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:** | ***2018.006S*** | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)**1 new species (*Mischivirus D*) in the genus *Mischivirus*** |
|  |
| **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): |       |

|  |
| --- |
| **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:** **2018.006S.N.v1.Mischivirus\_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 (*Mischivirus D*) in the genus *Mischivirus***

The genus *Mischivirus* presently comprises 3 species, *Mischivirus A* (host: *Miniopterus schreibersii* bats in China, 1 type), *Mischivirus B* (host: *Miniopterus schreibersii* bats in Hungary, 2 types) and *Mischivirus C* (host: *Hipposideros gigas* bats in Central Africa, 1 type). A novel, mischivirus-like picornavirus—canine picornavirus A128thr—has been detected in a respiratory swab collected from an American foxhound (*Canis lupus familiaris*) in December 1968 in USA (Norby et al., 2017).

**Relation to other picornaviruses:**

- Genome layout of Mischivirus D:

 5'-UTRIRES-II[L/1AB-1C-1D-2Anpg↓p/2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR

 (compare Fig. 1 of supporting material)

- Mischivirus D has typical hallmarks of picornaviruses:

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

 2A: **NPG887P** sequence motif,

 2Chel: **G1195**xx**G**x**GKS** motif of helicases,

 3BVPg: **Y1511-3** residue,

 3Cpro: **G1692**x**CG**x14**G**x**H** motif,

 3Dpol: **K1908DE**, **P2041SG**, **Y2080GDD**, **F2129LKR** motifs

- Phylogenetic analyses indicate a distinct clade that clusters with the known mischiviruses (compare Figs. 2-5 of supporting material). All mischiviruses cluster in the phylogenetic trees in a separate clade—with the exception of the 3Cpro tree (compare Fig. 4).

**Distinguishing features of *Mischivirus D*:**

1. *Mischivirus D* has a non-bat host.

2. *Mischivirus D* has a short **L protein** with little homology to the L proteins of mischiviruses A, B, and C and a short **2A protein** of only 17 amino acids.

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

- P1: nt divergence >0.48, aa divergence >0.54;

- 2Chel: nt divergence >0.36, aa divergence >0.42;

- 3Cpro: nt divergence >0.43, aa divergence >0.47;

- 3Dpol: nt divergence >0.38, aa divergence >0.34 (compare tables 1-8 of supporting material);

4. Within-species nt divergences of all known mischivirus B sequences are >0.32 in P1 gene region (aa divergence >0.28) and >0.26 in the 3D region (aa divergence >0.17).

**Species demarcation criteria:**

Within-species nt divergences of all known *Mischivirus B* sequences are >0.32 in P1 gene region (aa divergence >0.28) and >0.26 in the 3D region (aa divergence >0.17). Based on these results, preliminary species demarcation criteria were defined.

Members of a species of genus *Mischivirus*:

- 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 70% aa identity in the non-structural proteins 2C + 3CD.

**Exemplar:**

***Mischivirus D***, mischivirus D1 (canine picornavirus) [A128thr],

GenBank acc. no. KY512802

| **References:** |
| --- |
| Norby EE, Jarman RG, Keiser PB, Binn LN, Hang J. (2017). Genome sequence of a novel canine picornavirus isolated from American foxhound. Genome Announcement 5(20):e00338-17. |



**Figure 1:** Comparison of the genomes of mischiviruses and canine picornavirus A128thr (schematic depiction). The open reading frames are indicated by boxes. Positions of putative 3Cpro cleavage sites are indicated by ▼, the VP0 processing site by a ¶, and the site of termination/reinitiation of RNA translation at the NPGP sequence motif is indicated by an arrow (↓). The names and lengths of the deduced proteins are presented. The 5'-UTR and the 3'UTR of the canine picornavirus may be incomplete.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Fifty-two picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/ Senecavirus/Teschovirus/Torchivirus* 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*** and—if available—common names and types. 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). Fifty-two picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/ Senecavirus/Teschovirus/Torchivirus* 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*** and—if available—common names and types. 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 2,000,000 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). Fifty-two picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/ Senecavirus/Teschovirus/Torchivirus* 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*** and—if available—common names and types. 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). Fifty-two picornavirus sequences of the *Aphthovirus/Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Mischivirus/Mosavirus/ Senecavirus/Teschovirus/Torchivirus* 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*** and—if available—common names and types. 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 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**Table 1. Estimates of Evolutionary Divergence between P1 Nucleotide Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.503

[ 3] 0.486 0.320

[ 4] 0.482 0.319 0.029

[ 5] 0.483 0.318 0.030 0.014

[ 6] 0.481 0.318 0.027 0.010 0.014

[ 7] 0.480 0.319 0.028 0.008 0.014 0.007

[ 8] 0.484 0.319 0.206 0.202 0.204 0.202 0.201

[ 9] 0.511 0.484 0.487 0.489 0.487 0.489 0.488 0.499

[10] 0.529 0.525 0.520 0.523 0.523 0.522 0.521 0.516 0.532

[11] 0.535 0.525 0.512 0.509 0.508 0.509 0.509 0.520 0.531 0.156

[12] 0.530 0.540 0.526 0.523 0.521 0.524 0.525 0.523 0.521 0.249 0.254

[13] 0.553 0.549 0.549 0.550 0.550 0.549 0.548 0.561 0.562 0.539 0.540 0.533

[14] 0.556 0.541 0.553 0.554 0.555 0.553 0.553 0.563 0.541 0.538 0.539 0.547 0.418

[15] 0.544 0.552 0.550 0.549 0.546 0.548 0.549 0.547 0.553 0.525 0.525 0.525 0.463 0.443

The number of base differences per site from between sequences are shown. The analysis involved 15 nucleotide sequences. There were a total of 2733 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 2. Estimates of Evolutionary Divergence between P1 Amino Acid Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.564

[ 3] 0.551 0.267

[ 4] 0.551 0.267 0.001

[ 5] 0.551 0.267 0.001 0.000

[ 6] 0.552 0.265 0.002 0.001 0.001

[ 7] 0.550 0.268 0.004 0.002 0.002 0.004

[ 8] 0.543 0.277 0.148 0.148 0.148 0.149 0.148

[ 9] 0.586 0.554 0.547 0.545 0.545 0.545 0.545 0.558

[10] 0.642 0.616 0.608 0.608 0.608 0.607 0.605 0.611 0.627

[11] 0.639 0.610 0.598 0.598 0.598 0.597 0.598 0.604 0.625 0.043

[12] 0.643 0.612 0.607 0.607 0.607 0.608 0.604 0.613 0.619 0.157 0.169

[13] 0.668 0.647 0.650 0.650 0.650 0.650 0.648 0.655 0.665 0.659 0.659 0.653

[14] 0.670 0.645 0.655 0.655 0.655 0.655 0.655 0.657 0.655 0.643 0.639 0.656 0.444

[15] 0.667 0.668 0.662 0.662 0.662 0.662 0.665 0.655 0.678 0.648 0.644 0.642 0.526 0.506

The number of amino acid differences per site from between sequences are shown. The analysis involved 15 amino acid sequences. There were a total of 911 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 2Chel Nucleotide Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.414

[ 3] 0.408 0.248

[ 4] 0.408 0.255 0.024

[ 5] 0.409 0.254 0.024 0.004

[ 6] 0.408 0.248 0.027 0.018 0.020

[ 7] 0.409 0.255 0.023 0.005 0.005 0.019

[ 8] 0.418 0.246 0.042 0.041 0.043 0.042 0.042

[ 9] 0.367 0.407 0.405 0.406 0.404 0.406 0.404 0.396

[10] 0.441 0.473 0.484 0.489 0.488 0.482 0.487 0.486 0.476

[11] 0.450 0.479 0.488 0.488 0.488 0.487 0.490 0.489 0.464 0.211

[12] 0.449 0.480 0.494 0.490 0.492 0.489 0.494 0.492 0.468 0.217 0.035

[13] 0.469 0.504 0.481 0.484 0.484 0.482 0.483 0.483 0.482 0.521 0.487 0.496

[14] 0.468 0.492 0.485 0.485 0.484 0.484 0.482 0.478 0.487 0.510 0.498 0.498 0.303

[15] 0.459 0.495 0.477 0.477 0.478 0.478 0.477 0.478 0.488 0.501 0.483 0.478 0.288 0.332

The number of base differences per site from between sequences are shown. The analysis involved 15 nucleotide sequences. There were a total of 993 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 2Chel Amino Acid Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.421

[ 3] 0.430 0.193

[ 4] 0.430 0.193 0.000

[ 5] 0.430 0.193 0.000 0.000

[ 6] 0.430 0.193 0.000 0.000 0.000

[ 7] 0.430 0.193 0.000 0.000 0.000 0.000

[ 8] 0.437 0.199 0.012 0.012 0.012 0.012 0.012

[ 9] 0.440 0.407 0.416 0.416 0.416 0.416 0.416 0.416

[10] 0.560 0.556 0.587 0.587 0.587 0.587 0.587 0.590 0.552

[11] 0.557 0.543 0.571 0.571 0.571 0.571 0.571 0.575 0.555 0.058

[12] 0.557 0.543 0.571 0.571 0.571 0.571 0.571 0.575 0.555 0.055 0.006

[13] 0.547 0.573 0.567 0.567 0.567 0.567 0.567 0.570 0.585 0.582 0.566 0.566

[14] 0.531 0.539 0.536 0.536 0.536 0.536 0.536 0.539 0.560 0.569 0.585 0.585 0.227

[15] 0.531 0.567 0.576 0.576 0.576 0.576 0.576 0.576 0.560 0.575 0.569 0.569 0.265 0.330

The number of amino acid differences per site from between sequences are shown. The analysis involved 15 amino acid sequences. There were a total of 331 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 3Cpro Nucleotide Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.454

[ 3] 0.449 0.330

[ 4] 0.438 0.333 0.045

[ 5] 0.439 0.333 0.048 0.003

[ 6] 0.441 0.330 0.045 0.012 0.012

[ 7] 0.441 0.327 0.045 0.012 0.012 0.009

[ 8] 0.446 0.333 0.049 0.020 0.020 0.017 0.020

[ 9] 0.481 0.482 0.491 0.504 0.502 0.502 0.499 0.502

[10] 0.477 0.501 0.459 0.456 0.456 0.462 0.459 0.467 0.486

[11] 0.464 0.507 0.473 0.470 0.470 0.475 0.477 0.473 0.506 0.145

[12] 0.467 0.506 0.477 0.472 0.472 0.477 0.478 0.475 0.512 0.156 0.018

[13] 0.577 0.626 0.599 0.599 0.601 0.599 0.596 0.603 0.577 0.580 0.566 0.564

[14] 0.596 0.630 0.612 0.612 0.610 0.605 0.604 0.613 0.585 0.583 0.570 0.570 0.370

[15] 0.554 0.611 0.604 0.589 0.591 0.599 0.596 0.599 0.559 0.567 0.556 0.554 0.386 0.391

The number of base differences per site from between sequences are shown. The analysis involved 15 nucleotide sequences. There were a total of 657 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 6. Estimates of Evolutionary Divergence between 3Cpro Amino Acid Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.476

[ 3] 0.510 0.295

[ 4] 0.510 0.290 0.009

[ 5] 0.510 0.290 0.009 0.000

[ 6] 0.510 0.290 0.009 0.000 0.000

[ 7] 0.510 0.290 0.009 0.000 0.000 0.000

[ 8] 0.510 0.290 0.009 0.000 0.000 0.000 0.000

[ 9] 0.541 0.569 0.612 0.612 0.612 0.612 0.612 0.612

[10] 0.546 0.599 0.556 0.556 0.556 0.556 0.556 0.556 0.585

[11] 0.546 0.609 0.541 0.541 0.541 0.541 0.541 0.541 0.585 0.068

[12] 0.546 0.609 0.541 0.541 0.541 0.541 0.541 0.541 0.585 0.068 0.000

[13] 0.721 0.749 0.739 0.739 0.739 0.739 0.739 0.739 0.721 0.697 0.687 0.687

[14] 0.720 0.757 0.767 0.767 0.767 0.767 0.767 0.767 0.715 0.695 0.675 0.675 0.356

[15] 0.692 0.729 0.719 0.719 0.719 0.719 0.719 0.719 0.697 0.706 0.701 0.701 0.414 0.356

The number of amino acid differences per site from between sequences are shown. The analysis involved 15 amino acid sequences. There were a total of 219 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 7. Estimates of Evolutionary Divergence between 3Dpol Nucleotide Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.385

[ 3] 0.387 0.256

[ 4] 0.385 0.251 0.023

[ 5] 0.394 0.254 0.033 0.024

[ 6] 0.389 0.254 0.028 0.020 0.024

[ 7] 0.385 0.254 0.028 0.014 0.024 0.021

[ 8] 0.390 0.254 0.031 0.024 0.026 0.019 0.024

[ 9] 0.416 0.424 0.405 0.401 0.402 0.398 0.405 0.402

[10] 0.425 0.416 0.410 0.414 0.410 0.412 0.416 0.415 0.401

[11] 0.423 0.424 0.413 0.413 0.410 0.415 0.413 0.414 0.400 0.121

[12] 0.418 0.421 0.409 0.411 0.408 0.409 0.413 0.413 0.396 0.118 0.029

[13] 0.490 0.489 0.485 0.486 0.489 0.486 0.490 0.492 0.488 0.461 0.453 0.448

[14] 0.492 0.480 0.486 0.481 0.488 0.483 0.486 0.485 0.507 0.484 0.486 0.483 0.352

[15] 0.493 0.481 0.472 0.470 0.469 0.475 0.471 0.474 0.509 0.455 0.458 0.458 0.328 0.326

The number of base differences per site from between sequences are shown. The analysis involved 15 nucleotide sequences. There were a total of 1428 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 8. Estimates of Evolutionary Divergence between 3Dpol Amino Acid Sequences**

[ 1] #KY512802, Mischivirus D1, canine picornavirus [A128thr]

[ 2] #JQ814851, Mischivirus A1, Miniopterus schreibersii picornavirus

[ 3] #KP054273, Mischivirus B1, bat picornavirus [BatPV/V1/13/Hun]

[ 4] #KP054274, Mischivirus B1, bat picornavirus [BatPV/V8/13/Hun]

[ 5] #KP054275, Mischivirus B1, bat picornavirus [BatPV/V11/13/Hun]

[ 6] #KP054276, Mischivirus B1, bat picornavirus [BatPV/V12/13/Hun]

[ 7] #KP054277, Mischivirus B1, bat picornavirus [BatPV/V13/13/Hun]

[ 8] #KP054278, Mischivirus B2, bat picornavirus [BatPV/V14/13/Hun

[ 9] #KP100644, Mischivirus C1, African bat icavirus [PREDICT-06105]

[10] #MF327529, unassigned, Aimelvirus 1 [gpai001]

[11] #MF327530, unassigned, Aimelvirus 2 [gpai002]

[12] #MF327531, unassigned, Aimelvirus 3 [gpai003]

[13] #FJ438902, Cosavirus, Cosavirus A, human cosavirus A1 [0553]

[14] #FJ438907, Cosavirus, Cosavirus B, human cosavirus B1 [2263]

[15] #FJ438908, Cosavirus, Cosavirus D, human cosavirus D1 [5004]

[ 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 ]

[ 1]

[ 2] 0.347

[ 3] 0.360 0.163

[ 4] 0.358 0.161 0.004

[ 5] 0.358 0.161 0.009 0.004

[ 6] 0.358 0.161 0.004 0.002 0.006

[ 7] 0.358 0.161 0.004 0.000 0.004 0.002

[ 8] 0.358 0.161 0.004 0.000 0.004 0.002 0.000

[ 9] 0.400 0.398 0.388 0.385 0.385 0.385 0.385 0.385

[10] 0.445 0.430 0.445 0.443 0.439 0.443 0.443 0.443 0.432

[11] 0.439 0.426 0.447 0.445 0.441 0.445 0.445 0.445 0.439 0.051

[12] 0.443 0.430 0.445 0.443 0.439 0.443 0.443 0.443 0.437 0.056 0.017

[13] 0.538 0.534 0.536 0.536 0.538 0.536 0.536 0.536 0.564 0.502 0.504 0.504

[14] 0.573 0.545 0.560 0.560 0.560 0.560 0.560 0.560 0.582 0.546 0.546 0.548 0.280

[15] 0.556 0.540 0.547 0.547 0.547 0.547 0.547 0.547 0.569 0.531 0.535 0.533 0.302 0.295

The number of amino acid differences per site from between sequences are shown. The analysis involved 15 amino acid sequences. There were a total of 473 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