Infectious Diseases Labs

ID LABS

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Wednesday 20th March 2024
11:30 AM to 12:30 PM (SGT)

Venue: Diversity Room
Level 5 Immunos Building

Viral and Host Factors Driving Spontaneous Epstein-Barr Virus Reactivation

Epstein–Barr virus (EBV) is a cancer and autoimmune disease-associated gamma-herpesvirus that infects the majority of adults worldwide. After initial infection, EBV generally maintains a latent state in the host with minimal viral gene expression. However, aberrations in this prototypical latent viral state leading to increased lytic replication can cause upregulation of oncogenic factors, promoting EBV-associated diseases. For example, nasopharyngeal carcinoma and post-transplant lymphoproliferative disease have strong associations with EBV lytic replication. Another EBV-associated disease, endemic Burkitt lymphoma (BL), is an extremely fast-growing cancer found primarily in children in malaria-endemic regions of Sub-Saharan Africa. Nearly all endemic BL tumors are infected with EBV and the hallmark of the disease is high levels of oncogenic c-Myc expression due to an immunoglobulin/Myc translocation. In this study, we describe spontaneous lytic phenotypes in EBV strains isolated from Kenyan BL patient tumors. We specifically focus on a novel Type 1 spontaneously lytic EBV strain and describe viral and host factors that could contribute to this phenotype. We found that cells infected with spontaneous lytic strains have lower c-Myc protein stability and express high levels of the plasma cell marker SLAMF7. Additionally, spontaneous lytic strains have altered latency states, which appear to further promote their lytic phenotypes. The isolation of spontaneously lytic EBV strains from endemic BL tumors provides more evidence that EBV may not maintain a prototypically latent state in patients with EBV-associated diseases and raises the possibility that promiscuous lytic activity may contribute to the formation of these diseases

The Luftig laboratory studies viruses that cause cancer with an overarching goal of defining the basic molecular mechanisms underlying pathogenesis and leveraging these findings for diagnostic value and therapeutic intervention. Our work primarily focuses on the common herpesvirus, Epstein-Barr virus (EBV). Overall, EBV contributes to approximately 2% of all human cancers worldwide leading to nearly 200,000 deaths annually. We use cutting-edge, cross-disciplinary and highly collaborative approaches to characterize the temporal dynamics and single cell heterogeneity of EBV infection. With these strategies, we aim to discover fundamental molecular circuits underlying transcriptional control, viral manipulation of host signaling pathways, and metabolic regulation that collectively influence infected cell fate decisions. By understanding the nature of viral control of infected host cells, we are also well positioned to discover vulnerabilities in EBV-associated diseases and characterize new therapeutic interventions in cell-based and pre-clinical animal models.

Hosted by: Dr Mathew Tay

Webinar is open to all. No registration required

Questions? Contact us at **seminars@idlabs.a-star.edu.sg**

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