Systems Biology Research Symposium Oral Presentation Session

Biofilm Gene Association in Oral Streptococci by Systems Biology

<u>Ping Xu</u>^{1,2}, Xiuchun Ge¹, Yuetan Dou¹, Lei Chen¹, Xiaojing Wang¹, Jenishkumar R Patel¹ and Danail Bonchev^{2,3}.

¹The Philips Institute, ²The Center of the Study for Biological Complexity, ³The Department of Mathematics and Applied Mathematics, Virginia Commonwealth University, Richmond, Virginia 23298, USA

Presenter's email address: pxu@vcu.edu

Biofilm is a complex aggregation of microorganisms growing on a solid substrate. Pathogens in biofilms are resistant to harsh environmental stresses such as antibiotics, extreme pH shifts, oxidants, high osmolarity, and host immune system. Prevention of biofilm formation is critical to advancing public health systems against infectious diseases. To understand biofilm formation in *Streptococcus sanguinis*, we apply genome-wide gene-by-gene deletions for identification of all biofilm-related genes, and to construct a network that considers the cumulative contributions of biofilm genes. In building the network we proceeded from *S. sanguinis* microarray analysis and co-localization data from 30 streptococcal genomes. Network analysis will then provide information for the enrichment of pathways and biological processes in *S. sanguinis* with biofilm genes. Such integrative studies on streptococcal biofilm formation by systems biology methods may identify critical features of biofilm formation. Although many biofilm related genes have been intensively studied in other streptococci in the past two decades, there is no overview of gene relationships in this process. We anticipate that a comprehensive view of all associated genes in one organism will help to reveal the distinct genetics underlying biofilm processes and provide insight to biofilm formation that can not be gleaned from any single gene mutation.

The recent completion of *S. sanguinis* genome opens an opportunity to study biological characteristics of this organism. *S. sanguinis* is one of the viridans streptococci most commonly identified as a pioneer in dental plaques and a pathogen in infective endocarditis (IE). To study gene functions in this organism, we developed a method to systematically delete *S. sanguinis* ORFs across the genome. All ORFs in *S. sanguinis* genome have been precisely deleted and their functions in biofilm are being studied. The global network analysis of all associated genes in one organism will provide a comprehensive understanding on biofilm formation that can not be revealed by any single mutation.

Key words: systems biology, biofilm, Streptococcus sanguinis, networks