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:	***2015.015aM***	(to be completed by ICTV officers)

Short title: Removal of the species *Simian Virus 10* from the family *Paramyxoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)					
	1 ☒	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☐	**10** ☒

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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)	

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 15, 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 7: **REMOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.015aM***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Simian Virus 10

The present taxonomic position of these taxon/taxa:

Genus:	***Respirovirus***
Subfamily:	***Paramyxovirinae***
Family:	***Paramyxoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	**YES**

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Simian virus 10 (SV-10, also known as simian agent 10 [SA-10]), the only member of the species *Simian virus 10*, was obtained from ATCC and its genome completely sequenced. The virus was found to be closely related to, and indistinguishable from, human parainfluenzavirus 3 (HPIV-3; family Paramyxoviridae, subfamily *Paramyxovirinae*, genus *Respirovirus*; species *Human parainfluenzavirus 3*).
Details of the comparison between SV-10 and HPIV-3 include:

1. Identical genome nucleotide lengths.
2. Identical sets of genes (N, P/C/D, M, F, HN, L) with identical gene lengths, identical spacing, and almost-identical transcription and editing signals.
3. Identical sets of proteins with identical lengths except for minor differences for P and HN (which also have differences between certain HPIV-3 strains).
4. The percent nucleotide sequence identity between SV-10 and 5 strains of HPIV-3 was 96.0% to 98.6%, with the percent difference between SV-10 and the HPIV3 strains being in the same range as between the various HPIV-3 strains.

We conclude that SV-10 is a strain of HPIV-3 and does not warrant classification in a separate species from *Human parainfluenzavirus 3*.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Kumar et al, J Virol, 2010, 84:13068-13070 (see below).

P. L. Collins participated in this work as a US government employee and has not relinquished copyright; therefore, this article is supplied below.

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.

JOURNAL OF VIROLOGY, Dec. 2010, p. 13068–13070 Vol. 84, No. 24
0022-538X/10/$12.00 doi:10.1128/JVI.01928-10

Letter to the Editor

Identification of Simian Agent 10 as Human Parainfluenza Virus Type 3 Suggests Transmission of a Human Virus to an African Monkey[▽]

The use of nonhuman primates in biomedical research has led to the isolation of many simian viruses (4, 5). These viruses were given either consecutive SV (simian virus; for isolates from Asian monkeys) or SA (simian agent; for isolates from African monkeys) numbers (7, 10). SA10 was first isolated from the mouth of a samango monkey (*Cercopithecus mitis*) in 1963 (10). Based on serological findings (10), SA10 has long been classified as a distinct simian virus in the genus *Respirovirus* within the family *Paramyxoviridae* (2, 7).

We obtained SA10 from the ATCC and determined a complete consensus sequence for the genome using standard procedures (9). The genome of SA10 was determined to be 15,462 nucleotides (nt) in length (GenBank accession number HM583801), which is identical to that of human parainfluenza virus type 3 (HPIV3). Comparison with full-length genome sequences of other members of the family *Paramyxoviridae* showed that SA10 clustered with HPIV3. The extent of nucleotide sequence difference between SA10 and the various strains of HPIV3 is the same as that between the HPIV3 strains (Table 1).

The general features of the genome of SA10 (Fig. 1a) are identical to those of the genome of HPIV3. Like HPIV3, the P gene of SA10 contains an additional open reading frame (ORF) encoding the accessory C protein and a putative RNA editing site, ^{2498}UUUUUUCCCCC^{2508}, that is identical in position and sequence to that of HPIV3 (3). Like HPIV3, the insertion of two G residues at this site by the RNA editing mechanism would cause a frameshift and create an ORF encoding a D protein.

Furthermore, SA10 is identical to HPIV3 with regard to the nucleotide lengths of all of the genes, the exact spacing of each gene within the genome and within the respective hexamer subunits (8), and the lengths of the leader, trailer, and extragenic regions (Fig. 1a). The predicted lengths of the unmodified encoded proteins also are identical to those of various strains of HPIV3, with some heterogeneity in the predicted P and HN protein lengths, whereas the lengths of the other proteins are invariant among the HPIV3 strains and SA10. Analysis using 17 HPIV3 HN protein sequences showed that the SA10 HN protein sequence clustered with those of the HPIV3 strains (Fig. 1b). The cleavage site of SA10 is ^{104}DPRTKR ↓ F^{110}, which conforms to the furin cleavage site (underlining indicates the basic amino acids in the cleavage site).

The veritable identity of SA10 with HPIV3 suggests that SA10, rather than being a simian virus, is a strain of HPIV3. In particular, the few differences that occur between SA10 and various HPIV3 strains are of the same frequency as those occurring among the HPIV3 strains. A more likely possibility is that HPIV3 had been transmitted to the monkey from human handlers. A serologic survey of Indonesian macaques showed that nearly half of the sampled wild adult animals were seropositive for HPIV3, whereas no seropositive animals among the sampled wild infant, juvenile, and subadult animals were observed, implying that transmission can occur frequently, even to wild animals (6). In particular, human respiratory syncytial virus was originally isolated from captive chimpanzees and initially was called "chimpanzee coryza agent" (1) but was quickly recognized as a human pathogen and not a natural pathogen of chimpanzees. The present findings on SA10 clarify the taxonomy of *Paramyxoviridae*, illustrate that host range

TABLE 1. Nucleotide sequence identity among the complete genome sequences of the indicated viruses

Virus	% sequence identity among complete genome sequences of[a]:								
	SA10	HPIV3 strain					BPIV3	SPIV3	HPIV1
		14702	GP	LZ22	JS	ZHYMgz01			
SA10		98.6	96.6	96.0	97.4	96.0	78.5	78.2	60.8
HPIV3 14702			96.4	94.7	98.2	94.6	78.4	78.3	60.8
HPIV3 GP				95.0	97.1	94.8	78.4	78.3	60.6
HPIV3 LZ22					95.2	99.1	78.1	77.9	60.6
HPIV3 JS						95.1	78.3	78.1	60.7
HPIV3 ZHYMgz01							78.2	78.0	60.6
BPIV3								92.5	59.9
SPIV3									60.1

[a] BPIV3, bovine parainfluenza virus type 3; SPIV3, swine parainfluenza virus type 3.

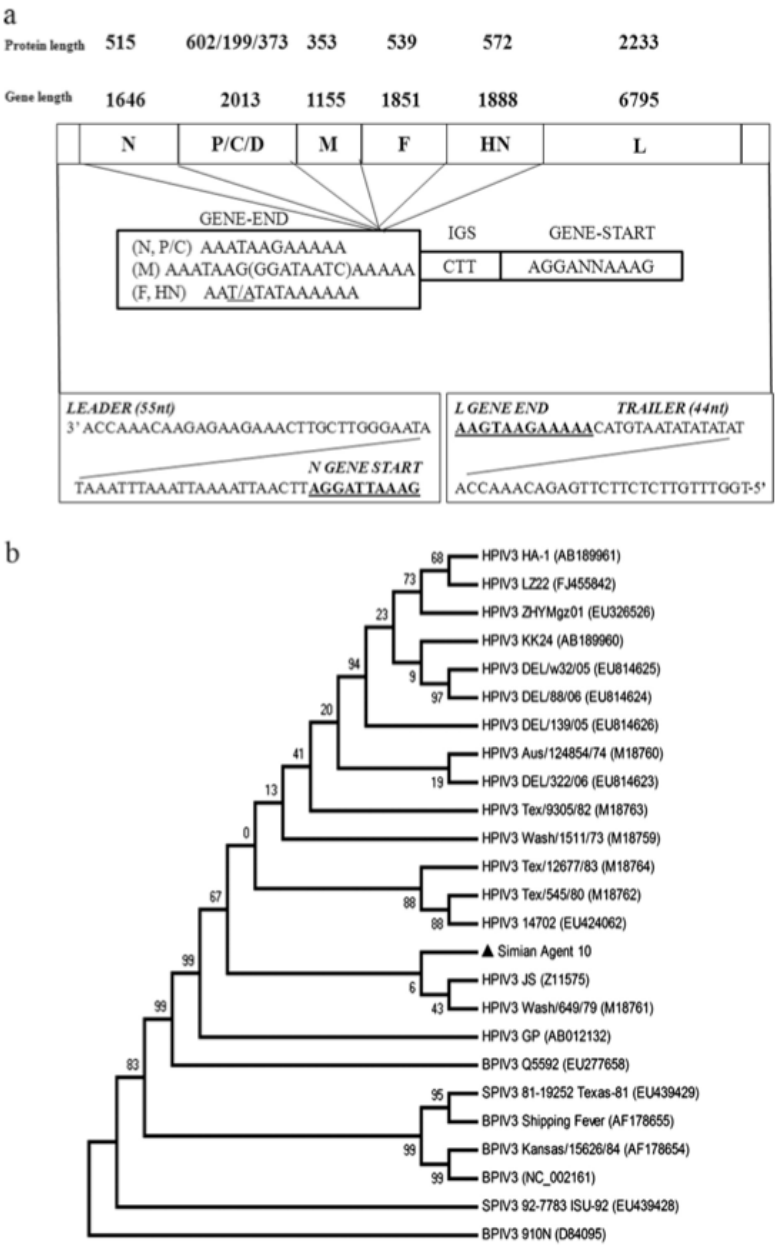

FIG. 1. SA10 genome map and phylogeny. (a) The genome of SA10 is shown in 3′-to-5′ orientation. The six genes are identified by their encoded proteins. The nucleotide length of each gene is shown above the map, as well as the amino acid length(s) of the unmodified predicted protein(s). The sequences of the 3′-extragenic leader and 5′-extragenic trailer regions are shown below the map. Also shown are the structures of the gene junctions, including the gene-end and gene-start transcription signals and the intergenic sequences (IGS). All sequences are positive sense. As is the case with HPIV3, the M gene of SA10 terminates with the elements of the gene-end sequence that appear to contain an insertion of 8 nt (in parentheses), as follows: 5′ AAATAAG(GGATAATC)AAAAA 3′. This is identical to HPIV3, with the difference of a single nucleotide [5′ AAATAAG(AGATAATC)AAAAA 3′, difference underlined] (11). (b) Phylogenetic tree of SA10 with the other 17 strains of HPIV3, 5 strains of bovine parainfluenza virus type 3 (BPIV3), and 2 strains of swine parainfluenza virus type 3 (SPIV3), based on the amino acid sequence of the HN protein and constructed as described above. The tree was constructed using the maximum parsimony method using MEGA 4 (Molecular Evolutionary Genetics Analysis 4) software (12), with bootstrap values calculated for 1,000 replicates.

identification can be ambiguous, and provide a cautionary tale for hasty virus classification.

Nucleotide sequence accession number. The sequence of SA10 has been deposited in GenBank under accession number HM583801.

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The views expressed herein do not necessarily reflect the official policies of the Department of Health and Human Services, nor does mention of trade names, commercial practices, or organizations imply endorsement by the U.S. Government.

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