

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2023.012S*** |  |
| **Short title:** Renaming 54 species with binomial names in the family *Coronaviridae*  |
|  |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Woo PCY, de Groot RJ, Haagmans B, Lau SKP, Neuman B, Perlman S, Sola I, van der Hoek L, Wong ACP, Yeh SH | pcywoo@nchu.edu.tw;R.J.deGroot@uu.nl;b.haagmans@erasmusmc.nl;skplau@hku.hk;bneuman@bio.tamu.edu;stanley-perlman@uiowa.edu;isola@cnb.csic.es;c.m.vanderhoek@amsterdamumc.nl;antonwcp@connect.hku.hk;shyeh@ntu.edu.tw |

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

|  |
| --- |
| PhD Program in Translational Medicine and Department of Life Sciences, National Chung Hsing University, Taichung 402, Taiwan [WPCY]Department of Biomolecular Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands [dGRJ]Department of Viroscience, Erasmus Medical Center, Rotterdam, The Netherlands [HB]Department of Microbiology, School of Clinical Medicine, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong [LSKP] [WACP]Department of Biology, Texas A&M University, College Station, Texas, 77843, United States [NB]Departments of Microbiology and Immunology, and Pediatrics, University of Iowa, Iowa City, IA 52242, United States [PS]Department of Molecular and Cell Biology, National Center for Biotechnology-Spanish, National Research Council (CNB-CSIC), Madrid, Spain [SI]Department of Medical Microbiology and Infection Prevention, Amsterdam UMC, Laboratory of Experimental Virology, Location University of Amsterdam, 1105 AZ Amsterdam, The Netherlands [vdHL]Department of Microbiology, College of Medicine, National Taiwan University, Taipei, Taiwan [YSH] |

**Corresponding author**

|  |
| --- |
| Patrick C.Y. Woo |

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

|  |
| --- |
| *Coronaviridae* Study Group |

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

|  |
| --- |
| All members have responded in agreement |

**ICTV Study Group votes on proposal**

|  |  |
| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Coronaviridae* Study Group | 10 | 0 | 0 |
|  |  |  |  |

**Authority to use the name of a living person**

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

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | 03 July 2023 |
| Date of this revision (if different to above) |  |

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

|  |
| --- |
|  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

|  |
| --- |
|  |

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

**Name of accompanying Excel module**

|  |
| --- |
| 2023.012S.N.v1.Coronaviridae\_54sprenamed.xlsx  |

**Abstract**

|  |
| --- |
| The family *Coronaviridae* includes viruses with positive-sense RNA genomes that are classified into three subfamilies, *Orthocoronavirinae*, *Letovirinae* and *Pitovirinae*. During the last two decades, a considerable number of novel viral species and strains have been identified in this family. To unify the use of binomial nomenclature in different viral families, we hereby propose to rename the 54 currently established species to binomial format. |

**Text of proposal**

|  |  |
| --- | --- |
|

|  |
| --- |
| The family *Coronaviridae*, being a monophyletic group of viruses in the order *Nidovirales*, are enveloped, positive-sense RNA viruses that are known to infect a wide spectrum of vertebrates. Viruses within this family are further classified into 3 subfamilies, *Letovirinae*, *Orthocoronavirinae* and *Pitovirinae*, with a total of 6 genera, 28 subgenera and 54 species currently identified. Over the last two decades since SARS epidemics, a significant number of viral genomes in this family have been sequenced and subsequently identified as novel species based on the species demarcation criteria supported by the computational framework DEmARC (DivErsity pArtitioning by hieRarchical Clustering). With an aim to comply with the mandated binomial species naming format, we have proposed the binomial nomenclature for the current species (n=54) in the family *Coronaviridae* with Latinized epithets. In cases of viruses which are well known by the general public and with detailed experimental studies, in order to have better synchronism, we have used epithets derived of host genus/species/common name, geographic location where virus was first isolated, well acknowledged disease name or artificial combined word describing special genomic feature.  |

 |

**Supporting evidence**

**References**