Insights into xylan degradation and haloalkaline adaptation through whole-genome analysis of *Alkalitalea saponilacus*, an anaerobic haloalkaliphilic bacterium capable of secreting novel halostable xylanase

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The obligately anaerobic haloalkaliphilic bacterium *Alkalitalea saponilacus* can use xylan as the sole carbon source and produce propionate as the main fermentation product. Using mixed carbon sources of 0.4% (w/v) sucrose and 0.1% (w/v) birch xylan, xylanase production from *A. saponilacus* was 3.2-fold greater than that of individual carbon sources of 0.5% (w/v) sucrose or 0.5% (w/v) birch xylan. The xylanase is halostable and exhibits optimal activity over a broad salt concentration (2–6% NaCl). Its activity increased approximately 1.16-fold by adding 0.2% (v/v) Tween 20. To understand the potential genetic mechanisms of xylan degradation and molecular adaptation to saline-alkali extremes, the complete genome sequence of *A. saponilacus* was performed with the pacBio single-molecule real-time (SMRT) and Illumina Misseq platforms. The genome contained one chromosome with a total size of 4,775,573 bps, and a G+C genomic content of 39.27%. Ten genes relating to the pathway for complete xylan degradation were systematically identified. Furthermore, various genes were predicted to be involved in isosmotic cytoplasm via the “compatible-solutes strategy” and cytoplasmic pH homeostasis though the “influx of hydrogen ions”. The halostable xylanase from *A. saponilacus* and its genomic sequence information provide some insight for potential applications in industry under double extreme conditions.

Biography

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