

A proteomic analysis of the hyperthermophilic archaeon *Thermoplasma acidophilum* grown under a rich medium culture condition

Sang-Eun Kim, Soowon Park, Hong Ju Lee and Sun Bok Lee

Department of Chemical Engineering and Division of Molecular Life and Sciences,
Pohang University Science and Technology, San 31, Hyoja Dong, Pohang 790-784, Korea
Tel: +82-54-279-5970, Fax: +82-54-279-5528

Abstract

Thermoplasma acidophilum is a thermoacidophilic archaeon that thrives at 59 °C and pH 2, which was isolated from self-heating coal refuse piles and solfatara fields.¹⁾ Species of the genus *Thermoplasma* do not possess a rigid cell wall, but are only delimited by a plasma membrane. The genome of *T. acidophilum* contains 1,564,906bp on a single chromosome and encodes 252 open reading frames, including a complete protein degradation pathway and various transport proteins.²⁾ However, how many of these proteins are expressed under certain conditions cannot be predicted alone from the genome sequence. Therefore, in this study, whole-cell proteins in cellular extracts of *T. acidophilum* were analyzed by two-dimensional gel electrophoresis method using immobilized pH gradient technology. Cells were grown under optimal culture conditions in the YE medium as reported previously.¹⁾ More than 160 spots were visualized by staining the gel with Colloidal Coomassie Blue G250. Among these proteins, 100 spots were analyzed by MALDI-TOF MS and the generated data were searched against the NCBI database using the ProFound tool, leading to the positive identification of 72 spots corresponding to 25 different proteins. Proteins were identified by matrix-assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry in combination with ProFound search engine. In total, 72 spots were able to be identified. Interestingly, nine of the identified proteins were present in the 2-DE map in more than one spot. This suggests that these proteins may suffer post-translational modifications but no further work was undertaken to characterize the anticipated modifications. The complete list of identified protein is presented in the supplementary material

References

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