Template for Taxonomic Proposal to the ICTV Executive Committee
Creating Species in an existing genus

Code[†] **2005.224V.04** To designate the following as species in the genus:

Mastadenovirus

belonging to the family° : ***Adenoviridae***

Simian adenovirus A
Simian adenovirus 3-VR1449 (SAdV-3/VR1449) AY598782

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Order	
Family	*Adenoviridae*
Genus	*Mastadenovirus*
Type Species	
Species in the Genus	
Tentative Species in the Genus	*Simian adenovirus*
Unassigned Species in the family	

New Taxonomic Order

Order	**none**
Family	*Adenoviridae*
Genus	*Mastadenovirus*
Type Species	
Species in the Genus	*Simian adenovirus A*
Tentative Species in the Genus	
Unassigned Species in the family	

ICTV-EC comments and response of the SG

Species demarcation criteria in the genus

Species designation depends on several of the following characteristics:

- Calculated phylogenetic distance (more than 5-10% based primarily on the distance matrix analysis of the protease, pVIII, hexon, and DNA polymerase aa sequence comparisons)
- DNA hybridization
- RFLP analysis
- Percentage of GC in the genome
- Oncogenicity in rodents
- Growth characteristics
- Host range
- Cross-neutralization
- Possibility of recombination
- Number of VA RNA genes
- Haemagglutination
- Genetic organization of the E3 region

Argumentation to justify the designation of new species in the genus

There is only a tentative species for monkey adenoviruses in spite that 20 serotypes (simian adenovirus 1 to 20) exist from Old World monkeys and 5 of them have been fully sequenced recently. The sequenced and fully annotated monkey adenoviruses are SAdV-1 and SAdV-3. Further three monkey adenovirus genomes are available in GenBank but they are non-annotated sequences from patents: SAdV-6 (under the obsolete name of SV-39 that means only simian virus 39), SAdV-7 (as SV-25), and SAdV-20 (ATCC VR541, GenBank Accession No. CQ982407). There are also chimpanzee adenovirus genomes but these viruses are official members of species *Human adenovirus B* (SAdV-21) and *Human adenovirus E* (SAdV-22 to 25). The present proposal aims at the establishment of *Simian adenovirus A* for SAdV-3 but most probably other SAdVs will be proposed to be its member later (first of all SAdV-4 and SAdV-6, but most likely also SAdV-9, 10, and 14) based on phylogenetic analysis (of partial sequences) and haemagglutination properties. (SAdV-1, 2, 5, 11, 12, 15, 19, and 20 will belong either to *Human adenovirus F* or to a newly established simian adenovirus species.)

Simian adenovirus A must be established because SAdV-3

- is from a new host (no species have been allocated yet for any monkey AdV);
- it has no cross-neutralization with any members of other species;
- phylogenetic calculation show a clear distance from any other accepted species (>10%);
- haemagglutination properties (group II) are different from those SAdVs that seem to belong to other species according to preliminary phylogenetic calculations (group I, III, and IV);
- it has one fiber gene that differentiates it from *Human adenoviruses F* and the similar simian adenoviruses with two fiber genes (SAdV-1, 11, 15);
- it lacks homologs of two E3 proteins, namely that of the 19K protein present in HAdV-B, C, D, and E, and the homolog of the 16K protein of HAdV-B, D, and E.

We propose the name *Simian adenovirus A* because it is in-line with the earlier naming policy in the Adenoviridae family, i.e., the name of the host is followed by a letter if there are more species under consideration with the same name.

List of created Species in the genus

Simian adenovirus A

References

Kovács GM, Davison AJ, Zakhartchouk AN, Harrach B (2004): Analysis of the first complete genome sequence of an Old World monkey adenovirus reveals a lineage distinct from the six human adenovirus species. J. Gen. Virol. 85 (10) 2799-2807

Annexes:

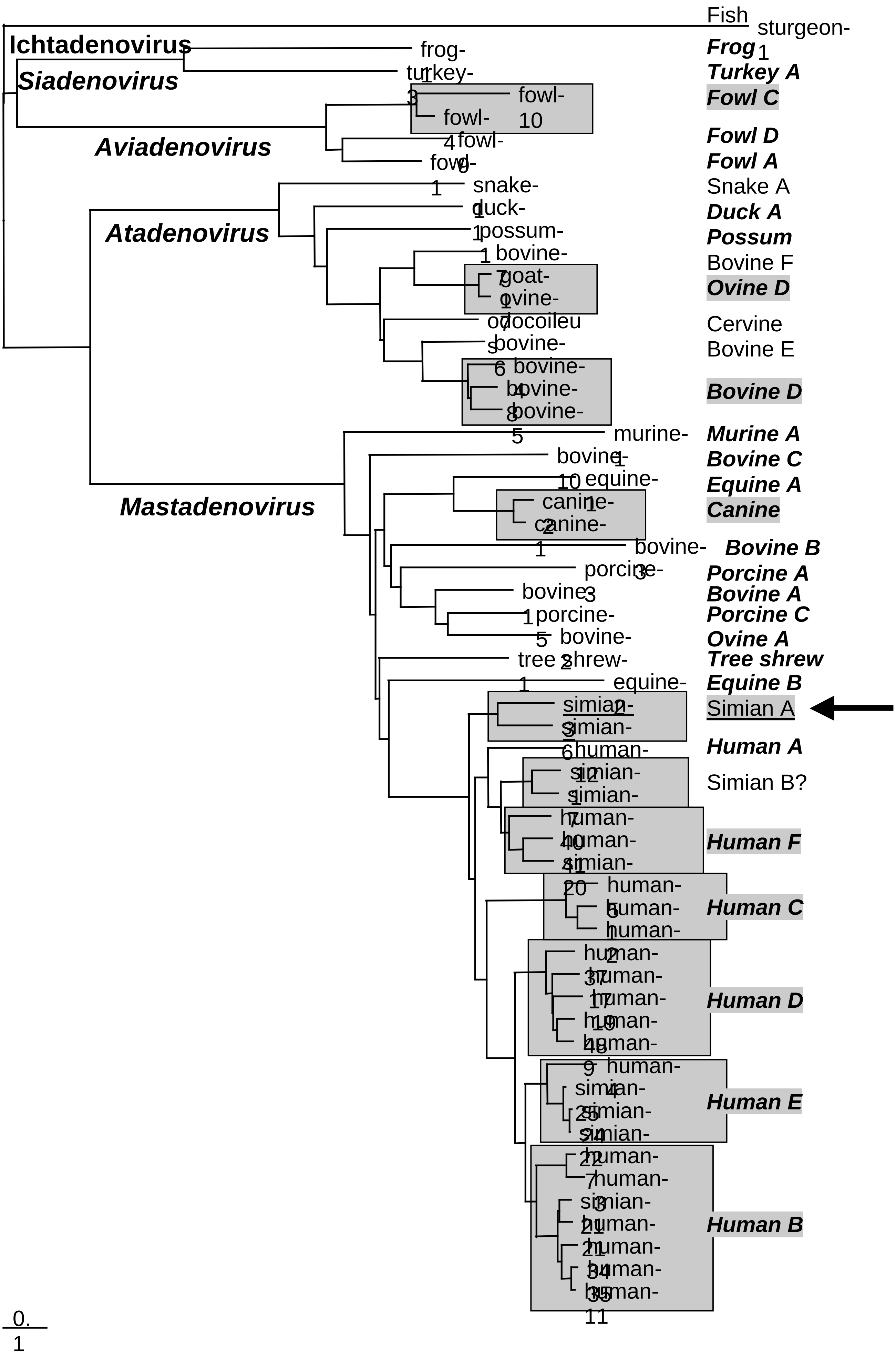
Ichtadenovirus
Siadenovirus
Aviadenovirus
Atadenovirus
Mastadenovirus
sturgeon-1
frog-1
turkey-3
fowl-10
fowl-4
fowl-9
fowl-1
snake-1
duck-1
possum-1
bovine-7
goat-1
ovine-7
odocoileus
bovine-6
bovine-4
bovine-8
bovine-5
murine-1
bovine-10
equine-1
canine-2
canine-1
bovine-3
porcine-3
bovine-1
porcine-5
bovine-2
tree shrew-1
equine-2
simian-3
simian-6
human-12
simian-1
simian-7
human-40
human-41
simian-20
human-5
human-1
human-2
human-37
human-17
human-19
human-48
human-9
human-4
simian-25
simian-24
simian-22
human-7
human-3
simian-21
human-21
human-34
human-35
human-11
Fish
Frog
Turkey A
Fowl C
Fowl D
Fowl A
Snake A
Duck A
Possum
Bovine F
Ovine D
Cervine
Bovine E
Bovine D
Murine A
Bovine C
Equine A
Canine
Bovine B
Porcine A
Bovine A
Porcine C
Ovine A
Tree shrew
Equine B
Simian A
Human A
Simian B?
Human F
Human C
Human D
Human E
Human B
0.1

Fig. 1. Distance matrix analysis of the hexon amino acid sequences (PROTDIST with categories model, then FITCH of the PHYILIP program package) demonstrates the genetic distance of the proposed new species. Adenovirus serotypes grouped into adenovirus species are boxed and labeled with the *accepted* or proposed names. Length of the sequences taken as homologous parts and analyzed was 811 residues. From the hexon sequences available in GenBank, that of HAdV-16 and SAdV-23 were excluded, as they are the results of homologous recombinations thus different parts of theses sequences show different clustering (the whole hexon sequence does not show the correct genetic relatedness). The aligned sequences are the full hexons or hexons only with some missing residues at their ends from GenBank (goat adenovirus 1, bovine adenovirus 5 to 8, odocoileus adenovirus 1 from black-tailed deer). Two hexon sequences have been assembled from partial sequences from GenBank (HAdV-19 and 37). They have some missing residues in the middle of the sequence. The sequence of bovine adenovirus strain Rus is unpublished. For bovine adenovirus 2, the amino acid sequence was deduced after the correction of a presumed reading frame shift error close to the 3' end of the gene deposited to GenBank.