This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.010-017V***	(to be completed by ICTV officers)

Short title: New genus Ichtadenovirus containing a new species in the family Adenoviridae; a new species in the genus Siadenovirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply)**:**	**1** ☒ **2** ☐ **3** ☐ **4** ☒ **5** ☒ **6** ☐ **7** ☐

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

Balázs Harrach, harrach@vmri.hu on behalf of the Adenoviridae Study Group

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

MODULE 4: **NEW GENUS**

(if more than one genus is to be created, please complete additional copies of this section)

Code	***2008.010V***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Adenoviridae***
Order:	

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	***2008.011V***	(assigned by ICTV officers)

To name the new genus: *Ichtadenovirus*

Code	***2008.012V***	(assigned by ICTV officers)

To assign the following as species in the new genus:

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

Sturgeon adenovirus A

Code	***2008.013V***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:

Sturgeon adenovirus A

Argument to justify the creation of a new genus:

White sturgeon adenovirus (WSAdV-1) is the only known fish adenovirus (AdV). Its host belongs to the subclass Chondrostei. Based on phylogenetic analysis of any of the proteins that are used routinely in phylogenetic calculations for AdVs, WSAdV-1 is clearly sufficiently distant from all other known adenoviruses to merit its establishment as a new species in a new genus. Partial genome sequencing (to date slightly exceeding 30.5 kbp) has encompassed the conserved central region lacking the pVIII and fiber genes on the right end of the genome, plus parts of the terminal regions, which have unique genetic contents. A striking genome organization difference from all other AdVs is the presence of two fiber genes near the left genome end.

Origin of the new genus name:

Icht: a truncated transliteration of the Greek ιχθυς, fish.

Argument to justify the choice of type species:

The proposed species is the single member of the proposed genus.

Species demarcation criteria in the genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

References:

Benkő M, Doszpoly A, LaPatra SE (2008) Sequence analysis of white sturgeon adenovirus reveals unique genome ends: Proposal for the establishment of a new adenovirus genus. Abstracts of the XIV. International Congress of Virology, Istanbul, Turkey, 10-15 August, p 90

Doszpoly A, Harrach B, Benkő M (2009) Genome analysis of a fish adenovirus confirms the proposal for a fifth adenovirus genus. Abstracts of the 9th International Adenovirus Meeting, Dobogókő, Hungary, 26-30 April, p 127

Harrach B (2008) Adenoviruses. General features. Mahy BWJ, van Regenmortel MHV (eds): Encyclopedia of Virology, 5 vols. Third Edition. Elsevier, Oxford vol 1, pp 1-9

Harrach B, Benkő M (2007) Phylogenetic analysis of adenovirus sequences. Wold WSM, Tollefson AE (eds) Adenovirus Methods and Protocols, Second Edition, vol. 2: Ad Proteins, RNA, Lifecycle, Host Interactions, and Phylogenetics. (Methods in Molecular Medicine, Vol. 131) Humana Press Inc., Totowa, NJ, USA pp 299-334

Kovács GM, LaPatra SE, D'Halluin JC, Benkö M (2003) Phylogenetic analysis of the hexon and protease genes of a fish adenovirus isolated from white sturgeon (*Acipenser transmontanus*) supports the proposal for a new adenovirus genus. Virus Research 98, 27-34

Annexes:

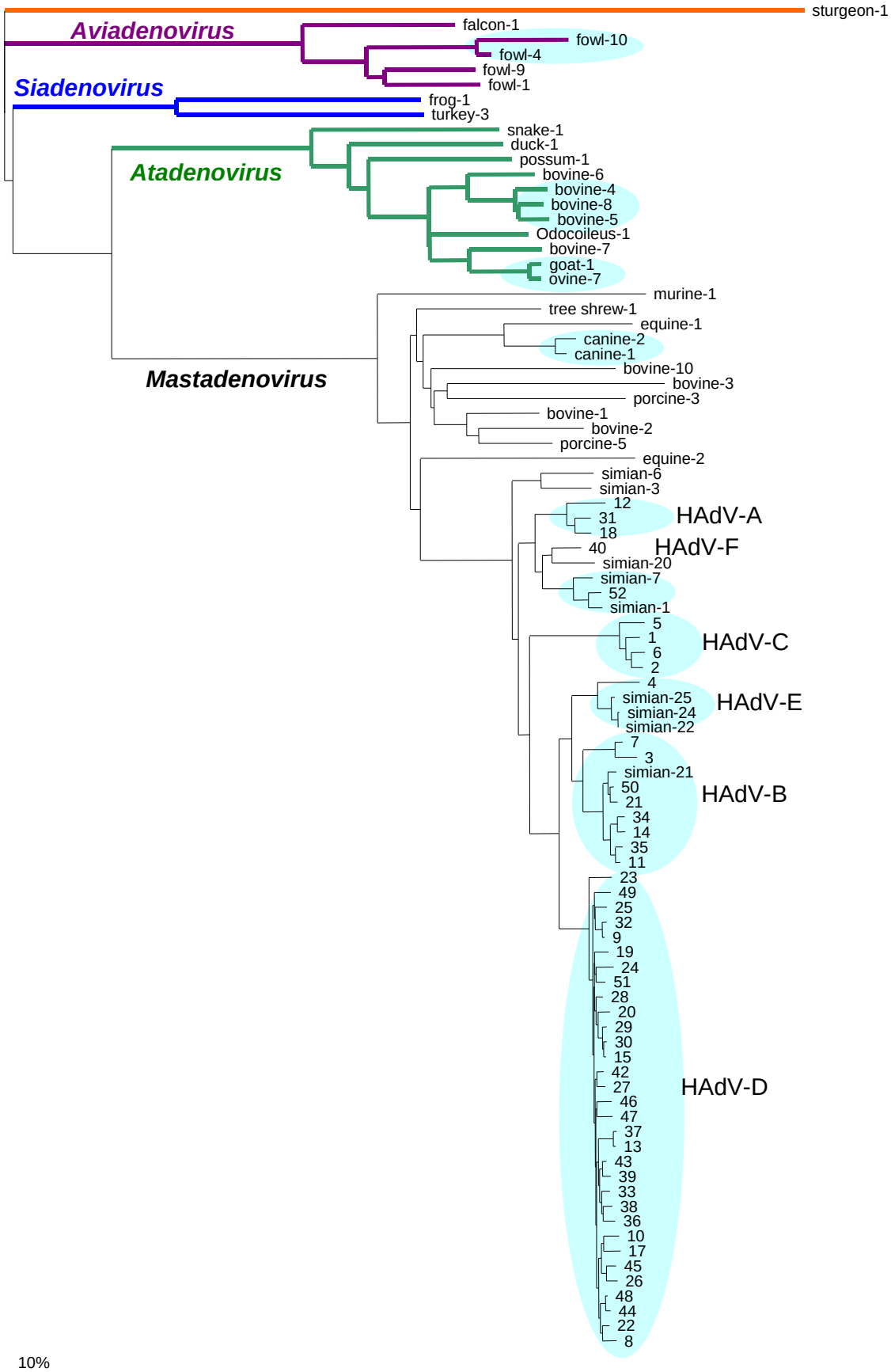
Adenovirus (AdV) infections have been described in a number of fish species, most often on the basis of electron microscopy. To date, a single virus isolate (white sturgeon adenovirus, WSAdV-1) has been obtained, from white sturgeon (*Acipenser transmontanus*). The gene content of the central region of the genome has been derived from DNA sequence data, and largely conforms to that found in every member of the four officially approved AdV genera. However, phylogenetic analyses have clearly indicated that WSAdV-1 represents a separate lineage. Moreover, recent sequence data have started to reveal a unique organization outside the conserved central region. Downstream from the IVa2 gene at the left end of the conserved central region, and in the same orientation, a large ORF is present. The encoded protein has significant similarity to bacterial and phage proteins of unknown functions. Further to the left, two complete and one partial protein-coding regions (in rightward orientation) have been identified. These complete genes are homologous to the fiber genes of other AdVs. To the right of the central conserved region, the gene arrangement is also very different from that in other AdVs. The pVIII, U exon and fiber genes are missing, and the genome contains at least eight ORFs with no known homologues. We propose that a novel genus be established for taxonomic classification of WSAdV-1 and possibly for additional fish AdVs. Since no similar AdV has been found in representatives of any other vertebrate classes, no serious counter-arguments arise against the formerly proposed name *Ichtadenovirus*.

Relevant GenBank accession numbers for WSAdV-1 are as follows.

1. AJ495768, 3449 bp, hexon and protease ORFs
2. AY082701, 415 bp, DNA polymerase ORF (partial)
3. Not yet submitted, ~30520 bp, four novel ORFs to the left of IVa2, through the central conserved region, to eight novel ORFs to the right of 33K

There are presently four genera in the family *Adenoviridae*. Two genera (*Mastadenovirus* and *Aviadenovirus*) comprise AdVs that probably coevolved with mammals and birds, respectively. The other two genera (*Atadenovirus* and *Siadenovirus*) are associated with a broader range of hosts. Atadenoviruses infect various ruminant and avian hosts, as well as a marsupial. All known Squamata (snake, lizard) AdVs also are atadenoviruses. The few known siadenoviruses were isolated or PCR amplified from birds, a frog and a tortoise. WSAdV-1 falls into a fifth clade on its own. However, AdV-like particles have been described in other fish species, and thus further members of this genus might emerge. On phylogenetic trees, the four genera and the fifth clade appear at considerable distances from each other (**Fig. 1**), thus justifying the establishment of a fifth genus

Fig. 1. Phylogenetic tree of AdVs based on a distance matrix analysis of hexon amino acid sequences. Protdist (categories matrix), Fitch (global rearrangements) programs of the PHYLIP 3.65 package. Unrooted tree with WSAdV-1 chosen as outgroup. AdVs are marked by the name of the host and the serotype number (or only by the serotype number in case of human AdVs (HAdVs)). AdVs that belong to the same species are grouped by light-blue ovals. HAdV species are indicated by their abbreviations.


sturgeon-1
Aviadenovirus
falcon-1
fowl-10
fowl-4
fowl-9
fowl-1
Siadenovirus
frog-1
turkey-3
snake-1
duck-1
possum-1
Atadenovirus
bovine-6
bovine-4
bovine-8
bovine-5
Odocoileus-1
bovine-7
goat-1
ovine-7
murine-1
tree shrew-1
equine-1
canine-2
canine-1
Mastadenovirus
bovine-10
bovine-3
porcine-3
bovine-1
bovine-2
porcine-5
equine-2
simian-6
simian-3
12
31
18
HAdV-A
40
HAdV-F
simian-20
simian-7
52
simian-1
5
1
6
2
HAdV-C
4
simian-25
simian-24
simian-22
HAdV-E
7
3
simian-21
50
21
34
14
35
11
HAdV-B
23
49
25
32
9
19
24
51
28
20
29
30
15
42
27
46
47
37
13
43
39
33
38
36
10
17
45
26
48
44
22
8
HAdV-D
10%

MODULE 5: **NEW SPECIES**

Code	***2008.015V***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Ichtadenovirus***
Subfamily:	
Family:	***Adenoviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Sturgeon adenovirus A

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

See the arguments above.

References:

Benkő M, Doszpoly A, LaPatra SE (2008) Sequence analysis of white sturgeon adenovirus reveals unique genome ends: Proposal for the establishment of a new adenovirus genus. Abstracts of the XIV. International Congress of Virology, Istanbul, Turkey,10-15 August, p 90

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, 10056-10059

Kovács GM, LaPatra SE, D'Halluin JC, Benkő M (2003) Phylogenetic analysis of the hexon and protease genes of a fish adenovirus isolated from white sturgeon (*Acipenser transmontanus*) supports the proposal for a new adenovirus genus. Virus Research 98, 27-34

Annexes:

See the arguments above.

MODULE 5: **NEW SPECIES**

Code	***2008.017V***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Siadenovirus***
Subfamily:	
Family:	***Adenoviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Raptor adenovirus A

Argument to justify the creation of the new species:

The genus *Siadenovirus* currently contains two species: *Frog adenovirus* and *Turkey adenovirus A*. A new siadenovirus has been found in several species of raptor (birds of prey). Because of the different host origin of this virus and its phylogenetic distance (>10%, calculated for various proteins) from the established species, the establishment of a new species is clearly merited.

References:

Kovács ER, Benkő M (2009) Confirmation of the existence of a novel siadenovirus species detected in raptors: partial sequence and phylogenetic analysis. 140, 64-70

Kovács ER, Harrach B, Benkő M (2009) Genome analysis of raptor adenovirus 1: a novel, non-isolated type, first member of a proposed new species in the genus *Siadenovirus*. Abstracts of the 9th International Adenovirus Meeting, Dobogókő, Hungary, 26-30 April, p 71

Zsivanovits P, Monks DJ, Forbes NA, Ursu K, Raue R, Benkő M (2006) Presumptive identification of a novel adenovirus in a Harris hawk (*Parabuteo unicinctus*), a Bengal eagle owl (*Bubo bengalensis*), and a Verreaux's eagle owl (*Bubo lacteus*). J Avian Med Surgery 20, 105-112

Annexes:

Sporadic deaths in raptors associated with a novel AdV (raptor adenovirus 1, RAdV-1) have been reported in two separate aviaries in England. Necropsy findings in a Harris hawk and two eagle owls included hepatomegaly, splenomegaly and renomegaly, as well as proventricular and ventricular dilation, ulceration and erythema. Histological findings in all three birds were hepatic necrosis, hepatitis, splenic necrosis, and proventricular and ventricular ulceration and necrosis. Basophilic inclusion bodies were seen in the above mentioned organs, as well as in the pancreas and the kidneys of one (Verreaux's) eagle owl. These pathological findings were thought to be consistent with those caused by AdVs. Attempts to detect aviadenoviruses or turkey haemorrhagic enteritis virus (*Turkey adenovirus*

A in genus *Siadenovirus*) by PCR failed. However, the "pan-adenovirus" nested PCR was positive, and the sequence seemed to be from a novel siadenovirus. Supposing that a new virus was present, molecular techniques (PCR) were applied and eventually the full genome (26.3 kbp) has been sequenced. The genome organization is identical with that of the two classified siadenoviruses. Further cases in the two bird collections were prevented by changing the homologous diet (day-old chicks and quails) to a heterologous one (newborn mice), and thus the causative role of the virus in the losses was indicated indirectly. Unfortunately, no test material was available from the homologous diet. PCR and sequencing confirmed that the same virus was present in the samples from all three dead birds. PCR tests for other viruses (herpesviruses, polyomaviruses and circoviruses) were negative. Attempts to isolate RAdV-1 in cell culture have not yet succeeded, and the true host must be considered as undetermined.

Relevant GenBank accession number:

EU715130, 12554 bp, DNA polymerase ORF (partial) to DNA-binding protein ORF (partial)

Naming the virus

Raptor adenovirus 1 was named for the type of birds from which it was detected. As it was found in different bird species at the same time, there was no possibility to select a single species (the first identified host) as the basis for the name for this virus. Furthermore, it must be noted that even these birds may not be the natural host.

Phylogenetics

Initial phylogenetic analysis of the partial sequence of DNA polymerase implied a new siadenovirus type. This was confirmed unambiguously by phylogenetic analyses based on several genes in the 12554 bp sequence (see **Fig. 2**).

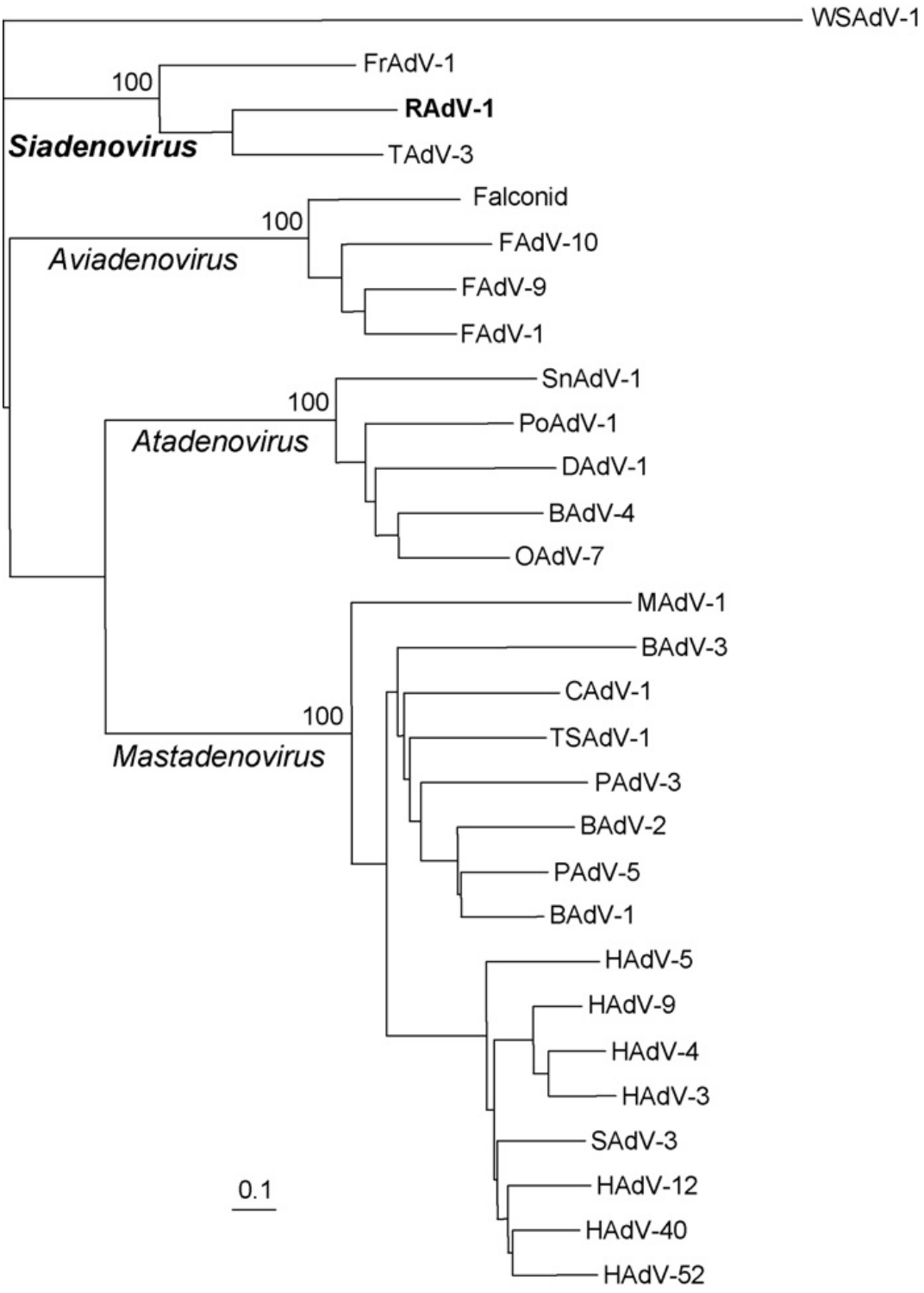


Fig. 2. Phylogenetic tree constructed by distance matrix analysis from an amino acid sequence alignment of the main capsid protein, hexon. RAdV-1 is shown in bold. Numbers at the nodes of the four main lineages refer to the level of confidence as determined by bootstrap analysis. Host abbreviations: B, bovine; C, canine; D, duck; F, fowl; Falcon-1, Northern Aplomado falcon; Fr, frog; H, human; M, murine; O, ovine; P, porcine; Po, possum; R, raptor; S, simian; Sn, snake; T, turkey; TS, tree shrew; WS, white sturgeon.