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:** | ***2018.008S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **1 new picornavirus genus (*Poecivirus*) with 1 species (*Poecivirus A*)** | | | |
|  | | | |
| **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): | | |  |

|  |
| --- |
| **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:** **2018.008S.N.v1.Poecivirus** |

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 (*Poecivirus A*) in the new genus *Poecivirus***

A novel, picornavirus—poecivirus [BCCH-449]—has been detected in tissue samples (mandible) collected from diseased black-capped chickadees (*Poecile atricapillus*) between 2001 and 2015 in Anchorage and the Matanuska-Sustna Valley, Alaska, USA (Zylberberg et al. 2016). The virus is suspected to cause the avian keratin disorder (AKD). Sequencing of the virus genome revealed a megrivirus-like virus. The virus was also detected in northwestern crows (*Corvus caurinus*) and redbreasted nuthatches (*Sitta canadensis*) with AKD-consistent pathology.

The genus *Megrivirus* presently comprises 5 species, *Megrivirus A* to *E*. The hosts of all known megriviruses are birds. Despite great similarities to megriviruses, the *Picornaviridae* Study Group favours creation of a new genus, *Poecivirus*, with *Poecivirus A* as its only species.

**Relation to picornaviruses:**

- Genome layout of poecivirus:

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

(compare Fig. 1 of supporting material)

- Poecivirus has typical hallmarks of picornaviruses:

- capsid protein 1AB, 1C, 1D: **rhv** domain with drug-binding site,

- 2Chel: **G1199**xx**G**x**GKS** motif of helicases,

- 3BVPg: **Y1562-3** residue,

- 3Cpro: **G1735**x**CG**x14**G**x**H** motif,

- 3Dpol: **K1952DE**, **P2084SG**, **Y2121GDD**, **F2170LKR** motifs

**Distinguishing features of poecivirus**

Despite phylogenetic relationship of poecivirus and megriviruses, high divergence and significant differences in genome layout justify creation of a new poecivirus genus:

1. **Phylogenetic analyses** of P1, 2Chel and 3Cpro genome regions indicate a branch at the root of the megrivirus clade; the 3Dpol tree, however, reveals clustering of poecivirus and harrier megrivirus (compare Figs. 2-5 of supporting material).

2. **Amino acid identities:**

Analysis of amino acid identities indicate an intermediate position of poecivirus relative to megriviruses and the remaining genera of picornavirus supergroup 2 (*Dicipivirus/Gallivirus/Kobu-virus/Megrivirus/Oscivirus/Passerivirus/Rosavirus/Sakobuvirus/Salivirus/Sicinivirus*).

- P1: 21-23% aai in comparison to megriviruses

<19% aai in comparison to other members of supergroup 2 genera

- 2Chel: 37-43% aai in comparison to megriviruses

<35% aai in comparison to other members of supergroup 2 genera

- 3Cpro: 33-37% aai in comparison to megriviruses

<30% aai in comparison to other members of supergroup 2 genera

-3Dpol: 47-51% aai in comparison to megriviruses

<44% aai in comparison to other members of supergroup 2 genera

The five megrivirus species show lower values of between-species/within-genus divergence than poecivirus-megrivirus comparisons (compare Tables 2-5 of supporting material).

3. Although poecivirus exhibits a typical picornavirus genome layout, comparison of the poecivirus genome to megrivirus genomes reveals significant differences:

- P1: Poecivirus 1AB protein is >90 aa shorter than the megrivirus 1AB; the poecivirus 1C is 70-80 aa longer than the megrivirus 1C.

-2A: 2A of poecivirus has no similarity to any known picornavirus protein. Whereas the known megriviruses have one to four 2A proteins with the last one showing the H-box/NC sequence motif, the single 2A protein of poecivirus lacks such a sequence motif.

**Table 1: Lengths of structural and nonstructural proteins**

***Poecivirus A Megrivirus A Megrivirus B Megrivirus C Megrivirus D Megrivirus E***

(KU977108) (KS663628) (KC876003) (KF961186) (KY488458) (MF405436)

L - - - - - 131 aa

1AB 293 aa\* 423 aa 389 aa 384 aa 377 aa 380 aa

1C 250 aa\* 166 aa 168 aa 181 aa 177 aa 176 aa

1D 223 aa 257 aa 250 aa 247 aa 348 aa\* 226 aa

2A 114 aa\* 241-135-198 aa 184-103-196 aa 220-104-199 aa 181 aa 104-132-205 aa

2B 182 aa 190 aa 190 aa 192 aa 190 aa 191 aa

2Chel 356 aa 345 aa 346 aa 372 aa 343 aa 344 aa

3A 141 aa 179 aa 182 aa 150 aa 156 aa 179 aa

3BVPg 27 aa 29 aa 28 aa 27 aa 26 aa 28 aa

3Cpro 192 aa 202 aa 197 aa 202 aa 194 aa 200 aa

3Dpol 482 aa 474 aa 474 aa 472 aa 493 aa 474 aa

\* The red colour indicates a significant difference.

**Species demarcation criteria:**

not applicable

**Type species of genus:**

***Poecivirus A***, poecivirus A1 [BCCHZ-449], GenBank acc. no. KU977108

**Origin of name:**

**poeci** refers to the host ***Poeci****le atricapillus* (black-capped chickadee)

| **References:** |
| --- |
| Zylberberg M, Van Hemert C, Dumbacher JP, Handel CM, Tihan T, DeRisi JL. 2016. Novel picornavirus associated with avian keratin disorder in Alaskan birds. mBio 7(4):e00874-16. |



**Figure 1:** Comparison of the genome organisation of poecivirus and the megrivirus species (schematic depiction). The open reading frames are indicated by boxes. 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/Rosavirus/Sakobuvirus/ Salivirus/Sicinivirus* supergroup (SG2) 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 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/Rosavirus/Sakobuvirus/ Salivirus/Sicinivirus* supergroup (SG2) 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 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/Rosavirus/Sakobuvirus/ Salivirus/Sicinivirus* supergroup (SG2) 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 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/Rosavirus/Sakobuvirus/ Salivirus/Sicinivirus* supergroup (SG2) 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 6,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**Table 2. Estimates of Evolutionary Divergence between Picornavirus P1 AA Sequences**

[ 1] KU977108, Poecivirus A [BCCH-449]

[ 2] KC663628, MeV-A2, duck megrivirus [LY]

[ 3] KY369299, MeV-A3, goose megrivirus [W18]

[ 4] KY369300, MeV-B3CP-Apol, goose\_megrivirus [HN56]

[ 5] KC876003, MeV-B1, mesivirus 1 [HK21]

[ 6] KC811837, MeV-B2, mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]

[ 7] KF961186, MeV-C1, chicken megrivirus [chicken/B21-CHV/2012/HUN]

[ 8] KF961187, MeV-C1, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]

[ 9] KJ690629, MeV-C1, chicken proventriculitis\_virus [CPV/Korea/03]

[10] KF979336, MeV-C2, chicken picornavirus 5 [27C]

[11] KF979335, MeV-A1CP-Cpol, chicken picornavirus 4 [5C]

[12] HM751199, MeV-A1CP-Cpol, turkey\_hepatitis\_virus [2993D]

[13] KF961188, MeV-A1CP-Cpol, turkey\_megrivirus [turkey/B407-THV/2011/HUN]

[14] HQ189775, MeV-A1CP-C, turkey hepatitis virus [0091.1]

[15] KY488458, MeV-D, harrier picornavirus [harrier/MR-01/HUN/2014]

[16] MF405436, MeV-E, penguin megrivirus

[17] JF973686, Rosavirus A1, rosavirus [M-7]

[18] JQ691613, Gallivirus A [turkey/M176/2011/HUN]

[19] KF741227, Sicinivirus A [UCC001]

[20] GU182406, Passerivirus A, turdivirus\_1 [00356]

[21] KF387721, Sakobuvirus A [FFUP1]

[22] GQ179640, Salivirus A [NG-J1]

[23] AB010145, Aichivirus A1 [A846-88]

[24] JN819202, Cadicivirus A, canine\_picodicistrovirus [209]

[25] GU182408, Oscivirus A1, turdivirus\_2 [10717]

[26] KP770140, Ampivirus A [NEWT/2013/HUN]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 ]

[ 1]

[ 2] 0.79

[ 3] 0.78 0.31

[ 4] 0.78 0.54 0.50

[ 5] 0.77 0.58 0.57 0.47

[ 6] 0.78 0.59 0.60 0.50 0.25

[ 7] 0.79 0.66 0.66 0.64 0.64 0.64

[ 8] 0.78 0.66 0.65 0.63 0.64 0.63 0.08

[ 9] 0.78 0.65 0.65 0.63 0.63 0.63 0.09 0.03

[10] 0.77 0.66 0.66 0.61 0.63 0.63 0.25 0.25 0.25

[11] 0.78 0.32 0.34 0.54 0.56 0.58 0.62 0.62 0.62 0.63

[12] 0.77 0.32 0.34 0.53 0.56 0.58 0.63 0.63 0.63 0.64 0.10

[13] 0.78 0.31 0.34 0.53 0.55 0.57 0.63 0.63 0.63 0.64 0.09 0.06

[14] 0.77 0.32 0.34 0.53 0.55 0.57 0.63 0.63 0.63 0.64 0.11 0.07 0.08

[15] 0.78 0.62 0.64 0.59 0.61 0.63 0.66 0.66 0.65 0.66 0.62 0.62 0.61 0.61

[16] 0.78 0.63 0.65 0.64 0.62 0.63 0.52 0.53 0.52 0.51 0.63 0.63 0.63 0.63 0.63

[17] 0.84 0.83 0.83 0.81 0.80 0.82 0.84 0.84 0.84 0.83 0.81 0.80 0.81 0.81 0.83 0.83

[18] 0.86 0.84 0.84 0.84 0.83 0.83 0.83 0.83 0.83 0.81 0.83 0.84 0.84 0.84 0.85 0.84 0.84

[19] 0.86 0.83 0.84 0.83 0.82 0.84 0.85 0.84 0.84 0.84 0.82 0.83 0.82 0.83 0.83 0.84 0.82 0.79

[20] 0.87 0.80 0.80 0.82 0.82 0.81 0.83 0.84 0.83 0.83 0.78 0.79 0.79 0.79 0.83 0.82 0.82 0.77 0.69

[21] 0.84 0.79 0.79 0.81 0.81 0.81 0.83 0.83 0.83 0.82 0.80 0.80 0.80 0.80 0.82 0.81 0.80 0.80 0.75 0.76

[22] 0.82 0.81 0.80 0.81 0.80 0.81 0.82 0.82 0.81 0.81 0.81 0.81 0.81 0.81 0.83 0.80 0.80 0.80 0.76 0.74 0.57

[23] 0.82 0.81 0.79 0.83 0.81 0.82 0.81 0.82 0.81 0.83 0.80 0.80 0.81 0.81 0.81 0.80 0.78 0.80 0.75 0.73 0.57 0.59

[24] 0.85 0.82 0.81 0.79 0.81 0.80 0.84 0.84 0.84 0.84 0.82 0.81 0.82 0.81 0.82 0.82 0.66 0.83 0.83 0.79 0.78 0.78 0.77

[25] 0.86 0.84 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.82 0.84 0.82 0.83 0.82 0.82 0.79 0.74 0.75 0.75 0.81

[26] 0.91 0.89 0.89 0.88 0.89 0.88 0.89 0.90 0.89 0.89 0.88 0.87 0.87 0.88 0.89 0.88 0.89 0.91 0.89 0.88 0.88 0.88 0.87 0.89 0.89

The number of amino acid differences per site between sequences are shown. The analysis involved 26 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 1564 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 3. Estimates of Evolutionary Divergence between Picornavirus 2Chel AA Sequences**

[ 1] KU977108, Poecivirus A [BCCH-449]

[ 2] KC663628, MeV-A2, duck megrivirus [LY]

[ 3] KY369299, MeV-A3, goose megrivirus [W18]

[ 4] KY369300, MeV-B3CP-Apol, goose\_megrivirus [HN56]

[ 5] KC876003, MeV-B1, mesivirus 1 [HK21]

[ 6] KC811837, MeV-B2, mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]

[ 7] KF961186, MeV-C1, chicken megrivirus [chicken/B21-CHV/2012/HUN]

[ 8] KF961187, MeV-C1, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]

[ 9] KJ690629, MeV-C1, chicken proventriculitis\_virus [CPV/Korea/03]

[10] KF979336, MeV-C2, chicken picornavirus 5 [27C]

[11] KF979335, MeV-A1CP-Cpol, chicken picornavirus 4 [5C]

[12] HM751199, MeV-A1CP-Cpol, turkey\_hepatitis\_virus [2993D]

[13] KF961188, MeV-A1CP-Cpol, turkey\_megrivirus [turkey/B407-THV/2011/HUN]

[14] HQ189775, MeV-A1CP-C, turkey hepatitis virus [0091.1]

[15] KY488458, MeV-D, harrier picornavirus [harrier/MR-01/HUN/2014]

[16] MF405436, MeV-E, penguin megrivirus

[17] JF973686, Rosavirus A1, rosavirus [M-7]

[18] JQ691613, Gallivirus A [turkey/M176/2011/HUN]

[19] KF741227, Sicinivirus A [UCC001]

[20] GU182406, Passerivirus A, turdivirus\_1 [00356]

[21] KF387721, Sakobuvirus A [FFUP1]

[22] GQ179640, Salivirus A [NG-J1]

[23] AB010145, Aichivirus A1 [A846-88]

[24] JN819202, Cadicivirus A, canine\_picodicistrovirus [209]

[25] GU182408, Oscivirus A1, turdivirus\_2 [10717]

[26] KP770140, Ampivirus A [NEWT/2013/HUN]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 ]

[ 1]

[ 2] 0.57

[ 3] 0.57 0.03

[ 4] 0.57 0.03 0.01

[ 5] 0.63 0.36 0.36 0.36

[ 6] 0.63 0.37 0.37 0.38 0.03

[ 7] 0.60 0.35 0.35 0.35 0.42 0.42

[ 8] 0.60 0.35 0.35 0.35 0.41 0.42 0.01

[ 9] 0.63 0.36 0.36 0.36 0.43 0.44 0.00 0.00

[10] 0.60 0.34 0.34 0.34 0.41 0.42 0.02 0.02 0.02

[11] 0.60 0.34 0.34 0.34 0.41 0.42 0.03 0.03 0.03 0.01

[12] 0.61 0.34 0.35 0.34 0.42 0.42 0.05 0.05 0.05 0.03 0.03

[13] 0.61 0.34 0.35 0.34 0.42 0.43 0.05 0.04 0.05 0.03 0.03 0.02

[14] 0.61 0.34 0.35 0.34 0.42 0.42 0.05 0.04 0.05 0.03 0.03 0.00 0.02

[15] 0.60 0.45 0.45 0.45 0.47 0.46 0.47 0.47 0.49 0.46 0.46 0.45 0.46 0.45

[16] 0.57 0.31 0.32 0.32 0.38 0.38 0.34 0.33 0.34 0.33 0.33 0.34 0.34 0.34 0.46

[17] 0.69 0.65 0.65 0.65 0.64 0.64 0.66 0.65 0.67 0.65 0.65 0.65 0.66 0.65 0.66 0.64

[18] 0.70 0.70 0.69 0.69 0.67 0.68 0.67 0.67 0.69 0.67 0.68 0.68 0.68 0.68 0.68 0.68 0.68

[19] 0.70 0.67 0.68 0.67 0.68 0.68 0.67 0.67 0.68 0.67 0.67 0.67 0.67 0.67 0.70 0.68 0.66 0.55

[20] 0.70 0.71 0.71 0.71 0.70 0.70 0.69 0.69 0.71 0.68 0.68 0.68 0.69 0.68 0.72 0.69 0.67 0.54 0.53

[21] 0.67 0.71 0.72 0.72 0.72 0.72 0.71 0.71 0.72 0.71 0.71 0.70 0.70 0.70 0.71 0.70 0.66 0.62 0.56 0.58

[22] 0.72 0.72 0.72 0.72 0.71 0.71 0.72 0.72 0.74 0.72 0.72 0.72 0.72 0.72 0.73 0.71 0.65 0.56 0.54 0.56 0.55

[23] 0.72 0.70 0.70 0.70 0.68 0.68 0.69 0.68 0.70 0.68 0.68 0.69 0.69 0.69 0.70 0.69 0.67 0.59 0.55 0.56 0.55 0.54

[24] 0.72 0.69 0.70 0.69 0.70 0.70 0.70 0.70 0.72 0.70 0.70 0.70 0.70 0.70 0.72 0.71 0.67 0.72 0.71 0.72 0.74 0.74 0.74

[25] 0.70 0.66 0.66 0.66 0.65 0.65 0.68 0.68 0.69 0.68 0.68 0.68 0.68 0.68 0.68 0.69 0.67 0.60 0.62 0.63 0.62 0.65 0.62 0.73

[26] 0.83 0.81 0.81 0.81 0.80 0.81 0.83 0.83 0.84 0.83 0.83 0.83 0.83 0.83 0.83 0.82 0.79 0.82 0.81 0.81 0.82 0.81 0.79 0.84 0.80

The number of amino acid differences per site between sequences are shown. The analysis involved 26 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 449 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 4. Estimates of Evolutionary Divergence between Picornavirus 3Cpro AA Sequences**

[ 1] KU977108, Poecivirus A [BCCH-449]

[ 2] KC663628, MeV-A2, duck megrivirus [LY]

[ 3] KY369299, MeV-A3, goose megrivirus [W18]

[ 4] KY369300, MeV-B3CP-Apol, goose\_megrivirus [HN56]

[ 5] KC876003, MeV-B1, mesivirus 1 [HK21]

[ 6] KC811837, MeV-B2, mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]

[ 7] KF961186, MeV-C1, chicken megrivirus [chicken/B21-CHV/2012/HUN]

[ 8] KF961187, MeV-C1, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]

[ 9] KJ690629, MeV-C1, chicken proventriculitis\_virus [CPV/Korea/03]

[10] KF979336, MeV-C2, chicken picornavirus 5 [27C]

[11] KF979335, MeV-A1CP-Cpol, chicken picornavirus 4 [5C]

[12] HM751199, MeV-A1CP-Cpol, turkey\_hepatitis\_virus [2993D]

[13] KF961188, MeV-A1CP-Cpol, turkey\_megrivirus [turkey/B407-THV/2011/HUN]

[14] HQ189775, MeV-A1CP-C, turkey hepatitis virus [0091.1]

[15] KY488458, MeV-D, harrier picornavirus [harrier/MR-01/HUN/2014]

[16] MF405436, MeV-E, penguin megrivirus

[17] JF973686, Rosavirus A1, rosavirus [M-7]

[18] JQ691613, Gallivirus A [turkey/M176/2011/HUN]

[19] KF741227, Sicinivirus A [UCC001]

[20] GU182406, Passerivirus A, turdivirus\_1 [00356]

[21] KF387721, Sakobuvirus A [FFUP1]

[22] GQ179640, Salivirus A [NG-J1]

[23] AB010145, Aichivirus A1 [A846-88]

[24] JN819202, Cadicivirus A, canine\_picodicistrovirus [209]

[25] GU182408, Oscivirus A1, turdivirus\_2 [10717]

[26] KP770140, Ampivirus A [NEWT/2013/HUN]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 ]

[ 1]

[ 2] 0.63

[ 3] 0.65 0.01

[ 4] 0.64 0.01 0.01

[ 5] 0.66 0.44 0.44 0.44

[ 6] 0.67 0.45 0.44 0.45 0.02

[ 7] 0.68 0.59 0.59 0.60 0.59 0.58

[ 8] 0.66 0.58 0.58 0.58 0.57 0.56 0.02

[ 9] 0.66 0.58 0.58 0.58 0.57 0.56 0.01 0.00

[10] 0.67 0.58 0.58 0.58 0.57 0.56 0.02 0.02 0.02

[11] 0.67 0.58 0.58 0.58 0.57 0.56 0.02 0.02 0.01 0.00

[12] 0.67 0.58 0.58 0.58 0.57 0.56 0.03 0.03 0.03 0.02 0.01

[13] 0.66 0.59 0.59 0.60 0.58 0.57 0.06 0.05 0.06 0.05 0.05 0.03

[14] 0.67 0.58 0.58 0.58 0.58 0.57 0.04 0.04 0.03 0.02 0.02 0.00 0.04

[15] 0.63 0.59 0.58 0.59 0.61 0.62 0.66 0.66 0.66 0.66 0.66 0.66 0.66 0.66

[16] 0.67 0.43 0.44 0.43 0.47 0.46 0.63 0.61 0.61 0.61 0.61 0.62 0.64 0.62 0.58

[17] 0.72 0.67 0.66 0.67 0.69 0.69 0.71 0.72 0.72 0.72 0.72 0.72 0.71 0.72 0.70 0.69

[18] 0.77 0.74 0.74 0.74 0.79 0.79 0.79 0.78 0.78 0.78 0.78 0.79 0.79 0.79 0.79 0.79 0.83

[19] 0.78 0.78 0.79 0.78 0.77 0.77 0.81 0.81 0.81 0.81 0.81 0.81 0.81 0.81 0.82 0.74 0.84 0.66

[20] 0.75 0.77 0.78 0.77 0.72 0.72 0.78 0.79 0.79 0.78 0.78 0.78 0.78 0.78 0.78 0.75 0.78 0.70 0.60

[21] 0.75 0.78 0.79 0.78 0.76 0.77 0.77 0.76 0.76 0.76 0.76 0.76 0.76 0.76 0.72 0.80 0.83 0.75 0.69 0.73

[22] 0.81 0.76 0.76 0.76 0.78 0.78 0.80 0.79 0.79 0.79 0.79 0.79 0.80 0.79 0.75 0.76 0.81 0.74 0.75 0.75 0.71

[23] 0.80 0.80 0.80 0.80 0.78 0.78 0.84 0.83 0.82 0.82 0.82 0.83 0.84 0.83 0.76 0.73 0.85 0.70 0.70 0.72 0.69 0.65

[24] 0.73 0.71 0.70 0.71 0.70 0.69 0.74 0.74 0.74 0.74 0.74 0.74 0.74 0.74 0.68 0.69 0.67 0.83 0.81 0.80 0.85 0.80 0.80

[25] 0.81 0.79 0.79 0.79 0.79 0.78 0.77 0.78 0.78 0.77 0.78 0.77 0.78 0.76 0.79 0.78 0.78 0.75 0.79 0.77 0.78 0.73 0.77 0.83

[26] 0.86 0.85 0.85 0.85 0.82 0.82 0.85 0.85 0.85 0.85 0.85 0.85 0.84 0.85 0.80 0.83 0.88 0.87 0.88 0.89 0.86 0.88 0.84 0.86 0.90

The number of amino acid differences per site between sequences are shown. The analysis involved 26 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 251 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison

**Table 5. Estimates of Evolutionary Divergence between Picornavirus 3Cpol AA Sequences**

[ 1] KU977108, Poecivirus A [BCCH-449]

[ 2] KC663628, MeV-A2, duck megrivirus [LY]

[ 3] KY369299, MeV-A3, goose megrivirus [W18]

[ 4] KY369300, MeV-B3CP-Apol, goose\_megrivirus [HN56]

[ 5] KC876003, MeV-B1, mesivirus 1 [HK21]

[ 6] KC811837, MeV-B2, mesivirus 2 [pigeon/GALII5-PiMeV/2011/HUN]

[ 7] KF961186, MeV-C1, chicken megrivirus [chicken/B21-CHV/2012/HUN]

[ 8] KF961187, MeV-C1, chicken megrivirus [chicken/CHK-IV-CHV/2013/HUN]

[ 9] KJ690629, MeV-C1, chicken proventriculitis\_virus [CPV/Korea/03]

[10] KF979336, MeV-C2, chicken picornavirus 5 [27C]

[11] KF979335, MeV-A1CP-Cpol, chicken picornavirus 4 [5C]

[12] HM751199, MeV-A1CP-Cpol, turkey\_hepatitis\_virus [2993D]

[13] KF961188, MeV-A1CP-Cpol, turkey\_megrivirus [turkey/B407-THV/2011/HUN]

[14] HQ189775, MeV-A1CP-C, turkey hepatitis virus [0091.1]

[15] KY488458, MeV-D, harrier picornavirus [harrier/MR-01/HUN/2014]

[16] MF405436, MeV-E, penguin megrivirus

[17] JF973686, Rosavirus A1, rosavirus [M-7]

[18] JQ691613, Gallivirus A [turkey/M176/2011/HUN]

[19] KF741227, Sicinivirus A [UCC001]

[20] GU182406, Passerivirus A, turdivirus\_1 [00356]

[21] KF387721, Sakobuvirus A [FFUP1]

[22] GQ179640, Salivirus A [NG-J1]

[23] AB010145, Aichivirus A1 [A846-88]

[24] JN819202, Cadicivirus A, canine\_picodicistrovirus [209]

[25] GU182408, Oscivirus A1, turdivirus\_2 [10717]

[26] KP770140, Ampivirus A [NEWT/2013/HUN]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 ]

[ 1]

[ 2] 0.51

[ 3] 0.51 0.03

[ 4] 0.51 0.03 0.01

[ 5] 0.51 0.34 0.34 0.33

[ 6] 0.51 0.34 0.34 0.34 0.01

[ 7] 0.52 0.33 0.32 0.33 0.38 0.39

[ 8] 0.52 0.33 0.33 0.33 0.38 0.38 0.00

[ 9] 0.52 0.34 0.33 0.33 0.38 0.39 0.00 0.01

[10] 0.52 0.33 0.33 0.33 0.38 0.38 0.01 0.01 0.01

[11] 0.53 0.34 0.33 0.34 0.38 0.39 0.01 0.01 0.02 0.01

[12] 0.53 0.33 0.33 0.33 0.38 0.38 0.02 0.02 0.03 0.02 0.02

[13] 0.53 0.33 0.33 0.33 0.38 0.38 0.02 0.02 0.03 0.02 0.02 0.01

[14] 0.53 0.33 0.33 0.33 0.38 0.38 0.02 0.01 0.02 0.02 0.02 0.01 0.01

[15] 0.49 0.45 0.44 0.44 0.46 0.46 0.45 0.45 0.45 0.45 0.45 0.45 0.46 0.45

[16] 0.51 0.27 0.27 0.26 0.30 0.30 0.32 0.32 0.32 0.32 0.33 0.33 0.32 0.32 0.43

[17] 0.58 0.62 0.62 0.62 0.61 0.61 0.60 0.60 0.60 0.60 0.60 0.60 0.60 0.60 0.62 0.61

[18] 0.61 0.59 0.59 0.59 0.55 0.56 0.59 0.58 0.59 0.59 0.59 0.59 0.59 0.59 0.58 0.56 0.58

[19] 0.62 0.58 0.58 0.58 0.56 0.56 0.56 0.56 0.56 0.56 0.56 0.56 0.56 0.56 0.58 0.55 0.57 0.40

[20] 0.62 0.58 0.58 0.58 0.57 0.57 0.58 0.58 0.58 0.58 0.58 0.58 0.58 0.58 0.59 0.56 0.59 0.37 0.36

[21] 0.62 0.59 0.59 0.59 0.55 0.55 0.56 0.56 0.57 0.57 0.57 0.57 0.57 0.57 0.54 0.56 0.61 0.46 0.40 0.39

[22] 0.64 0.60 0.60 0.60 0.62 0.62 0.60 0.60 0.60 0.60 0.60 0.61 0.61 0.60 0.62 0.61 0.62 0.52 0.53 0.53 0.50

[23] 0.58 0.58 0.58 0.58 0.57 0.57 0.57 0.57 0.57 0.57 0.57 0.57 0.57 0.57 0.57 0.55 0.56 0.46 0.45 0.42 0.43 0.47

[24] 0.66 0.67 0.68 0.68 0.65 0.66 0.64 0.65 0.64 0.65 0.65 0.65 0.65 0.65 0.67 0.66 0.50 0.64 0.63 0.64 0.66 0.66 0.64

[25] 0.57 0.56 0.55 0.55 0.54 0.54 0.55 0.55 0.55 0.55 0.55 0.55 0.55 0.55 0.55 0.53 0.56 0.50 0.47 0.46 0.46 0.56 0.44 0.64

[26] 0.79 0.80 0.80 0.80 0.78 0.78 0.79 0.79 0.79 0.79 0.79 0.79 0.79 0.79 0.79 0.80 0.80 0.77 0.79 0.79 0.79 0.81 0.80 0.78 0.81

The number of amino acid differences per site from between sequences are shown. The analysis involved 26 amino acid sequences. The coding data was translated assuming a Standard genetic code table. All ambiguous positions were removed for each sequence pair. There were a total of 575 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [1].

\_\_\_ within type comparison, \_\_\_ between types/within species comparison,

\_\_\_ between species/within genus comparison, \_\_\_ between genera comparison