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SIgN Immunology Seminar



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Systems Biology of Infection and Immunity-Deadly Virus Infections in the 21st Century: Successes, Challenges, Ebola and Networks to Nowhere

Host
Dr Lisa Ng
Singapore Immunology Network, A*Star

Date
Tuesday
5 July 2016

Time
11am – 12pm

Venue
SIgN Seminar Room
Immunos Building
Level 4
Biopolis

My laboratory is using systems biology and novel computational methods to understand and model the host response to highly pathogenic viruses, including Ebola virus; H5N1, H7N9, and pandemic influenza viruses; MERS coronavirus; and human and simian immunodeficiency viruses. We are also using these methods to study the early innate response to vaccination and to illuminate the events that lead to protective immune outcomes. Our approaches take particular advantage of next-generation RNA-sequencing and innovative experimental systems, such as the Collaborative Cross mouse genetics platform, to examine global patterns of host gene expression and the role of host genetic variation on infection outcome. Our studies using the Collaborative Cross have recently resulted in the development of a first-of-its-kind mouse model of Ebola hemorrhagic fever. We have shown that different recombinant inbred mouse lines exhibit distinct disease phenotypes after mouse-adapted Ebola virus infection. Phenotypes range from complete resistance to lethal disease to severe hemorrhagic fever and 100% mortality. RNA-seq is also expanding our views to encompass the uncharted territory of noncoding RNAs, where we have observed changes in the expression of diverse classes of small and long noncoding RNAs in response to virus infection. These findings suggest that a detailed knowledge of noncoding RNA regulation and function will be necessary for a full understanding of transcriptional control and viral pathogenesis. Our goal is to exploit these systems to provide molecular signatures for diagnostic or prognostic assays and a rational basis for antiviral drug and vaccine development.