208d Development of a Mechanistic Model for Sugar-Utilization Regulatory Systems

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Lignocellulosic biomass such as agricultural and wood residues, crops, and byproduct streams provides a low cost and uniquely sustainable resource for producing many fuels and chemicals. The microbial transformation of its constituent sugars (5-and 6-carbon sugars) into commodity chemicals is one of the most important steps in this process. The process requires an organism, such as *E. coli*, that is capable of fermenting sugar mixtures containing 5- and 6-carbon sugars. When *E. coli* is grown on sugar mixtures, the delayed and frequently incomplete consumption of other sugars due to the presence of glucose results in low yields and productivities of the desired product. *E. coli* possesses sophisticated regulatory systems (referred to as sugar-utilization regulatory systems, SURS) that control the utilization of different sugars. SURS regulate the preferential utilization of specific sugars from a sugar mixture, the induction of several genes due to the presence of glucose and the direction of carbon flow.

Our laboratories have been involved in developing a modeling framework to integrate genomic information in the overall metabolic flux analysis scheme. The concept is very powerful as it is one of the very few attempts to render static databases into one that is dynamic. That is, the proposed framework should allow one to capture the cellular behaviors in response to environmental/genetic perturbations. This is in sharp contrast to the traditional FBA analysis that normally starts with predetermined metabolic networks (maps). In this presentation, we will describe our recent efforts in the development of such a model for the sugar-utilization regulatory systems. Our preliminary model considers the elements such as glucose uptake through PTS, glucose metabolism through glycolysis, and the regulatory molecules that play a significant role in altering xylose utilization.