

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

Code<sup>†</sup>  To designate the following as species in the genus:

belonging to the family<sup>°</sup> :

*Snake adenovirus A*  
Snake adenovirus 1 (SnAdV-1) AY082603

<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

## Author(s) with email address(es) of the Taxonomic Proposal

Mária Benko (chair of Adenoviridae SG) and Balázs Harrach  
([benko@vmri.hu](mailto:benko@vmri.hu), [harrach@vmri.hu](mailto:harrach@vmri.hu))

## Old Taxonomic Order

Order  
Family *Adenoviridae*  
Genus *Atadenovirus*  
Type Species  
Species in the Genus  
Tentative Species in the Genus  
Unassigned Species in the family

## New Taxonomic Order

Order none  
Family *Adenoviridae*  
Genus *Atadenovirus*  
Type Species  
Species in the Genus *Snake 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 (>5-10%)
- Host range
- DNA hybridization
- Percentage of G+C in the genome
- Cross-neutralization
- Organization of the right-hand end of the genome

## Argumentation to justify the designation of new species in the genus

Presently, there is only a tentative species for snake adenovirus 1 (SnAdV-1), originally isolated from corn snake, but later identified also in python, boa and rat snake. However, SnAdV-1 is clearly different from any other adenovirus, and its full genome sequence has been determined recently. Additional snake adenovirus types and other reptilian adenoviruses have also been identified by PCR amplification of partial DNA-polymerase sequences. The phylogenetic analysis of those short sequences suggests the possible need of establishing further snake and other reptilian adenovirus species in the future, and all of them belong to the genus *Atadenovirus*. The present proposal aims at the establishment of *Snake adenovirus A* for the allocation of the well-characterized SnAdV-1.

*Snake adenovirus A* is to be established because SnAdV-1

- is from a new host (no species have been allocated yet for any reptilian AdV);
- it has no cross-neutralization with any members of other species;
- phylogenetic calculation show a clear distance from any other accepted species (>10%);
- it has a unique ORF (in its so called E4 region at the right-hand end of the genome) that has been found only in this virus;
- it has one gene (105R) in this region that does not occur in any of the so far officially accepted atadenoviruses but in the tree shrew adenovirus belonging to mastadenoviruses;
- it has a single RH (right-hand) gene typical for atadenoviruses; the phylogenetically closest duck adenovirus 1 has already two homologous RH genes, while the ruminant atadenoviruses (bovine adenovirus type 4 and ovine adenovirus 7) have four or five RH genes;

We propose the name *Snake 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

*Snake adenovirus A*

## References

1. Benkő M, Élő P, Ursu K, Ahne W, LaPatra ES, Thomson D, Harrach B (2002): First molecular evidence for the existence of distinct fish and snake adenoviruses. *J. Virol.* 76 (19) 10056-10059
2. Farkas SL, Benkő M, Élő P, Ursu K, Dán Á, Ahne W, Harrach B (2002): Genomic and phylogenetic analyses of an adenovirus isolated from a corn snake (*Elaphe guttata*) imply common origin with the members of the proposed new genus *Atadenovirus*. *J. Gen. Virol.* 83 (10) 2403-2410

## Annexes:



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 these 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, ordoileus 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.