

Dynamic Metabolic Flux Analysis of *Shewanella oneidensis* MR-1 Central Metabolisms

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Abstract: *Shewanella oneidensis* MR-1 have received significant attention because of their versatile carbon metabolisms and potential to engage in bioremediation of toxic metal compounds and microbial fuel cell applications. In active growth phase using lactate as the carbon source, MR-1 shows a dynamic metabolism. MR-1 produces a significant amount of pyruvate and acetate when the lactate is excess in the medium. When the energy favorable carbon source (lactate) is depleted, MR-1 will utilize the waste product (pyruvate and acetate) for their growth. In response to the switch of carbon sources during the growth, the central metabolism (TCA cycle, glyoxylate shunt and futile pathways) of MR-1 also changes. To describe this dynamic metabolism, we combine the enzyme kinetic modeling with the isotopomer analysis to quantitatively understand the regulation of metabolic network and profile the flux distribution as the function of the time. Using MATLAB based ODE tool box, we can solve the dynamic metabolism and predict the growth/extracellular metabolites production. Meanwhile, we may improve the model predictions using the constraints from the labeling information. The isotopomer information can also provide us the insight into the regulation of central metabolic pathways during MR-1 growth. Such isotopomer assisted dynamic flux model may be potentially used in other biological systems including the biofuel producers or microbial communities.