This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2018.002S*** | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)**Change the name of species *Avian sapelovirus* (genus *Sapelovirus)* to *Anativirus A* and move it to a new genus named *Anativirus*.** |
|  |
| **Author(s):** |
| Roland Zell, Alexander E. Gorbalenya, Tapani Hovi, Andrew M.Q. King, Nick J. Knowles, A. Michael Lindberg, M. Steven Oberste, Ann C. Palmenberg, Gabor Reuter, Peter Simmonds, Tim Skern, Caroline Tapparel, Katja C. Wolthers, Patrick C.Y. Woo |
| **Corresponding author with e-mail address:** |
| Roland Zell (roland.zell@med.uni-jena.de)  |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Picornaviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 15/06/2018 |
| Date of this revision (if different to above): |       |

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| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

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| --- |
| **Name of accompanying Excel module:** **2018.002S.N.v1.Anativirus** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
 |

**Rename the species *Avian sapelovirus* (genus *Sapelovirus*) to *Anativirus A.* Create 1 new picornavirus genus (*Anativirus*) and move *Anativirus A* from the genus *Sapelovirus* to *Anativirus*.**

The picornavirus supergroup 3 (SG3) presently comprises three genera *Enterovirus*, *Sapelovirus*, *Rabovirus* as well as a number of c. 50 yet unassigned sapelo-like viruses. Characteristic features of these three genera are the sequence similarities of the P1 capsid protein precursor, 2Chel, 3Cpro and 3Dpol proteins. One additional feature concerns the 2A protein. Its function was revealed for enteroviruses only: 2A is a chymotrypsin-like proteinase (2Apro) with a cysteine residue in the catalytic triade. Alignment of 2A sequences of SG3 picornaviruses indicates that also the sapelovirus and rabovirus 2A protein could have proteinase function. However, members of *Avian sapelovirus,* one of three acknowledged sapelovirus species, lack this proteinase. In addition, the leader protein of avian sapeloviruses is very long compared to the leader proteins of *Sapelovirus A* and *B*. These findings and available sequence data of c. 50 sapelo-like viruses suggest a revision of the *Sapelovirus* genus.

This is the first of a number of proposals aimed to develop a revised and up-to-date taxonomy of *Sapelovirus* and unassigned sapelo-like viruses. The present proposal recommends to create a novel picornavirus genus, to be named *Anativirus*, that comprises the avian sapeloviruses. For consistency, the species *Avian sapelovirus* should be renamed (proposed name: *Anativirus A*).

**Relation of anativiruses to other picornaviruses:**

- Anativiruses have a typical picornavirus layout:

 5'-UTRIRES-IV[L-1A-1B-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

 (compare Fig. 1 of supporting material)

- Anativiruses possess typical hallmarks of picornaviruses:

 capsid proteins: 1B, 1C, 1D have **rhv** domains with drug-binding site,

 2Chel: **G**xx**G**x**GKS** motif of helicases,

 3BVPg: **Y-3** residue,

 3Cpro: **C**x**CG**x14**G**x**H** motif,

 3Dpol: **KDE**, **PSG**, **YGDD**, **FLKR** motifs

- Phylogenetic analyses indicate a distinct clade that clusters with picornaviruses of SG 3 (*Enterovirus, Rabovirus, Sapelovirus*) in the P1, 2C, 3C and 3D trees (compare Figs. 2-5 of supporting material).

**Distinguishing features of anativiruses compared to sapelo-, entero- and raboviruses:**

- Whereas sapeloviruses A and B as well as the entero- and raboviruses have a 2A protein with a GxCGx10G motif and a length of c. 150-280 amino acids, anativiruses lack a 2A protein with a proteinase motif. Anativiruses have a very short 2A peptide with a length of only 6 amino acids. Due to the lack of 2Apro activity, a Q1301/G cleavage site is assumed at the N-terminus of the anativirus 2A peptide (Fig. 1).

- Anativiruses have long leader protein (451 aa).

- Anativiruses have a long 3' untranslated region (238 nt)

- Great divergence of P1, 2Chel, 3Cpro and 3Dpol justify assignment of anativiruses to a novel genus (campare Table 1).

**Table 1: Amino acid divergence\***

 ***Anativirus A* (duck picornavirus TW90A)**

 **P1 2Chel 3Cpro 3Dpol**

phacovirus [Pf-CHK1/PhV] (unassigned) 0.57 0.56 0.55 0.47

chicken picornavirus [UCC/PhV] (unassigned)\*\* 0.58 0.56 0.56 -

quail picornavirus [QPV1/HUN/2010] (unassigned) 0.56 0.57 0.55 0.47

pigeon picornavirus B [03/641] (unassigned) 0.63 0.57 0.54 0.47

pigeon picornavirus B [GAL-7/2010/HUN] (unassigned) 0.63 0.57 0.54 0.47

pigeon picornavirus A [03/603-7] (unassigned)\*\* - - 0.55 0.47

***Sapelovirus A*** (porcine sapelovirus [V13]) 0.56 0.60 0.55 0.44

***Sapelovirus B*** (simian sapelovirus 1 [2383]) 0.58 0.56 0.52 0.37

***Sapelovirus B*** (simian sapelovirus 2 [VRDL1]) 0.59 0.57 0.53 0.37

***Sapelovirus B*** (simian sapelovirus 3 [WUHARV sapelovirus 1]) 0.58 0.56 0.52 0.38

***Rabovirus A*** (rabovirus A1 [Berlin/Jan2011/0572]) 0.60 0.60 0.57 0.43

***Enterovirus A*** (enterovirus A71 [BrCr]) 0.65 0.60 0.57 0.48

***Enterovirus B*** (coxsackievirus B1 [Japan]) 0.66 0.60 0.62 0.46

***Enterovirus C*** (human poliovirus 1 [Mahoney]) 0.66 0.61 0.60 0.46

***Enterovirus D*** (enterovirus D68 [Fermon]) 0.66 0.64 0.64 0.46

***Enterovirus E*** (enterovirus E1 [LC-R4]) 0.63 0.60 0.59 0.46

***Enterovirus F*** (enterovirus F1 [BEV-261]) 0.64 0.62 0.60 0.47

***Enterovirus G*** (enterovirus G1 [UKG/410/73]) 0.65 0.62 0.60 0.46

***Enterovirus H*** (enterovirus H1 [A-2 plaque virus]) 0.63 0.61 0.58 0.47

***Enterovirus I*** (enterovirus I1 [19CC]) 0.64 0.61 0.61 0.46

***Enterovirus J*** (enterovirus J1 [1631]) 0.64 0.60 0.61 0.45

***Enterovirus K*** (enterovirus K1 [rodent/Ee/Pico V/NX2015]) 0.63 0.65 0.64 0.48

***Enterovirus L*** (enterovirus L1 [SEV-gx]) 0.65 0.60 0.62 0.45

***Rhinovirus A*** (human rhinovirus A9 [ATCC VR-489]) 0.69 0.63 0.66 0.45

***Rhinovirus B*** (human rhinovirus B3 [FEB]) 0.68 0.62 0.61 0.47

***Rhinovirus C*** (human rhinovirus C3 [HRV-QPM]) 0.70 0.63 0.65 0.48

\* number of amino acid differences per site

\*\* only partial sequence available

**Type species of the genus:**

Duck picornavirus strain TW90A (GenBank acc. no. AY563023)

**Species demarcation criteria:**

not applicable

**Origin of name:**

**Anati**virus, from the ***Anati****dae*, the family of birds that includes ducks, geese and swans.

| **References:** |
| --- |
| Tseng CH, Tsai HJ. 2007. Sequence analysis of a duck picornavirus isolate indicates that it together with porcine enterovirus 8 and simian picornavirus type 2 should be assigned to a new picornavirus genus. Virus Res 129(2):104-114. |



**Figure 1:** Comparison of the genome organisation of anativirus and the sapeloviruses (schematic depiction). The open reading frames are indicated by boxes. The names and lengths of the deduced proteins are presented. Positions of putative 3Cpro cleavage sites are indicated by a ▼. The 1AB processing site is indicated by a ¶ and the putative 2Apro cleavage site by a ↓.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Seventy-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, ***species names*** and—if available—types and common names (in round brackets). Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 13,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 3:**  Phylogenetic analysis of picornavirus **2Chel** using Bayesian tree inference (MrBayes 3.2). Seventy-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, ***species names*** and—if available—types and common names (in round brackets). Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 16,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 4:**  Phylogenetic analysis of picornavirus **3Cpro** using Bayesian tree inference (MrBayes 3.2). Seventy-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, ***species names*** and—if available—types and common names (in round brackets). Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 14,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 5:**  Phylogenetic analysis of picornavirus **3Dpol** using Bayesian tree inference (MrBayes 3.2). Seventy-eight picornavirus sequences of the *Enterovirus/Rabovirus/Sapelovirus* supergroup (SG3) were retrieved from GenBank; the newt ampivirus sequence served as outgroup [Note: the supergroup does not imply a taxonomic entity but reflects phylogenetic clustering of the respective genera observed in different tree inference methods (NJ, ML, Bayesian MCMC)]. Presented are GenBank accession numbers, ***genus*** ***names***, ***species names*** and—if available—types and common names (in round brackets). Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 21,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.