



Taxonomic Changes for Human and Animal Viruses, 2018 to 2020

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ABSTRACT The classification of viruses is relevant to a number of scientific and clinical disciplines, including the practice of diagnostic virology. Here, we provide an update to our previous review of taxonomic changes for disease-causing viruses in humans and vertebrate animals, covering changes between 2018 and 2020. Recent advances in virus taxonomy structure by the International Committee on Taxonomy of Viruses inform this update.

KEYWORDS virology, taxonomy, classification

The use of next-generation sequencing and other contemporary, high-throughput molecular methods has accelerated the discovery of new viruses and both minor and major variants of previously known viruses. Recognizing these viruses and having them correctly referenced in the scientific literature are increasingly demanding and important challenges. This is especially relevant when it comes to disease-causing viruses in humans and animals as related to their correct diagnostic identification and epidemiologic study. As a contribution to this effort, we reviewed the scientific literature for the identification of new viruses and changes in viral taxonomy.

METHODS

The International Committee on Taxonomy of Viruses (ICTV) website was reviewed to identify recent taxonomic changes (<https://ictv.global/taxonomy>). Changes listed in this review were limited to viruses affecting humans and vertebrate animals. The Scopus publication abstract database (Elsevier) was also reviewed using individual terms and combinations of each term that included but were not limited to virus, new, novel, disease, and identification. Other databases that were reviewed included PubMed Central, Google Scholar, and Microsoft Academic. Papers that were identified were individually reviewed and selected based on whether there was adequate evidence of a new disease-causing virus or a significant disease-causing variant. Single identifications and individual case reports were excluded. Changes listed are limited to viruses with pathogenic potential in their host species or zoonotic potential.

RESULTS AND DISCUSSION

The Scopus and other reviews produced hundreds of potentially new viruses, most involving plants and insects. Very few were identified that involved humans or animals and met the selection criteria. Other potential novel viruses have been described in the literature, but there were insufficient data to classify them at this time. We encourage research groups to continue their investigation of these viruses so that they can be classified and officially recognized by the ICTV.

Most notably, in 2016, the ICTV Executive Committee formed a working group to examine the rank structure of virus taxonomy. In 2019, the ICTV approved a new 15-rank classification hierarchy of virus taxonomy, as detailed in Fig. 1 (1, 2). The background, rationale, and impact of this change are reviewed by the ICTV Executive

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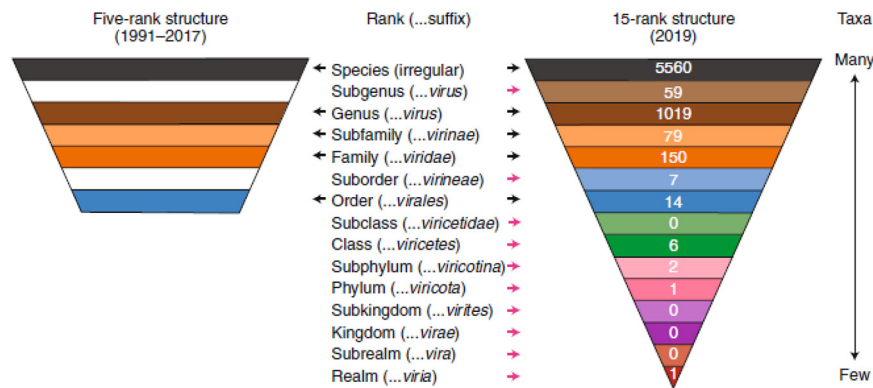


FIG 1 New 15-rank classification hierarchy of virus taxonomy approved by the ICTV in 2019. (Reproduced from reference 1, which is licensed under a Creative Commons Attribution 4.0 International License [http://creativecommons.org/licenses/by/4.0/], with permission from Alexander E. Gorbalenya and the publisher.)

Committee via a consensus statement (2). This expanded on the previous five-rank hierarchy of species, genus, subfamily, family, and order in place since 1991. The 15-rank hierarchy spans low intrataxon virus divergence (species) to high divergence (realm) and can accommodate taxa at any level of virus divergence. The 2019 ICTV virus taxonomy release (ratified March 2020) included 7 new virus families, 175 genera, and 614 species (https://ictv.global/reports/). The 2019 ICTV taxonomy release is available at https://ictv.global/taxonomy. The 15-rank hierarchy includes a newly created realm, *Riboviria*, encompassing RNA viruses. As noted by the ICTV, how this will influence the activities of the various communities within microbiology will be largely up to them. In the case of clinical microbiology, the genus and species designations are notably important for the accurate diagnosis and communications of research findings. Both genus and species classifications are expanding and being more finely divided as sequence analyses and other molecular traits are becoming commonplace in the discovery of novel viruses and the reclassification of established genus and species identities.

The most high-profile taxonomic change is the virus responsible for coronavirus disease 2019 (COVID-19), named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the ICTV in 2020 (3). SARS-CoV-2, together with SARS-CoV, falls in the *Sarbecovirus* subgenus of the *Betacoronavirus* genus. The clinical relevance of virus sequencing has recently been highlighted by the SARS-CoV-2 D614G genome spike protein variant that has become the dominant genotype potentially associated with a

TABLE 1 Selected taxonomic updates and proposed updates of viruses affecting vertebrate animals^a

Update(s)	Yr	Reference(s) or source
Name change from <i>Odokoileus hemionus</i> deer adenovirus 1 (OdAdV-1) to cervid adenovirus 1, with the species name <i>Cervid atadenovirus A</i>	2017	5
Novel nidovirus “Bellinger River virus” (BRV); BRV is the first nidovirus in the proposed <i>Barnivirus</i> genus that has been isolated from a nonsquamate reptile and is phylogenetically placed between the recognized python nidoviruses and the shingleback lizard nidovirus	2018	6
Create 1 new genus, <i>Boosepivirus</i> , with 3 species, <i>Boosepivirus A</i> , <i>Boosepivirus B</i> , and <i>Boosepivirus C</i>	2015	7
Create 8 new genera and 12 new species within the family <i>Poxviridae</i> , rename 1 species, and move 3 species	2019	8, 9
Create 3 new species in the genus <i>Sripuvirus</i> , family <i>Rhabdoviridae</i> , infecting reptiles and amphibians	2018	10
Rename the genus <i>Banyangvirus</i> to <i>Bandavirus</i> (a portmanteau of Bhanja virus and Dabie Mountain virus); change the species name <i>Huaiyangshan banyangvirus</i> to <i>Dabie bandavirus</i> , and change the genus name components of the remaining species in the genus from <i>banyangvirus</i> to <i>bandavirus</i>	2019	https://talk.ictvonline.org/taxonomy/p/taxonomy-history?taxnode_id=201906224 (accessed 20 July 2020)

^aBased on data from the International Committee on Taxonomy of Viruses (ICTV) 2019 taxonomy release (https://talk.ictvonline.org/taxonomy/ [accessed 24 August 2020]).

TABLE 2 New viruses with potential pathogenesis in host species or zoonotic potential

Family	Genus	Species	Animal host(s)	Pathogenesis(es)	Reference
Adenoviridae	Mastadenovirus	Bottlenose dolphin adenovirus 2 (BdAdV-2)	Bottlenose dolphin	Acute anorexia, diarrhea, and lethargy	11
Adenoviridae	Atadenovirus	Helodermatid adenovirus 2	Bearded dragon, Gila monsters, death adder	Necrotizing hepatitis	12
Adenoviridae	Aviadenovirus	Fowl adenovirus serotype 4 (FAdV-4)	Domestic poultry	Liver and kidney necrosis, hydropericardium	13
Poxviridae	Chordopoxvirinae	Brazospox virus	Northern pygmy mice	Pox proliferative epidermal lesions on the tail and feet	14
Rhabdoviridae	Ephemerovirus	Mavingoni virus	Cattle	Anorexia, nasal discharge, hyperthermia, lameness (cattle "flu")	15
Orthornavirae	Nidovirales	Pacific salmon nidovirus	Salmon	Inflammation of the spleen and liver as well as tubule necrosis and hyperplasia in the kidney	16
Flaviviridae	Pestivirus	Dongyang pangolin virus (DYPV)	Pangolins	Anorexia, systemic edema, multiorgan hemorrhage, and necrosis	17
Reoviridae	Coltivirus	Lishui pangolin virus (LSPV)	Pangolins	Anorexia, systemic edema, multiorgan hemorrhage, and necrosis	17
Paramyxoviridae	Respirovirus	Giant squirrel virus	Squirrels	Hemorrhagic-necrotizing pneumonia	18

TABLE 3 New and renamed viruses infecting humans from the International Committee on Taxonomy of Viruses 2019 taxonomy release^a

Family	Genus	Species	Change	Description of pathogenesis	Reference(s) or source
Polyomaviridae	Alphapolyomavirus	Human polyomavirus 14	New	Found in healthy blood donors	19
Phenuiviridae	Phlebovirus	Alenquer phlebovirus	New	Amazon region of Brazil; rare human infections based on serosurvey	20
Phenuiviridae	Phlebovirus	Ntepes phlebovirus	New	Kenya; neutralizing antibodies found in ~14% of human serum samples; isolated from sand flies	21
Phenuiviridae	Phlebovirus	Sicilian phlebovirus	New	Causes a self-limiting, acute, febrile disease; transmitted by sand fly	22
Phenuiviridae	Phlebovirus	Toscana phlebovirus	New	Causes meningitis, encephalitis; transmitted by sand fly	22
Phenuiviridae	Phlebovirus	Naples phlebovirus	Renamed; previous name, Sandfly fever Naples	Causes myalgia, fever; transmitted by sand fly	22
Phenuiviridae	Bandavirus	Heartland bandavirus	Renamed; previous name, Heartland banyangvirus (species); Banyangvirus (genus)	Causes fever, malaise, myalgia, headache; transmitted by the Lone Star tick, <i>Amblyomma americanum</i>	https://talk.ictvonline.org/taxonomy/p/taxonomy-history?taxnode_id=201906607 (accessed 20 July 2020)
Picornaviridae	Cardiovirus	Cardiovirus D	New	Scaffold virus; associated with gastrointestinal and respiratory illness in children	23, 24
Anelloviridae	Alphatorquevirus	Torque teno virus (TTV) (TTV1–TTV29)	New	TTV1 is the type species; high prevalence; no known direct or indirect link to pathogenicity	25
Anelloviridae	Betatorquevirus	Torque teno mini virus (TTMV) (TTMV1–TTMV12)	New	TTMV1 is the type species; no known direct or indirect link to pathogenicity	25
Reoviridae	Coltivirus	Colorado tick fever coltivirus	Renamed; previous name, Colorado tick fever virus (species)	Causes biphasic, febrile illness; transmitted by the wood tick <i>Dermacentor andersoni</i>	26

^aBased on data from the International Committee on Taxonomy of Viruses (ICTV) 2019 taxonomy release (<https://talk.ictvonline.org/taxonomy/> [accessed 24 August 2020]), which predates the discovery and classification of SARS-CoV-2.

transmission fitness advantage over the original D614 (4). As such, in the case of clinical microbiology, increasing the definition of a species among closely related viruses may not provide sufficient detail in accounting for strain variants associated with clinical significance. Additional taxonomic updates are provided in Tables 1 to 3.

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