

Human adenovirus type identification

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Dear editor

The published paper in your journal entitling “Human adenovirus type 8 epidemic keratoconjunctivitis with large corneal epithelial full-layer detachment: an endemic outbreak with uncommon manifestations” has come into our attention.¹ The article provides interesting clinical presentation of corneal epithelial layer detachment among 25% (4 out of 16 human adenovirus [HAdV]-positive cases) of patients diagnosed with epidemic keratoconjunctivitis (EKC).

However, we have some opinions about the article that are stated below:

First, we have noticed that the authors have used the combination of hexon gene sequence and BLASTN for the typing of HAdV. Due to the appearance of many recombinant types of HAdVs, especially the EKC causing ones, for the last few years, many isolates were wrongly diagnosed as HAdV-8 by serological method. For example, type HAdV-54 was diagnosed as HAdV-8 due to cross reaction in neutralization test.² Even this was described as genome type HAdV-8I due to its misidentification as HAdV-8.^{3,4} Nowadays, HAdV-54 has become the major agent of EKC in Japan, although a few HAdV-8 is still being isolated in some places.⁵⁻⁹ Another EKC causing recombinant type HAdV-53 carries the fiber gene of HAdV-8, penton of HAdV-37, and the hexon of HAdV-22.⁹

Therefore, current recommended type identification method of HAdV is sequencing of the penton (P)-hexon (H)-fiber (F) genes (molecular typing) or whole genome sequence.¹⁰

Second, the authors used the term HAdV-8 genotype on the basis of HAdV-8 hexon sequence followed by BLASTN. Now a days, PCR amplification and sequencing of variable regions within the hexon, penton base, and fiber genes is designated as molecular typing method.

The term genotype is used for the recognition of a new type by full genome sequence. A genotype number is assigned where sequence data reveal that either i) the virus isolate encodes novel hexon (loops 1 and 2), penton base (hypervariable region), and fiber (knob) sequences, or ii) is a recombinant with one or two of these regions derived from previously designated genotypes, or iii) is a recombinant that has a unique combination of these three regions derived from previously recognized genotypes.¹⁰

Third, in the discussion, the authors described HAdV-8C–H genome types as genotypes. Traditionally, genome types of HAdV are designated by the restriction endonuclease cleavage pattern analysis of viral DNA.¹¹

We hope the authors will perform the currently recommended methods to confirm the identity of their EKC causing HAdVs.

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Disclosure

The authors report no conflicts of interest in this work.

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