

Reconstruction of a Genome-Scale Metabolic Model to Simulate Uncoupled Growth of *Zymomonas mobilis*

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Abstract : *Zymomonas mobilis* is known as an example of the uncoupled growth phenomenon. This microorganism also has a unique metabolism that degrades glucose by the Entner–Doudoroff (ED) pathway. In this paper, a genome-scale metabolic model including 434 genes, 757 reactions and 691 metabolites was reconstructed to simulate uncoupled growth and study its effect on flux distribution in the central metabolism. The model properly predicted that ATPase was activated in experimental growth yields of *Z. mobilis*. Flux distribution obtained from model indicates that the major carbon flux passed through ED pathway that resulted in the production of ethanol. Small amounts of carbon source were entered into pentose phosphate pathway and TCA cycle to produce biomass precursors. Predicted flux distribution was in good agreement with experimental data. The model results also indicated that *Z. mobilis* metabolism is able to produce biomass with maximum growth yield of 123.7 g (mol glucose)⁻¹ if ATP synthase is coupled with growth and produces 82 mmol ATP gDCW⁻¹h⁻¹. Coupling the growth and energy reduced ethanol secretion and changed the flux distribution to produce biomass precursors.

Keywords : genome-scale metabolic model, *Zymomonas mobilis*, uncoupled growth, flux distribution, ATP dissipation

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