Center for Inference and Dynamics of Infectious Diseases Seminar

Virus-inclusive single cell RNA sequencing reveals the molecular signature of dengue virus infection in cell lines and human blood

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Eastlake E3-200/201 Combo

Fred Hutchinson Cancer Research Center

Light refreshments will be served; registration not necessary to attend this event

Abstract: Dengue virus (DENV) infects millions of people annually and can cause severe manifestations including hemorrhage and shock. However, a thorough understanding of the host response to DENV is lacking, partly because conventional approaches ignore heterogeneity in virus abundance across cells. In this talk, I will introduce viscRNA-Seq (virus-inclusive single cell RNA-Seq), an approach to probe the host transcriptome together with intracellular viral RNA at the single cell level. I applied viscRNA-Seq to monitor DENV infection in cultured cells and peripheral blood cells from dengue infected human subjects.

Longitudinal sampling of cultures cells enabled the identification of host factors that play pro- or antiviral roles. In blood cells from dengue patients, interferon response genes were upregulated in a cell-specific manner prior to severe symptoms. The majority of DENV-RNA containing cells were naive IgM B cells expressing the CD69 and CXCR4 receptors and antiviral genes, followed by monocytes. Unexpected patterns of genetic diversity were detected in the viral genome and the host antibody repertoire. ViscRNA-Seq enables a multi-faceted molecular elucidation of viral infection in cell lines and human tissues and the discovery of novel virus-host genetic interactions.

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Contact: Trevor Bedford (trevor@bedford.io) with questions
http:www.cidid.org, ***NOTE***: event will live-stream Webcast link