SIgN Immunology Seminar

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Strategy and platforms for tackling infectious disease

Host
Prof Ren Ee Chee
Singapore Immunology Network, A*Star

Date
Tuesday
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Time
2pm – 3pm

Venue
Aspiration
Matrix Building
Level 2M
Biopolis

There is an urgent need to find new therapeutics for the treatment and prevention of bacterial-mediated disease. The revolution in biology resulting from Next Generation (NexGen) DNA sequencing technologies has given us enormous insights into the genomic content and organization of microbial genomes. There is an expectation that this genomic information can be 'translated' into targets for new therapeutics. While the bioinformatics analysis of candidate genomes can result in the identification of putative therapeutic targets, robust empirical methodologies are required for hypothesis testing. Analysing mutants is a key component of any genetic-based strategy and screening pools of transposon (Tn) mutants has proven to be a reliable method for linking genotype with phenotype. While analysing mutants individually has resulted in the successful identification of therapeutic targets, parallel processing of larger numbers is required to exploit the massive amount of genome information now available. Several methods have been developed to increase the number of Tn mutants that can be analysed in a single experiment. Studies using signature-tagged mutagenesis (STM) have been carried out with Tn-mutant libraries passaged through a diverse range of environments. While STM has proven to be an extremely reliable technology, it is limited in the number of mutants that can be analysed in a single experiment. To address this problem, I have been involved in the development of more powerful array, (Transposon-mediated differential hybridisation (TMDH; Chaudhuri, R.R., et al., BMC Genomics, 2009. **10**: p. 291; Chaudhuri, R.R., et al. PLoS Pathog, 2009. **5**(7): p. e1000529., and sequencing approaches (Langridge, G.C., et al., Genome Res, 2009. **19**(12): p. 2308-16; Chaudhuri RR,. 2013. PLoS Genet, 2013. Apr;9(4):e1003456) that can analyse genome-wide panels of mutants in a single experiment. In this presentation I will describe the development of a 'proteogenomic' strategy that links the data from genome-wide Tn-mutagenesis experiments with microbial proteomics for the identification of candidate targets relevant for the development of therapeutics.