



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2013.003aV	(to be completed by ICTV officers)			
Short title: Change all species names in the family <i>Adenoviridae</i> to incorporate a genus designation (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input checked="" type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

Author(s) with e-mail address(es) of the proposer:

Andrew Davison (andrew.davison@glasgow.ac.uk)

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Adenoviridae

ICTV-EC or Study Group comments and response of the proposer:

Study Group chair comments: There were 8 opinions from the 10 members. Six were in favour of the proposal and 2 were not sure (but definitely not against it). Almost everybody feels that the new naming system would provide useful excess information. However, many are afraid that the usage of "officially approved" naming and abbreviations will continue to be compromised.

In summary, the *Adenoviridae* SG authorized the submission of the proposal.

Date first submitted to ICTV:

19 June 2013

Date of this revision (if different to above):

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2013.003aV	(assigned by ICTV officers)
Title of proposal: Change all species names in the family <i>Adenoviridae</i> to incorporate a genus designation		

Text of proposal:

Adenovirus species names consist of three parts: (i) a host-derived term, (ii) the word “adenovirus”, and (iii) an upper case letter. In line with the use of non-Latinized binomials in many other virus families, it is proposed that a genus-specific prefix be added to the word “adenovirus” in all species names. Nothing else in the names would change. This would bring clarity as to which genus a species belongs, particularly since certain host animals (bovines, ovines and turkeys) are associated with species of different genera, and it can be difficult to remember which species is in which genus. Adenovirus genera are very likely to remain stable taxa in the long term, and the names have the advantage that they also convey the family designation.

To avoid confusion, the upper case letter would remain the same. A potential disadvantage of this is that this letter will no longer be sequential within a genus (e.g. the first bovine species in the genus *Atadenovirus* would be *Bovine atadenovirus D*, and there would be no *Bovine atadenovirus A*, *Bovine atadenovirus B* or *Bovine atadenovirus C*). However, the letter should be considered only as a label, not conveying anything about the completeness of series. In any case, not all present series are complete (there is no species *Ovine adenovirus C* yet, as it has been maintained as tentative species for the partially sequenced ovine AdV-6, however the category of “tentative species” was abolished, and the full genome sequence of BAdV-6 is still lacking).

It is important to emphasize that this proposal would affect species names only. It would not extend to virus/strain/isolate names (e.g. human adenovirus 5) or to informal usages and abbreviations (e.g. “species C” or “HAdV-C”), which are beyond the remit of the ICTV. These names would remain the same as they are at present.

This list of proposed changes is below.

GENUS	PRESENT NAME	PROPOSED NAME
<i>Atadenovirus</i>	<i>Bovine adenovirus D</i>	<i>Bovine atadenovirus D</i>
<i>Atadenovirus</i>	<i>Duck adenovirus A</i>	<i>Duck atadenovirus A</i>
<i>Atadenovirus</i>	<i>Ovine adenovirus D</i>	<i>Ovine atadenovirus D</i>
<i>Atadenovirus</i>	<i>Possum adenovirus A</i>	<i>Possum atadenovirus A</i>
<i>Atadenovirus</i>	<i>Snake adenovirus A</i>	<i>Snake atadenovirus A</i>
<i>Aviadenovirus</i>	<i>Falcon adenovirus A</i>	<i>Falcon aviadenovirus A</i>
<i>Aviadenovirus</i>	<i>Fowl adenovirus A</i>	<i>Fowl aviadenovirus A</i>
<i>Aviadenovirus</i>	<i>Fowl adenovirus B</i>	<i>Fowl aviadenovirus B</i>
<i>Aviadenovirus</i>	<i>Fowl adenovirus C</i>	<i>Fowl aviadenovirus C</i>
<i>Aviadenovirus</i>	<i>Fowl adenovirus D</i>	<i>Fowl aviadenovirus D</i>
<i>Aviadenovirus</i>	<i>Fowl adenovirus E</i>	<i>Fowl aviadenovirus E</i>

<i>Aviadenovirus</i>	<i>Goose adenovirus A</i>	<i>Goose aviadenovirus A</i>
<i>Aviadenovirus</i>	<i>Turkey adenovirus B</i>	<i>Turkey aviadenovirus B</i>
<i>Ichtadenovirus</i>	<i>Sturgeon adenovirus A</i>	<i>Sturgeon ichtadenovirus A</i>
<i>Mastadenovirus</i>	<i>Bat adenovirus A</i>	<i>Bat mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Bat adenovirus B</i>	<i>Bat mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Bovine adenovirus A</i>	<i>Bovine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Bovine adenovirus B</i>	<i>Bovine mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Bovine adenovirus C</i>	<i>Bovine mastadenovirus C</i>
<i>Mastadenovirus</i>	<i>Canine adenovirus A</i>	<i>Canine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Equine adenovirus A</i>	<i>Equine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Equine adenovirus B</i>	<i>Equine mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Human adenovirus A</i>	<i>Human mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Human adenovirus B</i>	<i>Human mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Human adenovirus C</i>	<i>Human mastadenovirus C</i>
<i>Mastadenovirus</i>	<i>Human adenovirus D</i>	<i>Human mastadenovirus D</i>
<i>Mastadenovirus</i>	<i>Human adenovirus E</i>	<i>Human mastadenovirus E</i>
<i>Mastadenovirus</i>	<i>Human adenovirus F</i>	<i>Human mastadenovirus F</i>
<i>Mastadenovirus</i>	<i>Human adenovirus G</i>	<i>Human mastadenovirus G</i>
<i>Mastadenovirus</i>	<i>Murine adenovirus A</i>	<i>Murine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Murine adenovirus B</i>	<i>Murine mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Murine adenovirus C</i>	<i>Murine mastadenovirus C</i>
<i>Mastadenovirus</i>	<i>Ovine adenovirus A</i>	<i>Ovine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Ovine adenovirus B</i>	<i>Ovine mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Porcine adenovirus A</i>	<i>Porcine mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Porcine adenovirus B</i>	<i>Porcine mastadenovirus B</i>
<i>Mastadenovirus</i>	<i>Porcine adenovirus C</i>	<i>Porcine mastadenovirus C</i>
<i>Mastadenovirus</i>	<i>Simian adenovirus A</i>	<i>Simian mastadenovirus A</i>
<i>Mastadenovirus</i>	<i>Tree shrew adenovirus A</i>	<i>Tree shrew mastadenovirus A</i>
<i>Siadenovirus</i>	<i>Frog adenovirus A</i>	<i>Frog siadenovirus A</i>
<i>Siadenovirus</i>	<i>Great tit adenovirus A</i>	<i>Great tit siadenovirus A</i>
<i>Siadenovirus</i>	<i>Raptor adenovirus A</i>	<i>Raptor siadenovirus A</i>
<i>Siadenovirus</i>	<i>Skua adenovirus A</i>	<i>Skua siadenovirus A</i>
<i>Siadenovirus</i>	<i>Turkey adenovirus A</i>	<i>Turkey siadenovirus A</i>

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

