SPOTLIGHT

Articles of Significant Interest Selected from This Issue by the Editors

Requirements for Membrane Pore Formation by the Reovirus Myristoylated μ1N Peptide

An infecting nonenveloped virus must perforate or otherwise disrupt cellular membranes to gain access to the cytoplasm. Orthoreoviruses, when activated, can introduce pores into cell membranes. This process is accompanied by release of an N-terminally myristoylated, 42-residue peptide known as μ1N, generated by autolytic cleavage of the outer-layer protein, μ1. Zhang et al. (p. 7004–7014) found that synthetic myristoylated μ1N is sufficient to produce pores in liposomes, red blood cells, and murine L cells. These findings suggest that μ1N peptides, like various bacterial toxins, oligomerize to form a β-barrel in the membrane.

Semen-Derived Fibrils Promote Infection by the Human Retrovirus XMRV

XMRV is a newly identified human retrovirus present in a subset of men with prostate cancer. Hong et al. (p. 6995–7003) show that fibrils of prostatic acid phosphatase fragments present in semen (also called semen-derived enhancer of virus infection or SEVI) greatly increase the infectivity of XMRV at the level of viral attachment and entry. In addition, XMRV RNA is detected in prostatic secretions of some men with prostate cancer. These results suggest that SEVI and XMRV interact in human semen to promote dissemination of the virus among humans.

Pathogenesis of Lethal Severe Acute Respiratory Syndrome Coronavirus Infection

Several respiratory viruses cause acute respiratory distress syndrome (ARDS) and severe disease in the elderly. However, an understanding of the molecular mechanisms leading to age-related disease susceptibility is incomplete. Rockx et al. (p. 7062–7074) used systems biology approaches with severe acute respiratory syndrome coronavirus (SARS-CoV)-infected young and aged mice to characterize disease progression as distinguishable gene expression profiles, correlating with viral spike variation and lethality. These findings establish SARS-CoV-infected aged mice as a virally induced ARDS model and identify candidate genes and pathways for future studies of the mechanism of SARS-CoV lethality and potential ARDS therapeutic targets.

Mathematical Modeling of the Primary Adaptive Immune Response to Influenza Virus

Influenza A viruses infect millions of persons worldwide each year. Although most adults have cross-reactive immunity to new influenza virus strains, viral mutations occasionally give rise to pandemic-type variants in which a primary rather than recall immune response drives clearance of the virus. Lee et al. (p. 7151–7165) have developed an extensive differential equation model of the adaptive immune response to a primary influenza virus infection. This model predicts many known features of primary influenza virus infection and quantifies the importance of virus-specific CD8⁺ T cells over antibody in a primary immune response.

Progress toward a Vaccine for the Common Cold

Development of a traditional vaccine for the common cold has been thwarted by the existence of at least 100 serotypes of human rhinovirus. Katpally et al. (p. 7040–7048) show that it may be possible to leverage an Achilles’ heel in rhinovirus to generate a broadly active peptide vaccine. A highly conserved, internal capsid protein is transiently exposed through a ‘breathing’ process. Antibodies directed to portions of this peptide can elicit cross-serotypic neutralization, providing a new approach for the development of a serotype-independent rhinovirus vaccine.