

Plan Overview

A Data Management Plan created using DMPTool

Title: The role of the apical sodium-dependent bile acid transporter (ASBT) in facilitating norovirus infection

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Project abstract:

Based on the cell tropism of diarrheagenic murine noroviruses for immune cells, the well-established affinity of the norovirus VP1 capsid protein to bind bile acids, and our preliminary data demonstrating reduced MNV infection and disease in *Asbt*^{-/-} mice, we hypothesize that ingested MNV virions bind bile acids in the gut lumen, the virion-bile acid complexes bind ASBT and trigger receptor-mediated endocytosis, vesicular transport shuttles the complexes across the epithelial cell to be released basally, and the complexes then encounter target immune cells. This model will be rigorously tested using a combination of in vivo and ex vivo model systems.

Start date: 06-01-2023

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The role of the apical sodium-dependent bile acid transporter (ASBT) in facilitating norovirus infection

The majority of data generated in this proposal will be virus titer data, fecal scores, and real-time quantitative polymerase chain reaction (PCR) values. Due to the nature of our in vivo studies using neonatal mice, we infect total litters per condition regardless of litter size. A minimum of 3 litters totaling at least 10 pups is analyzed for each condition. In general, 4 conditions will be compared: wild-type mock-inoculated, wild-type MNV-infected, Asbt^{-/-}, mock-inoculated, and Asbt^{-/-}, MNV-infected. In subaim 2a, images will be acquired using a slide scanner and analyzed for the presence of viral and host mRNAs and protein.

In this proposed project, the cleaned, item-level spreadsheet data for all variables will be shared openly, along with example quantifications and transformations from initial raw data. Final files used to generate specific analyses to answer the Specific Aims and related results will also be shared. The rationale for sharing only cleaned data is to foster ease of data reuse.

RNAscope ISH probes and methods used to identify viral genome-positive cells in tissue sections and individual cell types of organoids will be shared in the methods sections of peer-reviewed publications.

Tissue sections will be imaged using a Aperio Scanscope CS and Leica's Aperio ImageScope 12.4.3 slide scan software. No other specialized tools, software, or code are needed.

No consensus standards exist.

All data sets generated in this study will be small and do not require repositories for storage. The data will be provided in the results and supplemental sections of peer reviewed manuscripts.

All data are stored in standard lab notebooks and in a university-level OneDrive storage cloud.

Data will be made available as pre-prints or at the time of publication. Raw data sets will be stored in the lab for a minimum of 10 years after publication.

There are no anticipated factors or limitations that will affect the access, distribution or reuse of the scientific data generated by the proposal.

Controlled access will not be used. The data that is shared will be shared by unrestricted download.

No data from humans will be collected in this study.

Lead PI, Stephanie Karst, will be responsible for the day-to-day oversight of lab/team data management activities and data sharing. Broader issues of DMS Plan compliance oversight and reporting will be handled by the PI and Co-I team as part of general University of Florida stewardship, reporting, and compliance processes.
