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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.009S*** | |  |
| **Short title:** Create five new genera (*Hemipivirus*, *Myrropivirus*, *Pemapivirus*, *Symapivirus*, *Tropivirus*), each with one species (*Hemipivirus A*, *Myrropivirus A*, *Pemapivirus A*, *Symapivirus A*, *Tropivirus A*) | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Zell R, Gorbalenya AE, Hovi T, Knowles NJ, Lindberg M, Oberste S, Palmenberg AC, Reuter G, Simmonds P, Skern T, Tapparel C, Wolthers K, Woo P | | roland.zell@med.uni-jena.de; a.e.gorbalenya@lumc.nl; tapani.hovi@thl.fi; nick.knowles@pirbright.ac.uk; michael.lindberg@lnu.se; soberste@cdc.gov; acpalmen@wisc.edu; reuter.gabor@gmail.com; peter.simmonds@ndm.ox.ac.uk; timothy.skern@meduniwien.ac.at; caroline.tapparel@unige.ch; k.c.wolthers@amc.uva.nl; pcywoo@hkucc.hku.hk | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | Jena University Hospital [RZ]  Leiden University Medical Center [AEG]  National Institute for Health and Welfare [TH]  The Pirbright Institute [NJK]  Linnaeus University Kalmar [ML]  Centers for Disease Control and Prevention [SO]  University of Wisconsin [ACP]  University of Pécs [GR]  University of Oxford [PS]  Medical University of Vienna [TS]  University of Geneve [CT]  Universiteit van Amsterdam [KW]  University of Hong Kong [PW] | | | | |
| **Corresponding author** | | | |
| **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: | | | 21/05/2019 |
| Date of this revision (if different to above): | | |  |

|  |
| --- |
| **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:** **2019.009S.N.v1.5newgen\_Hemipi-Myrropi-Pemapi-Symapi-Tropivirus.xlsx** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_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, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Create five new genera (*Hemipivirus***, ***Myrropivirus***, ***Pemapivirus***, ***Symapivirus***, ***Tropivirus*), each with one species (*Hemipivirus A***, ***Myrropivirus A***, ***Pemapivirus A***, ***Symapivirus A***, ***Tropivirus A*)**

Novel picornaviruses of reptiles and fish have been described by Shi et al. (2018).

These viruses with similarity to picornaviruses of supergroup 2 were detected in pooled tissue samples of the following hosts:

|  |  |  |  |
| --- | --- | --- | --- |
| **Virus name** | **Host** | **Specimens** | **Proposed genus/species** |
| Hainan oriental leaf-toed gekko picornavirus | *Hemidactylus bowringii* | gut, liver, lungs | ***Hemipivirus****/Hemipivirus A* |
| Chinese water snake picornavirus | *Myrrophis chinensis* | gut, liver, lungs | ***Myrropivirus****/Myrropivirus A* |
| Chinese softshell turtle picornavirus  Chinese broad-headed pond turtle picornavirus | *Pelodiscus sinensis*  *Mauremys (Chinemys) megalocephala* | gut, liver, lungs | ***Pemapivirus****/Pemapivirus A* |
| Wenling triplecross lizardfish picornavirus | *Synodus macrops* | gut, liver, gill | ***Symapivirus****/Symapivirus A* |
| Guangdong Chinese water skink picornavirus | *Tropidophorus sinicus* | gut, liver, lungs | ***Tropivirus****/Tropivirus A* |

However, the new viruses differ significantly from the known picornaviruses of supergroup 2. No virus was isolated yet.

**A. Genus *Hemipivirus***

**Relation to other picornaviruses:**

- Hemipiviruses have a typical picornavirus genome layout:

5'-UTR[L-1AB-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

- Hemipiviruses possess typical hallmarks of picornaviruses:

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

2A: H-box/NC sequence motif,

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 distinct branches that cluster with sequences of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus*) in the P1 and 3CD trees (compare Figs. 1 & 2 of supporting material).

**Distinguishing features of hemipiviruses compared to other viruses of picornavirus**

**supergroup 2:**

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 33 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from 77.9 to 85.7% for P1, 63.7-71.9% for 2Chel, 66.7-85.1% for 3Cpro and 52.8-65.5% for 3Dpol (compare Table 1). Divergence to sequences of other picornavirus supergroups is even greater.

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

**hemipivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*Dicipivirus Cadicivirus A* 0.828 0.708 0.743 0.655

*Cadicivirus B* 0.844 0.676 0.738 0.652

*Gallivirus Gallivirus A* 0.853 0.680 0.806 0.627

*Kobuvirus Aichivirus A* 0.803 0.706 0.810 0.615

*Aichivirus B* 0.790 0.706 0.828 0.597

*Aichivirus C* 0.789 0.699 0.790 0.607

*Aichivirus D* 0.818 0.719 0.794 0.613

*Aichivirus E* 0.792 0.645 0.851 0.600

*Aichivirus F* 0.779 0.664 0.800 0.578

*Livupivirus Livupivirus A* 0.805 0.678 0.828 0.620

*Ludopivirus*† *Ludopivirus A*† 0.804 0.707 0.818 0.615

*Megrivirus Megrivirus A* 0.855 0.678 0.672 0.615

*Megrivirus B* 0.853 0.688 0.667 0.585

*Megrivirus C* 0.845 0.696 0.718 0.598

*Megrivirus D* 0.843 0.701 0.709 0.587

*Megrivirus E* 0.843 0.684 0.665 0.608

*Myrropivirus*† *Myrropivirus A*† 0.841 0.655 0.723 0.528

*Oscivirus Oscivirus A* 0.830 0.662 0.833 0.557

*Passerivirus Passerivirus A* 0.796 0.685 0.799 0.608

*Passerivirus B* 0.817 0.680 0.777 0.592

*Poecivirus Poecivirus A* 0.852 0.712 0.734 0.604

*Rafivirus Rafivirus A* 0.808 0.681 0.844 0.619

*Rafivirus B* 0.803 0.652 0.790 0.626

*Rafivirus C*† 0.799 0.710 0.780 0.631

*Rosavirus Rosavirus A* 0.841 0.670 0.712 0.597

*Rosavirus B* 0.846 0.666 0.743 0.607

*Rosavirus C* 0.830 0.670 0.738 0.593

*Sakobuvirus Sakobuvirus A* 0.799 0.694 0.801 0.586

*Salivirus Salivirus A* 0.789 0.690 0.840 0.648

*Sicinivirus Sicinivirus A* 0.812 0.693 0.816 0.583

*Pemapivirus*† *Pemapivirus A*† 0.864 0.708 0.768 0.572

*Tropivirus*† *Tropivirus A*† 0.825 0.637 0.745 0.595

*Symapivirus*† *Symapivirus A*† 0.857 0.711 0.827 0.641

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

**Hemipivirus A**, hemipivirus A1 (Hainan oriental leaf-toed gecko picornavirus) strain LPXYC213122, GenBank acc. no. MG600089

**Species demarcation criteria:**

not applicable

**Origin of name:**

**hemipivirus:** derived from ***Hemi****dactylus bowringii* (host) and **pi**corna**virus**

**A. Genus *Myrropivirus***

**Relation to other picornaviruses:**

- Myrropiviruses have a typical picornavirus genome layout:

5'-UTR[L-1AB-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Figure 1 in Supporting Material)

- Myrropiviruses possess typical hallmarks of picornaviruses:

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

2A2: H-box/NC sequence motif,

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

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

3Cpro: **C**x**CG**x11**G**x**H** motif,

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

- Phylogenetic analyses indicate a distinct branch that clusters with sequences of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus*) in the P1 and 3CD trees (compare Figs. 1 & 2 of supporting material).

**Distinguishing features of myrropivirus A1 compared to other viruses of picornavirus**

**supergroup 2:**

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 33 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from 71.1 to 82.4% for P1, 60.0-73.5% for 2Chel, 68.9-82.4% for 3Cpro and 52.8-63.1% for 3Dpol (compare Table 4). Divergence to sequences of other picornavirus supergroups is even greater.

**Table 4: Amino acid divergence\***

**myrropivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*Dicipivirus Cadicivirus A* 0.711 0.704 0.741 0.576

*Cadicivirus B* 0.725 0.702 0.725 0.595

*Gallivirus Gallivirus A* 0.786 0.674 0.813 0.575

*Kobuvirus Aichivirus A* 0.792 0.709 0.801 0.580

*Aichivirus B* 0.794 0.679 0.791 0.588

*Aichivirus C* 0.788 0.700 0.814 0.579

*Aichivirus D* 0.796 0.717 0.797 0.610

*Aichivirus E* 0.792 0.681 0.824 0.574

*Aichivirus F* 0.788 0.678 0.801 0.590

*Livupivirus Livupivirus A* 0.753 0.639 0.824 0.546

*Ludopivirus*† *Ludopivirus A*† 0.796 0.673 0.809 0.588

*Megrivirus Megrivirus A* 0.823 0.638 0.717 0.619

*Megrivirus B* 0.775 0.633 0.670 0.576

*Megrivirus C* 0.824 0.643 0.712 0.609

*Megrivirus D* 0.805 0.667 0.714 0.578

*Megrivirus E* 0.802 0.673 0.728 0.580

*Oscivirus Oscivirus A* 0.778 0.647 0.813 0.532

*Passerivirus Passerivirus A* 0.809 0.685 0.790 0.571

*Passerivirus B* 0.803 0.705 0.757 0.570

*Poecivirus Poecivirus A* 0.810 0.726 0.690 0.601

*Rafivirus Rafivirus A* 0.771 0.665 0.809 0.581

*Rafivirus B* 0.793 0.660 0.789 0.572

*Rafivirus C*† 0.786 0.681 0.759 0.583

*Rosavirus Rosavirus A* 0.728 0.626 0.705 0.557

*Rosavirus B* 0.720 0.600 0.689 0.544

*Rosavirus C* 0.733 0.622 0.710 0.562

*Sakobuvirus Sakobuvirus A* 0.790 0.717 0.807 0.560

*Salivirus Salivirus A* 0.779 0.688 0.814 0.631

*Sicinivirus Sicinivirus A* 0.814 0.696 0.821 0.560

*Hemipivirus*†  *Hemipivirus A*† 0.738 0.655 0.723 0.529

*Pemapivirus*† *Pemapivirus A*† 0.759 0.655 0.726 0.528

*Tropivirus*† *Tropivirus A*† 0.781 0.622 0.732 0.565

*Symapivirus*† *Symapivirus A*† 0.807 0.735 0.773 0.603

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Myrropivirus A***, myrropivirus A1 (Guangdong Chinese water snake picornavirus) strain LPSF20501, GenBank acc. no. MG600081

**Species demarcation criteria:**

not applicable

**Origin of name:**

**myrropivirus**: derived from ***Myrro****phis chinensis* (host) and **pi**corna**virus**

**C. Genus *Pemapivirus***

**Relation to other picornaviruses:**

- Pemapiviruses have a typical picornavirus genome layout:

5'-UTR[L-1AB-1C-1D/2A1-2A2H-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Figure 1 in Supporting Material)

- Pemapiviruses possess typical hallmarks of picornaviruses:

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

2A2: H-box/NC sequence motif,

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

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

3Cpro: pemapivirus A1 with **C**x**CG**x14**G**x**H** motif,

pemapivirus A2 with **C**x**CG**x15**G**x**H** motif,

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

- Phylogenetic analyses indicate distinct branches that cluster with sequences of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus*) in the P1 and 3CD trees (compare Figs. 1 & 2 of supporting material).

- By convention, picornavirus types and species are distinguished on the basis of genus-specific amino acid divergences. p-Distances greater 30% indicate different species. Chinese softshell turtle picornavirus and Chinese broad-headed pond turtle picornavirus exhibit divergences of 30.4% for the polyprotein, 31.3% for P1 and 39.8% for VP1 sequences which may be borderline. Thus, the study group decided to await additional sequences before proposing a second pemapivirus species.

**Distinguishing features of pemapiviruses compared to other viruses of picornavirus**

**supergroup 2:**

- Pemapiviruses have two 2A proteins, the 2A1 protein is unique and has unknown function;

2A2 has a H-box/NC sequence motif.

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 33 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from 72.8 to 86.0% for P1, 64.0-76.1% for 2Chel, 72.4-87.3% for 3Cpro and 49.4-60.5% for 3Dpol (compare Table 2). Divergence to sequences of other picornavirus supergroups is even greater.

**Table 2: Amino acid divergence\***

**pemapivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*Dicipivirus Cadicivirus A* 0.763 0.751 0.750 0.600

*Cadicivirus B* 0.768 0.725 0.740 0.575

*Gallivirus Gallivirus A* 0.860 0.725 0.836 0.527

*Kobuvirus Aichivirus A* 0.776 0.728 0.868 0.543

*Aichivirus B* 0.796 0.746 0.842 0.521

*Aichivirus C* 0.784 0.752 0.853 0.529

*Aichivirus D* 0.783 0.761 0.842 0.554

*Aichivirus E* 0.799 0.713 0.820 0.546

*Aichivirus F* 0.795 0.733 0.813 0.530

*Livupivirus Livupivirus A* 0.762 0.726 0.803 0.516

*Ludopivirus*† *Ludopivirus A*† 0.797 0.710 0.840 0.576

*Megrivirus Megrivirus A* 0.818 0.677 0.721 0.605

*Megrivirus B* 0.804 0.640 0.701 0.565

*Megrivirus C* 0.831 0.683 0.767 0.603

*Megrivirus D* 0.830 0.674 0.755 0.563

*Megrivirus E* 0.821 0.674 0.725 0.582

*Myrropivirus*† *Myrropivirus A*† 0.752 0.655 0.739 0.530

*Oscivirus Oscivirus A* 0.821 0.720 0.829 0.494

*Passerivirus Passerivirus A* 0.803 0.738 0.818 0.546

*Passerivirus B* 0.827 0.733 0.840 0.560

*Poecivirus Poecivirus A* 0.807 0.729 0.763 0.597

*Rafivirus Rafivirus A* 0.771 0.699 0.801 0.533

*Rafivirus B* 0.771 0.692 0.827 0.524

*Rafivirus C*† 0.779 0.696 0.814 0.535

*Rosavirus Rosavirus A* 0.754 0.661 0.724 0.525

*Rosavirus B* 0.772 0.666 0.729 0.525

*Rosavirus C* 0.761 0.658 0.734 0.538

*Sakobuvirus Sakobuvirus A* 0.792 0.728 0.852 0.537

*Salivirus Salivirus A* 0.786 0.749 0.810 0.584

*Sicinivirus Sicinivirus A* 0.831 0.736 0.873 0.549

*Hemipivirus*† *Hemipivirus A*† 0.728 0.708 0.768 0.573

*Tropivirus*† *Tropivirus A*† 0.785 0.699 0.724 0.530

*Symapivirus*† *Symapivirus A*† 0.812 0.744 0.785 0.587

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Pemapivirus A***, pemapivirus A1 (Chinese softshell turtle picornavirus) strain WHJYGF74978, GenBank acc. no. MG600106

A second genome sequence, representing another type is available: pemapivirus A2 (Chinese broad-headed pond turtle picornavirus) strain WHWGC151314, GenBank acc. no. MG600108

**Species demarcation criteria:**

not applicable

**Origin of name:**

**pemapivirus**: derived from ***Pe****lodiscus sinensis* and ***Ma****uremys megalocephaas* (known hosts)

and **pi**corna**virus**

**D. Genus *Symapivirus***

**Relation to other picornaviruses:**

- Symapiviruses have a typical picornavirus genome layout:

5'-UTR[L-1AB-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Figure 1 in Supporting Material)

- Symapiviruses possess typical hallmarks of picornaviruses:

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

2A2: H-box/NC sequence motif,

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

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

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

3Dpol: **KDE**, **ASG**, **YGDD**, **FLKR** motifs.

- Phylogenetic analyses indicate a distinct branch that clusters with sequences of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus*) in the P1 and 3CD trees (compare Figs. 1 & 2 of supporting material).

**Distinguishing features of symapivirus A1 compared to other viruses of picornavirus**

**supergroup 2:**

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 33 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from 76.7 to 85.7% for P1, 67.9-76.0% for 2Chel, 72.9-84.0% for 3Cpro and 52.1-65.2% for 3Dpol (compare Table 5). Divergence to sequences of other picornavirus supergroups is even greater.

**Table 5: Amino acid divergence\***

**symapivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*Dicipivirus Cadicivirus A* 0.801 0.722 0.807 0.652

*Cadicivirus B* 0.798 0.723 0.768 0.614

*Gallivirus Gallivirus A* 0.851 0.713 0.790 0.569

*Kobuvirus Aichivirus A* 0.767 0.685 0.845 0.528

*Aichivirus B* 0.788 0.682 0.823 0.521

*Aichivirus C* 0.779 0.703 0.801 0.523

*Aichivirus D* 0.812 0.718 0.796 0.539

*Aichivirus E* 0.800 0.687 0.812 0.546

*Aichivirus F* 0.802 0.691 0.800 0.538

*Livupivirus Livupivirus A* 0.821 0.708 0.762 0.555

*Ludopivirus*† *Ludopivirus A*† 0.801 0.717 0.820 0.549

*Megrivirus Megrivirus A* 0.830 0.739 0.800 0.621

*Megrivirus B* 0.826 0.736 0.775 0.613

*Megrivirus C* 0.841 0.748 0.778 0.593

*Megrivirus D* 0.857 0.748 0.771 0.597

*Megrivirus E* 0.840 0.736 0.800 0.596

*Myrropivirus*† *Myrropivirus A*† 0.807 0.735 0.758 0.608

*Oscivirus Oscivirus A* 0.821 0.725 0.751 0.554

*Passerivirus Passerivirus A* 0.813 0.679 0.794 0.531

*Passerivirus B* 0.839 0.693 0.811 0.541

*Poecivirus Poecivirus A* 0.857 0.760 0.756 0.623

*Rafivirus Rafivirus A* 0.793 0.702 0.840 0.561

*Rafivirus B* 0.793 0.701 0.802 0.559

*Rafivirus C*† 0.805 0.729 0.801 0.592

*Rosavirus Rosavirus A* 0.789 0.711 0.762 0.580

*Rosavirus B* 0.799 0.714 0.729 0.621

*Rosavirus C* 0.802 0.715 0.762 0.604

*Sakobuvirus Sakobuvirus A* 0.784 0.691 0.839 0.541

*Salivirus Salivirus A* 0.783 0.688 0.830 0.591

*Sicinivirus Sicinivirus A* 0.844 0.698 0.837 0.558

*Hemipivirus*† *Hemipivirus A*† 0.815 0.712 0.804 0.640

*Pemapivirus*† *Pemapivirus A*† 0.810 0.744 0.765 0.586

*Tropivirus*† *Tropivirus A*† 0.829 0.733 0.772 0.608

\* number of amino acid differences per site

† proposed taxa

**Type species of genus:**

***Symapivirus A***, symapivirus A1 (Wenling triplecross lizardfish picornavirus) strain XYHYC185246, GenBank acc. no. MG600076

**Species demarcation criteria:**

not applicable

**Origin of name:**

**symapivirus**: derived from ***Sy****nodus* ***ma****crops* (host) and **pi**corna**virus**

**E. Genus *Tropivirus***

**Relation to other picornaviruses:**

- Tropiviruses have a typical picornavirus genome layout:

5'-UTR[L-1AB-1C-1D/2AH-box/NC-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

(compare Figure 1 in Supporting Material)

- Tropiviruses possess typical hallmarks of picornaviruses:

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

2A2: H-box/NC sequence motif,

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

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

3Cpro: **C**x**CG**x13**G**x**H** motif,

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

- Phylogenetic analyses indicate a distinct branch that clusters with sequences of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus*) in the P1 and 3CD trees (compare Figs. 1 & 2 of supporting material).

**Distinguishing features of tropivirus A1 compared to other viruses of picornavirus**

**supergroup 2:**

- **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 33 acknowledged and proposed species of picornavirus supergroup 2. The amino acid divergences range from 75.3 to 84.6% for P1, 60.9-73.0% for 2Chel, 64.9-86.2% for 3Cpro and 49.8-64.7% for 3Dpol (compare Table 3). Divergence to sequences of other picornavirus supergroups is even greater.

**Table 3: Amino acid divergence\***

**tropivirus A1 vs. member of ... P1 2Chel 3Cpro 3Dpol**

*Dicipivirus Cadicivirus A* 0.763 0.657 0.730 0.571

*Cadicivirus B* 0.785 0.660 0.692 0.581

*Gallivirus Gallivirus A* 0.846 0.693 0.862 0.585

*Kobuvirus Aichivirus A* 0.758 0.701 0.837 0.611

*Aichivirus B* 0.779 0.705 0.809 0.617

*Aichivirus C* 0.786 0.686 0.810 0.610

*Aichivirus D* 0.787 0.710 0.844 0.645

*Aichivirus E* 0.770 0.660 0.850 0.575

*Aichivirus F* 0.769 0.681 0.849 0.590

*Livupivirus Livupivirus A* 0.792 0.642 0.775 0.571

*Ludopivirus*† *Ludopivirus A*† 0.775 0.685 0.843 0.596

*Megrivirus Megrivirus A* 0.794 0.639 0.770 0.647

*Megrivirus B* 0.788 0.640 0.744 0.628

*Megrivirus C* 0.805 0.637 0.769 0.646

*Megrivirus D* 0.764 0.648 0.773 0.637

*Megrivirus E* 0.797 0.650 0.754 0.634

*Myrropivirus*† *Myrropivirus A*† 0.782 0.622 0.743 0.566

*Oscivirus Oscivirus A* 0.820 0.667 0.842 0.586

*Passerivirus Passerivirus A* 0.814 0.694 0.757 0.592

*Passerivirus B* 0.831 0.700 0.740 0.602

*Poecivirus Poecivirus A* 0.824 0.697 0.743 0.623

*Rafivirus Rafivirus A* 0.783 0.644 0.844 0.598

*Rafivirus B* 0.786 0.682 0.811 0.609

*Rafivirus C\*\** 0.782 0.672 0.784 0.638

*Rosavirus Rosavirus A* 0.775 0.620 0.649 0.498

*Rosavirus B* 0.776 0.609 0.692 0.519

*Rosavirus C* 0.753 0.620 0.659 0.510

*Sakobuvirus Sakobuvirus A* 0.786 0.695 0.838 0.613

*Salivirus Salivirus A* 0.770 0.701 0.862 0.634

*Sicinivirus Sicinivirus A* 0.845 0.694 0.842 0.594

*Hemipivirus*† *Hemipivirus A*† 0.760 0.637 0.745 0.594

*Pemapivirus*† *Pemapivirus A*† 0.786 0.669 0.724 0.530

*Symapivirus*† *Symapivirus A*† 0.830 0.730 0.778 0.606

\* number of amino acid differences per site

\*\* to be proposed

**Type species of genus:**

***Tropivirus A***, tropivirus A1 (Guangdong Chinese water skink picornavirus) strain ZGLXR119682, GenBank acc. no. MG600091

**Species demarcation criteria:**

not applicable

**Origin of name:**

**tropivirus**: derived from ***Tro****pidophorus sinicus* (host) and **pi**corna**virus**

| **References:** |
| --- |
| Shi M, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, Eden JS, Shen JJ, Liu L, Holmes EC, Zhang YZ. 2018. The evolutionary history of vertebrate RNA viruses. Nature 556:197-202. |

**Supporting material:**



**Legend to Figure 1:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Eighty picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus* supergroup were retrieved from GenBank; the entero- and cardiovirus sequences 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. The proposed names are printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Seventy-nine picornavirus sequences of the *Dicipivirus/Gallivirus/Kobuvirus/Livupivirus/Megrivirus/Oscivirus/Passerivirus/ Poecivirus/Sakobuvirus/Salivirus/Sicinivirus/Rafivirus/Rosavirus* supergroup were retrieved from GenBank; the entero- and cardiovirus sequences 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. The proposed name is printed in red and indicated by a dot (●). Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.