

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

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| **Code assigned:** | **2020.002S** |  |
| **Short title:** Create three new genera (*Danipivirus*, *Pygoscepivirus*, *Rajidapivirus*) including three new species (*Picornavirales*: *Picornaviridae*) |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Picornaviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 02/06/2020 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.002S.A.v1.Danipi-Pygoscepi-Rajidapivirus\_3ng3nsp.xlsx |

**Abstract**

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| Novel picornaviruses collected from tissue samples of the zebrafish (*Danio rerio*) and the sharpspine skate (*Okamejei acutispina*) as well as faecal samples of the gentoo penguin (*Pygoscelis papua*) exhibit unique properties of their genome organisation and sequence diversity. No viable virus was obtained. The viruses were named danipivirus, rajidapivirus and pygoscepivirus, respectively, after their hosts. The three viruses exhibit the genome layout of typical picornaviruses (i.e., 5'-UTRIRES[L/1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) but constitute the prototypes of three proposed genera each with one species.  |

**Text of proposal**

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| **Create three new genera, *Danipivirus*, *Pygoscepivirus*, *Rajidapivirus*, each with one species *Danupivirus A*, *Pygoscelivirus A*, *Rajidapivirus A***Novel picornaviruses have been identified in metagenomic studies. The zebrafish picornavirus (ZfPV) was detected in gut tissue of laboratory zebrafish (*Danio rerio*, wildtype AB line) kept in many laboratories worldwide (Altan et al. 2019). Pingu virus was discovered in cloacal swabs collected from gentoo penguins (*Pygoscelis papua*) of King George Island (de Souza et al. 2019). The Wenling sharpspine skate picornavirus was found in organ pools comprising gut, liver and gill of the sharpspine skate (*Okamejei acutispina*) caught in the East China Sea (Shi et al. 2018). These three picornaviruses are related to picornaviruses of supergroup 2 (*Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/ Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/ Poecivirus/Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus*) but distinguishing features justify creation of three new species of the new genera.

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| **Virus name** | **host** | **proposed genus/species** |
| zebrafish picornvirus | zebrafish (*Danio rerio*) | *Danipivirus/Danipivirus A* |
| pingu virus | gentoo penguin (*Pygoscelis papua*) | *Pygoscepivirus/Pygoscepivirus A* |
| Wenling sharpspine skate picornavirus | Wenling sharpspine skate (*Okamejei acutispina*) | *Rajidapivirus/Rajidapivirus A* |

The three viruses are characterised by short L proteins (c. 100 aa) with unknown function, uncleaved 1AB capsid protein and short 2A proteins (61-84 aa) with unknown function. The genome of danipivirus A1 (zebrafish picornavirus) has a length of 8298 nucleotides; the open reading frame (orf) encodes a single polyprotein of 2429 amino acids (aa). The genome of pygoscepivirus A1 (pingu virus) has a length of 7601 nucleotides encoding a polyprotein of 2192 aa. The rajidapivirus A1 (Wenling sharpspine skate picornavirus) has a length of 7947 nucleotides and an orf of 2322 aa. The sequence diversities of the P1, 2Chel and 3Cpro is high (50-88%) in comparisons with the respective proteins of other picornavirus species. For the 3Dpol, danipivirus A1 and rajidapivirus A1 show high diversities (57.8-69.1%) whereas the pygoscepivirus 3D protein exhibits lower diversity ranging from 40.0 to 65.2%. The P1 and 3D sequences of the three viruses cluster with sequences of the picornavirus supergroup 2 and constitute distinct branches in phylogenetic trees.**Relation to other picornaviruses:**- The danipiviruses, pygoscepiviruses and rajidapiviruses have a typical picornavirus genome layout: Zebrafish picornavirus:  5'-UTRIRES[L-1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR pingu picornavirus: 5'-UTRIRES[L-1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR Wenling sharpspine skate picornavirus: 5'-UTRIRES[L-1AB-1C-1D/2A-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR (compare Fig. 1 of supporting material)- The danipiviruses, pygoscepiviruses and rajidapiviruses possess typical hallmarks of picornaviruses:  **capsid proteins:** 1AB, 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 distinct branches of each of the three viruses though clustering with sequences of the picornavirus supergroup 2 (*Dicipivirus/Hemipivirus/ Gallivirus/Kobuvirus/Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/ Passerivirus/Pemapivirus/Poecivirus/Rafivirus/Rosavirus/Sakobuvirus/Salivirus/ Sicinivirus/Symapivirus/Tropivirus*) in the P1 and 3D trees (compare Figs. 2 & 3 of supporting material).**Distinguishing features:**- The three viruses comprise distinct branches in **phylogenetic analyses** (maximum likelihood trees). The pygoscepivirus A1 (pingu picornavirus) clusters with passeri-, sicini- and galliviruses in both phylogenetic trees. However, whereas these viruses have an 2A protein with similarity to H-box/NC proteins, the pygoscepivirus 2A lacks this similarity.- The three viruses exhibit **unique L** (96-104 aa) and **2A proteins** (61-84 aa). The function of both proteins is unknown. - Pygoscepivirus A1 (zebrafish picornavirus) has a very long **3A protein** (242 aa).- **Sequence divergences** (uncorrected p-distances) of orthologous proteins P1, 2Chel, 3Cpro and 3Dpol is high in pairwise comparisons with 40 acknowledged and proposed species of picornavirus supergroup 2. - **Danipivirus A1 (zebrafish picornavirus):** The amino acid divergences range from79.1 to 87.0% for P1, 71.2-77.0% for 2Chel,75.4-86.6% for 3Cpro and 57.8-67.3% for 3Dpol (compare Table 1). - **Pygoscepivirus A1 (pingu picornavirus):** The amino acid divergences range from 78.6 to 88.0% for P1, 50.9-75.4% for 2Chel,65.0-86.7% for 3Cpro and 40.0-65.2% for 3Dpol (compare Table 2). - **Rajidapivirus A1 (Wenling sharpspine skate picornavirus):** The amino acid divergences range from 77.6 to 86.6% for P1, 71.9-79.8% for 2Chel,78.2-86.7% for 3Cpro and 64.9-69.1% for 3Dpol (compare Table 3). These values justify the creation of new picornavirus genera.**Type species of the genera:** ***Danipivirus A***, danipivirus A1 (zebrafish picornavirus) strain IDEXX/ZfPV-1/2017/USA, GenBank acc. no. MH368041***Pygoscepivirus A***, pygoscepivirus A1 (pingu virus) strain 991, GenBank acc. no. MH255796***Rajidapivirus A***, rajidapivirus A1 (Wenling sharpspine skate picornavirus), strain DHBYCGS18742, GenBank acc. no. MG600093**Species demarcation criteria:**not applicable**Origin of name:****Danipivirus**: refers to ***Danio***, the genus name of the zebrafish host (*Danio rerio*), and **pi**corna**virus****Pygoscepivirus** refers to ***Pygoscelis***, one of seven penguin genera, and **pi**corna**virus****Rajidapivirus** refers to ***Rajidae***, a family of skates (cartilaginous fish), and **pi**corna**virus** |

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**Supporting evidence**

**Table 1: Diversities of orthologous proteins \***

**Danipivirus A1 (zebrafish picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Kobuvirus Aichivirus A* 81.0% 72.0% 82.6% 60.9%

 *Aichivirus B* 80.5% 71.4% 81.6% 60.7%

 *Aichivirus C* 81.1% 72.9% 83.2% 59.6%

 *Aichivirus D* 82.5% 75.1% 82.2% 62.1%

 *Aichivirus E* 79.6% 73.8% 83.2% 61.0%

 *Aichivirus F* 80.2% 73.2% 84.2% 59.9%

 *grey squirrel kobuvirus* 81.4% 74.4% 80.0% 63.5%

*Dicipivirus Cadicivirus A* 84.3% 74.1% 83.6% 64.9%

 *Cadicivirus B* 84.7% 73.4% 82.5% 66.5%

*Gallivirus Gallivirus A* 85.3% 75.4% 81.5% 59.4%

*Hemipivirus Hemipivirus A* 82.7% 71.2% 80.0% 67.2%

*Livupivirus Livupivirus A* 80.7% 70.5% 86.5% 60.7%

*Ludopivirus Ludopivirus A* 79.1% 75.5% 81.1% 62.6%

*Megrivirus Megrivirus A* 83.9% 75.7% 78.7% 62.7%

 *Megrivirus B* 86.5% 73.3% 80.1% 61.3%

 *Megrivirus C* 85.1% 74.3% 82.5% 64.1%

 *Megrivirus D* 84.5% 75.4% 79.2% 63.7%

 *Megrivirus E* 83.4% 75.7% 79.7% 61.0%

*Myrropivirus Myrropivirus A* 84.9% 71.8% 80.6% 66.2%

*Oscivirus Oscivirus A* 85.7% 75.0% 83.2% 57.8%

*Passerivirus Passerivirus A* 82.4% 72.9% 75.4% 58.0%

 *Passerivirus B* 83.5% 75.0% 76.0% 59.7%

*Pemapivirus Pemapivirus A* 85.7% 75.9% 82.7% 62.2%

 *Chinese broad-headed pond turtle picornavirus 1* 85.6% 76.8% 79.6% 63.0%

*Poecivirus Poecivirus A* 86.5% 76.9% 80.3% 65.1%

*Rafivirus Rafivirus A* 81.3% 72.9% 84.3% 59.4%

 *Rafivirus B* 81.9% 74.1% 85.9% 58.3%

 *Rafivirus C* 81.3% 73.8% 84.7% 61.2%

*Rosavirus Rosavirus A* 83.6% 74.3% 86.4% 65.2%

 *Rosavirus B* 84.1% 73.1% 85.9% 65.4%

 *Rosavirus C* 83.2% 73.5% 85.3% 65.2%

*Sakobuvirus Sakobuvirus A* 81.0% 77.0% 84.3% 60.4%

*Salivirus Salivirus A* 81.8% 72.5% 78.1% 63.8%

*Sicinivirus Sicinivirus A* 86.1% 73.5% 80.3% 59.2%

*Symapivirus Symapivirus A* 85.6% 74.5% 81.1% 60.1%

*Tropivirus Tropivirus A* 84.5% 73.4% 86.6% 61.3%

 Yili teratoscincus roborowskii picornavirus 1 83.1% 73.3% 84.6% 62.8%

unassigned Wenling sharpspine skate picornavirus 87.0% 75.0% 81.1% 59.8%

unassigned pingu picornavirus 83.9% 75.4% 85.9% 67.3%

\* number of amino acid differences per site

**Table 2: Derversities of orthologous proteins \***

**Pygoscepivirus A1 (pingu picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Kobuvirus Aichivirus A* 78.7% 54.9% 69.1% 45.6%

 *Aichivirus B* 78.6% 54.8% 69.1% 47.0%

 *Aichivirus C* 79.7% 53.9% 65.9% 43.5%

 *Aichivirus D* 81.0% 61.4% 72.5% 48.6%

 *Aichivirus E* 79.7% 55.9% 72.1% 44.7%

 *Aichivirus F* 80.3% 55.6% 74.2% 43.2%

 *grey squirrel kobuvirus* 80.4% 52.8% 67.6% 49.5%

*Dicipivirus Cadicivirus A* 87.4% 70.1% 84.4% 63.0%

 *Cadicivirus B* 86.1% 70.4% 81.1% 60.4%

*Gallivirus Gallivirus A* 82.2% 56.0% 64.1% 41.7%

*Hemipivirus Hemipivirus A* 84.8% 68.1% 85.8% 62.6%

*Livupivirus Livupivirus A* 79.9% 65.2% 78.7% 52.8%

*Ludopivirus Ludopivirus A* 81.5% 50.9% 77.6% 50.5%

*Megrivirus Megrivirus A* 83.7% 66.9% 76.3% 59.4%

 *Megrivirus B* 85.8% 64.1% 75.6% 57.0%

 *Megrivirus C* 87.0% 64.7% 82.4% 57.4%

 *Megrivirus D* 83.6% 68.1% 77.9% 58.5%

 *Megrivirus E* 85.1% 66.6% 78.0% 57.0%

*Myrropivirus Myrropivirus A* 84.5% 68.5% 81.9% 59.8%

*Oscivirus Oscivirus A* 82.3% 61.4% 77.5% 46.9%

*Passerivirus Passerivirus A* 80.0% 53.3% 65.0% 40.0%

 *Passerivirus B* 79.1% 52.1% 69.9% 41.5%

*Pemapivirus Pemapivirus A* 84.9% 71.6% 83.4% 55.1%

 *Chinese broad-headed pond turtle picornavirus 1* 86.4% 71.0% 86.7% 56.8%

*Poecivirus Poecivirus A* 85.2% 66.6% 81.3% 61.1%

*Rafivirus Rafivirus A* 81.5% 67.4% 80.6% 52.1%

 *Rafivirus B* 81.2% 69.3% 79.4% 50.6%

 *Rafivirus C* 83.1% 68.2% 80.8% 53.3%

*Rosavirus Rosavirus A* 84.3% 65.4% 86.7% 56.6%

 *Rosavirus B* 85.5% 66.6% 84.5% 57.4%

 *Rosavirus C* 84.4% 63.2% 83.4% 58.8%

*Sakobuvirus Sakobuvirus A* 80.7% 58.0% 68.7% 46.2%

*Salivirus Salivirus A* 83.0% 56.8% 71.6% 53.9%

*Sicinivirus Sicinivirus A* 82.1% 53.6% 66.8% 42.3%

*Symapivirus Symapivirus A* 84.4% 67.6% 79.3% 54.4%

*Tropivirus Tropivirus A* 86.4% 66.0% 85.1% 57.0%

 Yili teratoscincus roborowskii picornavirus 1 88.0% 68.8% 84.2% 56.6%

unassigned Wenling sharpspine skate picornavirus 86.6% 73.4% 82.3% 65.2%

unassigned zebrafish picornavirus 87.0% 75.4% 81.1% 59.8%

\* number of amino acid differences per site

**Table 3: Derversities of orthologous proteins \***

**Rajidapivirus A1 (Wenling sharpspine skate picornavirus) vs. P1 2Chel 3Cpro 3Dpol**

*Kobuvirus Aichivirus A* 80.1% 73.3% 82.1% 67.3%

 *Aichivirus B* 80.7% 73.0% 81.8% 67.1%

 *Aichivirus C* 82.5% 72.3% 80.0% 67.0%

 *Aichivirus D* 81.8% 75.1% 82.3% 69.1%

 *Aichivirus E* 81.5% 73.0% 81.6% 65.6%

 *Aichivirus F* 78.1% 73.7% 83.7% 65.6%

 *grey squirrel kobuvirus* 78.3% 75.5% 78.2% 67.0%

*Dicipivirus Cadicivirus A* 85.0% 77.6% 86.2% 69.0%

 *Cadicivirus B* 83.3% 74.4% 83.4% 68.9%

*Gallivirus Gallivirus A* 84.4% 71.9% 85.1% 66.9%

*Hemipivirus Hemipivirus A* 84.4% 76.2% 83.1% 68.4%

*Livupivirus Livupivirus A* 77.6% 75.3% 86.6% 65.2%

*Ludopivirus Ludopivirus A* 79.9% 75.5% 80.3% 66.8%

*Megrivirus Megrivirus A* 85.3% 74.2% 82.2% 69.0%

 *Megrivirus B* 84.6% 73.9% 81.6% 65.5%

 *Megrivirus C* 83.9% 73.2% 80.6% 67.9%

 *Megrivirus D* 83.9% 75.4% 78.4% 67.9%

 *Megrivirus E* 85.2% 73.5% 81.0% 68.5%

*Myrropivirus Myrropivirus A* 82.7% 74.3% 83.8% 65.2%

*Oscivirus Oscivirus A* 82.1% 74.1% 82.6% 65.8%

*Passerivirus Passerivirus A* 83.0% 76.6% 83.8% 66.8%

 *Passerivirus B* 84.0% 73.9% 85.5% 65.6%

*Pemapivirus Pemapivirus A* 82.7% 79.8% 86.7% 66.7%

 *Chinese broad-headed pond turtle picornavirus 1* 83.4% 78.9% 85.2% 67.2%

*Poecivirus Poecivirus A* 85.2% 76.4% 81.8% 65.4%

*Rafivirus Rafivirus A* 78.0% 74.3% 85.7% 67.2%

 *Rafivirus B* 79.0% 75.8% 84.1% 66.1%

 *Rafivirus C* 78.6% 76.2% 82.3% 66.2%

*Rosavirus Rosavirus A* 83.4% 76.5% 84.1% 65.8%

 *Rosavirus B* 81.9% 75.9% 82.4% 67.3%

 *Rosavirus C* 83.0% 74.5% 85.7% 67.2%

*Sakobuvirus Sakobuvirus A* 81.7% 73.0% 79.9% 67.3%

*Salivirus Salivirus A* 80.3% 73.1% 84.0% 67.4%

*Sicinivirus Sicinivirus A* 83.4% 72.7% 86.0% 65.8%

*Symapivirus Symapivirus A* 84.4% 79.5% 84.6% 67.2%

*Tropivirus Tropivirus A* 84.35 78.5% 84.6% 66.4%

 Yili teratoscincus roborowskii picornavirus 1 82.0% 76.9% 82.6% 64.9%

unassigned pingu picornavirus 86.6% 73.4% 82.3% 65.2%

unassigned zebrafish picornavirus 83.9% 75.0% 85.9% 67.3%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of danipivirus A1, pygoscepivirus A1 and rajidapivirus A1 (schematic depiction). The open reading frames are indicated by a box. Position of putative 3Cpro cleavage sites are indicated by a ▼. The names and lengths of the deduced proteins are presented. The 5’-UTR may be incomplete.



**Figure 2:** Phylogenetic analysis of picornavirus P1 protein using Bayesian tree inference (MrBayes 3.2). Eighty-three picornavirus sequences of the *Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/ Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/Poecivirus/ Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus* supergroup were retrieved from GenBank; the cardiovirus 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, species names, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Genus names are presented at the right. 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.



**Figure 3:** Phylogenetic analysis of picornavirus 3D protein using Bayesian tree inference (MrBayes 3.2). Eighty-three picornavirus sequences of the *Dicipivirus/Hemipivirus/Gallivirus/Kobuvirus/ Livupivirus/Ludopivirus/Megrivirus/Myrropivirus/Oscivirus/Passerivirus/Pemapivirus/Poecivirus/ Rafivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus/Symapivirus/Tropivirus* supergroup were retrieved from GenBank; the cardiovirus 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, species names, type and—if available—common names in round brackets. Designations of isolates are given in square brackets. Genus names are presented at the right. Yet unassigned viruses are printed in blue. The proposed name is printed in red and indicated by a dot (●). Asterisks (\*) indicate incomplete genomes. 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.

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