

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

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| **Code assigned:** | **2022.002S** |  |
| **Short title:** Create eight new species in the genus *Pestivirus* (*Flaviviridae*) |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Sent to *Hepaciviridae* SG chair and SC chair on 15th December 2021 and 19th April 2022  |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 | 19/04/2022 |
| 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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| 2022.002S.N.v1.Pestivirus\_8nsp.xlsx |

**Abstract**

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| Eight additional species proposed for the genus *Pestivirus* (family *Flaviviridae*) based on phylogeny, pathology and host species of newly reported pestiviruses. |

**Text of proposal**

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| As a result of an analysis of sequences of recently reported novel pestiviruses (Table 1) we propose to establish eight additional species (*Pestivirus* *L*, *Pestivirus M*, *Pestivirus* *N*, *Pestivirus* *O*, *Pestivirus* *P*, *Pestivirus* *Q*, *Pestivirus* *R,* and *Pestivirus S*), expanding the number of pestivirus species to 19 [6]. This proposal is an extension of previous work in which reference sequences and species demarcation criteria were proposed on the basis of phylogenetic and distance comparisons between complete genome sequences [7]. We have only proposed new species where a complete coding sequence is available. Current species demarcation criteria in the genus take into account nucleotide and deduced amino acid sequence relatedness, antigenic relatedness and host of origin (https://talk.ictvonline.org/ictv-reports/ictv\_online\_report/positive-sense-rna-viruses/w/flaviviridae/361/genus-pestivirus).**Table 1.** Recently reported pestivirus sequences.

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| **Proposed Species** | **Virus Name** | **Abbrevi-ation 1** | **Host****Species** | **Isolates** |  | **Ref.** |
| **GenBank** | **Region2** | **Length [b]** |
| *Pestivirus* *L* | Linda virus | LindaV | *Sus scrofa* | Austria1 | KY436034 | CG | 12,614 | [4] |
| *Pestivirus* *M* | Phocoenapestivirus | PhoPeV | *Phocoena phocoena* | PhoPeV-1 | MK910227 | CG | 11,880 | [3] |
| PhoPeV-2 | MK910228 | CG  | 11,880 | [3] |
| PhoPeV-3 | MK910229 | CG | 12,060 | [3] |
| *Pestivirus* *N* | Tunisian sheep-like pestivirus | TSV | *Capra aegagrus hircus* | 70292/2007/EN | MZ664273 | CCS | 12,268 | [5] |
| *Ovis gmelini aries* | 92019/2007/AG | MZ664274 | CG | 12,286 | [5] |
| *Pestivirus* *O* | ovine/ITpestivirus | ovIT PeV | *Ovis gmelini aries* | 338710-2/2017 | MK618725 | PG | 11,143 | [8] |
| 338710-3/2017 | MK618726 | CCS | 12,173 | [8] |
| 1756/2017 | MG770617 | CCS | 12,173 | [8] |
| *Pestivirus* *P* | pangolinpestivirus | DYPV | *Amblyomma javanense* | DYAJ1 | MK636874 | CG | 12,443 | [2] |
| *Manis javanica* | DYCS | MK636875 | CG | 12,446 | [2] |
| *Pestivirus* *Q* | rodent pestivirus | RtNn-PeV | *Niviventer niviventer* | HuB2014 | KY370101 | CCS | 13,220 | [10] |
| *Pestivirus* *R* | rodent pestivirus | RtAp-PeV | *Apodemus peninsulae* | JL2014 | KY370100 | CCS | 12,768 | [10] |
| n.a. | rodent pestivirus | RtNe-PeV | *Niviventer excelsior* | SC2014 | KY370099 | PG | 11,644 | [10] |
| n.a. | rodent pestivirus | RtAd-PeV | *Apodemus draco* | SAX2015 | KY370102 | PG | 11,551 | [10] |
| n.a. | rodent pestivirus | RtNn-PeV | *Niviventer niviventer* | SAX2015 | KY370103 | PG | 11,435 | [10] |
| *Pestivirus* *S* | bat pestivirus | BtSk-PeV | *Scotophilus kuhlii* | 1/GX2017 | MH282908 | CCS | 11,921 | [9] |
| n.a. | bat pestivirus | 3/GX2017 | MH282910 | PG | 7266 | [9] |
| n.a. | bat pestivirus | 4/GX2017 | MH282911 | PG | 7132 | [9] |

n.a., not assigned (no complete cds available); 1 Given is the first proposed or commonly used abbreviation. 2 CG complete genome, CCS complete coding sequence, PG partial genomeMembers of additional species proposed here are generally distinguished by the phylogeny of (Figure 1B) and distances between complete coding sequences (Table 2), with members of different species belonging to well-demarcated clades and having distances of >0.24 (nucleotide) or >0.15 (amino acid). Most of the viruses assigned to new species are genetically very distinct from members of the previously approved species *Pestivirus* *A* through *Pestivirus* *K*. Members of different species are also generally distinguished on the basis of the phylogeny or distance comparisons for a highly conserved part of NS5B (NS5B3312–3837), with distances of >0.13 as the demarcation point. An advantage of using NS5B3312–3837 region is that this region is not prone to large-scale insertion or deletion and so no additional editing of sequences is required. **Table 2.** Minimum p-distances between members of selected pestivirus species.

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|  | **Minimum p-Distances** |
| **CDS** | **Polyprotein** | **NS5B3312–3837** |
| *Pestivirus A* | *Pestivirus B* | >0.30 | >0.24 | >0.17 |
| *Pestivirus* *C* | *Pestivirus D* | >0.29 | >0.21 | >0.14 |
| *Pestivirus* *C* | *Pestivirus I* | >0.28 | >0.20 | >0.14 |
| *Pestivirus* *D* | *Pestivirus I* | >0.28 | >0.19 | >0.14 |
| *Pestivirus L* | *Pestivirus* *F* | 0.35 | 0.31 | 0.22 |
| *Pestivirus* *M* | *Pestivirus* *F*, *Pestivirus* *L* | >0.37 | >0.36 | >0.22 |
| *Pestivirus* *N* | *Pestivirus* *C* | >0.24 | >0.16 | >0.09 |
| *Pestivirus* *N* | *Pestivirus I* | >0.26 | >0.18 | >0.13 |
| *Pestivirus* *N* | *Pestivirus* *O* | 0.23 | >0.14 | 0.11 |
| *Pestivirus* *O* | *Pestivirus* *C* | >0.22 | >0.14 | >0.11 |
| *Pestivirus* *P* | *Pestivirus* *F*, *Pestivirus* *M* | >0.41 | >0.47 | >0.33 |
| *Pestivirus* *Q* | *Pestivirus* *R* | 0.40 | 0.42 | 0.33 |
| *Pestivirus* *Q* | *Pestivirus J* | 0.30 | 0.22 | 0.17 |
| *Pestivirus* *R* | *Pestivirus* *Q* | 0.40 | 0.42 | 0.33 |
| *Pestivirus R* | *Pestivirus J* | 0.40 | 0.42 | 0.31 |
| *Pestivirus* *S* | *Pestivirus* *K* | >0.40 | >0.40 | >0.29 |
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**Figure 1.** Phylogenetic analysis of pestivirus sequences. (**A**) Maximum likelihood tree was based on the conserved partial NS5B peptide (positions 3312–3837 in the polyprotein of BVDV-1 (*Pestivirus A)* reference strain SD-1). With one exception (KY370103, indicated by asterisk), the sequences were derived from complete coding sequences. For clarity, the clades for viruses in the species *Pestivirus A*, *Pestivirus B*, *Pestivirus C*, *Pestivirus D*, *Pestivirus H,* and *Pestivirus K* are collapsed. Proposed species are indicated using red. Pestivirus sequences identified in non-ungulate hosts are highlighted (grey shaded box). Bootstrap values >70% are shown. (**B**) A subset of pestiviruses closely related to TSV (*Pestivirus* *N*) and ovIT PeV (*Pestivirus* *O*) was analyzed separately by Maximum likelihood analyses for complete coding sequences or (**C**) polyprotein sequences. Figure reproduced from [6].Members of the proposed species *Pestivirus N* and *Pestivirus O* are not as divergent from CSFV isolates in the species *Pestivirus C* for either complete coding region sequences or for the NS5B3312–3837 region. These viruses are also antigenically related [1]. Nevertheless, we argue that these isolates represent three different species for the following reasons:1. Phylogenetic analysis of complete coding nucleotide or polyprotein sequences (Figure 1B, 1C) or NS5B3312–3837 sequences (Figure 1A) shows that ovIT PeV (*Pestivirus O*) shares a common branch with, but is distinct from, CSFV (*Pestivirus C*). Similarly, TSV (*Pestivirus N*) shares a common branch with both ovIT PeV and CSFV, but is distinct from both.
2. Natural infection with CSFV (*Pestivirus C*) is confined to pigs, while ovIT PeV (*Pestivirus O*) and TSV (*Pestivirus N*) have only been detected in small ruminants. Both viruses have been known for more than 15 years.
3. Experimental infection of pigs with TSV (*Pestivirus N*) results in no CSF-like symptoms [39], while studies on porcine cells *in vitro* revealed rather inefficient replication. Pigs exposed to infection with ovIT PeV (*Pestivirus O*) showed only mild, unspecific clinical signs and pathological alterations, with very limited replication, these features resembling the outcome of horizontal infections of pigs with other ruminant pestiviruses, e.g., BVDV-1 (*Pestivirus A*) or BDV (*Pestivirus D*) [1, 5].
4. Regulatory considerations in the control of CSF require a clear differentiation of CSFV from other pestiviruses.
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