

# Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020)

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## Abstract

This article reports the changes to virus classification and taxonomy approved and ratified by the International Committee on Taxonomy of Viruses (ICTV) in March 2020. The entire ICTV was invited to vote on 206 taxonomic proposals approved by the ICTV Executive Committee at its meeting in July 2019, as well as on the proposed revision of the ICTV Statutes. All proposals and the revision of the Statutes were approved by an absolute majority of the ICTV voting membership. Of note, ICTV has approved a proposal that extends the previously established realm *Riboviria* to encompass nearly all RNA viruses and reverse-transcribing viruses, and approved three separate proposals to establish three realms for viruses with DNA genomes.

## Introduction

Changes to virus taxonomy (the universal scheme of virus classification of the International Committee on Taxonomy of Viruses [ICTV]) take place annually and are the result of a multi-stage process. In accordance with the ICTV Statutes (<http://ictv.global/statutes.asp>), proposals submitted to the ICTV Executive Committee (EC) undergo a review process that involves input from the ICTV Study Groups (SGs) and Subcommittees (SCs), other interested virologists, and the EC. After final approval by the EC, proposals are presented for ratification to the full ICTV membership by publication on the ICTV website (<http://ictv.global>) followed by an electronic vote.

The latest set of proposals approved by the EC was made available on the ICTV website in February 2020 (see <https://ictv.global/proposals-2019/> for all proposals combined into a single zip file, and use the links provided in the References to access individual proposals). A list of proposals was

then emailed on February 19, 2020 to the 164 members of the ICTV, namely the EC Members, Life Members, ICTV Subcommittee Members including the SG Chairs, and ICTV National Representatives. Members were then requested to vote on whether to ratify the taxonomic proposals; voting closed on March 21, 2020.

## Changes to virus taxonomy and to the Statutes of the International Committee for Taxonomy of Viruses

All proposals [1–206] were ratified by ICTV members, in every case receiving an absolute majority of votes, between 55% and 62% of eligible voters. A summary of the taxonomy changes enacted by the proposals is provided in Table 1. Each proposal is cited and listed in the References to acknowledge the authors' efforts and to provide links to the specific proposals on the ICTV website. These documents remain available for those who wish to see the full details of the proposals.

A notable taxonomic change approved in this ratification is the extension of the realm *Riboviria*, a clade of viruses that use cognate RNA-directed RNA polymerases (RdRps) for their replication, to include also the reverse-transcribing

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**Table 1** Summary of taxonomic changes approved in March 2020

Rank	Total, MSL-34 <sup>a</sup>	New	Moved	Abolished	Renamed	Merged	Split	Total, MSL-35 <sup>b</sup>
Realm	1	3	0		0 0	0	0	4
Kingdom	0	9	0		0 0	0	0	9
Phylum	1	15	1		0 0	0	0	16
Subphylum	2	0	0		0 0	0	0	2
Class	6	30	0		0 0	0	0	36
Order	14	41	6		0 0	0	0	55
Suborder	7	1	0		0 0	0	0	8
Family	150	18	66		0 0	0	0	168
Subfamily	79	25	1	1 (promoted)	0	0	1	103
Genus	1,019	408	44		6 7	0	2	1,421
Subgenus	59	10	2		1 0	0	0	68
Species	5,560	1,044	104		13 83	1	0	6,590

<sup>a</sup>Total numbers of taxa in the ICTV Master Species List prior to 2020 ratification

<sup>b</sup>Total numbers of taxa now recognized, as reported in the ICTV Master Species List #35

viruses that use a homologous replication enzyme [6, 207–210]. In the current taxonomy, all available primary taxonomic ranks for this realm are filled. Three novel realms for distinct subsets of viruses with DNA genomes were established as well, i.e., *Monodnaviria*, comprising viruses of prokaryotes and eukaryotes with single-strand DNA genomes that utilize the rolling-circle replication mechanism and encode replication initiation endonucleases of the HUH superfamily; *Varidnaviria*, comprising viruses of prokaryotes and eukaryotes with double-strand DNA genomes and single vertical jelly-roll or double jelly-roll capsid proteins; and *Duplodnaviria*, comprising viruses of prokaryotes and eukaryotes with double-strand DNA genomes and HK97-fold capsid proteins [3–5]. A detailed justification for the establishment of these realms has been published recently [211].

To ensure that the ICTV maintains the expertise and flexibility needed to meet the challenges of virus taxonomy in the future, and to clarify the procedures for electing the Executive Committee, a working group established by the Executive Committee of the ICTV has proposed amendments to the ICTV Statutes. The amended Statutes were also ratified in the ICTV-wide vote and then approved in April 2020 by the Virology Division of the International Union of Microbiological Societies, which is the parent organization of the ICTV. The new Statutes can be found at <https://ictv.global/statutes.asp>. The key effects of adopting the new Statutes include: enlargement of the Executive Committee from 19 to 23 Members representing the diversity of virologists in geography, demography and expertise; establishment of a single nomination procedure and timeframe for all positions on the Executive Committee except Virus Subcommittee Chairs; and increased participation by ICTV Members in elections to the EC

by allowing ballots other than those cast in person at the Plenary Meeting.

## Conclusion

All proposals submitted for ratification were ratified by an absolute majority of the ICTV, and the changes proposed are now part of official ICTV taxonomy. New ICTV Statutes are now in force as well. An up-to-date list of all approved taxa can be found on the ICTV online website: <https://ictv.global/msl/>.

## Compliance with ethical standards

**Conflict of interest** The authors declare no conflicts of interest. A.R.M. is a Program Director at the U.S. National Science Foundation (NSF); the statements and opinions expressed herein are made in a personal capacity and do not constitute endorsement by NSF or the government of the United States. Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture. USDA is an Equal Opportunity Provider and Employer. The content of this publication does not necessarily reflect the views or policies of the US Department of Health and Human Services or of the institutions and companies affiliated with the authors. This work was supported in part through Laulima Government Solutions, LLC's prime contract with the US National Institute of Allergy and Infectious Diseases (NIAID) under Contract No. HHSN272201800013C. J.H.K. performed this work as an employee of Tunnell Government Services (TGS), a subcontractor of Laulima Government Solutions, LLC under Contract No. HHSN272201800013C. N.J.K. is partially supported by core funding provided by the Biotechnology and Biological Sciences Research Council, UK. B.E.D. is supported by Netherlands Organization for Scientific Research (NWO) Vidi grant 864.14.004 and European Research Council (ERC) Con-

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