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Key Interests

Adenovirus | Evolution | Genomics | Bioinformatics | Zoonosis | Viral Pathogens | Co-infection | Proteomics

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SELECT PUBLICATIONS

› J. Zhang *et al*., A survey of recent adenoviral respiratory pathogens in Hong Kong reveals emergent and recombinant human adenovirus type 4 (HAdV-E4) circulating in civilian populations. *Viruses* 11(2), E129 (2019).

› G. Singh *et al*., Divergent evolution of E1A CR3 in human adenovirus species D. *Viruses* 11(2), E143 (2019).

› A. M. Ismail *et al*., Adenoviromics: mining the human adenovirus species D genome. *Front Microbiol* 9, 2178 (2018).

› D. Seto *et al*., Using the whole genome sequence to characterize and name human adenoviruses. *J Virol* 85, 5701-2 (2011).

Research Focus

Adenoviruses infect all vertebrates and are important pathogens that affect different and multiple physiological systems. Human adenoviruses were among the first pathogens to be isolated and studied, and are models for understanding human health and biology. Paradoxically, they are also tools for medicine and research. We are interested in how these pathogens evolve and arise using a genomics and bioinformatics approach. We have found that they can co-infect to exchange genome elements, forming novel pathogens, and also are zoonotic, resulting in emergent human pathogens.

Current Projects

■ Evolution and host adaptation of zoonotic adenoviral human respiratory pathogen: HAdV-4 is one of the first respiratory pathogens to be isolated (1952) and studied. Genomic analysis reveals it is a chimpanzee virus, with recent isolates (2001, 2002, and 2018) containing a recombination of a viral replication motif that permits optimal viral replication in human cells.

■ Data mining adenovirus genomes: Proteins comprising proteomes of the diverse members of the human adenovirus genotypes have presumably evolved to be compatible and optimal with regards to the specific tissues and organs they infect. In comparative analyses of adenoviral pathogens from the respiratory tract versus the ocular tissues, we find that protein homologs are optimized differently, for example as noted in the analysis of a critical (gene expression) regulatory protein, E1A. This may help in understanding how similar pathogens affect different cells and result in different pathologies.