

Predicting the next eye pathogen; analysis of a novel adenovirus

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The ongoing dance between a virus and its host distinctly shapes how the virus evolves. While human adenoviruses typically cause mild infections, recent reports have described newly characterized adenoviruses that can cause severe, sometime fatal, human infections.

Researchers from the Massachusetts Eye and Ear and Harvard Medical School, Provincial Laboratory for Public Health, School of [Systems Biology](#), George Mason University, and the Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center report a systems biology approach to show how evolution has affected the disease potential of a recently identified novel human adenovirus. Their approach is based on the belief that understanding viral evolution and pathogenicity is essential to our capacity to foretell the potential impact on human disease for new and emerging viruses. Their study is now published in *mBio*.

Since the first adenovirus was characterized in 1953, 69 human adenoviruses (HAdVs) have been recognized as unique types. Analysis of whole-[genome sequence data](#) for existing and new HAdVs confirmed a critical role for homologous recombination in adenovirus evolution, leading to new and sometime serious [human infections](#). The emergence of new HAdV types, with several associated with severe eye infection, promoted the investigators to apply a systems biology approach to try to predict the ocular tropism of a previously uncharacterized and highly novel HAdV, isolated by nasopharyngeal swab from a 4-month-old boy with several bronchiolitis.

A combined genomic, bioinformatics and biological analysis identified a unique deletion in a key protein of the viral capsid and further suggested the potential of the virus to cause severe ocular infection. The results point toward a possible approach for predicting pathogenicity for newly identified and recently emergent [human pathogens](#).

Provided by Massachusetts Eye and Ear Infirmary

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