KSBB, *Proceeding of Current Biotechnology and Bioengineering*(XVII) : October, 2005

Proteomic analysis of the hyperthermophilic archaeon *Thermoplasma acidophilum* grown under normal conditions

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Abstract

Thermoplasma acidophilum is a thermoacidophilic archaeon that thrives at 59 °C and pH 2. *Thermoplasma acidophilum* does 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 1509 open reading frames, including a complete protein degradation pathway and various transport proteins. 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. More than 200 spots were visualized by staining the 2-DE gel with Colloidal Coomassie Blue G250. Among these proteins, 141 spots were analyzed by MALDI-TOF MS and the generated data were searched against the NCBInr database using Mascot tools. This leads to the identification of 103 spots corresponding to 66 different proteins. Interestingly, 36 of the identified proteins have been detected at more than one position on the 2D gels. This suggests that these archaeal proteins are subject to regulation by post-translational modifications.

References

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