S8-4

Comparison of Genome Structure and Global Gene Expression Profiles Between *Zymomonas mobilis* Type Strain ZM1 and Highly Ethanologenic ZM4 Strain

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Global expression profiles of *Z. moblilis* were analyzed with the DNA microarray containing all predicted *Z. moblilis* ZM4 ORF during the cell growth. At the early stage of growth, especially starting point of exponential growth stage, ribosomal proteins and translation elongation factors were highly expressed. On the contrary, at the late stage of growth, ATP synthetase, alcohol dehydrogenase and heat shock proteins were actively expressed. These results imply that ethanol production, ATP synthesis and cell growth were tightly related to each other. The higher expression of heat shock proteins was due to the accumulation of ethanol of which concentration was more than 40g/L.

Z. mobilis ZM4 (ATCC31821) shows almost two fold higher specific ethanol production rate and glucose uptake rate than *Z. mobilis* type strain ZM1 (ATCC10988). We found that *Z. mobilis* ZM4 strain has more 54 open reading frames by co-hybridizing labeled *Z. mobilis* ZM4 and ZM1 DNA to microarray. Among the 54 ORFs, we found four kinds of membrane transport proteins, and four proteins involved in type IV secretory system, alcohol related dehydrogenase and several transcriptional regulators. These ORFs might be responsible for the higher specific ethanol production rate and glucose uptake rate of ZM4 strain than those of *Z. mobilis* ZM1 type strain. The overall patterns of global expression profiles of *Z. mobilis* ZM1 and ZM4 were very similar except for the fact that many of additional 54 ORFs in *Z. mobilis* ZM4 strain were actively transcripted.