

Zymomonas mobilis:
**A Merging Block-Buster for the Production of Value-Added
Primary Metabolites from Renewable Resources**

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Abstract

The strains of *Zymomonas mobilis* have been isolated from samples of tropical countries and studied on the unique energetic metabolism of carbohydrates, the Enter-Doudoroff Pathway. From the late of 1970s, the bacterium has been focused as an promising microorganism to produce fuel ethanol, of which advantages over the conventional used yeasts due to the higher rates of substrate uptake and ethanol production. Further researches have been carried out to construct super strains to utilizing extended ranges of substrates and to be tolerant to higher concentration of ethanol. The full genome of *Z. mobilis* ZM was completely sequenced and some of them were clearly annotated molecular constructions of strains producing useful metabolites are being progressed with utilizing the genomic data. The backgrounds, achievements, and current dynamic researches with new paradigms in R&D using strains of *Z. mobilis* are reviewed.

From the kinetic studies and designing bioprocesses, it was clear that *Z. mobilis* offered an attractive alternative as a suitable microorganism for higher productivity ethanol fermentations. These include: (1) higher ethanol and lower biomass yield on glucose and fructose, but not sucrose, (2) higher specific rates of glucose uptake and ethanol production at relatively high concentration of ethanol, (3) higher specific growth rate at relatively high concentration of glucose and ethanol, (4) ability to grow anaerobically and not to require the controlled addition of oxygen for maintaining viability, (5) the potential for genetic manipulation of strains of *Z. mobilis* to extend the substrate range and to overcome some drawbacks.

Since the genetic knowledge and tool on this organism have not been well advanced, it is not so efficient in the construction of strains for overcoming the draw backs. It is thought that *Z. mobilis* would be applied immediately without any lag period or hesitation for commercial production of ethanol. In this sense, The entire sequence of the *Z. mobilis* ZM4 (ATCC31821) genome was determined (Seo *et*

al., 2005).

It consists of 2,056,416 base pairs with an average G+C content of 46.33% forming a circular chromosome with 1,998 predicted genes (open reading frames, ORFs) and three ribosomal RNA transcription units (supplementary information at www.macrogen.com /zymomonas; GenBank accession no. AE008692). The 1,998 predicted coding ORFs cover 87% of the genome, and each ORF has an average length of 898 bp. Among these, 1,346 (67.4%) could be assigned as putative functions, 258 (12.9%) were matched to conserved hypothetical coding sequences of unknown function, and the remaining 394 (19.7%) showed no similarities to known genes in other organisms.

The results presented in this paper provide a platform for the molecular construction of strains with enhanced industrial potential not only by enhancing the production rate using hexose substrates but also by introducing genes allowing the use of other renewable carbohydrates or cellulosic resources as the carbon source. Further studies may allow us to elucidate metabolism-wide control mechanisms explaining alcohol sensitivity and tolerance of *Z. mobilis* ZM4 and to construct strains producing various value-added primary metabolites beyond ethanol itself.