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:** | ***2019.025M*** |  |
| **Short title:** Create three new genera, create five new species and move/rename four species in the family *Paramyxoviridae* |
|  |
| **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 |
| Balkema-Buschmann A, Dundon WG, Duprex WP, Easton AJ, Fouchier RAM, Kurath G, Lamb RA, Lee B, Rima BK, Rota PA, Wáng L (王林发), Jin Q, Wu Z | anne.buschmann@fli.de;W.Dundon@iaea.org; pduprex@pitt.edu;A.J.Easton@warwick.ac.uk; r.fouchier@erasmusmc.nl; gkurath@usgs.gov; ralamb@northwestern.edu; benhur.lee@mssm.edu; b.rima@qub.ac.uk; prota@cdc.gov; linfa.wang@duke-nus.edu.sgzdsys@vip.sina.comwuzq2009@ipbcams.ac.cn) |
| **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]) |
| Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany [ABB]Animal Production and Health Laboratory, International Atomic Energy Agency, Austria [WGD]University of Pittsburgh, School of Medicine, Pittsburgh, Pennsylvania, USA [WPD]School of Life Sciences, University of Warwick, Coventry, UK [AJE]Department of Viroscience, Erasmus University Medical Centre Rotterdam, the Netherlands [RAMF]US Geological Survey Western Fisheries Research Center, Seattle, Washington, USA [GK]Department of Molecular Biosciences, Northwestern University, Evanston, Ill, USA [RAL]Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, NY, USA [BL]Centre for Experimental Medicine, The Queen's University of Belfast, Northern Ireland [BKR]National Center for Immunization and Respiratory Diseases, CDC, Atlanta, Georgia, USA [PAR]Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore [LFW]Institute of Pathogen Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China [JQ and ZW]; |

 |
| **Corresponding author** |
| Rima BK; b.rima@qub.ac.uk |
| **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) | **ICTV *Paramyxoviridae* Study Group** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | June 19, 2019 |
| Date of this revision (if different to above): |       |

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

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

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| **Name of accompanying Excel module:** 2019.025M.A.v1.Paramyxoviridae\_3gen5sp4rensp.xlsx |
| **Supporting material:**This TP contains a proposal to recognize five new paramyxovirus species based on the recent decision of the ICTV *Paramyxoviridae* Study Group to classify viruses in this family on the basis of the similarity of the sequences of their RNA-directed RNA polymerase protein (RdRP formerly known as L). Application of the published species demarcation criterion that a branch length of >0.03 in a maximum likelihood tree derived from a Clustal W alignment of the amino acid sequences of the RdRP protein of the viruses justifies the classification of these new viruses as members of new species. This TP also contains a proposal for dealing with a confusion related to the numbering of a species in the *Avulavirinae.* A new virus derived from the urine of a bat has been described by Rebecca Johnson et al. (1) which has been named Alston virus by the authors. The name derives from the location Alstonville where the virus was isolated. Phylogenetic analysis (see Figure 1) shows that the sequence of the RdRP of Alston virus fulfills the classification criterion and hence it is proposed to be a member of a new species to be named *Mammalian orthorubulavirus 6* as it is closely related to the virus PIV5 in the species *Mammalian orthorubulavirus 5*. A second new virus derived from a Pacific salmon has been described by James Winton et al. (2) which has been named Pacific salmon paramyxovirus by the authors. The name is derived from the ocean in which the salmon from which the virus was isolated, was found. Phylogenetic analysis (see Figure 1) shows that the sequence of the RdRP of this virus fulfills the classification criterion and hence it is proposed to be a member of a new species to be *Oncorhynchus* *aquaparamyxovirus* in the genus *Aquaparamyxovirus* as it is closely related to, but distinct from, Atlantic salmon paramyxovirus. The authors describe two variants of the virus but their RdRP sequences do not satisfy the species demarcation criterion. We have therefore chosen the Trask river (PSPV-A) isolate from 1982 as the exemplar. Consequentially, it is also proposed that the species *Salmon aquaparamyxovirus* will be renamed *Salmo aquaparamyxovirus.*A third new paramyxovirus, Hervey virus, has been described (3) and submitted to the database with accession number KU672593. The name is derived from Hervey Bay where the virus was isolated from urine samples from bats. No protein accession is available for the RdRP (L) protein but the coding sequence is from nucleotide 8323 to 15121. Phylogenetic analysis (see Figure 1) shows that this virus should be classified as a new species in the genus *Pararubulavirus* in the subfamily *Rubulavirinae*.A fourth group of new, unnamed, paramyxoviruses has been described as the founding members of a novel genus “*Shaanvirus*” (4, 5). A coding-complete genome sequence is available for one of these viruses (Gen Bank accession number MG230624). This virus was isolated from a bat urine sample of Schreibers’s long-fingered bats (*Miniopterus schreibersii*). Phylogenetic analysis (see Fig.1) shows that this virus should be classified as a member of the genus *Jeilongvirus* in the subfamily *Orthoparamyxovirinae*. To honor the original suggestion for a genus name, “*Shaanvirus*”, we propose to name this virus “Shaan virus”, which is to be classified as a member of the species *Miniopteran jeilongvirus*. |
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The fifth element of this proposal introduces a correction in the species list excel file which indicates that a virus named as avian paramyxovirus 17 in the NCBI database should be recognized as a member of a new species *Avian* o*rthoavulavirus 21* in the *Orthoavulavirus* genus. This has been suggested by a TP provided by Dr Shabbir (2019.014M.N.v1\_Avulavirus\_1newsp) and accepted by the Study Group. Figure 1 again shows that this virus’s RdRP sequence fulfils the criterion for establishing a new species in the family.

Finally, the Study group has been requested to create genera for three established species not currently assigned to subfamilies. In line with the previously assigned species names the genera are proposed to be named *Cynoglossusvirus*, *Hoplichthysvirus*, and *Scoliodonvirus*.

Figure 1 Molecular Phylogenetic analysis by Maximum Likelihood method



The evolutionary history was inferred by using the Maximum Likelihood method based on the JTT matrix-based model. The tree with the highest log likelihood (-254158.30) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 77 amino acid sequences. There were a total of 2731 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

\* referred to in this TP

\* referred to in two other current TPs concerning the family *Paramyxoviridae* by Shabbir *et al.* re *Avian avulavirus 21* [2019.014M.N.v1\_Avulavirus\_1newsp (1)] and Forth, Hoper and Beer re *giant squirrel respirovirus* [2019.019M.N.v2.1newsp\_Squirrel\_respirovirus]

| **References:** |
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| 1. Rebecca I. Johnson, Mary Tachedjian, Brenton Rowe, Bronwyn A. Clayton, Rachel Layton, Jemma Bergfeld, Lin-Fa Wang and Glenn A. Marsh (2018). Alston Virus, a Novel Paramyxovirus Isolated from Bats Causes Upper Respiratory Tract Infection in Experimentally Challenged Ferrets. Viruses 10, 675; doi:10.3390/v10120675.
2. James R. Winton, William N. Batts, Rachel L. Powers, Maureen K. Purcell (2019). Complete Genome Sequences of the Index Isolates of Two Genotypes of Pacific Salmon Paramyxovirus. Microbiology Resource Announcements 8 (10) e01521-18
3. Kohl C, Tachedjian M, Todd S, Monaghan P, Boyd V, Marsh GA, et al. (2018). Hervey virus: Study on co-circulation with Henipaviruses in Pteropid bats within their distribution range from Australia to Africa. PLoS ONE 13(2): e0191933.
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5. Ji Yeong Noh, Dae Gwin Jeong, Sun-Woo Yoon, Ji Hyung Kim, Yong Gun Choi, Shien-Young Kang & Hye Kwon Kim (2018). Isolation and characterization of novel bat paramyxovirus B16-40 potentially belonging to the

proposed genus *Shaanvirus.* SCIENTIFIC REPORTS *8:12533*  DOI:10.1038/s41598-018-30319-7 |