Division of Biology Presents:

Identification of Novel Virus-Host Interactions using Proteomics and Genomics

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A dynamic relationship exists between viruses and their hosts in which each exploit the other’s vulnerabilities. A window is opened into the established condition, which evolved over millennia, by taking advantage of loss-of-function mutations in either the virus or host. Two examples of this approach will be presented here. In the first example, mass spectrometry was used to identify a poxviral protein that is necessary for replication in type 1 interferon-treated cells as well as the interacting interferon-induced host protein. In the second example, a human genome-wide RNAi screen was used to identify a protein that inhibits the replication of the modified vaccinia virus Ankara (MVA) vaccine strain and an interacting viral protein that can defend against this host protein was found in wild-type strains. In both examples, CRISPR-Cas9 was used to engineer permissive cell lines.

If you would like to visit with Dr. Bernard Moss, please contact Candy Hernandez at candyh@ksu.edu.

Coffee & cookies served preceding the seminar in Ackert Hall, Room 225