

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

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| **Code assigned:** | **2020.007S** |  |
| **Short title:** Create one new species (*Mischivirus E*) in the genus *Mischivirus* (*Picornavirales*: *Picornaviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Picornaviridae* Study Group |

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

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

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

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

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

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

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2020.007S.R.Mischivirus\_1nsp.xlsx |

**Abstract**

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| The *Mischivirus* genus presently comprise four species, *Mischivirus A* to *D*. The known mischiviruses have been detected in faecal samples of bats (mischiviruses A1, B1 and C1) and dogs (mischivirus D1). A novel mischivirus-like virus from the faeces of the Asian house shrew (*Suncus murinus*) exhibits an identical genome layout (5'-UTRIRES[L-1A-1B-1C-1D-2Anpg↓p-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR) and significant sequence similarity to justify assignment to the genus *Mischivirus*, but a new species, *Mischivirus E*: The between-species amino acid divergences range from 52.2 to 59.2% for P1, 44.9-48.8% for 2Chel, 51.2-59.0% for 3Cpro and 31.3-40.5% for 3Dpol in comparisons to other mischiviruses. Divergence to sequences of other picornavirus genera is considerably greater. |

**Text of proposal**

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| |  | | --- | | **Create a new species, *Mischivirus E*, in the genus *Mischivirus***  The *Mischivirus* genus presently comprise four species, *Mischivirus A* to *D*. The known mischiviruses have been detected in faecal samples of bats (mischiviruses A1, B1 and C1) and dogs (mischivirus D1). A novel mischivirus-like virus was detected in faeces from the Asian house shrew (*Suncus murinus*) in the Zheijang province, China (W.-P. Guo & Y.-Z. Zhang, 2017, unpublished). No viable virus was isolated. Despite significant similarities to the known mischiviruses, the Suncus murinus mischivirus exhibits differences which justify assignment to a new species.  **Relation to other picornaviruses:**  1. The Suncus murinus mischivirus has a typical picornavirus genome layout:  5'-UTRIRES[L-1A-1B-1C-1D-2Anpg↓p-2B-2Chel/3A-3BVPg-3Cpro-3Dpol]3'UTR  (compare Fig. 1 of supporting material)  2. The Suncus murinus mischivirus possesses typical hallmarks of picornaviruses:  **capsid proteins:** 1B, 1C, 1D have **rhv** domains with drug-binding site,  **2Chel:** **G**xx**G**x**GKS** motif of helicases,  **3BVPg:** **Y-3** residue,  **3Cpro:** **C**x**CG**x14**G**x**H** motif,  **3Dpol:** **KDE**, **PSG**, **YGDD**, **FLKR** motifs  3. **Phylogenetic analyses** indicate a distinct branch that clusters with sequences of the mischiviruses and the picornavirus supergroup 1 (*Ailurivirus/Aphthovirus/Bopivirus/ Cardiovirus/Cosavirus/Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/ Mupivirus*/*Senecavirus/Teschovirus/Torchivirus/Tottorivirus*) in the P1 and 3CD trees (compare Figs. 2 & 3 of supporting material).  4. **Divergence:** Comparisons to other mischiviruses show <56% diversity for the polyprotein, <61% for P1 and <46% for 2C+3CD (Table 1) suggesting a new mischivirus species, *Mischivirus E*, with 1 type, mischivirus E1 (GenBank acc. nos. MF352410).  **Distinguishing features of the Suncus murinus mischivirus compared to other viruses of picornavirus supergroup 1:**  1. The Suncus murinus mischivirus has characteristic features of the **L, 1A,** and **1B** proteins (compare Fig. 1):  - the L protein are remarkably short (41 aa) compared to the L proteins of other mischiviruses (68-97 aa), its function is unknown;  - the 1A protein is shorter (44 aa) compared to the 1A proteins of other mischiviruses (61-64 aa);  - the 1B protein exhibits an unusually long puff region (elongated by 21 aa between beta-strand E and alpha-helix B).  2. **Sequence divergence** (uncorrected p-distances) of orthologous proteins is high in pairwise comparisons with 37 acknowledged and proposed species of picornavirus supergroup 1. The amino acid divergences range from 54.2 to 60.6% for P1, 44.9-48.8% for 2Chel, 51.2-55.8% for 3Cpro and 31.3-40.5% for 3Dpol in comparisons to other mischiviruses (compare Table 1). Divergence to sequences of other picornaviruses of supergroup 1 is even greater (6-28%).  **Species demarcation criteria:**  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 virus of species:**  ***Mischivirus E***, mischivirus E1 (Suncus murinus mischivirus) strain Wencheng-Sm294, GenBank acc. no. MF352410 | |

**Supporting evidence**

**Table 1: Diversities**

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|  | **MiV-A1** | **MiV-B1** | **MiV-C1** | **MiV-D1** | **MiV-E1** |
| **Polyprotein** | | | | | |
| **MiV-A1** | - |  |  |  |  |
| **MiV-B1** | 0.266 | - |  |  |  |
| **MiV-C1** | 0.544 | 0.547 | - |  |  |
| **MiV-D1** | 0.523 | 0.524 | 0.558 | - |  |
| **P1 protein** | | | | | |
| **MiV-A1** |  |  |  |  |  |
| **MiV-B1** | 0.280 | - |  |  |  |
| **MiV-C1** | 0.559 | 0.562 | - |  |  |
| **MiV-D1** | 0.572 | 0.548 | 0.592 | - |  |
| **MiV-E1** | 0.542 | 0.533 | 0.599 | 0.606 | - |
| **2C+3CD protein** | | | | | |
| **MiV-A1** | - |  |  |  |  |
| **MiV-B1** | 0.201 | - |  |  |  |
| **MiV-C1** | 0.438 | 0.443 | - |  |  |
| **MiV-D1** | 0.405 | 0.421 | 0.443 | - |  |
| **MiV-E1** | 0.423 | 0.425 | 0.454 | 0.446 | - |

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

**Suncus murinus mischivirus vs. P1 2Chel 3Cpro 3Dpol**

*Mischivirus* *Mischivirus A* 53.5% 45.2% 57.5% 33.4%

*Mischivirus B* 52.2% 48.0% 59.0% 31.3%

*Mischivirus C* 58.9% 48.8% 51.2% 40.5%

*Mischivirus D* 59.2% 44.9% 56.7% 39.4%

*Ailurivirus* *Ailurivirus A* 63.2% 58.2% 61.4% 45.6%

*Aphthovirus* *Bovine rhinitis A virus* 75.2% 66.3% 80.9% 56.1%

*Bovine rhinitis B virus* 75.4% 64.0% 79.3% 56.1%

*Equine rhinitis A virus* 68.0% 64.7% 77.7% 53.7%

*Foot-and-mouth disease virus* 75.6% 63.3% 81.0% 56.7%

*Bopivirus* *Bopivirus A* 68.6% 65.6% 85.2% 61.6%

*Cardiovirus* *Cardiovirus A* 62.7% 53.5% 68.8% 45.4%

*Cardiovirus B* 62.6% 55.1% 68.0% 47.0%

*Cardiovirus C* 65.9% 52.1% 68.3% 47.2%

*Cardiovirus D* 62.2% 53.6% 69.9% 49.0%

*Cardiovirus E* 63.3% 56.4% 71.2% 47.6%

*Cardiovirus F* 63.5% 53.4% 69.1% 47.4%

*Cosavirus* *Cosavirus A* 68.4% 52.6% 74.8% 54.5%

*Cosavirus B* 66.8% 51.1% 74.1% 54.9%

*Cosavirus D* 69.4% 55.8% 76.2% 52.3%

*Cosavirus E* 68.6% 53.3% 77.7% 56.2%

*Cosavirus F* 67.1% 53.3% 77.2% 53.8%

*Erbovirus* *Erbovirus A* 66.9% 66.9% 81.4% 53.2%

*Hunnivirus* *Hunnivirus A* 73.0% 63.9% 76.6% 57.8%

*Malagasivirus* *Malagasivirus A* 71.5% 65.7% 78.9% 57.8%

*Malagasivirus B* 70.9% 65.5% 80.8% 58.7%

*Mosavirus* *Mosavirus A* 64.6% 56.9% 75.8% 61.5%

*Mosavirus B* 63.1% 59.2% 80.2% 61.1%

Mupivirus *Mupivirus A1* 63.0% 55.9% 70.2% 48.7%

*Senecavirus* *Senecavirus A* 68.0% 61.6% 66.3% 44.6%

*Teschovirus* *Teschovirus A* 74.7% 65.8% 80.4% 60.3%

*Teschovirus B* 74.0% 65.2% 78.9% 61.0%

*Torchivirus* *Torchivirus A* 67.5% 61.9% 72.4% 58.3%

*Tottorivirus* *Tottorivirus A* 75.1% 67.6% 78.9% 57.1%

unassigned Burpengary virus 71.0% 65.0% 77.0% 52.8%

unassigned Hainan black-spectacled toad picornavirus 68.7% 68.3% 79.2% 56.3%

unassigned Zheijiang banded bullfrog picornavirus 71.7% 71.7% 76.4% 57.3%

\* number of amino acid differences per site

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**Figure 1:** Genome organisation of mischiviruses (schematic depiction). The genome of the Suncus murinus mischivirus is compared to the genomes of the exemplar viruses of other mischiviruses. The open reading frame is indicated by a box. Position of putative 3Cpro cleavage sites are indicated by a ▼ and the VP0 processing site by a ¶. The names and lengths of the deduced proteins are presented. The 5’-UTR may be incomplete.



**Figure 2:** Phylogenetic analysis of picornavirus P1 protein using Bayesian tree inference (MrBayes 3.2). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/ Cosavirus/Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Mupivirus/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 (●). \* indicates incomplete genomes. Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.



**Figure 3:** Phylogenetic analysis of picornavirus 3CD protein using Bayesian tree inference (MrBayes 3.2). Seventy-six picornavirus sequences of the *Ailurivirus/Aphthovirus/Bopivirus/Cardiovirus/ Cosavirus/Erbovirus/Hunnivirus/Malagasivirus/Mischivirus/Mosavirus/Mupivirus/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 (●).\* indicates incomplete genomes. Numbers at nodes indicate posterior probabilities obtained after 2,000,000 generations. The optimal substitution model (GTR+G+I) was determined with MEGA 5. The scale indicates substitutions/site.

**References**

W.-P. Guo & Y.-Z. Zhang, 2017, unpublished