NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

BIOLOGY COLLOQUIUM

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Hosted by A/P Ge Ruowen

A Million Genomes Ahead



By Jun Wang

Executive Director, BGI (previously known as the Beijing Genomics Institute), Shenzhen, China

While it is definitely a question whether different types of cancer have similar genomic alterations, we do not even have sufficient samples to understand a single type of cancer. Individuals with different genetic and environmental factors, such as carcinogen exposure, commensal or pathogenic bacteria and viruses, life style and mental health, all have to be sampled, both horizontally and longitudinally. The interpretation of cancer genomes relies on the scale and quality of the sequencing data, innovative handling of such big data and detailed clinical and pre-clinical information. Early and routine tests would be possible with accurate and ultra-low input next-generation sequencing technologies, which necessitate development of non-invasive sampling approaches. Each sample should be analyzed in a multi-omic fashion to be truly reliable and informative. Single-cell sequencing is necessary for elucidating the heterogeneity and reconstructing the evolution of a cancer sample. Biological investigations with optimized humanized mouse models and conditional reprogramming tumors cells would be instrumental for development and evaluation of drugs. While we envision a million 'personalized' cancer genomes to come, the hope is to integrate the large-scale, multi-dimensional data in order to stratify each patient or at-risk individual, for efficient diagnosis, prognosis and treatment.

Artwork by Ann Nee, DBS, NUS