

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

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| **Code assigned:** | **2020.011M** |  |
| **Short title:** Create one new species (*Avian metaavulavirus 22*)in the genus *Metaavulavirus* (*Mononegavirales*: *Paramyxoviridae*) | | |
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**Author(s) and email address(es)**

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| Balkema-Buschmann A, Dundon WG, Duprex WP, Easton AJ, Fouchier RAM, Kurath G, Lamb RA, Lee B, Rima BK, Rota PA, Wang LF (王林发) | [anne.buschmann@fli.de](mailto:anne.buschmann@fli.de);  [W.Dundon@iaea.org](mailto:W.Dundon@iaea.org);  [pduprex@pitt.edu](mailto:pduprex@pitt.edu);  [A.J.Easton@warwick.ac.uk](mailto:A.J.Easton@warwick.ac.uk);  [r.fouchier@erasmusmc.nl](mailto:r.fouchier@erasmusmc.nl);  [gkurath@usgs.gov](mailto:gkurath@usgs.gov);  [ralamb@northwestern.edu](mailto:ralamb@northwestern.edu);  [benhur.lee@mssm.edu](mailto:benhur.lee@mssm.edu);  [b.rima@qub.ac.uk](mailto:b.rima@qub.ac.uk);  [prota@cdc.gov](mailto:prota@cdc.gov);  [linfa.wang@duke-nus.edu.sg](mailto:linfa.wang@duke-nus.edu.sg) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| 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] |

**Corresponding author**

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| Rima BK; [b.rima@qub.ac.uk](mailto:b.rima@qub.ac.uk) |

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

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| ICTV *Paramyxoviridae* Study Group |

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

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| n/a |

**Submission dates**

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| Date first submitted to SC Chair | July 31, 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.011M.R.Metaavulavirus\_1nsp.xlsx |

**Abstract**

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| This TP contains a proposal to create a new species in the genus *Metaavulavirus*. The second element of this proposal introduces a correction in the species list. |

**Text of proposal**

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| |  | | --- | | **Supporting material:**  This TP contains a proposal to create a new species in the genus *Metaavulavirus*. In a paper by Liu et al. (1), the authors suggest the need for a new species in the aforementioned genus based on a virus that they named avian paramyxovirus (APMV) 21 and that was isolated from turtle doves. They proposed the name *Avian metaavulavirus 21* for the species However, a species of that name has been established already for a distinct avian paramyxovirus 21 and so both species and virus names should be renumbered. The authors carried out a phylogenetic analysis of the amino acid sequence of the RdRP (L) protein according to the instructions provided by the ICTV *Paramyxoviridae* Study Group in 2019. 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 APMV/dove/Taiwan/AHR133/2009, abbreviated now APMV-22, as a member of a new species to be named Avian *metaavulavirus 22*. | |

**Supporting evidence**

The cited paper provides all the appropriate supporting material and a phylogenetic analysis in Fig 3. The SG repeated the analysis for and included all 21 current avulavirinds in a tree (Fig 1).

A screenshot of a cell phone

Description automatically generated



**Fig 1 Phylogenic tree of all proposed and established 22 members of the *Avulavirinae***

Evolutionary analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model. The tree with the highest log likelihood (-263728.35) is shown. The percentage of 500 bootstrapped 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 the JTT model, and then selecting the topology with superior log likelihood value. This analysis involved 22 amino acid sequences. There were a total of 2745 positions in the final dataset. Evolutionary analyses were conducted in MEGA X with a gap generation penalty value of 5.0 and an extension penalty of 1.0.

**References**

1 Yu-Pin Liu, Shu-Ting Kuo, Chwei-Jang Chiou, Calogero Terregino, Hsiang-Jung Tsai. Novel avian metaavulavirus isolated from birds of the family *Columbidae* in Taiwan. Veterinary Microbiology 236, 108377e. doi.org/10.1016/j.vetmic.2019.07.029