

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | A proposal to classify viruses at a below-species rank |
| **Code assigned:**  | 2025.001G |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Peter | Simmonds | Nuffield Department of Medicine, University of Oxford, Oxford, UK | Peter.Simmonds@ndm.ox.ac.uk | X |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - | **X** |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| N/A |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  02/07/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:**  |
| *Brief description of current situation:* Viruses are mandatorily classified into genus and species ranks in the ICTV taxonomy, and optionally can be further assigned as members of one or more higher ranks, namely family, order, class, phylum, kingdom and realm, and sub-categories of each of these. However, distinct viruses classified into the same species cannot currently be classified into separate below-species ranks. This lack of engagement prevents ICTV involvement in the formal definition and assignment criteria of viruses that are required for clinical, phytosanitary and regulatory purposes. *Proposed changes:* We propose the creation of a single below-species rank to which viruses can be optionally assigned. Proposals for the creation of sub-species ranks and assignment of viruses to these would proceed through formal taxonomy proposals and ratification by the ICTV membership. The additional rank would be incorporated into the ICTV Master Species List and Virus Metadata Resource with regulated nomenclature (italicized type, letters only from the Latin alphabet and numbers but without diacritics or accents) and an optional designator (*eg.* type, isolate, subspecies). Below-species names may be derived from existing names of viruses, such as *Enterovirus coxsackiepol* type *Poliovirus 1.* Assignments would be based on practical utility. Classification of one or more viruses into below-species ranks (*eg. Betacoronavirus pandemicum* isolate *SARS coronavirus 2*) does not imply that all members of the species, such as other bat sarbecovirus in this example, should have to be similarly classified. *Justification:* Classifications at the species level often lack sufficient precision to adequately describe viruses, such as HIV-1 and polioviruses, even though formal taxonomic assignments are frequently essential for adequate clinical descriptions, biocontainment and import/export trade regulations. An authoritative classification framework enables these category distinctions to be officially defined and recorded by the ICTV and made accessible to the clinical, veterinary and plant virus communities and to wider regulatory authorities.  |

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| **Text of General Proposal:**  |
| *Background:* A critique of the use of the species term in virus taxonomy and a proposal to create a below species rank for viruses was recently published (1), PDF provided as a supplementary file. The current taxonomy proposal formalizes the outline contained within that article for the creation of a below-species rank by the ICTV. In doing so, the proposal seeks to address several practical issues in the current virus taxonomy framework that have caused problems and sometime confusion in the virology community, and incompatibilities in the way virus classification information is stored and presented in biological databases. In particular, certain virus entities, such as HIV-1, SARS-CoV-2 as well as polioviruses and enterovirus D68 in distinction from other enteroviruses, have important regulatory and biocontainment restrictions that differ from other members of the species to which they are assigned. In situations where clarity in their identification and nomenclature is absolutely essential, the proposers believe it is important for the ICTV, as the primary internationally recognised agency for virus classification, to provide an adequate taxonomic description and assignment criteria for these entities. The widespread informal community-assigned classifications and the widespread use of different virus names in non-English languages for viruses in these categories is quite incompatible with the drafting of international regulations for containment and trade, and hinders communication of clinical, veterinary and agricultural virus pathogen descriptions in different languages. There is furthermore considerable variability in the accessibility and means by which currently described below-species classifications hare made available and updated – some are described in consensus papers (*eg.* (2-5), some are listed on community websites (*eg.* https://picornaviridae.com), while many represent traditionally used categories without available records of how their original assignments were made – for example dengue virus types 1-4. To address this, a simple extension of virus classification below the level of species is proposed. These changes will require a relatively minor revision of the International Code of Virus Classification and Nomenclature (ICVCN) to create the additional below-species rank and incorporate this into the Master Species List and related taxonomy records. Proposals for the addition or conversion existing below-species classification to newly created below-species ranks will be invited from the relevant study groups where these are required for scientific, clinical and regulatory purposes. *Proposed* *changes:* The following principles and practical steps to produce a below-species ranks are proposed as follows: 1. Below-species assignments and their taxon nomenclature should become part of the remit of the ICTV.
2. Virus variants within a species can be optionally assigned to a single below-species rank where there is a justified need.
3. Some existing virus names may be repurposed in the nomenclature of below-species taxa.
4. The below-species designations will form a third part (suffix) to the species/scientific name of the species.
5. Several approved designator terms to describe below-species taxa will be available, and may include subspecies (ssp.), type, genotype, serotype, isolate, and potentially others.
6. Names used for below-species categories will be written in italicized type, comprise letters only from the Latin alphabet and numbers but without diacritics or accents.
7. Below-species taxon names should not be abbreviated after first use.
8. The criteria used for assignment, their nomenclature and any required updating of below-species assignments will be managed by the relevant ICTV Study Group.
9. Changes and additions to assignments at the below-species rank should be actively solicited from the wider virus community and carry its support.

Typically, below-species classification should match existing virus/type/strain assignments, nomenclature, and usage to minimize disruption to pre-existing classifications. The number of species where subdivision into a below-species rank and affected by the proposal is relatively small; most species have one-to-one equivalence to the virus assigned to it. For example, the term measles virus is encapsulated in its assignment to *Morbillivirus hominis* and Ebola virus with *Orthoebolavirus zairense.* In neither case would a formal taxonomic recognition of their component strains would be required. However, this can be readily reviewed by the relevant Study Group should it became important to record clinical and regulatory (*eg.* BSL categorisation) differences between them. Contrastingly, adequate taxonomic descriptions of, as examples, hepatitis E virus, enterovirus types, primate lentiviruses and sarbecoviruses are required in each case because the species assignments lack sufficient granularity to adequately define the properties of their members required by the virology and wider communities using the ICTV taxonomy framework. As viruses classified below the level of species represent taxa, the Master Species List (MSL) maintained by the ICTV (https://ictv.global/msl) would therefore need to expand to include the range of designated genotypes, isolates, subspecies *etc.* of species that will be formally assigned by the relevant Study Groups. This will require the additional data fields for designator and assigned names for taxa in below-species listings. Regulation of below-species nomenclature should come within the remit of the relevant ICTV Study Group. Additions and changes to virus classifications below the level of species will require submission of formal taxonomy proposals through the ICTV Executive Committee and ratification with oversight from the relevant Study Group. As most of the relevant classifications are already in place and widely standardised in the virus community and there is a choice of designators to match existing assignments, it would be relatively simple for Study Groups to formalise these into formal below-species taxonomic categories.*Justification:* The changes proposed are designed to enable a formally recorded terminology below the species level and to create a nomenclature that better follows the usage of classification terms used in public databases and elsewhere in biology. *Compatibility with existing taxon and virus nomenclature.* The addition of a taxonomic layer simply adds to the range of taxonomic assignments possible for viruses, creating a classification for viruses assigned to the same species where they need to clearly differentiated from each other. The adoption of a below-species rank will not create incompatibilities with existing references to viruses used in the existing virological literature. For example, poliovirus type 3 (PV-3) is still a member of *Enterovirus coxsackiepol*, even though it can now be more precisely described taxonomically as *Enterovirus coxsackiepol* type *poliovirus 3*. Existing assignments would remain valid, and there would therefore be no terminological schism in the virological literature before and after their adoption. *Compatibility with existing biological databases*. Below-species classification for some viruses will formalize an existing system of below-species classification provided for certain viruses by GenBank and other INSDC databases. For example, an assignment such as *Enterovirus coxsackiepol* type *poliovirus1* would closely match its designation on GenBank as *Enterovirus coxsackiepol*,(serotype) Poliovirus 1and have assigned the taxid 12080 (in distinction to taxid 138950 for the species):<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Tree&id=12080>The assignment of below-species taxa would be therefore largely compatible with the below-species assignments and virus name annotations for GenBank and other INSDC records. This would also avoid the current need (rarely met) for records to maintain both species assignment and virus names for each entry – a practice that is unnecessary and indeed largely absent in sequence records for all other biological organisms. *Compatibility with taxonomy of other organisms.* As previously discussed (6), the recent change of virus species names to a binomial format has resolved major compatibility problems for virus entries in biological databases where the two elements in the name are often by default assigned to genus and species epithet fields (for example, by changing the previous species term *Measles virus* to *Morbillivirus hominis*). The proposed creation of a formal below-species taxonomic level would enable virus assignments at this rank to be similarly incorporated into the sub-species field available in biological databases. *Accountability.*Since every relevant division of viruses, including those at a below-species rank, will be represented as taxa, information on the criteria for assignment and their approval will be stored in and accessible from the MSL and associated taxonomic records held by the ICTV. Very much as currently recorded for species and higher rank taxa, these will provide definitive information on the approval process for below-species assignments, including the criteria under which the taxon was defined and assigned, its nomenclature, dates of approval, and information on those involved in the decision. The existence of formal records will provide the basis for future modification and expansion of below-species taxonomy as this develops. *Providing a classification more suitable for regulatory purposes.* The greater precision and range of taxonomic names may also be used to update currently erroneous and poorly constructed regulatory documents, including the UK ACDP list of containment restrictions for microbiological pathogens (7) (see Table 1A in (1)). As described in a previous section, the list of biological agents uses a complicated and often erroneous combination of virus names and virus species terms, leading to practical problems in using the document for laboratory management. The proposed substitution of species (or scientific) names (Table 1B) immediately clarifies the reference of the virus terms to defined taxa at species and below-species levels. Its revised format becomes substantially similar to the species and subspecies terms used for bacterial, amoebic and fungal pathogens listed in the same ACDP document. Review of other regulatory lists, such as the Biosafety in Microbiological and Biomedical Laboratories document from the US Centers for Disease Control (8) that are based only on virus community assigned virus names, non-taxonomic terms such as arboviruses and a frequent dependence on over-broad virus family level divisions, should be considered. The nomenclature of viruses identified as “Priority Pathogens” by the World Health Organization (9) is a similar hotchpotch of virus species names and various type suffixes (such as “genotype HEV3” where the parent species (*Paslahepevirus balayani*) lacks the granularity to adequately describe the pathogen. *Flexibility in Virus Community Usage.* The existence of precisely defined taxonomic names for every classified virus will provide much greater clarity of reference that is independent of their common virus names and their language-specific variants. Biocontainment regulations in France, for example, could list VIH-1 (virus de l'immunodéficience humaine de type 1) as long as term was provided with the taxonomic synonym (such as *Lentivirus humimdef1* isolate *HIV1*) on first mention. The advantages of clarity and flexibility provided through below-species assignments would similarly legitimize the introduction of essential virus names such as SARS-CoV-2 for the causative agent of COVID-19 by the ICTV *Coronaviridae* Study Group (10). The existence of a below-species rank would enable the synonym, *Sarbecovirus pandemicum* isolate *SARS coronavirus 2* to be provided. In the event, the virus name proposal was entirely outside of the remit of the Study Group when it was first proposed in 2020. Adoption of a below-species rank by the ICTV will avoid similar problems in the future, for example in the instance of a high pathogencity avian influenza outbreak, where the species term, *Alphainfluenzavirus influenzae*, would be similarly inadequate to distinguish the causative strain, *eg.* HPAI*-*H5N1,from seasonal influenza A viruses.  |

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| **References:** |
| 1. Simmonds P. A critique of the use of species and below-species taxonomic terms for viruses-time for change? Virus evolution. 2024;10(1):veae096,10.1093/ve/veae096.2. Simmonds P, Gorbalenya AE, Harvala H, Hovi T, Knowles NJ, Lindberg AM, et al. Recommendations for the nomenclature of enteroviruses and rhinoviruses. Arch Virol. 2020;165(3):793-7,10.1007/s00705-019-04520-6.3. Smith DB, Simmonds P, International Committee on Taxonomy of Viruses Hepeviridae Study G, Jameel S, Emerson SU, Harrison TJ, et al. Consensus proposals for classification of the family Hepeviridae. J Gen Virol. 2014;95(Pt 10):2223-32,10.1099/vir.0.068429-0.4. Simmonds P, Bukh J, Combet C, Deleage G, Enomoto N, Feinstone S, et al. Consensus proposals for a unified system of nomenclature of hepatitis C virus genotypes. Hepatology. 2005;42(4):962-73,10.1002/hep.20819.5. Kuhn JH, Becker S, Ebihara H, Geisbert TW, Johnson KM, Kawaoka Y, et al. Proposal for a revised taxonomy of the family Filoviridae: classification, names of taxa and viruses, and virus abbreviations. ArchVirol. 2010;155(12):2083-1036. Postler TS, Clawson AN, Amarasinghe GK, Basler CF, Bavari S, Benko M, et al. Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. Syst Biol. 2017;66(3):463-73,10.1093/sysbio/syw096.7. The Approved List of biological agents 2023 [Available from: <https://www.hse.gov.uk/pubns/misc208.pdf>.8. Biosafety in Microbiological and Biomedical Laboratories 2020 [Available from: <https://www.cdc.gov/labs/pdf/SF__19_308133-A_BMBL6_00-BOOK-WEB-final-3.pdf>.9. Pathogens Prioritization; a Scientific Framework for Epidemic and Pandemic Research Preparedness 2024 [Available from: <https://cdn.who.int/media/docs/default-source/consultation-rdb/prioritization-pathogens-v6final.pdf?sfvrsn=c98effa7_7&download=true>.10. Gorbalenya AE, Baker SC, Baric RS, de Groot RJ, Drosten C, Gulyaeva AA, et al. The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. Nat Microbiol. 2020;5(4):536-44,10.1038/s41564-020-0695-z. |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.001G.N.v1.Review and background of proposal.pdf | Published review by author or proposal advancing the argument for a below-species rank, and a review of the related conceptual issue of the object and category reference of species and virus terms  |