Subject: Thesis Defense: Sian Lum, MS Biology
Date: Wednesday, June 25, 2025 at 2:20:08 PM Eastern Daylight Time
From: SSB Faculty List on behalf of Diane St. Germain
To: SSB-FACULTY-LIST-L@LISTSERV.GMU.EDU

Thesis Defense Announcement
To: The George Mason University Community

Candidate: Sian Lum
Program: M.S. in Biology

Date: July 7, 2025

Time: 11:00 AM Eastern Time (US and Canada)

Location: IABR Room 1004, Science & Tech campus

and via Zoom

Join Zoom Meeting
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Committee Chair: Dr. Ramin Hakami

Committee members: Dr. Massimo Caputi, Dr. Yuntao Wu

Title: Characterization of IFN-B Stimulating RNA Species Associated With Small Extracellular Vesicles Released During RVFV Infection

Abstract: Extracellular vesicles, including small extracellular vesicles (sEV), such as “exosomes” have been found to play a central role in intercellular communication. Recently, sEVs have attracted more attention as their critical functions in a variety of diseases, including infectious diseases, has become better understood. However, there are still significant gaps in our knowledge regarding how sEV derived from an infectious origin (EXi) can alter host immunity. In particular, much remains to be elucidated for innate immune regulation of EXi during infection with cytoplasmic RNA viruses such as SARS-CoV-2 or Rift Valley fever virus (RVFV), which is a Category A priority pathogen. Using our model of RVFV infection, our laboratory previously showed that EXi induce interferon beta (IFN-B) in naïve recipient cells through activation of RIG-I, ultimately leading to autophagy to protect the cells against infection. Also, based on the findings, it was hypothesized that viral RNA genome pieces that are packaged into EXi are responsible for RIG-I activation. In support of this, subsequent work in our laboratory showed that RNA purified from EXi-RVFV induces IFN-B in naïve recipient cells through RIG-I activation. In this work, we have begun characterizing the viral RNA genome pieces that are incorporated into the EXi, with the ultimate goal of identifying the species that lead to IFN-B activation. As part of this effort, RNAseq analysis of the EXi-associated RNA was performed and the short viral RNA genome sequences that are present were identified by software analysis of the RNAseq data. To verify the presence of these viral RNA sequences, we have designed and validated the specificity of various primer pairs, focusing initially on the sequences corresponding to the L genome segment of RVFV. In addition, we have shown that in vitro transcribed L segment by itself is capable of giving robust IFN-B activation and begun producing truncated versions of the L segment by in vitro transcription (IVT) to analyze for the ability to induce IFN-B. Collectively, our data provide further support of our model that short viral RNA genome species within EXi-RVFV activate innate immune response against RVFV in local and distal naïve cells and set the stage for identification of these species in future studies. These findings provide deeper insights into the exact mechanisms of how sEVs produce a protective response against RVFV, helping to form a basis for devising novel and effective countermeasures in the future.
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