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:** | ***2018.012S*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **1 new picornavirus genus (*Tottorivirus*) with 1 species (*Tottorivirus 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:** **2018.012S.N.v1.Tottorivirus** |

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 (*Tottorivirus A*) in a new genus (*Tottorivirus*)**

A novel picornavirus named porcine picornavirus Japan (PPVJ) has been detected in a faecal specimen of a 2-months old healthy piglet collected in the Tottori prefecture, Japan. No virus was isolated yet.

**Relation to other picornaviruses:**

- Tottoriviruses have a typical picornavirus genome layout:

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

(compare Fig. 1 of supporting material)

- Tottoriviruses possess typical hallmarks of picornaviruses:

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

2A: **NPGP** 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 a distinct branch (compare Figs. 2-5 of supporting material). Closest relatives are the lesaviruses, hunniviruses and teschoviruses.

**Distinguishing features of tottoriviruses compared to the closest relatives:**

1. Tottoriviruses have **unique L, 2B, 3A proteins**;

2. **Sequence divergence** (uncorrected p-distances) of all relevant genome regions is high in pairwise comparisons:

- P1: nt divergence >0.52, aa divergence >0.59;

- 2Chel: nt divergence >0.52, aa divergence >0.63;

- 3Cpro: nt divergence >0.58, aa divergence >0.67;

- 3Dpol: nt divergence >0.45, aa divergence >0.48 (compare tables 1-8 of supporting material);

**Type species of genus:**

***Tottorivirus A***, porcine picornavirus Japan [Tottori-WOL], GenBank acc. no. LC113907

**Origin of name:**

**tottori**: place name, refers to the **Tottori** prefecture, Japan, where the faecal sample was collected

**Species demarcation criteria:**

not applicable

| **References:** |
| --- |
| Naoi Y, Kishimoto M, Masuda T, Ito M, Tsuchiaka S, Sano K, Yamasato H, Omatsu T, Aoki H, Furuya T, Katayama Y, Oba M, Okada T, Shirai J, Mizutani T, Nagai M. 2016. Characterization and phylogenetic analysis of a novel picornavirus from swine feces in Japan. Arch Virol 161:1685-1690. |



**Figure 1:** Comparison of the genome organisation of porcine picornavirus Japan (proposed genus: *Tottorivirus*), lesavirus 1, *Hunnivirus A* and *Teschovirus A* (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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.544

[ 3] 0.540 0.282

[ 4] 0.545 0.253 0.280

[ 5] 0.546 0.353 0.352 0.345

[ 6] 0.535 0.394 0.400 0.377 0.377

[ 7] 0.535 0.392 0.399 0.376 0.378 0.216

[ 8] 0.540 0.387 0.397 0.374 0.376 0.221 0.039

[ 9] 0.523 0.492 0.499 0.495 0.503 0.499 0.481 0.481

[10] 0.531 0.485 0.501 0.485 0.499 0.497 0.500 0.498 0.397

[11] 0.572 0.533 0.548 0.527 0.548 0.532 0.538 0.539 0.555 0.546

The number of base differences per site from between sequences are shown. The analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 2766 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.632

[ 3] 0.630 0.187

[ 4] 0.635 0.149 0.160

[ 5] 0.631 0.299 0.310 0.305

[ 6] 0.631 0.368 0.378 0.368 0.349

[ 7] 0.623 0.361 0.381 0.361 0.343 0.126

[ 8] 0.622 0.357 0.377 0.355 0.341 0.125 0.008

[ 9] 0.595 0.559 0.564 0.555 0.575 0.551 0.541 0.535

[10] 0.598 0.536 0.534 0.534 0.550 0.536 0.527 0.524 0.396

[11] 0.684 0.631 0.639 0.630 0.632 0.631 0.636 0.636 0.658 0.635

The number of amino acid differences per site from between sequences are shown. The analysis involved 11 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 922 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.537

[ 3] 0.523 0.226

[ 4] 0.542 0.278 0.286

[ 5] 0.537 0.296 0.281 0.226

[ 6] 0.535 0.288 0.271 0.239 0.124

[ 7] 0.545 0.283 0.279 0.224 0.126 0.117

[ 8] 0.540 0.287 0.276 0.221 0.125 0.107 0.028

[ 9] 0.538 0.460 0.476 0.470 0.481 0.471 0.470 0.460

[10] 0.536 0.461 0.458 0.475 0.472 0.464 0.468 0.471 0.324

[11] 0.565 0.483 0.470 0.452 0.479 0.482 0.483 0.482 0.465 0.498

The number of base differences per site from between sequences are shown. The analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 1011 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.633

[ 3] 0.633 0.090

[ 4] 0.630 0.217 0.207

[ 5] 0.655 0.232 0.232 0.180

[ 6] 0.646 0.214 0.211 0.173 0.037

[ 7] 0.642 0.207 0.211 0.183 0.053 0.028

[ 8] 0.639 0.207 0.211 0.176 0.046 0.028 0.006

[ 9] 0.669 0.542 0.536 0.537 0.547 0.537 0.534 0.531

[10] 0.667 0.533 0.536 0.547 0.566 0.559 0.553 0.550 0.245

[11] 0.650 0.586 0.567 0.561 0.580 0.574 0.574 0.571 0.585 0.573

The number of amino acid differences per site from between sequences are shown. The analysis involved 11 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 337 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.593

[ 3] 0.557 0.207

[ 4] 0.595 0.160 0.229

[ 5] 0.586 0.313 0.316 0.281

[ 6] 0.583 0.311 0.293 0.272 0.096

[ 7] 0.602 0.293 0.298 0.258 0.100 0.067

[ 8] 0.592 0.295 0.300 0.258 0.103 0.071 0.037

[ 9] 0.580 0.535 0.541 0.551 0.557 0.550 0.545 0.551

[10] 0.581 0.506 0.488 0.516 0.535 0.519 0.526 0.524 0.321

[11] 0.599 0.577 0.590 0.567 0.573 0.574 0.569 0.569 0.545 0.549

The number of base differences per site from between sequences are shown. The analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 648 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.695

[ 3] 0.680 0.149

[ 4] 0.695 0.125 0.173

[ 5] 0.709 0.266 0.285 0.237

[ 6] 0.705 0.260 0.264 0.221 0.048

[ 7] 0.710 0.255 0.255 0.226 0.063 0.024

[ 8] 0.705 0.260 0.260 0.221 0.058 0.019 0.005

[ 9] 0.735 0.634 0.614 0.644 0.652 0.644 0.644 0.649

[10] 0.739 0.617 0.617 0.642 0.635 0.627 0.627 0.632 0.271

[11] 0.773 0.682 0.697 0.692 0.700 0.701 0.711 0.706 0.640 0.663

The number of amino acid differences per site from between sequences are shown. The analysis involved 11 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 216 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.473

[ 3] 0.459 0.189

[ 4] 0.470 0.156 0.173

[ 5] 0.465 0.200 0.212 0.160

[ 6] 0.467 0.216 0.222 0.166 0.056

[ 7] 0.466 0.207 0.220 0.162 0.057 0.060

[ 8] 0.464 0.211 0.215 0.159 0.056 0.060 0.018

[ 9] 0.467 0.425 0.420 0.410 0.415 0.422 0.420 0.423

[10] 0.452 0.414 0.415 0.419 0.422 0.419 0.423 0.427 0.310

[11] 0.527 0.481 0.486 0.480 0.477 0.477 0.470 0.474 0.483 0.478

The number of base differences per site from between sequences are shown. The analysis involved 11 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 1392 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] #LC113907, swine picornavirus Japan [Tottori-WOL]

[ 2] #JQ941880, Hunnivirus A1 (bovine hungarovirus) [BHUV1/2008/HUN]

[ 3] #HM153767, Hunnivirus A2 (ovine hungarovirus) [OHUV1/2009/HUN]

[ 4] #KX156157, Hunnivirus A6 (rodent hunnivirus) [rodent/Rn/PicoV/SX2015\_2]

[ 5] #KJ950971, Hunnivirus A4 (Norway rat hunnivirus) [NrHuV/NYC-E21]

[ 6] #KT944214, Hunnivirus A7 (rat hunnivirus) [05VZ-75-RAT099]

[ 7] #KT944212, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT106]

[ 8] #KT944213, Hunnivirus A8 (rat hunnivirus) [83GR-70-RAT130]

[ 9] #KM396707, lesavirus 1 [Mis101308/2012]

[10] #KM396708, lesavirus 2 [Nai108015/2012]

[11] #AF231769, Teschovirus A1, porcine teschovirus 1 [Talfan]

[ 1 2 3 4 5 6 7 8 9 10 11 ]

[ 1]

[ 2] 0.492

[ 3] 0.503 0.110

[ 4] 0.484 0.081 0.094

[ 5] 0.498 0.116 0.121 0.088

[ 6] 0.503 0.125 0.132 0.094 0.024

[ 7] 0.501 0.121 0.125 0.092 0.029 0.039

[ 8] 0.503 0.123 0.123 0.090 0.026 0.037 0.007

[ 9] 0.491 0.432 0.439 0.425 0.431 0.432 0.430 0.430

[10] 0.478 0.434 0.436 0.432 0.433 0.428 0.434 0.430 0.243

[11] 0.579 0.517 0.530 0.512 0.511 0.510 0.514 0.514 0.524 0.531

The number of amino acid differences per site from between sequences are shown. The analysis involved 11 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 464 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