.27%. A number of genes related to xylan degradation and its complete xylan degradation pathway, xyn A gene of xylanase belonging to a glycoside hydrolase (GH) family 10 and its neighborhood genes were systematically identified. Furthermore, various genes involved in biosynthesis and transportation of osmolytes, as well as genes encoding monovalent cation/proton antiporters, multi-subunit sodium/proton antiporters, F0F1-ATP synthases, H^+-transporting ATPases, Na^+/solute symporters and K^+ transport systems were predicted. This genome sequence provides molecular information and elucidation for halo-stable xylanase production, and will be used in the biotechnology.

Biography

The focus of Baisuo Zhao research is bacterial taxonomy and microbial physiology, Molecular mechanisms of gene expression and mutagenesis. He is also interested in studies of molecular microbial ecology including the genetic and the functional diversity of microbial communities. His third research interest on Microbial Genomics & Metagenomics involves in genome analysis of pure isolates and metagenomics from extreme conditions, reactors etc.

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