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Toward an Integrated Human Adenovirus Designation System That Utilizes Molecular and Serological Data and Serves both Clinical and Fundamental Virology[▽]

The following proposals contribute toward elaborating a robust system for designating human adenovirus (HAdV) types. Our stance is that the system should be based on genomic sequence data, clinically relevant, easy to comprehend, and well integrated with the established immunotyping scheme. The main considerations are framing the criteria used to define a "type" and dealing with an increasing number of intertypic recombinants.

Type definition. The term "type," which has succeeded "serotype," will denote hexon type as defined by sequence analysis. For example, "HAdV-1" designates human adenovirus type 1, and "1" designates hexon identity. Only strains carrying novel hexon genes will be considered "candidate new types." Ideally, serology should be used to characterize the resulting antigenic phenotypes. The rationale for this proposal is that the major capsid protein, hexon, should remain the primary identifier because it contains the major neutralizing epitope, which is frequently targeted in molecular diagnosis. Designations that mask hexon identity risk misinterpretation because they do not reflect any specific characteristic of the virus. Moreover, if types are merely designated by sequential numbers according to the order in which novel genome sequences are reported, a huge increase in their number is likely. We note that the major capsid protein is effectively used as the target for molecular typing and naming of human papillomaviruses (L1) and human enteroviruses (VP1).

Intertypic recombinants. The designations of intertypic recombinant HAdVs (natural or engineered) will include the identity of the hexon gene (H) and also that of the fiber gene (F), which is responsible for hemagglutinin type and is a major determinant of tropism. These designations will replace those resulting from seroneutralization (SN) and hemagglutination inhibition (HI) assays, respectively. For example, HAdV-H7/F3 will designate a virus with a type 7 hexon and a type 3 fiber. The rationale for this proposal is that published data support a strong correlation between identities established by sequence analysis of hexon and fiber and SN and HI assays, respectively.

Further matters for consideration by the community. (i) Intertypic recombinant redesignation. Intertypic recombinants HAdV-29 and the recently described HAdV-D53, HAdV-B55, and HAdV-D56 will require redesignation. HAdV-52 will require investigation to confirm whether it is a human or simian AdV. If the former, it will meet the criteria to be considered a new type. HAdV-D54 meets the criteria to be considered a candidate new type but may need to be renamed.

(ii) Extent of sequences required. The extent of the sequences required for considering a candidate new type will need to be agreed upon. The options are hexon loop 1 (HVR1-6), hexon loops 1 and 2 (HVR1-7), or the complete hexon and fiber knob or complete fiber.

(iii) Unique identifier. Because recombinant HAdVs with different genome sequences may be correctly described by the same designation based on hexon and fiber types, a unique identifier will also be assigned to all recombinants. The strain name or the GenBank-assigned accession number are among the options.

(iv) Newly identified HAdVs. Laboratories that are capable of maintaining collections of reference strains and generating serological reagents will be invited to facilitate a thorough description of new HAdVs identified by sequencing.

(v) Type and GenBank accession numbers. Until decisions are reached on the definition of "type," the designation of intertypic recombinants, and items i through iii, new type numbers should not be assigned either in manuscripts by researchers or by GenBank.

The opinions in this report are those of the authors and do not necessarily represent the views of the Centers for Disease Control and Prevention.

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