This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

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

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

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

| **Code assigned:** | ***2019.018S*** |  |
| --- | --- | --- |
| **Short title:** Create one new species (*Teschovirus B*) in the genus *Teschovirus* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Zell R, Gorbalenya AE, Hovi T, Knowles NJ, Lindberg M, Oberste S, Palmenberg AC, Reuter G, Simmonds P, Skern T, Tapparel C, Wolthers K, Woo P | roland.zell@med.uni-jena.de; a.e.gorbalenya@lumc.nl; tapani.hovi@thl.fi; nick.knowles@pirbright.ac.uk; michael.lindberg@lnu.se; soberste@cdc.gov; acpalmen@wisc.edu; reuter.gabor@gmail.com; peter.simmonds@ndm.ox.ac.uk; timothy.skern@meduniwien.ac.at; caroline.tapparel@unige.ch; k.c.wolthers@amc.uva.nl; pcywoo@hkucc.hku.hk |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| Jena University Hospital [RZ]Leiden University Medical Center [AEG]National Institute for Health and Welfare [TH]The Pirbright Institute [NJK]Linnaeus University Kalmar [ML]Centers for Disease Control and Prevention [SO]University of Wisconsin [ACP]University of Pécs [GR]University of Oxford [PS]Medical University of Vienna [TS]University of Geneve [CT]Universiteit van Amsterdam [KW]University of Hong Kong [PW] |

 |
| **Corresponding author** |
| **Roland Zell** (roland.zell@med.uni-jena.de) |
| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Picornaviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 21/05/2019 |
| Date of this revision (if different to above): |       |

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

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** **2019.018S.N.v1.1newsp\_Teschovirus\_B.xlsx** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Create one new species (*Teschovirus B*) in the genus *Teschovirus***

The genus *Teschovirus* presently consists of only one species, *Teschovirus A* (host: pigs, wild boar). Two recent studies (Oba et al., 2018; Yang et al., 2018) described virus isolates/sequences that represent a novel species with three types.

**Relation to teschovirus and other picornaviruses:**

- Genome layout of novel teschoviruses:

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

- Members of *Teschovirus B* have typical hallmarks of picornaviruses:

 - long **L protein**,

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

 - **2A** has a **NPGP**-motif,

 - **2Chel** with **GxxGxGKS** motif of helicases,

 - **3BVPg** peptides with **Y-3** residue,

 - **3Cpro** with **GxCGx14GxH** motif,

 - **3Dpol** with KDE, PSG, YGDD and FLKR motifs,

- Members of *Teschovirus B* cluster with teschovirus A strains in **phylogenetic analyses** (compare Figs. 2 & 3 of supporting material). Interspecies recombinants have been described (LC386158, LC386159, LC386161).

**Distinguishing features of *Teschovirus B* compared to *Teschovirus A*:**

- All teschovirus genomes show high sequence similarity. 1D protein (VP1) is the most divergent protein (compare Table 1).

- **Sequence divergences** (uncorrected p-distances) of relevant genome regions suggest a distinct teschovirus species (compare Table 1).

**Table 1: Observed amino acid divergences**

*Teschovirus B* vs. P1\* VP1\* 2Chel 3Cpro 3Dpol

*Teschovirus A*  13-26% 44-51% 7-18% 19-26% 13-17%

\* recombinant strains of Teschovirus B were excluded

**Exemplar:**

*Teschovirus B*, teschovirus B1 strain HuN41, GenBank acc. no. MG875515.

**Species demarcation criteria:**

Members of a species of the genus *Teschovirus*:

- are less than 20% divergent in polyprotein aa sequence (compare Table 2, supporting material),

-are less than 30% divergent in P1 aa sequence (compare Table 3, supporting material),

-are less than 10% divergent in 2C+3CD aa sequence (compare Table 4, supporting material),

- share a common genome organization,

- share a natural host range.

| **References:** |
| --- |
| Oba M, Naoi Y, Ito M, Masuda T, Katayama Y, Sakaguchi S, Omatsu T, Furuya T, Yamasato H, Sunaga F, Makino S, Mizutani T, Nagai M. 2018. Metagenomic identification and sequence analysis of a Teschovirus A-related virus in porcine feces in Japan, 2014-2016. Infect Genet Evol 66:210-216.Yang T, Li R, Yao Q, Zhou X, Liao H, Ge M, Yu X. 2018. Prevalence of porcine teschovirus in Hunan, China: identification of novel viral species and genotypes. J Gen Virol 99:1261-1267. |

**Supporting Material:**



**Legend to Figure 1:**  Phylogenetic analysis of picornavirus **P1** using Bayesian tree inference (MrBayes 3.2). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/ Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus* supergroup were retrieved from GenBank; the enterovirus 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*, type and—if available—common names in round brackets. 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 (●). The box indicates recombinant teschovirus strains. Numbers at nodes indicate posterior probabilities obtained after 1,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Legend to Figure 2:**  Phylogenetic analysis of picornavirus **3CD** using Bayesian tree inference (MrBayes 3.2). Seventy-two picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/Cosavirus/Erbovirus/ Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Senecavirus/Teschovirus/Torchivirus/Tottorivirus* supergroup were retrieved from GenBank; the enterovirus 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*, type and—if available—common names in round brackets. 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 (●). The box indicates recombinant teschovirus strains. 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 2. Estimates of Evolutionary Divergence between Teschovirus Polyprotein Sequences**

[ 1] AF231769, *Teschovirus A*, teschovirus A1 [Talfan]

[ 2] LC386152, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im7/2016/G1]

[ 3] LC386153, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im9/2016/G1]

[ 4] AF296087, *Teschovirus A*, teschovirus A2 [T80]

[ 5] MF170936, *Teschovirus A*, teschovirus A2 [HuN32]

[ 6] AF296088, *Teschovirus A*, teschovirus A3 [O2b]

[ 7] AF296089, *Teschovirus A*, teschovirus A4 [PS36]

[ 8] AF296090, *Teschovirus A*, teschovirus A5 [F26]

[ 9] AF296091, *Teschovirus A*, teschovirus A6 [PS37]

[10] AF296092, *Teschovirus A*, teschovirus A7 [F43]

[11] AF296093, *Teschovirus A*, teschovirus A8 [UKG173/74]

[12] AF296094, *Teschovirus A*, teschovirus A9 [Vir2899/84]

[13] AF296095, *Teschovirus A*, teschovirus A10 [Vir460/88]

[14] AF296096, *Teschovirus A*, teschovirus A11 [Dresden]

[15] JN859128, *Teschovirus A*, teschovirus A12 [CC25]

[16] JQ429405, *Teschovirus A*, teschovirus A13 [wild boar/WB2C-TV/2011/HUN]

[17] LC386160, *Teschovirus A*, teschovirus A14 [JPN/MoI2-2-2/2015/G]

[18] MG875515, *Teschovirus B*, teschovirus B1 [HuN41]

[19] LC386154, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka1/2015/G]

[20] LC386155, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka2/2015/G]

[21] LC386156, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta1/2016/G]

[22] LC386157, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta2/2016/G]

[23] MG875516, *Teschovirus B*, teschovirus B3 [HuN42]

[24] LC386158, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/Ishi-Im1-1/2015/G]

[25] LC386159, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/MoI2-2-1/2015/G]

[26] LC386161, *Teschovirus B*, rec. teschovirus A16CP-Bpol [JPN/HkKa2-1/2015/G]

[ 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] 0.053

[ 3] 0.053 0.000

[ 4] 0.100 0.111 0.111

[ 5] 0.111 0.115 0.115 0.048

[ 6] 0.063 0.079 0.079 0.104 0.109

[ 7] 0.111 0.121 0.121 0.070 0.078 0.106

[ 8] 0.094 0.105 0.105 0.098 0.107 0.084 0.107

[ 9] 0.101 0.110 0.110 0.063 0.072 0.097 0.069 0.094

[10] 0.094 0.102 0.102 0.095 0.103 0.086 0.104 0.082 0.095

[11] 0.112 0.110 0.110 0.074 0.083 0.116 0.080 0.108 0.078 0.106

[12] 0.106 0.105 0.105 0.117 0.113 0.096 0.118 0.101 0.107 0.098 0.119

[13] 0.088 0.089 0.089 0.121 0.119 0.079 0.128 0.108 0.114 0.108 0.120 0.097

[14] 0.058 0.064 0.064 0.108 0.117 0.074 0.116 0.102 0.102 0.099 0.117 0.109 0.093

[15] 0.102 0.107 0.107 0.066 0.073 0.108 0.072 0.099 0.071 0.102 0.072 0.109 0.116 0.112

[16] 0.122 0.120 0.120 0.120 0.117 0.121 0.126 0.123 0.123 0.117 0.122 0.105 0.117 0.118 0.116

[17] 0.191 0.194 0.194 0.183 0.191 0.180 0.196 0.182 0.184 0.183 0.185 0.173 0.194 0.188 0.185 0.141

[18] 0.222 0.227 0.227 0.218 0.228 0.225 0.223 0.222 0.224 0.224 0.229 0.232 0.230 0.222 0.228 0.238 0.301

[19] 0.218 0.224 0.224 0.214 0.222 0.222 0.220 0.220 0.219 0.220 0.226 0.227 0.224 0.219 0.226 0.234 0.300 0.018

[20] 0.218 0.224 0.224 0.214 0.222 0.222 0.220 0.220 0.219 0.220 0.226 0.227 0.224 0.219 0.226 0.234 0.300 0.018 0.000

[21] 0.224 0.233 0.233 0.215 0.222 0.220 0.220 0.222 0.221 0.220 0.227 0.225 0.231 0.227 0.229 0.235 0.290 0.060 0.063 0.063

[22] 0.224 0.233 0.233 0.215 0.222 0.220 0.220 0.222 0.221 0.220 0.227 0.225 0.231 0.227 0.229 0.235 0.290 0.060 0.063 0.063 0.000

[23] 0.230 0.233 0.233 0.221 0.227 0.225 0.223 0.229 0.229 0.228 0.228 0.229 0.231 0.228 0.233 0.242 0.309 0.073 0.079 0.079 0.075 0.075

[24] 0.181 0.186 0.186 0.173 0.182 0.173 0.180 0.171 0.167 0.169 0.175 0.176 0.189 0.176 0.180 0.190 0.211 0.145 0.150 0.150 0.147 0.147 0.152

[25] 0.180 0.184 0.184 0.178 0.183 0.176 0.184 0.173 0.171 0.172 0.177 0.178 0.189 0.179 0.183 0.193 0.212 0.154 0.157 0.157 0.154 0.154 0.160 0.016

[26] 0.179 0.189 0.189 0.180 0.192 0.182 0.192 0.171 0.176 0.176 0.181 0.188 0.200 0.185 0.194 0.210 0.227 0.159 0.166 0.166 0.157 0.157 0.168 0.074 0.071

 within type comparison, between types/within species comparison,

 between species/within genus comparison, between genera comparison

Divergence estimates of recombinant teschovirus strains (lines 24-26) are printed in red.

**Table 3. Estimates of Evolutionary Divergence between Teschovirus P1 Sequences**

[ 1] AF231769, *Teschovirus A*, teschovirus A1 [Talfan]

[ 2] LC386152, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im7/2016/G1]

[ 3] LC386153, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im9/2016/G1]

[ 4] AF296087, *Teschovirus A*, teschovirus A2 [T80]

[ 5] MF170936, *Teschovirus A*, teschovirus A2 [HuN32]

[ 6] AF296088, *Teschovirus A*, teschovirus A3 [O2b]

[ 7] AF296089, *Teschovirus A*, teschovirus A4 [PS36]

[ 8] AF296090, *Teschovirus A*, teschovirus A5 [F26]

[ 9] AF296091, *Teschovirus A*, teschovirus A6 [PS37]

[10] AF296092, *Teschovirus A*, teschovirus A7 [F43]

[11] AF296093, *Teschovirus A*, teschovirus A8 [UKG173/74]

[12] AF296094, *Teschovirus A*, teschovirus A9 [Vir2899/84]

[13] AF296095, *Teschovirus A*, teschovirus A10 [Vir460/88]

[14] AF296096, *Teschovirus A*, teschovirus A11 [Dresden]

[15] JN859128, *Teschovirus A*, teschovirus A12 [CC25]

[16] JQ429405, *Teschovirus A*, teschovirus A13 [wild boar/WB2C-TV/2011/HUN]

[17] LC386160, *Teschovirus A*, teschovirus A14 [JPN/MoI2-2-2/2015/G]

[18] MG875515, *Teschovirus B*, teschovirus B1 [HuN41]

[19] LC386154, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka1/2015/G]

[20] LC386155, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka2/2015/G]

[21] LC386156, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta1/2016/G]

[22] LC386157, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta2/2016/G]

[23] MG875516, *Teschovirus B*, teschovirus B3 [HuN42]

[24] LC386158, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/Ishi-Im1-1/2015/G]

[25] LC386159, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/MoI2-2-1/2015/G]

[26] LC386161, *Teschovirus B*, rec. teschovirus A16CP-Bpol [JPN/HkKa2-1/2015/G]

[ 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] 0.086

[ 3] 0.086 0.000

[ 4] 0.236 0.236 0.236

[ 5] 0.230 0.233 0.233 0.076

[ 6] 0.131 0.151 0.151 0.232 0.224

[ 7] 0.249 0.252 0.252 0.147 0.155 0.240

[ 8] 0.209 0.213 0.213 0.219 0.214 0.181 0.234

[ 9] 0.218 0.222 0.222 0.124 0.136 0.210 0.143 0.197

[10] 0.221 0.210 0.210 0.223 0.211 0.186 0.232 0.180 0.204

[11] 0.239 0.233 0.233 0.143 0.147 0.239 0.153 0.221 0.147 0.227

[12] 0.211 0.221 0.221 0.238 0.233 0.183 0.239 0.193 0.214 0.192 0.243

[13] 0.168 0.179 0.179 0.251 0.247 0.141 0.264 0.211 0.230 0.217 0.249 0.216

[14] 0.105 0.104 0.104 0.226 0.235 0.140 0.245 0.205 0.210 0.207 0.230 0.213 0.174

[15] 0.225 0.233 0.233 0.136 0.133 0.231 0.140 0.211 0.135 0.228 0.147 0.232 0.249 0.227

[16] 0.238 0.237 0.237 0.233 0.228 0.231 0.244 0.231 0.241 0.224 0.238 0.216 0.247 0.227 0.230

[17] 0.236 0.246 0.246 0.225 0.232 0.218 0.240 0.221 0.224 0.224 0.230 0.222 0.248 0.229 0.232 0.175

[18] 0.353 0.353 0.353 0.346 0.354 0.364 0.361 0.352 0.360 0.362 0.361 0.364 0.360 0.347 0.359 0.364 0.356

[19] 0.350 0.353 0.353 0.341 0.350 0.362 0.357 0.353 0.355 0.357 0.358 0.361 0.356 0.347 0.359 0.365 0.356 0.013

[20] 0.350 0.353 0.353 0.341 0.350 0.362 0.357 0.353 0.355 0.357 0.358 0.361 0.356 0.347 0.359 0.365 0.356 0.013 0.000

[21] 0.362 0.367 0.367 0.341 0.342 0.355 0.355 0.354 0.356 0.354 0.356 0.352 0.364 0.361 0.363 0.359 0.342 0.127 0.124 0.124

[22] 0.362 0.367 0.367 0.341 0.342 0.355 0.355 0.354 0.356 0.354 0.356 0.352 0.364 0.361 0.363 0.359 0.342 0.127 0.124 0.124 0.000

[23] 0.374 0.369 0.369 0.355 0.357 0.370 0.366 0.371 0.375 0.372 0.363 0.361 0.364 0.364 0.374 0.375 0.365 0.166 0.160 0.160 0.157 0.157

[24] 0.250 0.250 0.250 0.240 0.244 0.242 0.262 0.231 0.228 0.231 0.230 0.229 0.263 0.237 0.243 0.250 0.237 0.349 0.347 0.347 0.351 0.351 0.363

[25] 0.249 0.248 0.248 0.245 0.245 0.243 0.263 0.233 0.227 0.231 0.230 0.231 0.256 0.238 0.247 0.251 0.238 0.351 0.348 0.348 0.353 0.353 0.365 0.013

[26] 0.276 0.280 0.280 0.281 0.292 0.282 0.311 0.253 0.260 0.269 0.264 0.276 0.301 0.274 0.291 0.313 0.279 0.379 0.382 0.382 0.382 0.382 0.400 0.161 0.161

 within type comparison, between types/within species comparison,

 between species/within genus comparison, between genera comparison

Divergence estimates of recombinant teschovirus strains (lines 24-26) are printed in red.

**Table 4. Estimates of Evolutionary Divergence between Teschovirus 2C-3CD Sequences**

[ 1] AF231769, *Teschovirus A*, teschovirus A1 [Talfan]

[ 2] LC386152, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im7/2016/G1]

[ 3] LC386153, *Teschovirus A*, teschovirus A1 [JPN/Ishi-Im9/2016/G1]

[ 4] AF296087, *Teschovirus A*, teschovirus A2 [T80]

[ 5] MF170936, *Teschovirus A*, teschovirus A2 [HuN32]

[ 6] AF296088, *Teschovirus A*, teschovirus A3 [O2b]

[ 7] AF296089, *Teschovirus A*, teschovirus A4 [PS36]

[ 8] AF296090, *Teschovirus A*, teschovirus A5 [F26]

[ 9] AF296091, *Teschovirus A*, teschovirus A6 [PS37]

[10] AF296092, *Teschovirus A*, teschovirus A7 [F43]

[11] AF296093, *Teschovirus A*, teschovirus A8 [UKG173/74]

[12] AF296094, *Teschovirus A*, teschovirus A9 [Vir2899/84]

[13] AF296095, *Teschovirus A*, teschovirus A10 [Vir460/88]

[14] AF296096, *Teschovirus A*, teschovirus A11 [Dresden]

[15] JN859128, *Teschovirus A*, teschovirus A12 [CC25]

[16] JQ429405, *Teschovirus A*, teschovirus A13 [wild boar/WB2C-TV/2011/HUN]

[17] MG875515, *Teschovirus B*, teschovirus B1 [HuN41]

[18] LC386154, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka1/2015/G]

[19] LC386155, *Teschovirus B*, teschovirus B1 [JPN/Ishi-Ka2/2015/G]

[20] LC386156, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta1/2016/G]

[21] LC386157, *Teschovirus B*, teschovirus B2 [JPN/Ishi-Ta2/2016/G]

[22] MG875516, *Teschovirus B*, teschovirus B3 [HuN42]

[23] LC386158, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/Ishi-Im1-1/2015/G]

[24] LC386159, *Teschovirus B*, rec. teschovirus A15CP-Bpol [JPN/MoI2-2-1/2015/G]

[25] LC386161, *Teschovirus B*, rec. teschovirus A16CP-Bpol [JPN/HkKa2-1/2015/G]

[ 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 ]

[ 1]

[ 2] 0.024

[ 3] 0.024 0.000

[ 4] 0.007 0.025 0.025

[ 5] 0.029 0.034 0.034 0.028

[ 6] 0.016 0.028 0.028 0.015 0.029

[ 7] 0.014 0.027 0.027 0.015 0.024 0.013

[ 8] 0.011 0.029 0.029 0.012 0.031 0.014 0.016

[ 9] 0.019 0.030 0.030 0.020 0.027 0.019 0.014 0.019

[10] 0.008 0.028 0.028 0.008 0.029 0.018 0.016 0.013 0.021

[11] 0.024 0.021 0.021 0.025 0.037 0.031 0.027 0.027 0.030 0.024

[12] 0.035 0.027 0.027 0.034 0.030 0.035 0.032 0.038 0.032 0.037 0.031

[13] 0.033 0.029 0.029 0.032 0.028 0.034 0.031 0.036 0.033 0.035 0.033 0.014

[14] 0.027 0.034 0.034 0.028 0.034 0.029 0.024 0.029 0.026 0.027 0.038 0.037 0.036

[15] 0.016 0.017 0.017 0.015 0.029 0.021 0.021 0.020 0.027 0.016 0.021 0.025 0.026 0.033

[16] 0.041 0.038 0.038 0.040 0.038 0.043 0.040 0.044 0.040 0.043 0.039 0.026 0.024 0.039 0.037

[17] 0.140 0.146 0.146 0.140 0.144 0.137 0.137 0.140 0.138 0.141 0.150 0.149 0.149 0.144 0.147 0.156

[18] 0.132 0.138 0.138 0.132 0.136 0.129 0.129 0.132 0.130 0.134 0.142 0.141 0.139 0.136 0.139 0.146 0.016

[19] 0.132 0.138 0.138 0.132 0.136 0.129 0.129 0.132 0.130 0.134 0.142 0.141 0.139 0.136 0.139 0.146 0.016 0.000

[20] 0.135 0.143 0.143 0.135 0.140 0.132 0.132 0.135 0.133 0.136 0.146 0.144 0.144 0.139 0.142 0.151 0.017 0.017 0.017

[21] 0.135 0.143 0.143 0.135 0.140 0.132 0.132 0.135 0.133 0.136 0.146 0.144 0.144 0.139 0.142 0.151 0.017 0.017 0.017 0.000

[22] 0.135 0.141 0.141 0.135 0.139 0.132 0.132 0.135 0.133 0.136 0.143 0.144 0.144 0.139 0.142 0.151 0.012 0.016 0.016 0.016 0.016

[23] 0.134 0.140 0.140 0.134 0.136 0.131 0.129 0.134 0.130 0.135 0.144 0.143 0.143 0.138 0.141 0.150 0.014 0.016 0.016 0.011 0.011 0.011

[24] 0.140 0.146 0.146 0.140 0.144 0.137 0.136 0.140 0.138 0.141 0.150 0.149 0.149 0.144 0.147 0.156 0.019 0.024 0.024 0.019 0.019 0.018 0.015

[25] 0.122 0.133 0.133 0.120 0.129 0.122 0.120 0.120 0.124 0.124 0.137 0.135 0.139 0.131 0.137 0.144 0.015 0.020 0.020 0.013 0.013 0.011 0.013 0.013

 within type comparison, between types/within species comparison,

 between species/within genus comparison, between genera comparison

Divergence estimates of recombinant teschovirus strains (lines 23-25) are printed in red.