Singaporean Society for Immunology

Sponsored by: STEMCELL™ TECHNOLOGIES

SgSI Seminar Series: Infection & Immunity

Date & Time: 24 March 2016 (Thursday), 4.30 - 5.45pm

*Venue: Breakthrough, Matrix Level 4, Biopolis

Host: Dr. Katja Fink, SIgN

Registration is based on first-come first-served. Click here to register now!

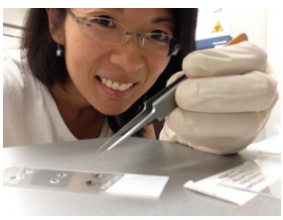
Dr. Charles-Antoine Dutertre

Senior Research Fellow

Duke-NUS

Deciphering Dendritic Cell Subsets along Mammalian Species: From Primates to Bats

Dendritic cells (DCs) are central actors of anti-viral immune responses. DCs are subdivided in discrete subsets that have specialized anti-viral functions such as antigen presentation, type-I and type-III interferon (IFN) production. In mice, $CD8\alpha^+$/$CD103^+$ DCs, which are also defined as $CADM1^+XCR1^+$, optimally cross-present antigens to $CD8^+$ T cells, respond strongly to TLR3 ligands and are the greatest source of type-III IFN (IFN-III). Homologous $CADM1^+XCR1^+$ DCs, commonly defined as $CD141^+$ DCs, have been identified in humans by comparative genomic and functional studies. However, the identification of such cells in other mammalian species is still elusive. Here, we identified in multiple Macaques species a DC population highly responsive to TLR3 stimulation, with strong phenotypic and transcriptional homology to human and murine $CADM1^+XCR1^+$ DCs. We also identified cells with a DC morphology that shared the phenotype ($Lin^-MHC\text{-}II^{hi}CADM1^+XCR1^+$) and gene expression signature of mouse, human and macaque $CADM1^+XCR1^+$ DCs in Bats. Interestingly, virus-infected Bat splenocytes have been demonstrated to produce high levels of IFN-III with no significant IFN-I induction. Since Bats are reservoirs of many zoonotic viruses such as Ebola and Nipah viruses, we will now investigate whether $CADM1^+$ DCs, by their IFN-III production and $CD8^+$ T cell-stimulatory capacities, could orchestrate the control of viruses in Bats.



Dr. Shuzhen Sim

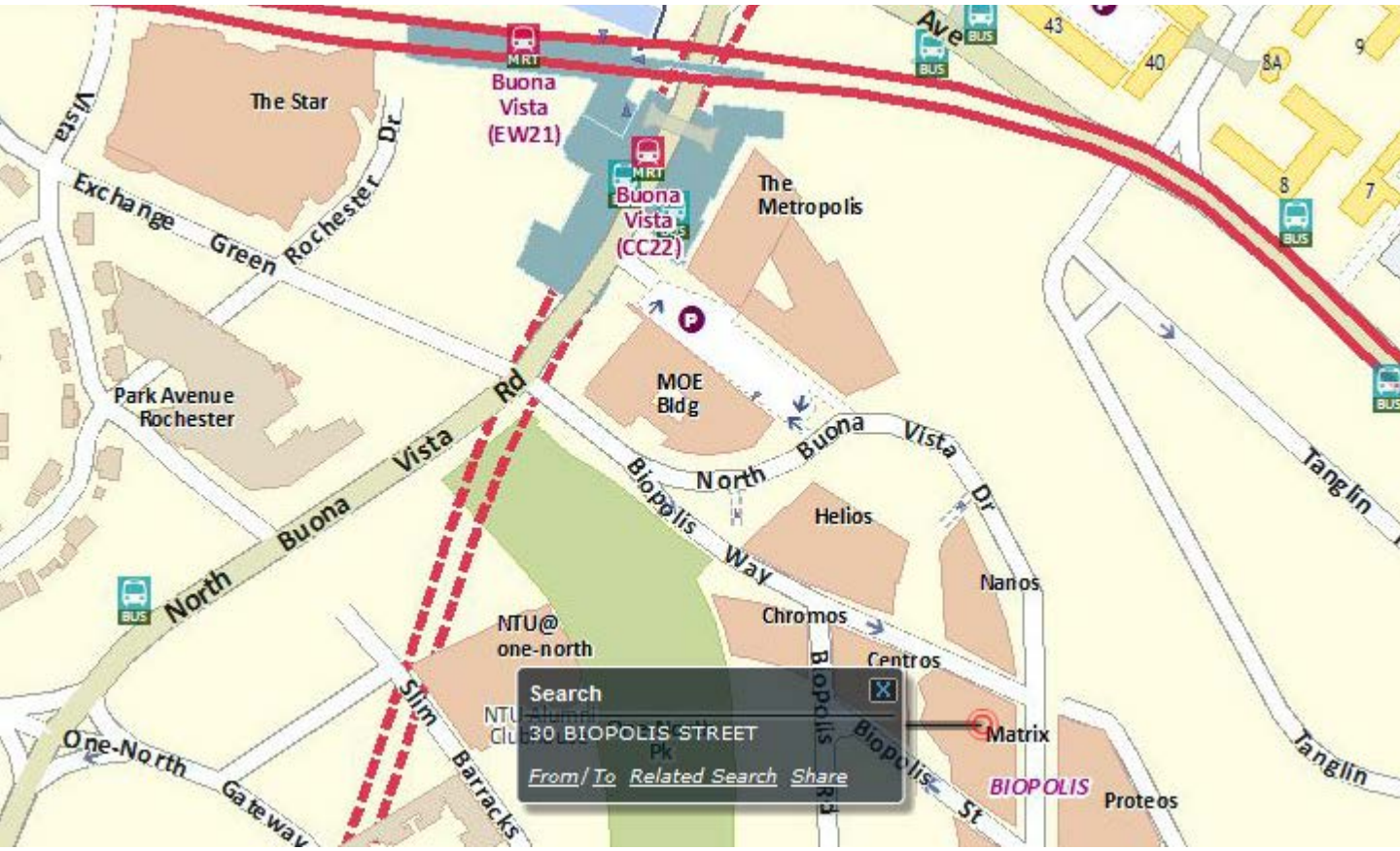
Research Fellow

GIS, A*STAR

Exploring host-pathogen interactions in *Aedes aegypti*, the primary mosquito vector of dengue virus

The ability of *Aedes aegypti* to become infected by and eventually transmit dengue virus (DENV) is dependent on the mosquito host response and on the infecting virus population. Broadly, our research focuses on trying to understand these host-pathogen interactions. From the host perspective, we are characterizing the impact of the mosquito gut microbiota on vector competence. Antibiotic treatment severely depletes *Ae. aegypti* gut bacterial loads, alters microbial 16S profiles, and renders mosquitoes more refractory to DENV infection; we use RNA-Seq to characterize the microbiota-modulated mosquito transcriptome, and to distinguish between microbiota-dependent and –independent host responses to DENV. From the virus perspective, we are characterizing the intrahost genetic diversity of DENV populations obtained directly from infected mosquitoes, using whole-genome deep sequencing and sensitive variant calling algorithms to detect low frequency viral variants. Comparing virus populations from human patients and matched mosquitoes has allowed us to track the horizontal transmission of variants and to detect host-specific selection pressures; we are now comparing virus populations from mosquitoes with normal and depleted gut microbiota. Through these analyses, we hope to develop a comprehensive picture of the complex interactions between the mosquito host response, DENV population dynamics, and microbial inhabitants of the mosquito gut.

*Address: 30 Biopolis Street, Singapore 138671
Nearest Bus Stop: Buses 91, 92, 95, 74, 191, 196, 198, 200 (walk 5 min)
Nearest MRT Station: Buona Vista CC22/EW21 (walk 5 min)



This seminar is sponsored by STEMCELL Technologies