

THE JOHN LAWRENCE SEMINARS



"SYSTEMS VIROLOGY: HOST-DIRECTED STRATEGIES FOR IDENTIFYING SIGNATURES, TARGETS, DRUGS, AND VACCINE STRATEGIES-- CAN WE HELP STOP THE INFLUENZA, AIDS, AND EBOLA EPIDEMICS?"

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My laboratory is using systems biology and novel computational approaches to understand and model integrated views of the host antiviral-response, vaccine efficacy, and viral pathogenesis. These approaches are also being used to molecularly phenotype drugs and adjuvants, providing new ways to evaluate efficacy, off-target effects, and mechanisms of action. Much of our work is focused on viruses responsible for worldwide pandemics, including influenza virus, hepatitis C virus, HIV, and Ebola. We are taking advantage of advances in metabolomics, lipidomics, computational biology, and next-generation sequencing, and are using innovative experimental systems, such as the Collaborative Cross mouse genetics platform. These approaches are expanding our views to encompass the uncharted territory of noncoding RNAs, where we have observed changes in the expression of diverse classes of small and long noncoding RNAs in response to infection, and the role of host genetic variation and its implications for personalized medicine. Most recently we have performed drug-repurposing studies, using sophisticated computational algorithms such as CANDOR. This integrated approach is designed to provide molecular signatures predictive of protective immunity or pathology, biomarkers for diagnostic or prognostic assays, and a rational basis for improvements to antiviral therapies and vaccines.

**TUES., NOV. 3RD
4:00 P.M.**

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**HOST:
BEN BROWN**