14th International Conference on **Microbial Interactions & Microbial Ecology**
&
11th Edition of International Conference on **Advances in Microbiology and Public Health**
August 19-20, 2019 Vienna, Austria

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 xylanse 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. saponilacusand its genomic sequence information provide some insight for potential applications in industry under double extreme conditions.

Biography

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