

**S5-1**

## Characterization and Analysis of the Genome Sequence of the Ethanologenic Bacterium *Zymomonas mobilis* ZM4

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A physical map of the *Zymomonas mobilis* ZM4 genome has been constructed from the results of reciprocal Southern hybridization with *Pme*I, *Pac*I, and *Not*I-digested genomic DNA fragments

*Zymomonas mobilis* ZM4 contains three ribosomal transcription units (*rrnA* to C operons) which are clustered around the 50 min region on the physical map of *Zymomonas mobilis* ZM4.

The phylogenetic tree, based on the 16S rRNA sequence, was constructed by neighbor-joining and maximum-parsimony methods.

We report the complete genome sequence of *Zymomonas mobilis* ZM4 (ATCC31821), an ethanologenic microorganism of interest for the production of fuel ethanol. The genome consists of 2,056,416 base pairs forming a circular chromosome with 1,998 open reading frames (ORFs) and three ribosomal RNA transcription units. The genome lacks recognizable genes for 6-phosphofructokinase, an essential enzyme in the Embden-Meyerhof-Parnas pathway, and for two enzymes in the tricarboxylic acid cycle, the 2-oxoglutarate dehydrogenase complex and malate dehydrogenase, so glucose can be metabolized only by the Entner-Doudoroff pathway. Whole genome microarrays were used for genomic comparisons with the *Z. mobilis* type strain ZM1 (ATVCC10988) revealing that 54 ORFs predicted to encode for transport and secretory proteins, transcriptional regulators and oxidoreductase in the ZM3 strain were absent from ZM1. Most of these ORFs were also found to be actively transcribed in association with ethanol production by ZM4.