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**

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| **Code assigned:** | ***2019.021S*** | |  |
| **Short title:** Create eight new species in the subfamily *Orthocoronavirinae* of the family *Coronaviridae* and four new species and a new genus in the subfamily *Serpentovirinae* of the family *Tobaniviridae* | | | |
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| **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 | |
| Ziebuhr J, Baker S, Baric RS, de Groot RJ, Drosten C, Gulyaeva AA, Haagmans BL, Neuman BW, Perlman S, Poon LLM, Sola I, Gorbalenya AE | | [john.ziebuhr@viro.med.uni-giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de);  [Sbaker1@luc.edu](mailto:Sbaker1@luc.edu);  [rbaric@email.unc.edu](mailto:rbaric@email.unc.edu);  R.J.deGroot@uu.nl;  christian.drosten@charite.de;  A.Gulyaeva@lumc.nl;  b.haagmans@erasmusmc.nl;  [bneuman@tamut.edu](mailto:bneuman@tamut.edu);  stanley-perlman@uiowa.edu;  [llmpoon@hkucc.hku.hk](mailto:llmpoon@hkucc.hku.hk);  isola@cnb.csic.es;  [A.E.Gorbalenya@lumc.nl](mailto:A.E.Gorbalenya@lumc.nl) | |
| **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]) | |  | | | | |
| **Corresponding author** | | | |
| John Ziebuhr: [john.ziebuhr@viro.med.uni-giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)  Alexander E. Gorbalenya, [A.E.Gorbalenya@lumc.nl](mailto:A.E.Gorbalenya@lumc.nl) | | | |
| **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) | | This proposal is filed by the **Coronavirus Study Group** in consultation with:  *Nidovirales* Study Group  *Arteriviridae* Study Group  *Mesoniviridae* Study Group | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
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|  | | | |
| Date first submitted to ICTV: | | | 1 June 2019 |
| Date of this revision (if different to above): | | | 15 October 2019 |

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| **ICTV-EC comments and response of the proposer:** |
| **Nick Knowles**:  Most things were approved, but there were a few issues that were picked up:   * 2019.020S-023S.N.v1.Nidovirales   + First line (species *Deltaarterivirus pejah*) - says move species (and also rename in comments), but it should be two different entries - a move of the subgenus (from one genus to another) and a rename only of the species (it stays within the subgenus *Pedartevirus*)   + *Shingleback nidovirus 1* - says move species, but it is a move of the subgenus   The other major thing was the use of partial (non-full-coding) genome sequences being used to propose new species.    Hebius snake nidovirus 1 (MG600021) 12.5 Kb  Murina bat coronavirus JTAC2 (KU182966) 25.7 Kb  Tropidophorus coronavirus 118981 (MG600026) 22.4 Kb  Sectovirus 2 (MG600031) 26 Kb    I realise that you might consider that each of these has enough data for classification, but the committee was adamant that (from this point on) new species should have at least complete coding sequences. These four species proposals need to be removed from the proposals (we had the same problem for a few picornavirus sequences).    Please can you let me have your updated proposals as soon as possible.  **All SGs concerned with nidoviruses**:   * The excel sheet with the *Nidovirales* taxonomy has been updated as requested. * The four nidovirus TPs submitted on June 1st, 2019 (including this TP) have been updated to indicate that four nidoviruses with incomplete coding sequences are not part of the proposed taxonomy. |

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

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| **Name of accompanying Excel module:** 2019.020S-023S.A.v1.Nidovirales.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:**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| additional material in support of this proposal  This and three accompanying proposals are based on analyses of the genomic diversity of viruses in the *Nidovirales* order and most closely related unclassified viruses performed by A. A. Gulyaeva, D. V. Samborskiy, I. A. Sidorov, and A. E. Gorbalenya (Gulyaeva et al & Gorbalenya, in preparation). The general framework of this analysis and its specific application to the group of viruses included in this particular proposal are separately summarized below.  **Computational Taxonomy Framework**. The analyses of the order *Nidovirales* included all publicly available (>3500; beginning of April 2019) (near) complete genome sequences of nidoviruses and most closely related unclassified viruses from diverse vertebrate and invertebrate hosts; many of these sequences are currently the only source of information about the respective viruses1-10. Sequences were analyzed in the computational comparative genomics framework DEmARC (DivErsity pArtitioning by hieRarchical Clustering)11,12 using profiles of multiple sequence alignments (MSA), Bayesian and Maximum-likelihood phylogenetic trees, and profiles of clustering cost (CC) function that were produced for weighted hierarchical clustering of pairwise patristic distances (PPD); DEmARC 1.41 was used for analysis (software is available upon request to AEG). All local minima of the CC profile (smallest CC values in a range of PPD values) were considered as candidate thresholds for demarcating ranks because they satisfied two requirements: (i) the clusters formed under these thresholds were monophyletic in the ML tree of the respective nidovirus subset, and (ii) all intra- and inter-cluster PPDs were (predominantly) smaller and (predominantly) larger, respectively, than the respective threshold. If *all* intra- and inter-cluster PPDs, respectively, were smaller and larger than the respective threshold, such clustering has a cost of zero (CC=0) according to DEmARC. We have also measured the persistence of a clustering as a range of PPD values over which this clustering was favored with the support of zero CC (CC=0). The respective “threshold PPD ranges” were considered best candidates for demarcation. Those thresholds that were supported independently by several datasets were predominantly used to set the demarcation criteria of a rank, as these assignments were less likely to be fortuitous due to biased virus sampling and/or residue selection.  Genome sequences were assigned to nidovirus taxa using either the Haygens tool (<http://veb.lumc.nl/HAYGENS/>) or by the authors who described the respective viruses. Assignments were verified by alignments and phylogenetic analyses of five replicative protein domains characteristic of nidoviruses (synteny of molecular markers), namely the 3CLpro, NiRAN, RdRp, ZBD and HEL1. As shown in **Fig. 1**, 15 groups of nidovirus lineages, ranging from separate families to the entire order plus an outgroup, were analyzed. For each group, the MSA of five concatenated replicative domains conserved in the *Nidovirales* were generated and used in phylogenetic and DEmARC analyses. For analyses involving viruses of an outgroup, tentatively called *Protonidovirales*, the MSA included the RdRp and HEL1 domains. These viruses also share the 3CLpro domain, which, however, was *not* included in the analysis due to its extreme divergence. Data from these analyses provided support for monophyletic clusters, levels and clusters of classification, agreement between phylogeny and classification for each virus group, and inter-group agreement regarding the classification levels.  **Application of the computational taxonomy framework to the *Coronaviridae* and *Tobaniviridae* families**. The current taxonomy of the *Coronaviridae* family includes two subfamilies, five genera, 24 subgenera, and 39 species (**Table 1**)13. The *Tobaniviridae* family currently includes four subfamilies, eight genera, nine subgenera, and 11 species (**Table 2**)13. They were delineated during prior DEmARC analyses of the genetic divergence in this family. The analyses used for this proposal included 973 new genome sequences. The “old” and “new” sequences were classified using a dataset that combined all established and candidate vertebrate nidoviruses excluding viruses in the *Arteriviridae* family. Unlike arteriviruses, these viruses encode replicative ExoN and/or O-MT domains in ORF1b (or its equivalent). They included the *Coronaviridae* and *Tobaniviridae* families (CoTo3 group in **Fig. 1**), and also six distantly related viruses, which were demarcated along as detailed in a separate taxonomy proposal (see 2019.023S.Ac.v1a.New\_Nidovirus\_Families.docx). The location of the 3CLpro, NiRAN, RdRp, ZBD and HEL1 domains used for the DEmARC analysis is shown for SARS-CoV and BRV, as representatives of the two families(**Fig. 2**). Among the candidate thresholds identified in this analysis (mostly supported with CC=0 or close to it), those thresholds were selected that observed the already established taxa. This was the case for all taxa at the subfamily and family ranks. At the species, subgenus and genus ranks, two taxa were merged (**Tables 1 and 2**). The taxa advancements (compared to the currently used taxonomy) are detailed (separately) for the different ranks in a phylogenetic tree of these viruses (**Fig. 3-6**).  ***Demarcation criteria***. We used either a range or a particular value of patristic pairwise distances (PPD) calculated using FastTree 2.1.4 SSE3 ML phylogeny based on an MSA of five concatenated domains (3CLpro, NiRAN, RdRp, ZBD and HEL) as the demarcation criterion for taxa at each of the following four ranks: subfamily, genus, subgenus, and species (**Tables 1 and 2**). They were selected as local minima in the CC distribution, commonly corresponding to the CC=0 or close to it (see above).  **Table 1** Demarcation thresholds for four ranks of the *Coronaviridae* family   |  |  |  |  |  | | --- | --- | --- | --- | --- | | **rank** | **Taxa #**  **current new** | **PPD range1** | **PUD (%) range2** | **Dataset used3** | | subfamily | 2 0 | 1.404-1.779 | 0.461-0.519 | CoTo3\_5d | | genus | 5 0 | 0.851-0.891 | 0.351-0.360 | CoTo3\_5d | | subgenus**4** | 24 3 | 0.193-0.223 | 0.133-0.147 | CoTo3\_5d | | species5 | 39 8 | 0.085-0.090 | 0.073-0.076 | CoTo3\_5d |   **1**The demarcation threshold is depicted as a range of PPD values for which the number of clusters (taxa) remained constant and the CC=0. PPD values account for repeated replacements of amino acid residues.  **2**The demarcation threshold is depicted as a range of PUD values, deduced from PPD values for which the number of clusters (taxa) remained constant and the CC=0. PUD values were calculated as the % of different residues in compared proteins.  **3**See Figure 1.  **4**Two subgenera, *Buldecovirus* and *Moordecovirus*, were merged into one - *Buldecovirus*.  5Two species, *Ferret coronavirus* (FRCoV) and *Mink coronavirus 1* (MCoV), were merged into one – *Mink coronavirus 1*.  **Table 2** Demarcation thresholds for four ranks of the *Tobaniviridae* family   |  |  |  |  |  | | --- | --- | --- | --- | --- | | **rank** | **Taxa #**  **current new** | **PPD range1** | **PUD (%) range2** | **Dataset used3** | | subfamily | 4 0 | 1.404-1.779 | 0.461-0.519 | CoTo3\_5d | | genus4 | 8 1 | 0.851-0.891 | 0.351-0.360 | CoTo3\_5d | | subgenus | 9 3 | 0.193-0.223 | 0.133-0.147 | CoTo3\_5d | | species | 11 4 | 0.085-0.090 | 0.073-0.076 | CoTo3\_5d |   **1**The demarcation threshold is depicted as a range of PPD values for which the number of clusters (taxa) remained constant and the CC=0. PPD values account for repeated replacements of amino acid residues.  **2**The demarcation threshold is depicted as a range of PUD values, deduced from PPD values for which the number of clusters (taxa) remained constant and the CC=0. PUD values were calculated as the % of different residues in compared proteins.  **3**See Figure 1.  4Two genera, *Tiruvirus* and *Pregotovirus*, were merged into one - *Pregotovirus*.    **Fig. 1**. Nidovirus phylogeny and subsets used to advance the taxonomy. Depicted is a phylogenetic tree of nidoviruses representing 113 established and newly proposed species (left) and 14 subsets of nidoviruses (right), which were analysed to build the taxonomy. For virus acronyms, see the accompanying spreadsheet; black and green indicate established and newly delineated species, respectively. The tree was reconstructed by IQ‑Tree 1.5.5 based on an MSA of five domains (3CLpro, NiRAN, RdRp, ZBD and HEL1) with the best fitting evolutionary model selected for each domain independently. Subsequently, the tree was midpoint-rooted. Branch support was estimated using the Shimodaira-Hasegawa-like approximate likelihood ratio test (SH-aLRT) with 1000 replicates and is depicted by shaded circles. DEmARC-based classifications of 14 subsets of nidoviruses and one group including all nidoviruses plus an outgroup including four viruses (protonidoviruses) were analyzed to verify and advance the taxonomy of the order. The taxonomic assignment of four nidoviruses included in this computational analysis, HHPAV, Mu-BatCoV\_JTAC2, TsinCoV\_118981 and GMRSToV, is deferred until complete genome sequences of the respective viruses become available.      **Fig. 2**. Domain combination used for phylogenetic and DEmARC analyses of the *Coronaviridae* and *Tobaniviridae* families. Shown are the locations of the conserved replicative domains (5d, 5 domains) used in the analysis of the CoTo3 group (see **Fig. 1**). The replicative domains are depicted in relation to the genome and the (other) open reading frames in the genomes of SARS coronavirus (SARS-CoV) and Breda torovirus (BRV), respectively. The results shown in **Figs. 3-6** were obtained using an MSA of this domain combination.    **Fig. 3.** Cluster partitioning of the phylogenetic tree (branch of the tree depicted in **Fig. 1**) of vertebrate nidoviruses, excluding the *Arteriviridae* family. For virus abbreviations, see the accompanying spreadsheet. The current and proposed **subgenus** structure of the *Coronaviridae* and *Tobaniviridae* is detailed on the right. The taxonomic assignment of three nidoviruses included in this computational analysis, Mu-BatCoV\_JTAC2, TsinCoV\_118981 and GMRSToV, is deferred until complete genome sequences of the respective viruses become available.    **Fig. 4.** Cluster partitioning of the phylogenetic tree (branch of the tree depicted in **Fig. 1**) of vertebrate nidoviruses, excluding the *Arteriviridae* family. For virus abbreviations, see the accompanying spreadsheet. The current and proposed **genus** structure of the *Coronaviridae* and *Tobaniviridae* is detailed on the right. The taxonomic assignment of three nidoviruses included in this computational analysis, Mu-BatCoV\_JTAC2, TsinCoV\_118981 and GMRSToV, is deferred until complete genome sequences of the respective viruses become available.    **Fig. 5.** Cluster partitioning of the phylogenetic tree (branch of the tree depicted in **Fig. 1**) of vertebrate nidoviruses, excluding the *Arteriviridae* family. For virus abbreviations, see the accompanying spreadsheet. The current and proposed **subfamily** structure of the *Coronaviridae* and *Tobaniviridae* is detailed on the right. The taxonomic assignment of three nidoviruses included in this computational analysis, Mu-BatCoV\_JTAC2, TsinCoV\_118981 and GMRSToV, is deferred until complete genome sequences of the respective viruses become available.    **Fig. 6.** Cluster partitioning of the phylogenetic tree (branch of the tree depicted in **Fig. 1**) of vertebrate nidoviruses, excluding the *Arteriviridae* family. For virus abbreviations, see the accompanying spreadsheet. The current and proposed family structure of the *Coronaviridae* and *Tobaniviridae* is detailed on the right. The taxonomic assignment of three nidoviruses included in this computational analysis, Mu-BatCoV\_JTAC2, TsinCoV\_118981 and GMRSToV, is deferred until complete genome sequences of the respective viruses become available. |
| 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. |

| **References:** |
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| 1. De Sabato L, Lelli D, Faccin F, Canziani S, Di Bartolo I, Vaccari G, Moreno A. 2019. Full genome characterization of two novel Alpha-coronavirus species from Italian bats. Virus Res 260:60-66.  2. Dervas E, Hepojoki J, Laimbacher A, Romero-Palomo F, Jelinek C, Keller S, Smura T, Hepojoki S, Kipar A, Hetzel U. 2017. Nidovirus-Associated Proliferative Pneumonia in the Green Tree Python (Morelia viridis). J Virol 91:e00718-17.  3. Dong X, Liu S, Zhu L, Wan X, Liu Q, Qiu L, Zou P, Zhang Q, Huang J. 2017. Complete genome sequence of an isolate of a novel genotype of yellow head virus from Fenneropenaeus chinensis indigenous in China. Arch Virol 162:1149-1152.  4. Papineau A, Berhane Y, Wylie TN, Wylie KM, Sharpe S, Lung O. 2019. Genome Organization of Canada Goose Coronavirus, A Novel Species Identified in a Mass Die-off of Canada Geese. Sci Rep 9:5954.  5. Shi M, Lin XD, Chen X, Tian JH, Chen LJ, Li K, Wang W, Eden JS, Shen JJ, Liu L, Holmes EC, Zhang YZ. 2018. The evolutionary history of vertebrate RNA viruses. Nature 556:197-202.  6. Wang W, Lin XD, Liao Y, Guan XQ, Guo WP, Xing JG, Holmes EC, Zhang YZ. 2017. Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. J Virol 91:e00764-17.  7. Wu Z, Lu L, Du J, Yang L, Ren X, Liu B, Jiang J, Yang J, Dong J, Sun L, Zhu Y, Li Y, Zheng D, Zhang C, Su H, Zheng Y, Zhou H, Zhu G, Li H, Chmura A, Yang F, Daszak P, Wang J, Liu Q, Jin Q. 2018. Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome 6:178.  8. Xu L, Zhang F, Yang W, Jiang T, Lu G, He B, Li X, Hu T, Chen G, Feng Y, Zhang Y, Fan Q, Feng J, Zhang H, Tu C. 2016. Detection and characterization of diverse alpha- and betacoronaviruses from bats in China. Virol Sin 31:69-77.  9. Yinda CK, Ghogomu SM, Conceicao-Neto N, Beller L, Deboutte W, Vanhulle E, Maes P, Van Ranst M, Matthijnssens J. 2018. Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. Virus Evol 4:vey008.  10. Zhuang QY, Wang KC, Liu S, Hou GY, Jiang WM, Wang SC, Li JP, Yu JM, Chen JM. 2015. Genomic Analysis and Surveillance of the Coronavirus Dominant in Ducks in China. PLoS One 10:e0129256.  11. Lauber C, Gorbalenya AE. 2012. Toward genetics-based virus taxonomy: comparative analysis of a genetics-based classification and the taxonomy of picornaviruses. J Virol 86:3905-3915.  12. Lauber C, Gorbalenya AE. 2012. Partitioning the genetic diversity of a virus family: approach and evaluation through a case study of picornaviruses. J Virol 86:3890-3904.  13. Ziebuhr J, Baric RS, Baker S, de Groot RJ, Drosten C, Gulyaeva A, Haagmans BL, Neuman BW, Perlman S, Poon LLM, Sola I, Gorbalenya AE. 2017. ICTV taxonomy proposal 2017.013S. Reorganization of the family *Coronaviridae* into two families, *Coronaviridae* (including the current subfamily *Coronavirinae* and the new subfamily *Letovirinae*) and the new family *Tobaniviridae* (accommodating the current subfamily *Torovirinae* and three other subfamilies), revision of the genus rank structure and introduction of a new subgenus rank. |
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