This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.010S*** | | | | (to be completed by ICTV officers) |
| **Short title:** Renaming four species and creating seven new species in the genus *Pestivirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Donald B. Smith, Gregor Meyers, Jens Bukh, Ernest A. Gould, Thomas Monath, A. Scott Muerhoff, Alexander Pletnev, Rebecca Rico-Hesse, Jack T. Stapleton, Peter Simmonds and Paul Becher | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Paul Becher paul.becher@tiho-hannover.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) | | | ***Flaviviridae*** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| Proposal written by the *Flaviviviridae* Study group | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 31 May 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.010S.N.v1.Pestivirus\_7sp4spren** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 3:** **NON-STANDARD**

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

|  |
| --- |
| non-standard proposal |
| ***Title of proposal:*** |
| **Text of proposal:** |
|  |

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal | |
| --- | --- |
| **References:** | |
| **Avalos-Ramirez, R., Orlich, M., Thiel, H. J. & Becher, P.** **(2001).** Evidence for the presence of two novel pestivirus species. *Virology* **286**, 456–65.  **Bauermann, F. V., Flores, E. F. & Ridpath, J. F.** **(2012).** Antigenic relationships between Bovine viral diarrhea virus 1 and 2 and HoBi virus. *J Vet Diagnostic Investig* **24**, 253–261.  **Becher, P., Orlich, M., Shannon, A. D., Horner, G., König, M. & Thiel, H. J.** **(1997).** Phylogenetic analysis of pestiviruses from domestic and wild ruminants. *J Gen Virol* **78**, 1357–1366. Microbiology Society.  **Becher, P., Avalos Ramirez, R., Orlich, M., Cedillo Rosales, S., König, M., Schweizer, M., Stalder, H., Schirrmeier, H. & Thiel, H.-J.** **(2003).** Genetic and antigenic characterization of novel pestivirus genotypes: implications for classification. *Virology* **311**, 96–104.  **Firth, C., Bhat, M., Firth, M. A., Williams, S. H., Frye, M. J., Simmonds, P., Conte, J. M., Ng, J., Garcia, J. & other authors**. **(2014).** Detection of zoonotic pathogens and characterization of novel viruses carried by commensal Rattus norvegicus in New York City. *MBio* **5**, e01933–14.  **Hause, B. M., Collin, E. A., Peddireddi, L., Yuan, F., Chen, Z., Hesse, R. A., Gauger, P. C., Clement, T., Fang, Y. & Anderson, G.** **(2015).** Discovery of a novel putative atypical porcine pestivirus in pigs in the USA. *J Gen Virol* **96**, 2994–2998. Microbiology Society.  **Kirkland, P. D., Frost, M. J., Finlaison, D. S., King, K. R., Ridpath, J. F. & Gu, X.** **(2007).** Identification of a novel virus in pigs—Bungowannah virus: A possible new species of pestivirus. *Virus Res* **129**, 26–34.  **Liu, L., Kampa, J., Belák, S. & Baule, C.** **(2009a).** Virus recovery and full-length sequence analysis of atypical bovine pestivirus Th/04\_KhonKaen. *Vet Microbiol* **138**, 62–68.  **Liu, L., Xia, H., Wahlberg, N., Belák, S. & Baule, C.** **(2009b).** Phylogeny, classification and evolutionary insights into pestiviruses. *Virology* **385**, 351–357.  **Neill, J. D., Ridpath, J. F., Fischer, N., Grundhoff, A., Postel, A. & Becher, P.** **(2014).** Complete Genome Sequence of Pronghorn Virus, a Pestivirus. *Genome Announc* **2**, e00575–14–e00575–14. American Society for Microbiology.  **Postel, A., Schmeiser, S., Oguzoglu, T. C., Indenbirken, D., Alawi, M., Fischer, N., Grundhoff, A. & Becher, P.** **(2015).** Close relationship of ruminant pestiviruses and classical Swine Fever virus. *Emerg Infect Dis* **21**, 668–72. Centers for Disease Control and Prevention.  **Postel, A., Hansmann, F., Baechlein, C., Fischer, N., Alawi, M., Grundhoff, A., Derking, S., Tenhündfeld, J., Pfankuche, V. M. & other authors**. **(2016).** Presence of atypical porcine pestivirus (APPV) genomes in newborn piglets correlates with congenital tremor. *Sci Rep* **6**, 27735. Nature Publishing Group.  **Postel, A., Meyer, D., Petrov, A. & Becher, P.** **(2017).** Recent emergence of a novel porcine pestivirus: interference with classical swine fever diagnosis? *Emerg Microbes Infect* **6**, e19. Nature Publishing Group.  **Ridpath J.F.** **(2013).** A need to define characteristics to be used in the taxonomy of the expanding pestivirus genus. *Berl Munch Tierarztl Wochenschr* **126**, 462–467.  **Schirrmeier, H., Strebelow, G., Depner, K., Hoffmann, B. & Beer, M.** **(2004).** Genetic and antigenic characterization of an atypical pestivirus isolate, a putative member of a novel pestivirus species. *J Gen Virol* **85**, 3647–3652. Microbiology Society.  **Simmonds, P., Becher, P., Bukh, J., Gould, E. A., Meyers, G., Monath, T., Muerhoff, S., Pletnev, A., Rico-Hesse, R. & other authors**. **(2017).** ICTV Virus Taxonomy Profile: Flaviviridae. *J Gen Virol* **98**, 2–3. Microbiology Society.  **Smith, D. B., Becher, P., Bukh, J., Gould, E. a., Meyers, G., Monath, T., Muerhoff, a. S., Pletnev, A., Rico-Hesse, R. & other authors**. **(2016).** Proposed update to the taxonomy of the genera Hepacivirus and Pegivirus within the Flaviviridae family. *J Gen Virol* **97**, 2894–2907. Microbiology Society.  **Stapleton, J. T., Foung, S., Muerhoff, A. S., Bukh, J. & Simmonds, P.** **(2011).** The GB viruses: a review and proposed classification of GBV-A, GBV-C (HGV), and GBV-D in genus Pegivirus within the family Flaviviridae. *J Gen Virol* **92**, 233–46. Microbiology Society.  **Tamura, K., Stecher, G., Peterson, D., Filipski, A. & Kumar, S.** **(2013).** MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Mol Biol Evol* **30**, 2725–9.  **Vilcek, S., Ridpath, J. F., Van Campen, H., Cavender, J. L. & Warg, J.** **(2005).** Characterization of a novel pestivirus originating from a pronghorn antelope. *Virus Res* **108**, 187–193.  **Vilček, Š. & Nettleton, P. F.** **(2006).** Pestiviruses in wild animals. *Vet Microbiol* **116**, 1–12. | |
|  | |
| **Annex:**  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. |

We propose renaming the existing four species in the genus *Pestivirus*, family *Flaviviridae*, (*Bovine viral diarrhea virus 1* (BVDV-1), *Bovine viral diarrhea virus 2* (BVDV-2), *Border disease virus* (BDV), and *Classical swine fever virus* (CSFV) (Becher *et al.*, 2003; Simmonds *et al.*, 2017)), and creating seven new species, using a host-independent scheme with the format *Pestivirus Y*. Demarcation of the four existing *Pestivirus* species is based on a range of criteria including divergence of complete coding nucleotide sequences by more than 25%, >10-fold differences in cross-neutralisation titres, and in some cases differing, although overlapping, host ranges (Becher *et al.*, 2003; Simmonds *et al.*, 2017). Additional related viruses have been isolated or sequenced from domestic animals (Hause *et al.*, 2015; Kirkland *et al.*, 2007; Liu *et al.*, 2009a; Postel *et al.*, 2015, 2016; Schirrmeier *et al.*, 2004) and wild species such as giraffe (Avalos-Ramirez *et al.*, 2001; Becher *et al.*, 1997), pronghorn antelope (Neill *et al.*, 2014; Vilcek *et al.*, 2005) and rat (Firth *et al.*, 2014), and proposed as additional species within the genus *Pestivirus* (Becher *et al.*, 2003; Liu *et al.*, 2009b; Ridpath J.F., 2013; Vilček & Nettleton, 2006).

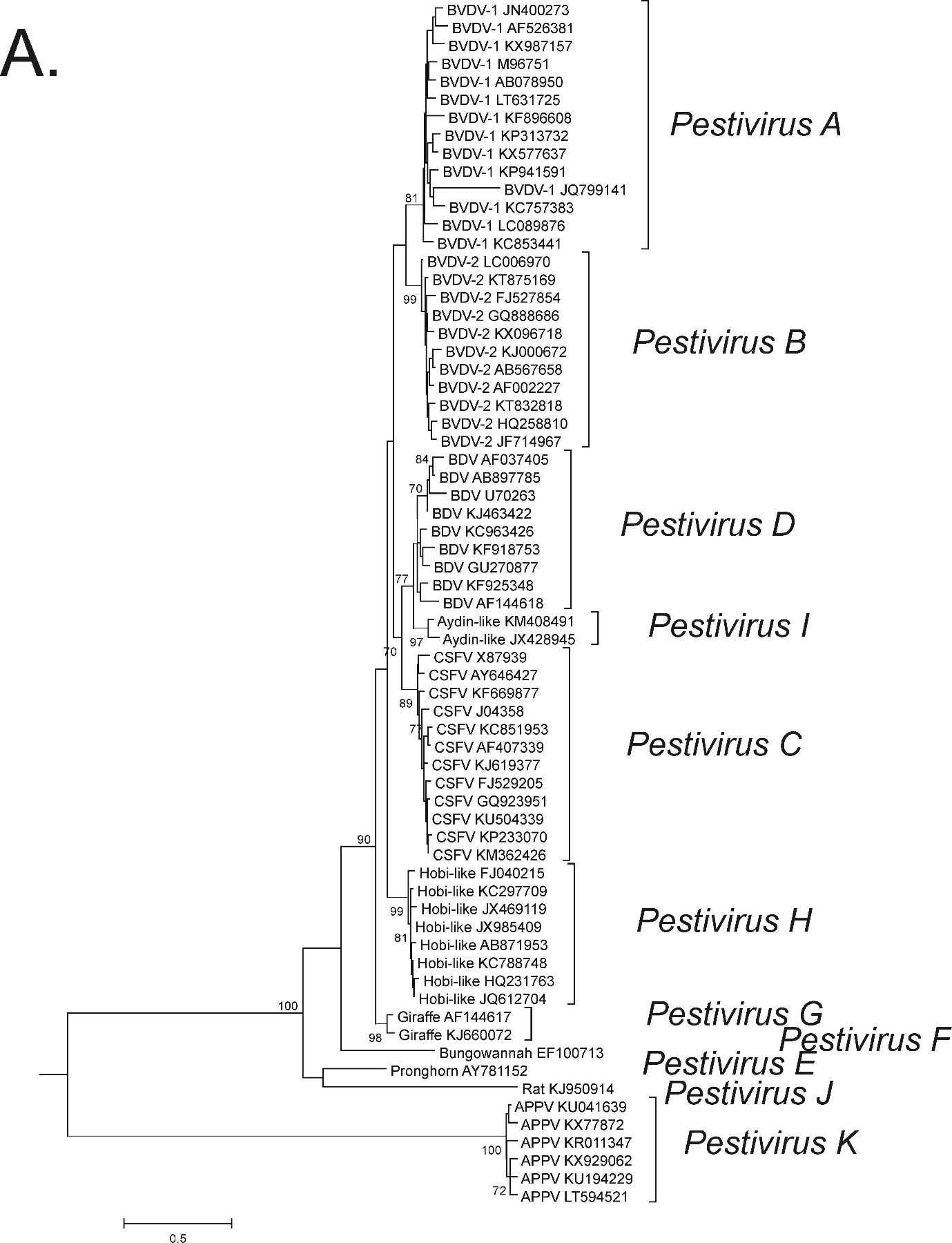
Pairwise amino acid p-distances between complete polyprotein sequences of members of the four existing *Pestivirus* species were < 0.15 for BVDV-1, < 0.11 for BVDV-2,, < 0.15 for BDV and < 0.13 for CSFV. Inter-species amino acid p-distances were > 0.2, respectively, supporting the existing taxonomy where BVDV-1, BVDV-2, CSFV and BDV belong to four different species (Becher *et al.*, 1997, 2003).

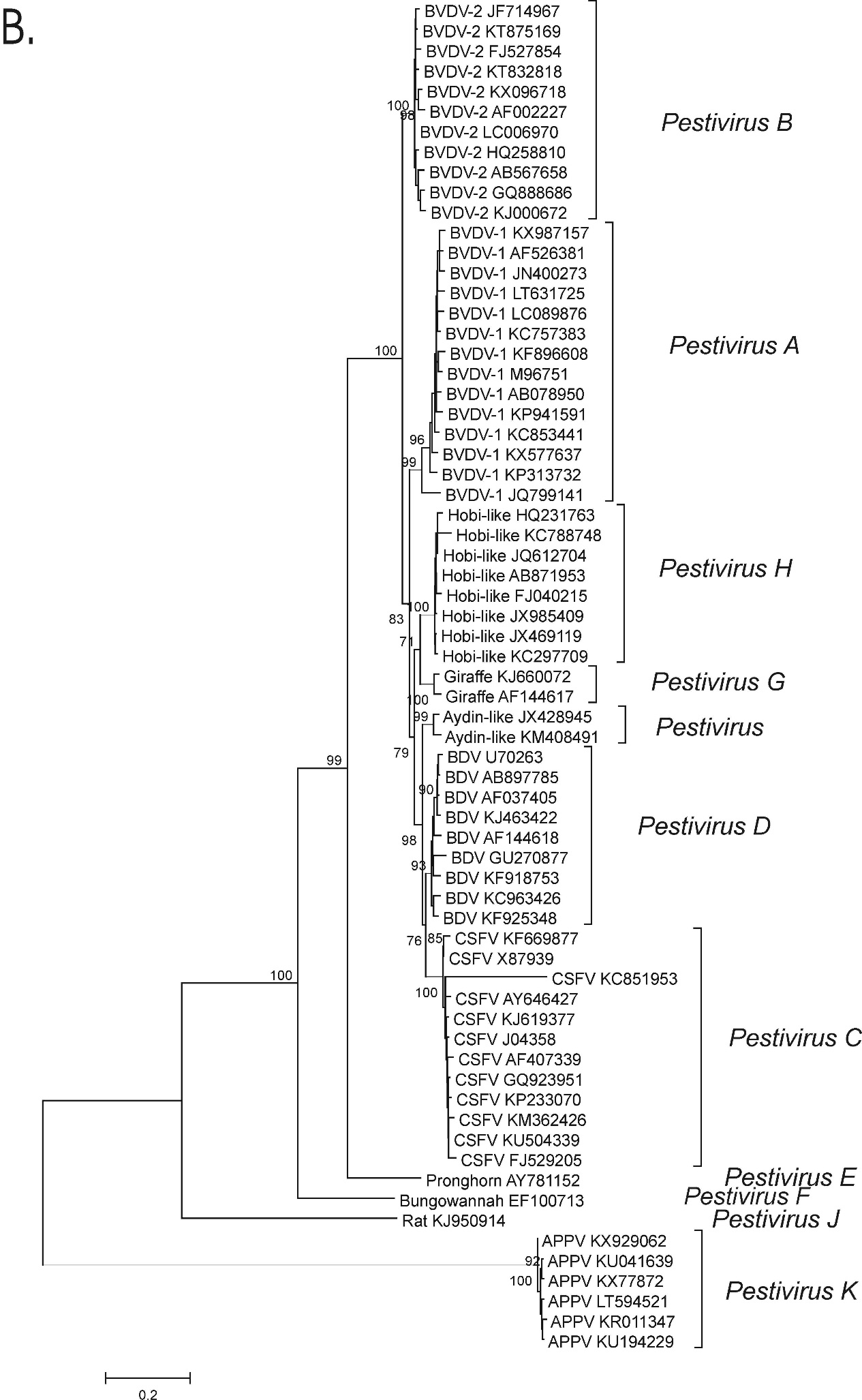
Similarly, amino acid p-distances were > 0.19 for comparisons between members of the four existing species and amongst giraffe pestivirus (AF144617), pronghorn antelope pestivirus (AY781152), Bungowannah virus (EF100713), Hobi-like pestivirus (FJ040215), rat pestivirus (KJ950914), atypical porcine pestivirus (KR011347) and Aydin-like pestivirus (JX428945) in comparisons with each other and members of the four existing *Pestivirus* species. Since some regions of the virus genome are difficult to align for these sequences, we carried out phylogenetic analysis on the most conserved regions of the virus polyprotein which were amino acid positions 189-418, 1547-2321 , 2397-2688 and 3312-3837 (numbered according to the first amino acid of the polyprotein of BVDV-1 SD-1, Accession number M96751) with support for eleven distinct clades (Figure 1). Although the antelope pestivirus, Bungowannah virus, atypical porcine pestivirus and rat pestivirus sequences were outside a clade comprising the four existing species, giraffe pestivirus, Hobi-like pestivirus and Aydin-like pestivirus, with the atypical porcine pestivirus and rat pestivirus sequences the most divergent, we consider all eleven clades to represent members of different *Pestivirus* species because of their common genome organisation, protein homology, and where known, virological, antigenic (Avalos-Ramirez *et al.*, 2001; Bauermann *et al.*, 2012; Becher *et al.*, 2003; Postel *et al.*, 2015, 2017) and pathological features ; hosts ranges are overlapping and incompletely described. Similar degrees of diversity are observed with other genera within the *Flaviviridae* and pestivirus sequences are monophyletic in a phylogenetic tree constructed using NS5B amino acid sequences (1).

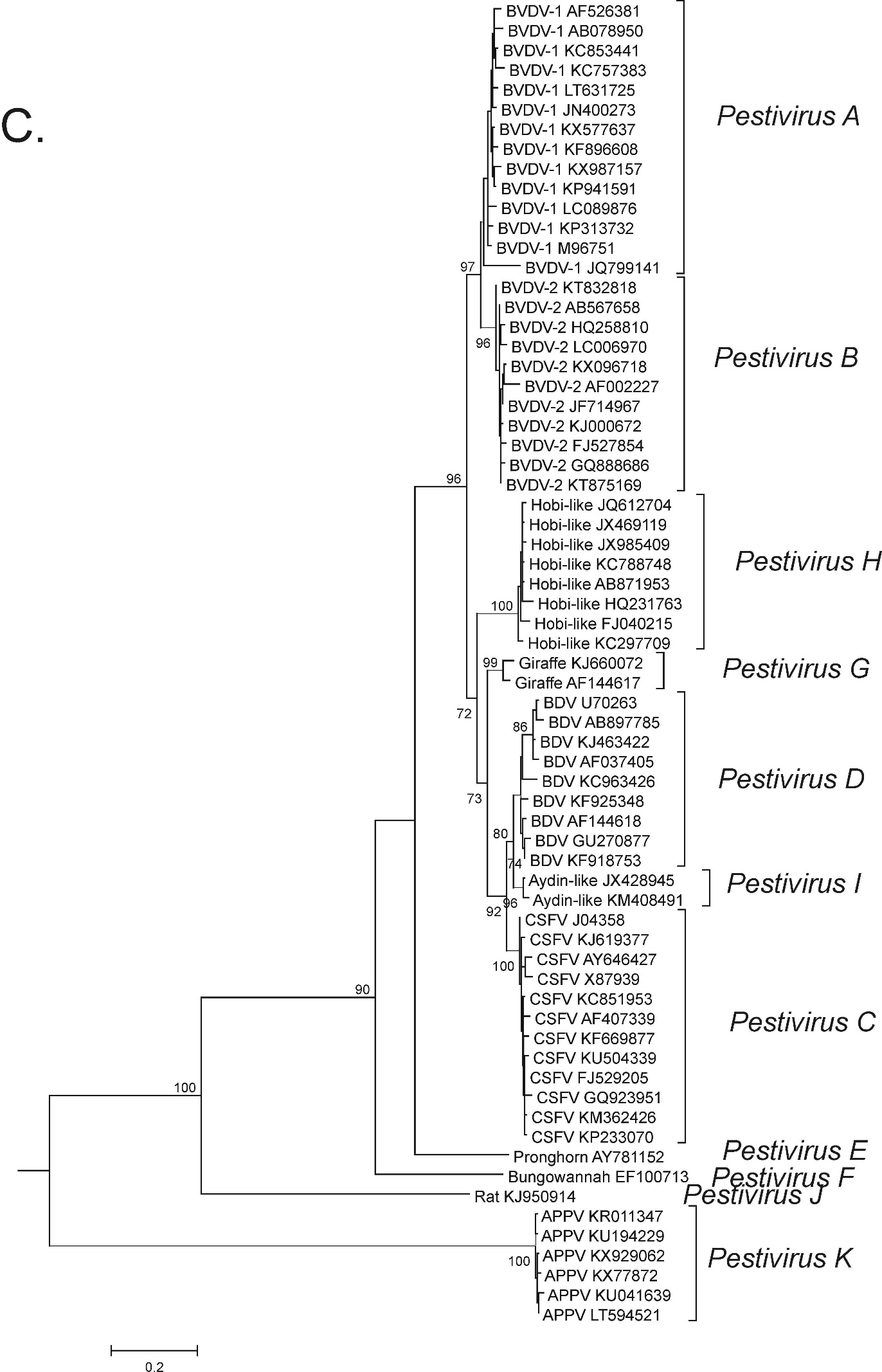
*Pestivirus* species names are currently derived from virus isolate names that describe host range and disease attributes. These names provide no clear distinction between the species name and the virus name apart from italicisation - the species *Border disease virus* includes the virus Border disease virus from sheep and goat, as well as reindeer pestivirus and variants infecting pigs, cattle, and bison.

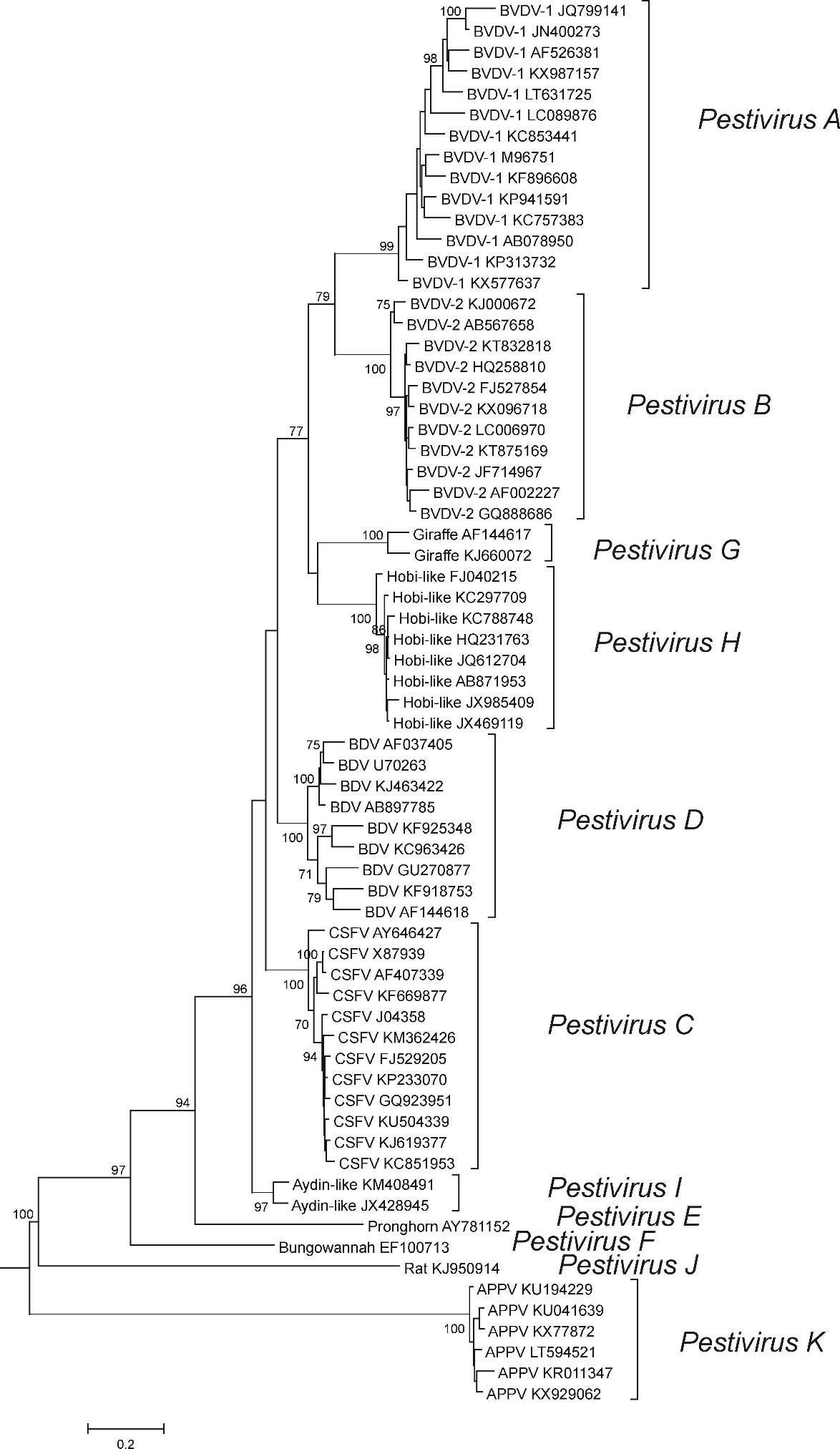
We propose adopting the naming scheme already used for both the *Hepacivirus* (Smith *et al.*, 2016) and *Pegivirus* (Stapleton *et al.*, 2011)genera within the *Flaviviridae* family. Hence, *Bovine viral diarrhea virus 1* – becomes *Pestivirus A, Bovine viral diarrhea virus 2* becomes *Pestivirus B, Classical swine fever virus* becomes *Pestivirus C* and *Border disease virus* becomes *Pestivirus D*. We have limited the addition of new species to those for which complete genomic or complete coding sequences are available.

We also propose changing the exemplar virus isolate name for *Bovine viral diarrhea virus 2* from C413 (Accession AF002227) to 890 (Accession U18059) and for *Classical swine fever virus* from Eystrup (Accession AF326963) to Alfort 187 (Accession X87939) since in both cases the proposed exemplar viruses have been more intensely studied in animal experiments and through the production of infectious clones than the previous exemplars.

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**D.**

**Figure 1**

Phylogenetic analysis of pestivirus polyprotein fragments. Phylogenetic trees were constructed using MEGA 6 (Tamura *et al.*, 2013) and based upon distances between amino acid sequences for amino acid positions positions A. 189-418, B. 1547-2321 and C. 2397-2688 D. 3312-3899 by maximum likelihood using a JTT+G model. Up to fifteen sequences were used for each species, choosing the most divergent sequences and eliminating sequences < 1% divergent, and comprised: BVDV1 (M96751, JQ799141, KP313732, KP941591, JN400273, KF896608, KC757383, KC853441, AB078950, AF526381, LC089876, KX577637, KX987157, LT631725), BVDV2 (AF002227, LC006970, KT875169, KT832818, KJ000672, HQ258810, JF714967, AB567658, FJ527854, GQ888686, KX096718), CSFV (X87939, J04358, FJ529205, AY646427, KF669877, KP233070, KM362426, KJ619377, KC851953, GQ923951, AF407339, KU504339), BDV (AF037405, AB897785, KJ463422, KF925348, KF918753, KC963426, GU270877, U70263, AF144618), Hobi-like (FJ040215, KC788748, KC297709, JX985409, JX469119, JQ612704, HQ231763, AB871953), Giraffe (AF144617, KJ660072), Aydin-like (KM408491, JX428945), Pronghorn (AY781152), Rat (KJ950914), Bungowannah (EF100713), APPV (KU041639, KR011347, KU194229, LT594521, KX77872, KX929062). Branches supported by >70% of bootstrap replicates are indicated.

**Table 1 Characteristics of proposed pestivirus species**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Existing**  **species**  **name** | **Proposed species**  **name** | **Virus names** | **Abbreviation** | **Type isolate** | **Genbank Accession** | **Host** | **Complete coding region sequences** | **Disease** |
| *Bovine viral diarrhea virus 1* | *Pestivirus A* | bovine viral diarrhea virus 1 | BVDV-1 | NADL | M31182 | Cattle, sheep, other ruminants, pig | 79 | Bovine viral diarrhea/ Mucosal disease (BVD/MD) |
| *Bovine viral diarrhea virus 2* | *Pestivirus B* | bovine viral diarrhea virus 2 | BVDV-2 | 890 | U18059 | Cattle, sheep, other ruminants pig | 99 | BVD/MD |
| *Classical swine fever virus* | *Pestivirus C* | classical swine fever virus, hog cholera virus | CSFV | Alfort 187 | X87939 | Pig | 96 | Classical swine fever |
| *Border disease virus* | *Pestivirus D* | Border disease virus,  reindeer pestivirus | BDV | X818 | AF037405 | Sheep, reindeer, chamois, other ruminants, pigs | 13 | Border disease  Hairy shaker syndrome  Fuzzy lamb syndrome |
|  | *Pestivirus E* | pronghorn antelope pestivirus | Pronghorn |  | AY781152 | Antelope | 1 | Unknown |
|  | *Pestivirus F* | Bungowannah virus | Bungo | Bungowan-nah | EF100713 | Pig | 1 | Porcine myocarditis syndrome |
|  | *Pestivirus G* | giraffe pestivirus | Giraffe | H138 | AF144617 | Giraffe, cattle | 2 | MD-like (giraffe) / unknown (cattle) |
|  | *Pestivirus H* | HoBi-like pestivirus, atypical ruminant pestivirus, bovine viral diarrhea virus 3, | Hobi-like, BVDV-3 | Th/04\_KhonKaen | FJ040215 | Cattle, buffalo | 12 | BVD/MD |
|  | *Pestivirus I* | Aydin-like pestivirus, |  | Aydin/04-TR | JX428945 | Sheep, goat | 2 | Abortions, congenital malformations |
|  | *Pestivirus J* | rat pestivirus |  | NrPV/NYC-D23 | KJ950914 | Rat | 1 | Unknown |
|  | *Pestivirus K* | atypical porcine pestivirus | APPV | 000515 | KR011347 | Pig | 6 | Congenital tremor |