

Venue: GIZA  
21<sup>st</sup> August 2007  
1515-1630 hr

## **Symposium 2C: Metagenomics**

### **S2C-1. Metagenomics: discovering microbial diversity**

Koh CL<sup>1</sup> and Chan KG<sup>2</sup>

<sup>1</sup>*DNA Centre @ NIE, NSSE AG, National Institute of Education, Nanyang Technological University, 1 Nanyang Walk, Singapore 637616, and* <sup>2</sup>*Division of Genetics and Molecular Biology, Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia.*

Metagenomics has been defined by Chen and Pachter (2005) as “the application of modern genomics techniques to the study of communities of microbial organisms directly in their natural environments, bypassing the need for isolation and laboratory cultivation of individual species.” In other words, metagenomics is a culture-independent analysis of a mixture of microbial genomes, termed the metagenome and extracted from a native ecosystem, by using a DNA sequencing approach. By analysing genes coding for small subunit ribosomal RNA (SSU rRNA) or SSU rDNA present in a metagenome, we are able to determine the microbiome and microbial diversity in it by comparing the SSU rDNA sequences with those in the nucleotide database at GenBank. Hence, metagenomics, which is both a research field and a set of research techniques, enables us to assess and identify the genetic diversity present in the genetic material from a native sample. For example, we can use metagenomics to unravel the complex indigenous microbial community or microbiome present in our mouth, dental plaque, phlegm, or gastrointestinal tract, during our normal and diseased states, leading to new insight into the role of microbes in human health and disease. Understanding how microbial community structure affects health and disease may contribute to better diagnosis, treatment, and prevention of disease.

### **S2C-2. Metagenomics: mining novel genes**

Chan KG<sup>1</sup> and Koh CL<sup>2</sup>

<sup>1</sup>*Division of Genetics and Molecular Biology, Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia, and* <sup>2</sup>*DNA Centre @ NIE, NSSE AG, National Institute of Education, Nanyang Technological University, 1 Nanyang Walk, Singapore 637616.*

Besides enabling us to assess and identify the microbiome and microbial diversity present in a metagenome extracted from a native sample, metagenomics is also a powerful tool that enables us to directly access or clone all functional genes in the microbial community from the native sample, which may comprise novel unculturable and underrepresented culturable microbes. These genes may encode products of biotechnological significance, e.g., new enzymes that degrade waste products or environmental pollutants and new enzymes that lead to the production of new antibiotics or vitamins. They may also encode products of medical importance, e.g., virulence-associated characteristics of various organisms, or products that perform the multitude of diverse metabolic pathways of microbes. We will review and discuss the processes involved in isolating and identifying various metabolic genes of both culturable and unculturable microbes in metagenomes extracted from microbial communities present in a myriad of ecosystems.

**S2C-3. Lab-on-Chips**

Liu WT

*Division of Environmental Science and Engineering, National University of Singapore, Singapore*

Abstract not available at time of printing.