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Research

Most of the research in our laboratory has used coronaviruses as models to study the genetics of RNA virus transcription, replication, persistence, and cross species transmission. We have also been using alphavirus vaccine vectors to develop novel candidate vaccines against caliciviruses. Specific areas of interest include:

1. Coronavirus Reverse Genetics and vaccine development.

We have developed infectious cDNAs from two coronaviruses. Specific applications include: a) studying critical cis and trans acting factors that regulate coronavirus subgenomic mRNA synthesis and replication, b) rearranging the coronavirus gene order to study genome evolution and function in coronavirus transcription and replication, c) identification of the minimal coronavirus genome, d) development of coronavirus replicon RNAs and coronavirus replicon particles for vaccine development, e) expression of heterologous genes from coronavirus vaccine vectors for

swine and other important species.

2. Norwalk like virus (Calicivirus) vaccine development.

We are using the alphavirus, Venezuelan equine encephalitis virus (VEE), as a vaccine vector for the Norwalk like viruses. Our research encompasses: a) expression of Norwalk and SnowMountain virus capsid proteins from VEE, b) biochemical and immunologic characterization of these recombinant proteins, c) vaccine testing in mice, and d) use a human challenge model to identify immunologic responses associated with protection from NLV reinfection.

3. RNA virus transcription, replication and recombination.

Our laboratory has had a longstanding interest in using genetic approaches to study coronavirus transcription, replication and RNA recombination.

4. RNA virus persistence, cross species transmission and virus-host coevolution.

Our laboratory has studied the mechanism for coronavirus persistence in vitro. This occurs by virus selection for resistant host cells that down regulate the expression of the host receptor needed for coronavirus docking and entry. The emergence of these resistant host cells subsequently selects for the coevolution of virus variants that recognize new receptors for docking and entry. Virus variants evolve with expanded host range through recognition of phylogenetic homologues of the normal coronavirus receptor. Consequently, we are studying the mechanisms of RNA virus-host cell coevolution and virus receptor interactions that regulate virus host range expansion.

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Complete list of publications

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