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Targeted gene deletions in metabolic pathways of the bacterium *Shewanella oneidensis*

The production of substances from biologically catalyzed reactions can be limited by either the amount of material in the feedstock required for respiration or the separation of the biomass produced. The bacterium, *Shewanella oneidensis* can carry out respiration using an external electron acceptor such as an electrode thus removing the need for a soluble oxidizing agent. *S. oneidensis* can also be metabolically directed using genetic techniques. Utilizing these features, *S. oneidensis* can be used for more efficient conversion of glycerol to ethanol than is possible in conventional systems such as *Escherichia coli*. The metabolism can be guided by eliminating pathways nonessential either to the organism or for production of ethanol. The pathways to be eliminated were determined from a model created through a comparison of *E. coli* and *S. oneidensis*. In accordance with the model, the genes *ldhA*, *gnd*, *sucA*, *pckA*, *pykA*, *sfcA*, and *aceA* need to be deleted to maximize flux towards ethanol. During the spring of 2008, I generated and began characterization of the metabolic mutations needed to test the current model. Mutations were generated using a vector and double recombination technique and metabolite production was monitored using growth curves and HPLC analysis. Preliminary growth analysis has shown that metabolite flux can be controlled through targeted gene deletion. This project is a forerunner to work in quantitatively characterizing combinations of these mutations in *S. oneidensis*.



Poster Number: Session: