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:** | ***2018.007S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **1 new species (*Passerivirus B*) in the genus *Passerivirus*** | | | |
|  | | | |
| **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](mailto: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**

|  |
| --- |
| **Name of accompanying Excel module:** **2018.007S.N.v1.Passerivirus\_sp** |

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. |

**Create 1 new species (Passerivirus B) in the genus *Passerivirus***

The genus *Passerivirus* presently consists of only 1 species, *Passerivirus A* (host: pale thrush, *Turdus pallidus*). A novel, passerivirus-like picornavirus—waxbill passerivirus [waxbill/DB01/HUN/2014]—has been detected in faecal specimens collected from estrildid finches (*Uraeginthus spec.*). The virus was detected in home-reared finches (3 diseased birds) associated with enteritis (Pankovics et al. 2018).

**Relation to other picornaviruses:**

- Genome layout of waxbill passerivirus:

5'-UTRIRES-V[L/1A-1B-1C-1D/2AH-box/NC-2B-2Chel/3A-3B1VPg-3B2VPg-3Cpro-3Dpol]3'UTR

(compare Fig. 1 of supporting material)

- waxbill passerivirus has typical hallmarks of picornaviruses:

- waxbill passerivirus has a L protein,

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

- 2A: **H-box/NC** sequence motif,

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

- 3BVPg: **Y-3** residue, passeriviruses have two putative 3BVPg peptides,

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

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

- Phylogenetic analyses indicate that waxbill passerivirus clusters with *Passerivirus A* (compare Figs. 2-5 of supporting material).

**Distinguishing features of waxbill passerivirus compared to *Passerivirus A*:**

1. Waxbill passerivirus has a different host compared to *Passerivirus A* (*Estrildidae* vs. *Turdidae*).

2. Waxbill passerivirus has a longer **L protein** (413 aa vs. >312 aa) of *Passerivirus A*.

3. **Sequence divergences** (uncorrected p-distances) of all relevant genome regions suggest a distinct species:

- P1: nt divergence 0.53, aa divergence 0.59;

- 2Chel: nt divergence 0.37, aa divergence 0.35;

- 3Cpro: nt divergence 0.35, aa divergence 0.33;

- 3Dpol: nt divergence 0.29, aa divergence 0.14 (compare Table 1);

**Table 1: Nucleotide and amino acid divergence\***

**P1 2Chel 3Cpro 3Dpol**

**Passerivirus B vs. nt aa nt aa nt aa nt aa**

*Passerivirus A* 0.530 0.593 0.371 0.349 0.354 0.328 0.285 0.144

*Cadicivirus A* 0.642 0.817 0.583 0.731 0.609 0.741 0.528 0.637

Cadicivirus B\*\* 0.643 0.799 0.594 0.726 0.650 0.778 0.556 0.635

*Gallivirus A* 0.640 0.783 0.486 0.570 0.572 0.694 0.399 0.374

*Kobuvirus A* 0.607 0.751 0.512 0.542 0.541 0.670 0.461 0.434

*Livupivirus A* 0.615 0.758 0.538 0.683 0.645 0.764 0.427 0.496

*Megrivirus A* 0.643 0.823 0.584 0.714 0.645 0.783 0.503 0.587

*Oscivirus A1* 0.637 0.794 0.553 0.629 0.595 0.753 0.419 0.450

Poecivirus A\*\* 0.660 0.826 0.590 0.715 0.625 0.775 0.517 0.615

Rafivirus A\*\* 0.630 0.796 0.592 0.709 0.645 0.845 0.468 0.509

Rafivirus B\*\* 0.618 0.784 0.611 0.713 0.647 0.828 0.484 0.513

*Rosavirus A* 0.670 0.839 0.562 0.666 0.659 0.785 0.513 0.595

Rosavirus B\*\* 0.668 0.835 0.552 0.675 0.622 0.762 0.530 0.602

Rosavirus C\*\* 0.684 0.834 0.549 0.667 0.623 0.784 0.546 0.607

*Sakobuvirus A* 0.618 0.750 0.499 0.547 0.586 0.711 0.427 0.417

*Salivirus A* 0.608 0.754 0.500 0.559 0.597 0.749 0.471 0.524

*Sicinivirus A* 0.594 0.717 0.482 0.512 0.468 0.527 0.385 0.365

\* number of base and amino acid differences per site

\*\* to be proposed

**Exemplar:**

***Passerivirus B***, passerivirus B1 (waxbill passerivirus) [waxbill/DB01/HUN/2014],

GenBank acc. no. MF977321

**Species demarcation criteria:**

Based on available sequence data, preliminary species demarcation criteria were defined.

Members of a species of genus *Passerivirus*:

- share a common genome organization,

- share greater than 70% aa identity in the polyprotein,

- share greater than 70% aa identity in the P1,

- share greater than 75% aa identity in the non-structural proteins 2C + 3CD.

| **References:** |
| --- |
| Pankovics P, Boros Á, Phan TG, Delwart E, Reuter G. A novel passerivirus (family Picornaviridae) in an outbreak of enteritis with high mortality in estrildid finches (Uraeginthus sp.) Arch Virol, 2018;163(4):1063-1071. |



**Figure 1:** Schematic depiction of the genome organisation of waxbill passerivirus (proposed species: *Passerivirus B*). The open reading frame is indicated by a box. Positions of putative 3Cpro cleavage sites are indicated by ▼. The names and lengths of the deduced proteins are presented.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Seventy-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/ Sakobuvirus/ Sicinivirus/Rosavirus* supergroup 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***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 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-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup 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***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 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-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup 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***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 4,000,000 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-five picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Megrivirus/Oscivirus/Passerivirus/Salivirus/Sakobuvirus/ Sicinivirus/Rosavirus* supergroup 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***, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Yet unassigned viruses are printed in blue. Proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 6,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.