

MetroHealth Medical Center

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Abstract Submission Form

Poster Title: Characterizing KSHV viral particles for Infection Models

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Kaposi's sarcoma-associated Herpesvirus (KSHV), also known as human herpesvirus-8 (HHV-8), belongs to the gammaherpesvirus subfamily and is one of seven known oncoviruses. KSHV infection can lead to two lymphoproliferative disorders: primary effusion lymphoma (PEL) and multicentric Castleman disease (MCD), as well as KSHV inflammatory cytokine syndrome. In addition, patients infected with HIV have been reported to have a much higher possibility of developing Kaposi's sarcoma (KS) by its etiological agent - KSHV. The traditional KSHV infection model begins by transmission through the saliva into the oropharynx region where the virus is able to replicate, then disseminates to the mucosal lymphoid tissues like the tonsils, and finally targets B-cells which serve as the primary viral reservoir. While KSHV infection is primarily associated with endothelial, epithelial, and B-cell tumors, researchers were also able to identify KSHV infection in T-cells, monocytes, macrophages, and in specific regions of the brain as well. The mechanism by which KSHV is able to drive infection to these other cell types is not fully understood. Previous data from our lab has shown that the TAR RNA from HIV-associated exosomes is a key element to enhance KSHV infection and that HIV-associated exosomes promotes KSHV infectivity in an EGFR-dependent fashion. This research project aims to characterize KSHV viral particles using various methods in order to create a reproducible infection model, which can be applied for studying KSHV infection tropism as well as for studying the mechanisms behind enhanced KSHV infectivity in a co-infection model with HIV and HIV-associated exosomes.