Articles of Significant Interest Selected from This Issue by the Editors

Metallosphaera Turreted Icosahedral Virus, a Founding Member of a New Family of Archaeal Viruses

Adding to the largely unexplored world of archaeal virology, Wagner et al. (e00925-17) describe a new archaeal virus, Metallosphaera turreted icosahedral virus (MTIV), isolated from a hot spring in Yellowstone National Park. Two strains of the virus were identified; each linear, double-stranded DNA (dsDNA) genome encodes 21 open reading frames (ORFs) distinct from other known viral genes. As determined by cryo-electron microscopy, the 70-nm, $T = 28$ icosahedron reveals an unusual structure with 42 turret-like projections, 12 from 5-fold axes and 30 hexameric units on 2-fold axes. Both virion structural properties and genome content support MTIV as the founding member of a new family of archaeal viruses.

Insights into Regulation of Reovirus Cell Entry

Capsids of nonenveloped and enveloped viruses adopt metastable conformations. Snyder and Danthi (e00898-17) identify a region within the reovirus $\mu 1$ protein that regulates capsid stability. Deletions within this domain allow unregulated structural transitions and impair viral replication. Replicative fitness is rescued by a second-site change that restores conformational flexibility. This work highlights the balance between the stabilizing and genome delivery functions of viral capsids.

TET2 Regulates the DNA Methylation State of Latent Epstein-Barr Virus

Epstein-Barr Virus (EBV) latent infection can alter the epigenetic programming of viral and cellular genes. Lu et al. (e00804-17) discovered that EBV-encoded transcriptional activator EBNA2 localizes to the TET2 gene and interacts with TET2 protein to direct hydroxymethyl cytosine modification at regulated sites in the EBV and host genomes. This epigenetic modification correlates with transcription activation and demethylation of viral and cellular genes required for host cell proliferation.

Histone-Like Protein from Adenovirus Blunts DNA Damage Response

The adenovirus genome is packaged with protein VII, a histone-like protein that associates with host chromatin and can shield incoming viral genomes from recognition by the cellular machinery of the DNA damage response (DDR). Avgousti et al. (e01089-17) discovered that protein VII on the host genome significantly blocks accumulation of DNA damage signaling marks. This study focuses on key elements in the damage response pathway and highlights how viral manipulation of chromatin influences access of DDR proteins to the host genome.
Persistence-Associated Mutations Enhance Chikungunya Virus Virulence

Chikungunya virus, a reemerging alphavirus, causes severe and often chronic musculoskeletal disease in humans. Virus-host interactions that determine disease severity are not well understood. Hawman et al. (e00816-17) identified a single amino acid substitution in the viral E2 glycoprotein and a deletion in the 3’ untranslated region of virus circulating in the serum of mice persistently infected with Chikungunya virus. Introducing these mutations into the parental strain enhances viral dissemination and disease severity in mice. These findings identify viral determinants of Chikungunya virus persistence and pathogenesis and provide new insight into pathogen-host interactions that dictate the outcome of infection.

The E2 K200R mutation and the deletion in the 3’ UTR enhance viral pathogenicity in mice.