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Using the Whole-Genome Sequence To Characterize and Name Human Adenoviruses▽

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We propose that human adenoviruses (HAdVs) be identified, characterized, and typed on the basis of complete genome sequence analyses rather than serological approaches. This idea has recently percolated through the community of adenovirologists. As a result, an open-floor discussion took place at the Ninth International Adenovirus Meeting (Dobogókő, Hungary, April 2009) on the need for a paradigm shift in recognizing and naming HAdVs in the future. An *ad hoc* committee then met to formulate the principles of the new approach. Recommendations 1 through 4 originated during the open-floor discussion and were discussed by the committee; recommendations 5 and 6 were developed by the authors to avoid conflicting claims and to deal with recombinants. These were reaffirmed at an NIH-sponsored and user-driven workshop of the

Human Adenovirus Working Group, which met at NCBI (Bethesda, MD) on February 3, 2011.

"Type" will succeed "serotype," reflecting the prevalence of genome sequence data usage; type is already in usage per International Committee on Taxonomy of Viruses (ICTV) definitions.

Previously named HAdVs will transition to the new format; e.g., "serotype HAdV-C1" will become "type HAdV-C1," where the letter "C" indicates the adenovirus species (currently species A through G). Each adenovirus type will have a unique, consecutively assigned number; i.e., there will not be an HAdV-D54 and an HAdV-C54.

Acceptance of a new type will require analysis of the complete genome sequence, including phylogenomics.

Serum neutralization will continue to be used as an additional criterion, per the ICTV definition. This should be by actual serum neutralization and hemagglutination inhibition, rather than by imputed derivation by limited DNA sequencing of the epitopes.

Naming priority will follow the order in which genome sequence data are released in the public sequence databases. Adherence to the Bermuda principles, whereby sequences are released as soon as possible, will be encouraged (see http://www.ornl.gov/sci/techresources/Human_Genome/publicat/hgn/v7n6/19intern.shtml).

Recombination is an accepted feature of HAdV evolution and will be accommodated. Recombinants will be classified as novel types if there are sufficient genomic, biological, or pathogenic differences from related types. Until a new recombinant genome is peer-reviewed and published, a provisional standardized name that reflects critical serological markers and similarities to established types in species, penton base, and serology-based motifs in hexon and fiber, plus the year and place of isolation, will be used for the recombinant. Thus, the provisional name for HAdV-D53 is HAdV-D/Hannover/[unique identifier]/2005/P37/H22/F8. "P" refers to the penton base, "H" to the hexon loop 1 region, and "F" to the fiber knob; numbers refer to the established type with the highest level of nucleotide identity in the respective regions. The unique identifier is

a lab designation or strain name, e.g., 2005-IAI-1 for HAdV-D53 isolate 1 and 2005-IAI-2 for HAdV-D53 isolate 2 should both genomes be deposited in GenBank.

Discoverers of “candidate” novel HAdV types should submit a FASTA file with the genome nucleotide sequence and the “evidence” to genomes@ncbi.nlm.nih.gov with the subject line “Human Adenovirus Working Group.” This file will be forwarded with submitter information removed to the NIH Human Adenovirus Working Group for a rapid, preliminary, confidential data review to coordinate the assignment of type number. This is not meant as a peer review but will prevent multiple genomes being assigned the same type number. Detailed information, including contact information for the working group members and current recommendations on typing parameters, may be found at http://hadvwg.gmu.edu. HAdV typing criteria are being refined, and input from the community is appreciated.

Revisions to the criteria used in establishing HAdV types must avoid compromising the stability and utility of the current system while accommodating changes in technology that reflect the nature of the data available. The effective replacement of serology by DNA sequencing and bioinformatics has recently been observed with the characterization of HAdV-G52, HAdV-D53, HAdV-D54, HAdV-B55, and HAdV-D56. These advances set the scene for the recognition of new HAdV types in the future.

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