

Reconstruction of sugar utilization pathways and regulons in the *Clostridium* genus

Chen Yang¹, Lei Zhang¹, Xiaoqun Nie¹ and Dmitry A. Rodionov²

¹Key Laboratory of Synthetic Biology, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, China

²Burnham Institute for Medical Research, Chinese Academy of Sciences, China

The Clostridia are a diverse group of Gram-positive bacteria that include several pathogens and many terrestrial species that produce solvents and organic acids through fermentation of a variety of carbon sources. However, the knowledge about carbohydrate utilization pathways and their regulation in *Clostridium* spp. is rather limited. Accurate projection of known carbohydrate catabolic pathways across diverse bacteria with complete genomes is quite challenging due to frequent variations in components of these pathways.

In this study we combine comparative genomics with experimental techniques to reconstruct sugar utilization pathways in *Clostridium* species directly from their genome sequences. The subsystems-based comparative genomic approach was used, which integrates the analysis of conserved operons and regulons with pathway reconstruction across a large variety of genomes. This approach allows us to significantly improve the accuracy of genomic annotations and to identify previously uncharacterized genes involved in clostridial sugar metabolism. The predicted gene functions are then experimentally verified through a combination of genetic and biochemical techniques. Comparison of the reconstructed catabolic pathways with *Bacillus subtilis* identified substantial variations including non-orthologous gene replacements and families of paralogous proteins with different substrate specificity. Our long-term goal is to build a comprehensive knowledge base of carbohydrate utilization pathways in various *Clostridium* species. This knowledge base is important for bioengineering and biomedical applications of *Clostridium* spp. as well as for analysis of metagenomic data.

Biography

Chen Yang is a professor in the Key Laboratory of Synthetic Biology, Chinese Academy of Sciences. She completed her B.S. in biochemical engineering from Zhejiang University in 1994 and Ph.D. in biochemical engineering and science from Kyushu Institute of Technology, Japan, in 2001. From 2001 to 2008 she was a postdoctoral fellow in Keio University, Japan, and then in Burnham Institute for Medical Research, USA. Dr. Yang has published over 20 papers in prestigious journals. Her current research is focused on comparative genomics and metabolic flux analysis in microorganisms.