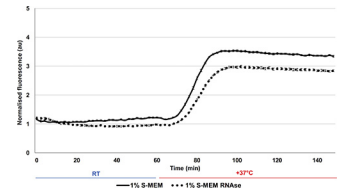




Articles of Significant Interest in This Issue

Physiological Factors Leading to Enterovirus Expansion and Uncoating

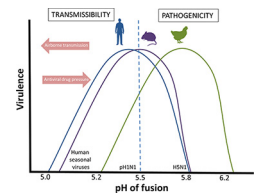
The mechanisms at work to uncoat enteroviruses are not well understood. Using real-time uncoating measurements and high-resolution structures, Ruokolainen et al. (e00599-19) found that albumin and a preset ion composition cause pocket factor release, capsid expansion, and fenestration, while the genome remains anchored to the capsid. Before entering cells, extracellular albumin primes the virus into a metastable yet infectious intermediate state. Ionic changes, likely within endosomes, contribute to uncoating and promote genome release after viral particle endocytosis. This work provides new insight into the uncoating of enteroviruses which may yield targets for therapeutic development.



Real-time uncoating measurement of enterovirus expanding at 37°C upon serum (or albumin) treatment.

Implications of Hemagglutinin pH Stability for Influenza Viruses

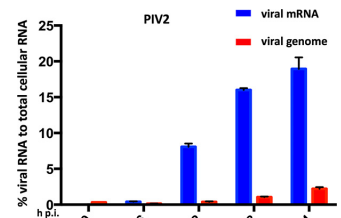
Influenza viruses vary with regard to hemagglutinin surface protein pH stability. Singanayagam et al. (e00058-19) discovered that hemagglutinin pH stability markedly affects virus infection outcomes in different experimental systems. Opposing pressures encountered in the environment inside and outside the cell determine pH stability that varies depending on viral and host factors as well as ecology. Understanding the consequences of pH stability for viral phenotypes has implications for the rational use of antiviral drugs, improvement of vaccines, and monitoring of pandemic risk.



Relationship between hemagglutinin pH stability, virulence, and transmission.

Patterns of Paramyxovirus Transcription and Replication Revealed by High-Throughput Sequencing

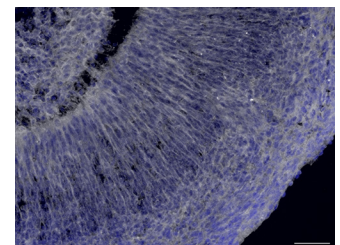
Polyadenylation selection is used to isolate mRNA from infected cells for transcriptional studies, but genomic RNA often copurifies with the poly(A)-selected mRNA. Wignall-Fleming et al. (e00571-19) found that directional sequencing is an advantageous method to distinguish between genomic RNA and mRNA/antigenomic RNA for paramyxoviruses. Directional sequencing of total cell RNA, after the physical removal of ribosomal and mitochondrial RNA, facilitates quantitative analysis of the abundance of genomic RNA and mRNA/antigenomes and of the presence of defective virus genomes. This approach sheds light on virus transcription and replication kinetics of several paramyxoviruses and may be used to study other RNA viruses.



Kinetic analysis of parainfluenza virus type 2 transcription and replication.

Human Cytomegalovirus Infection Impairs Calcium Responsiveness and Terminal Differentiation of Human Cortical Organoids

Human cytomegalovirus (HCMV) is a leading cause of congenital birth defects, and prenatal infection can cause severe neurological defects. Sison et al. (e00954-19) used human stem cell-derived three-dimensional cortical organoid tissue to investigate the effect of HCMV infection on the calcium-dependent processes of neural tissue development, neural differentiation, and cellular response to external stimuli. Infected neural cells lost calcium responsiveness and showed dramatic reductions in tissue organization and terminal differentiation. Organoids offer insight into the effects of HCMV infection in the developing human brain and may help identify novel therapeutic targets.



Neuronal differentiation and radial organization in human cortical organoids in the absence of HCMV infection.

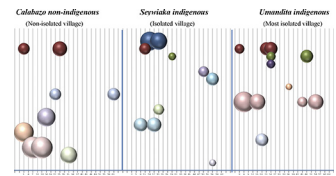
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<https://doi.org/10.1128/JVI.01080-19>

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Respiratory Virome Diversity Is Not Reduced by Extreme Geographic Isolation

The effects of geographic isolation on viral diversity are not well understood. Using metagenomics to analyze the respiratory virome of humans living in isolated communities, Altan et al. (e00681-19) compared viruses in nasal swabs of healthy young children from three villages with different levels of geographic and cultural isolation. The diversity of human viruses, with the exception of papillomaviruses, was not reduced in the more isolated villages. Frequent exposures to widely circulating viruses, particularly rhinoviruses, occur even in small populations with limited outside contacts. These findings provide potential clues about the global circulation of viruses and help explain viral diversity in isolated communities.



Virome in nasal swabs of children from different northern Colombian villages.