# THE ICTV AT SIXTY YEARS: CLASSIFYING THE WORLDWIDE VIROSPHERE

JUNE 25, 2026
EUROPEAN VIRUS BIOINFORMATICS CENTER
VIRUSES *IN SILICO*

Elliot J. Lefkowitz, PhD
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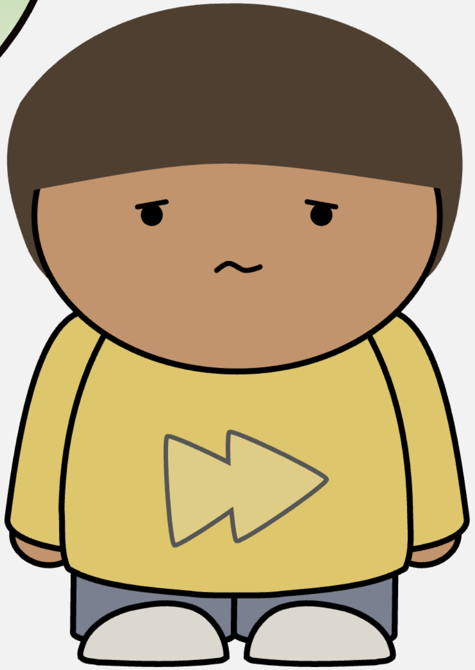
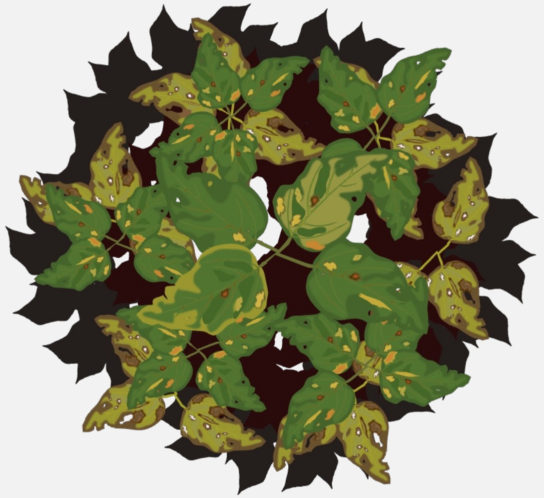
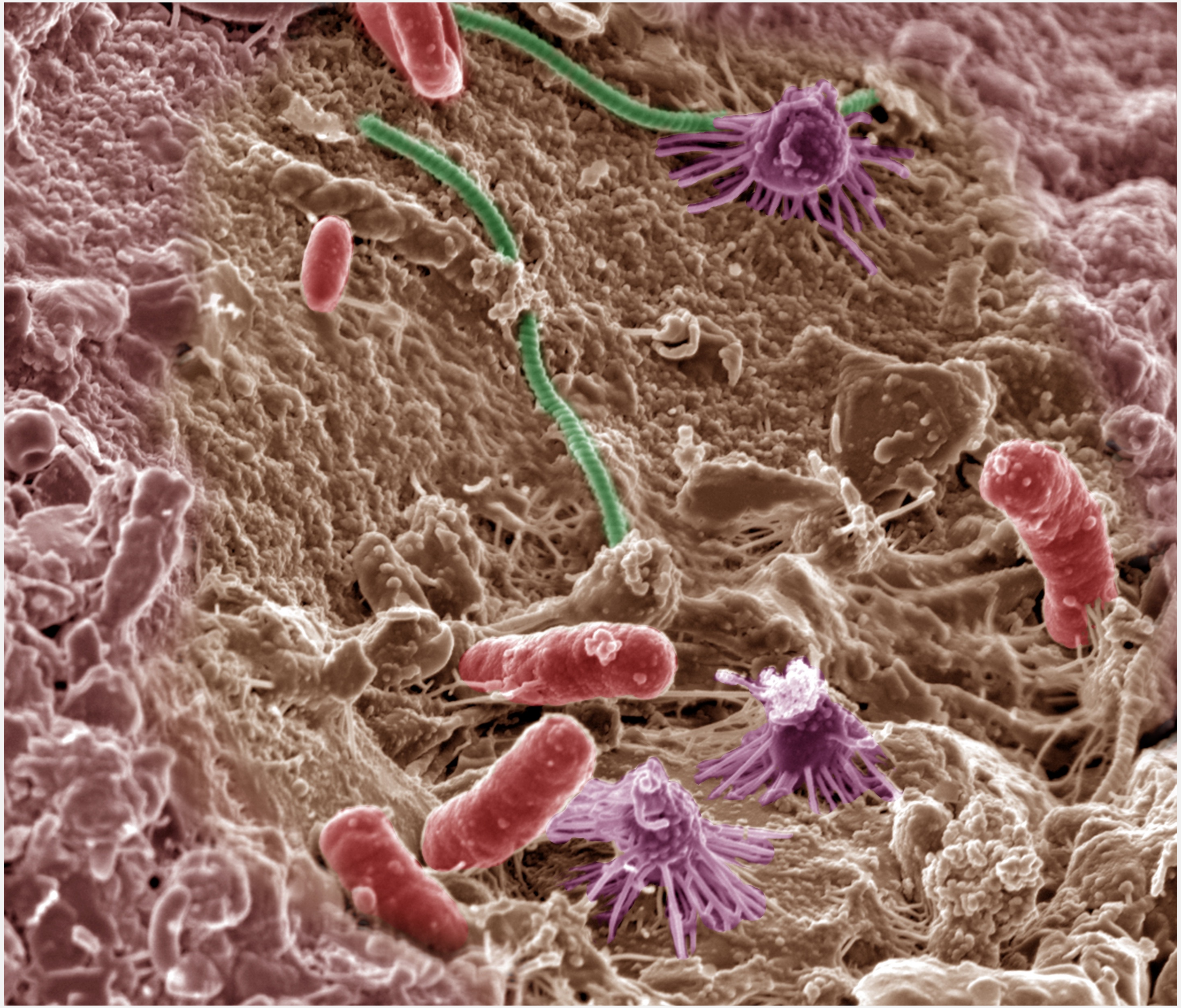
University of Alabama at Birmingham

# IT STARTS WITH...

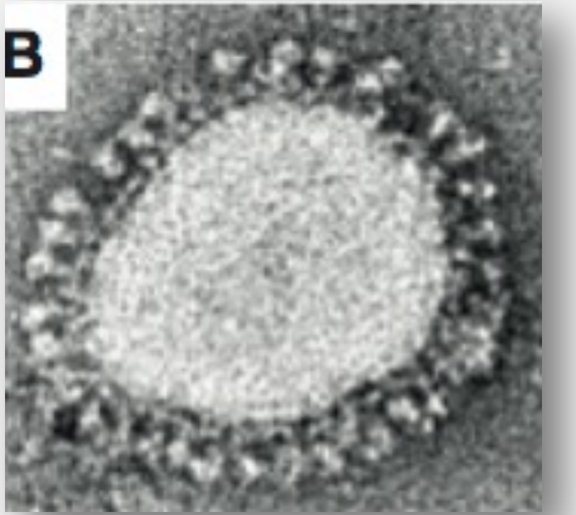


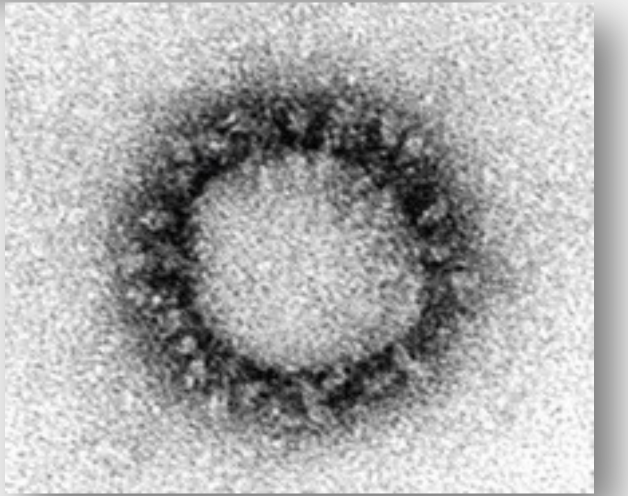


# …A DISCOVERY OF VIRUSES

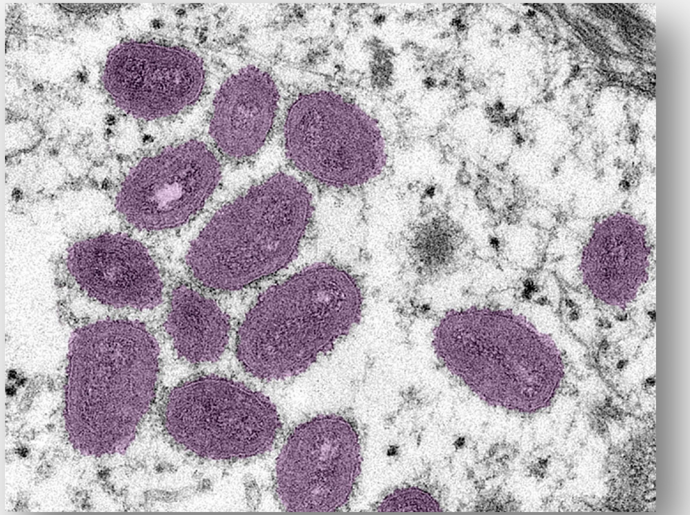


# WHICH ONE WOULD YOU LIKE TO GET?

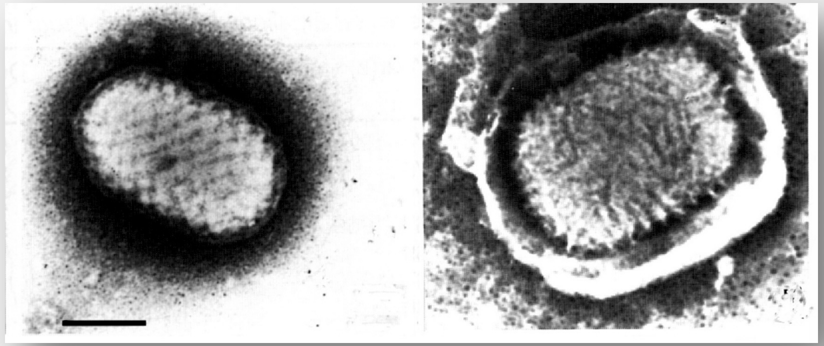


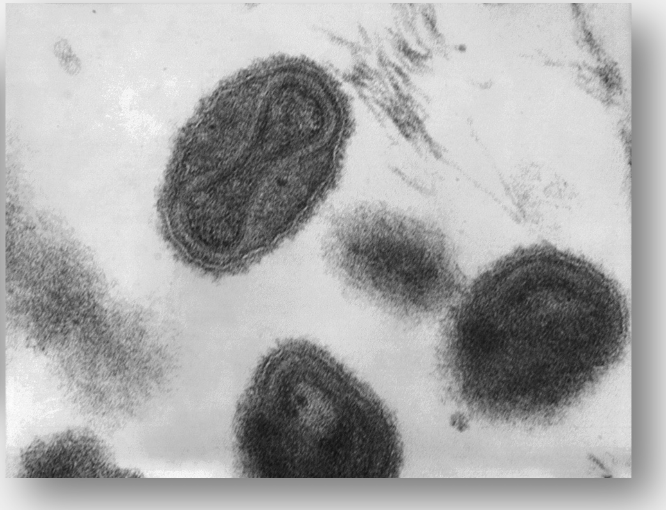


Dr Monica Birkhead, SVP CEZPD



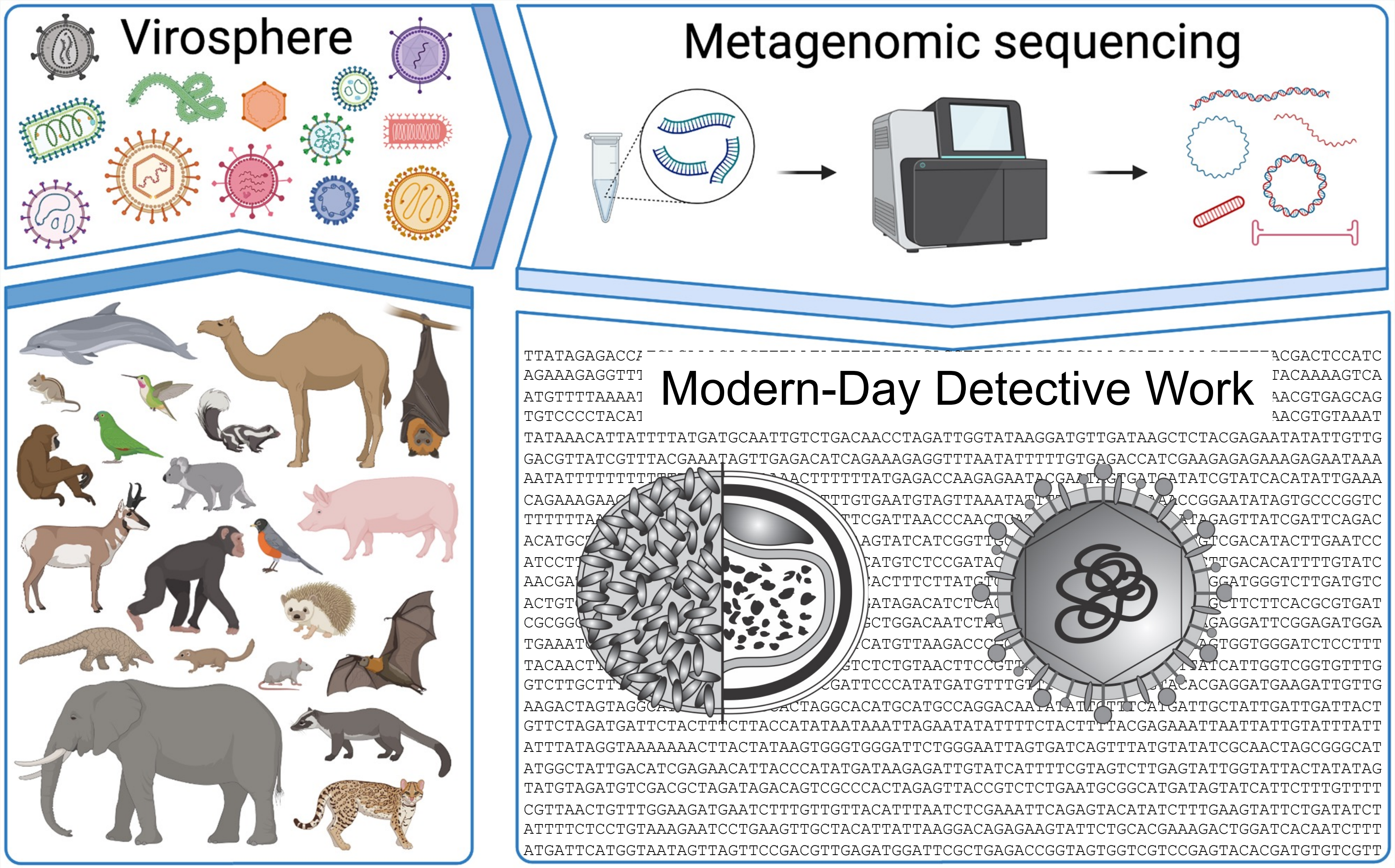
Int Dent J. 2022 PMID: 35934521





CDC/ Dr. Fred Murphy; Sylvia Whitfield

# METAGENOMICS

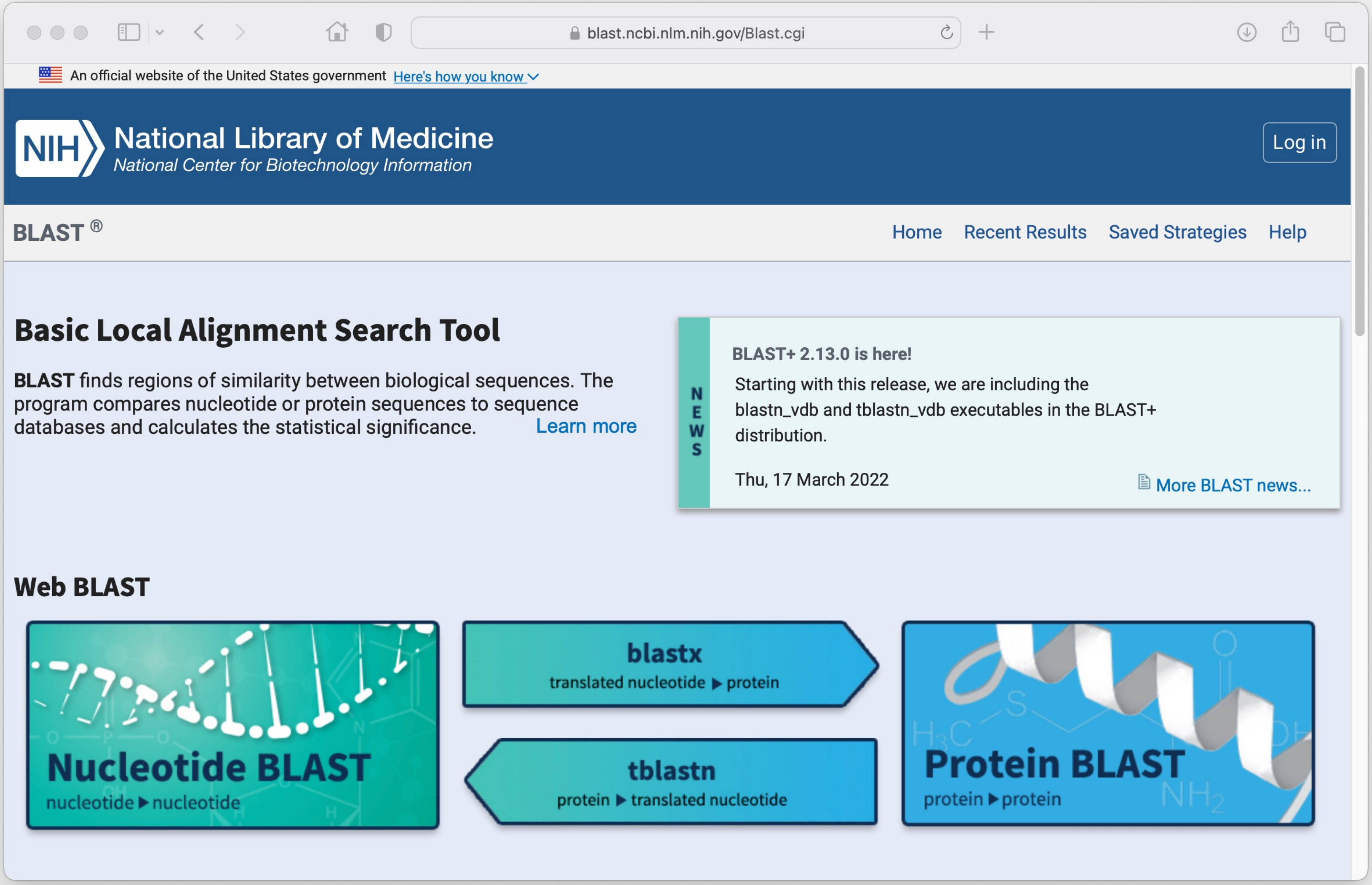


https://commons.wikimedia.org/wiki/File:Genomic_signatures_for_predicting_the_zoonotic_potential_of_novel_viruses_(graphical_summary).png

# NOW WHAT?

I have lots of sequence data

Let’s do Bioinformatics!



## Basic Local Alignment Search Tool

**BLAST** finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

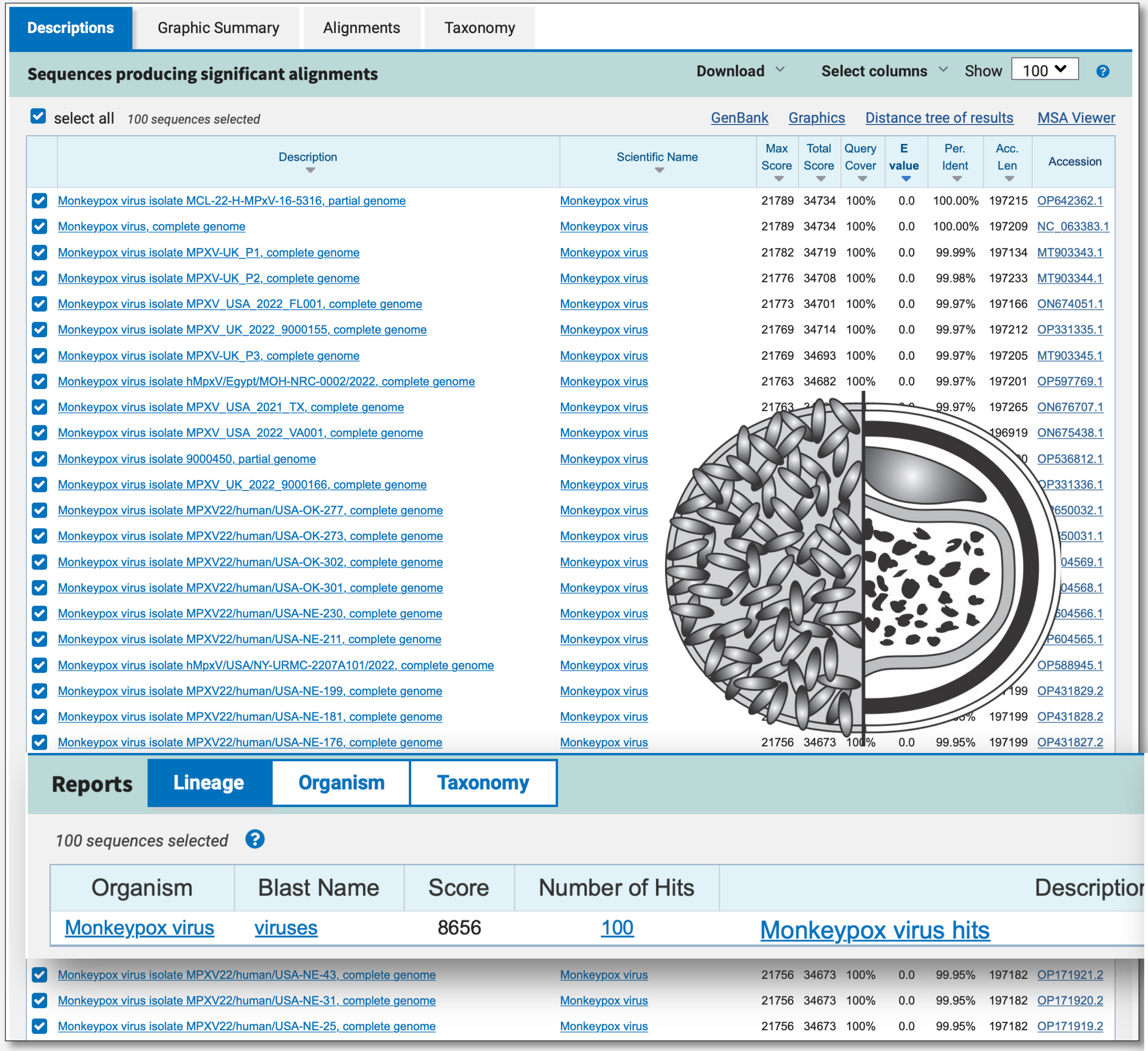
**BLAST+ 2.13.0 is here!**

Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 March 2022

### Web BLAST

# AND THE ANSWER IS…



**Sequences producing significant alignments**

☑ select all *100 sequences selected*

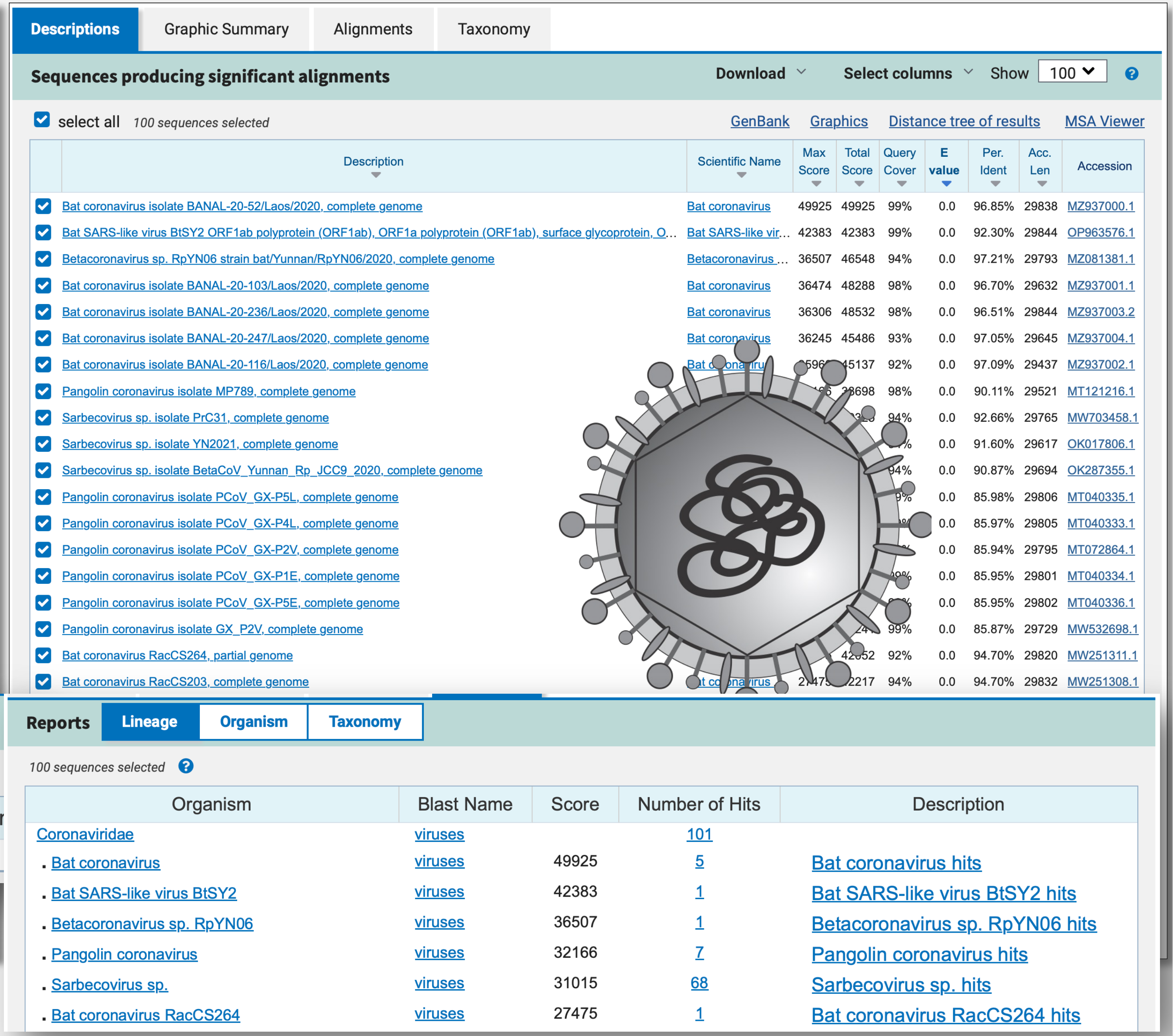
| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|---|
| ☑ | Monkeypox virus isolate MCL-22-H-MPxV-16-5316, partial genome | Monkeypox virus | 21789 | 34734 | 100% | 0.0 | 100.00% | 197215 | OP642362.1 |
| ☑ | Monkeypox virus, complete genome | Monkeypox virus | 21789 | 34734 | 100% | 0.0 | 100.00% | 197209 | NC_063383.1 |
| ☑ | Monkeypox virus isolate MPXV-UK_P1, complete genome | Monkeypox virus | 21782 | 34719 | 100% | 0.0 | 99.99% | 197134 | MT903343.1 |
| ☑ | Monkeypox virus isolate MPXV-UK_P2, complete genome | Monkeypox virus | 21776 | 34708 | 100% | 0.0 | 99.98% | 197233 | MT903344.1 |
| ☑ | Monkeypox virus isolate MPXV_USA_2022_FL001, complete genome | Monkeypox virus | 21773 | 34701 | 100% | 0.0 | 99.97% | 197166 | ON674051.1 |
| ☑ | Monkeypox virus isolate MPXV_UK_2022_9000155, complete genome | Monkeypox virus | 21769 | 34714 | 100% | 0.0 | 99.97% | 197212 | OP331335.1 |
| ☑ | Monkeypox virus isolate MPXV-UK_P3, complete genome | Monkeypox virus | 21769 | 34693 | 100% | 0.0 | 99.97% | 197205 | MT903345.1 |
| ☑ | Monkeypox virus isolate hMpxV/Egypt/MOH-NRC-0002/2022, complete genome | Monkeypox virus | 21763 | 34682 | 100% | 0.0 | 99.97% | 197201 | OP597769.1 |
| ☑ | Monkeypox virus isolate MPXV_USA_2021_TX, complete genome | Monkeypox virus | 21763 | [illegible] | [illegible] | [illegible] | 99.97% | 197265 | ON676707.1 |
| ☑ | Monkeypox virus isolate MPXV_USA_2022_VA001, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | 196919 | ON675438.1 |
| ☑ | Monkeypox virus isolate 9000450, partial genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | OP536812.1 |
| ☑ | Monkeypox virus isolate MPXV_UK_2022_9000166, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | OP331336.1 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-OK-277, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-OK-273, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-OK-302, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-OK-301, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-230, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-211, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] |
| ☑ | Monkeypox virus isolate hMpxV/USA/NY-URMC-2207A101/2022, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | OP588945.1 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-199, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | OP431829.2 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-181, complete genome | Monkeypox virus | [illegible] | [illegible] | [illegible] | [illegible] | [illegible] | 197199 | OP431828.2 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-176, complete genome | Monkeypox virus | 21756 | 34673 | 100% | 0.0 | 99.95% | 197199 | OP431827.2 |

**Reports** **Lineage** **Organism** **Taxonomy**

*100 sequences selected*

| Organism | Blast Name | Score | Number of Hits | Description |
|---|---|---|---|---|
| Monkeypox virus | viruses | 8656 | 100 | Monkeypox virus hits |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-43, complete genome | Monkeypox virus | 21756 | 34673 | 100% | 0.0 | 99.95% | 197182 | OP171921.2 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-31, complete genome | Monkeypox virus | 21756 | 34673 | 100% | 0.0 | 99.95% | 197182 | OP171920.2 |
| ☑ | Monkeypox virus isolate MPXV22/human/USA-NE-25, complete genome | Monkeypox virus | 21756 | 34673 | 100% | 0.0 | 99.95% | 197182 | OP171919.2 |



**Sequences producing significant alignments**

☑ select all *100 sequences selected*

| | Description | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. Ident | Acc. Len | Accession |
|---|---|---|---|---|---|---|---|---|---|
| ☑ | Bat coronavirus isolate BANAL-20-52/Laos/2020, complete genome | Bat coronavirus | 49925 | 49925 | 99% | 0.0 | 96.85% | 29838 | MZ937000.1 |
| ☑ | Bat SARS-like virus BtSY2 ORF1ab polyprotein (ORF1ab), ORF1a polyprotein (ORF1ab), surface glycoprotein, O… | Bat SARS-like vir… | 42383 | 42383 | 99% | 0.0 | 92.30% | 29844 | OP963576.1 |
| ☑ | Betacoronavirus sp. RpYN06 strain bat/Yunnan/RpYN06/2020, complete genome | Betacoronavirus … | 36507 | 46548 | 94% | 0.0 | 97.21% | 29793 | MZ081381.1 |
| ☑ | Bat coronavirus isolate BANAL-20-103/Laos/2020, complete genome | Bat coronavirus | 36474 | 48288 | 98% | 0.0 | 96.70% | 29632 | MZ937001.1 |
| ☑ | Bat coronavirus isolate BANAL-20-236/Laos/2020, complete genome | Bat coronavirus | 36306 | 48532 | 98% | 0.0 | 96.51% | 29844 | MZ937003.2 |
| ☑ | Bat coronavirus isolate BANAL-20-247/Laos/2020, complete genome | Bat coronavirus | 36245 | 45486 | 93% | 0.0 | 97.05% | 29645 | MZ937004.1 |
| ☑ | Bat coronavirus isolate BANAL-20-116/Laos/2020, complete genome | [illegible] | [illegible] | 45137 | 92% | 0.0 | 97.09% | 29437 | MZ937002.1 |
| ☑ | Pangolin coronavirus isolate MP789, complete genome | [illegible] | [illegible] | [illegible] | 98% | 0.0 | 90.11% | 29521 | MT121216.1 |
| ☑ | Sarbecovirus sp. isolate PrC31, complete genome | [illegible] | [illegible] | [illegible] | 94% | 0.0 | 92.66% | 29765 | MW703458.1 |
| ☑ | Sarbecovirus sp. isolate YN2021, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 91.60% | 29617 | OK017806.1 |
| ☑ | Sarbecovirus sp. isolate BetaCoV_Yunnan_Rp_JCC9_2020, complete genome | [illegible] | [illegible] | [illegible] | 94% | 0.0 | 90.87% | 29694 | OK287355.1 |
| ☑ | Pangolin coronavirus isolate PCoV_GX-P5L, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 85.98% | 29806 | MT040335.1 |
| ☑ | Pangolin coronavirus isolate PCoV_GX-P4L, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 85.97% | 29805 | MT040333.1 |
| ☑ | Pangolin coronavirus isolate PCoV_GX-P2V, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 85.94% | 29795 | MT072864.1 |
| ☑ | Pangolin coronavirus isolate PCoV_GX-P1E, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 85.95% | 29801 | MT040334.1 |
| ☑ | Pangolin coronavirus isolate PCoV_GX-P5E, complete genome | [illegible] | [illegible] | [illegible] | [illegible] | 0.0 | 85.95% | 29802 | MT040336.1 |
| ☑ | Pangolin coronavirus isolate GX_P2V, complete genome | [illegible] | [illegible] | [illegible] | 99% | 0.0 | 85.87% | 29729 | MW532698.1 |
| ☑ | Bat coronavirus RacCS264, partial genome | [illegible] | [illegible] | [illegible] | 92% | 0.0 | 94.70% | 29820 | MW251311.1 |
| ☑ | Bat coronavirus RacCS203, complete genome | [illegible] | [illegible] | [illegible] | 94% | 0.0 | 94.70% | 29832 | MW251308.1 |

**Reports** **Lineage** **Organism** **Taxonomy**

*100 sequences selected*

| Organism | Blast Name | Score | Number of Hits | Description |
|---|---|---|---|---|
| Coronaviridae | viruses | | 101 | |
| . Bat coronavirus | viruses | 49925 | 5 | Bat coronavirus hits |
| . Bat SARS-like virus BtSY2 | viruses | 42383 | 1 | Bat SARS-like virus BtSY2 hits |
| . Betacoronavirus sp. RpYN06 | viruses | 36507 | 1 | Betacoronavirus sp. RpYN06 hits |
| . Pangolin coronavirus | viruses | 32166 | 7 | Pangolin coronavirus hits |
| . Sarbecovirus sp. | viruses | 31015 | 68 | Sarbecovirus sp. hits |
| . Bat coronavirus RacCS264 | viruses | 27475 | 1 | Bat coronavirus RacCS264 hits |

# NOW WHAT?

I have lots of hits.

Let’s do Taxonomy!

# TAXONOMY

- Taxonomy = classification + nomenclature
- Classification ⟶ relationships
- Nomenclature ⟶ named point of reference
- Taxonomy ⟶ inferences on function
- Function leads to understanding and response
  - Diagnosis
  - Pathogenesis
  - Epidemiology
  - Treatments
  - Prophylactics

# BIOLOGICAL TAXONOMIES

- Rules of Nomenclature
  - International Code of Zoological Nomenclature
  - International Code of Nomenclature for algae, fungi, and plants
  - International Code of Nomenclature of Prokaryotes
  - International Code of Phylogenetic Nomenclature (PhyloCode)
  - BioCode, International rules for the scientific names of organisms
- Rules of Classification
  - All biological organisms except viruses
    - No specific entities or explicit rules guiding classification
    - Responsibility of discoverer or interested individuals/groups
- Rules of Classification and Nomenclature
  - Viruses
    - Sole responsibility of the International Committee on Taxonomy of Viruses (ICTV)
      - The International Code of Virus Classification and Nomenclature

# INTERNATIONAL COMMITTEE ON TAXONOMY OF VIRUSES: ICTV

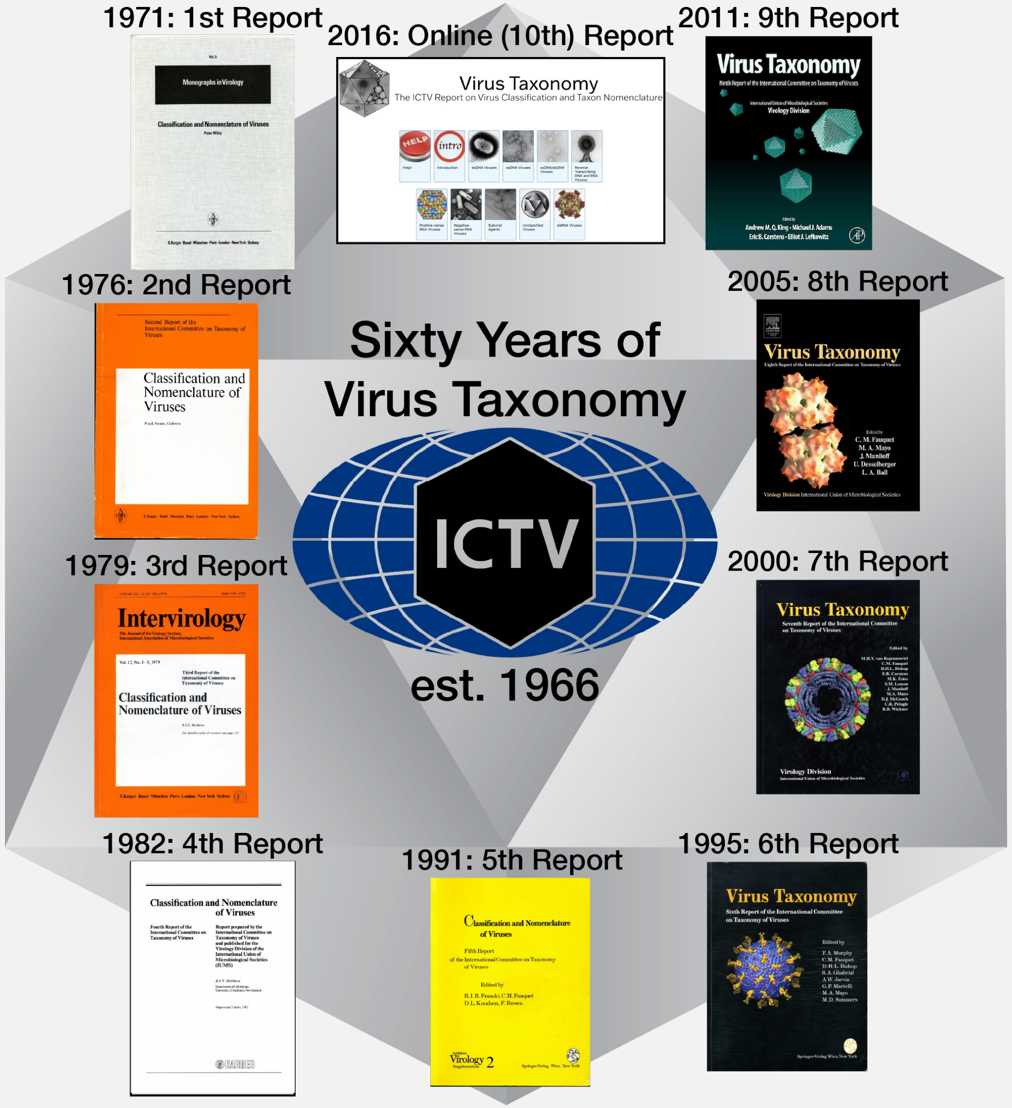
https://ictv.global

# CHARGE TO THE ICTV

**Established by the International Association of Microbiological Societies (IAMS) as the International Committee on Nomenclature of Viruses (ICNV) to create a universal system of classification and nomenclature for all viruses**

**The current charge to the ICTV by the International Union of Microbiological Societies, Virology Division is to:**

**Develop, refine, and maintain a universal virus taxonomy**



1971: 1st Report

2016: Online (10th) Report

2011: 9th Report

1976: 2nd Report

Sixty Years of Virus Taxonomy

2005: 8th Report

1979: 3rd Report

est. 1966

2000: 7th Report

1982: 4th Report

1991: 5th Report

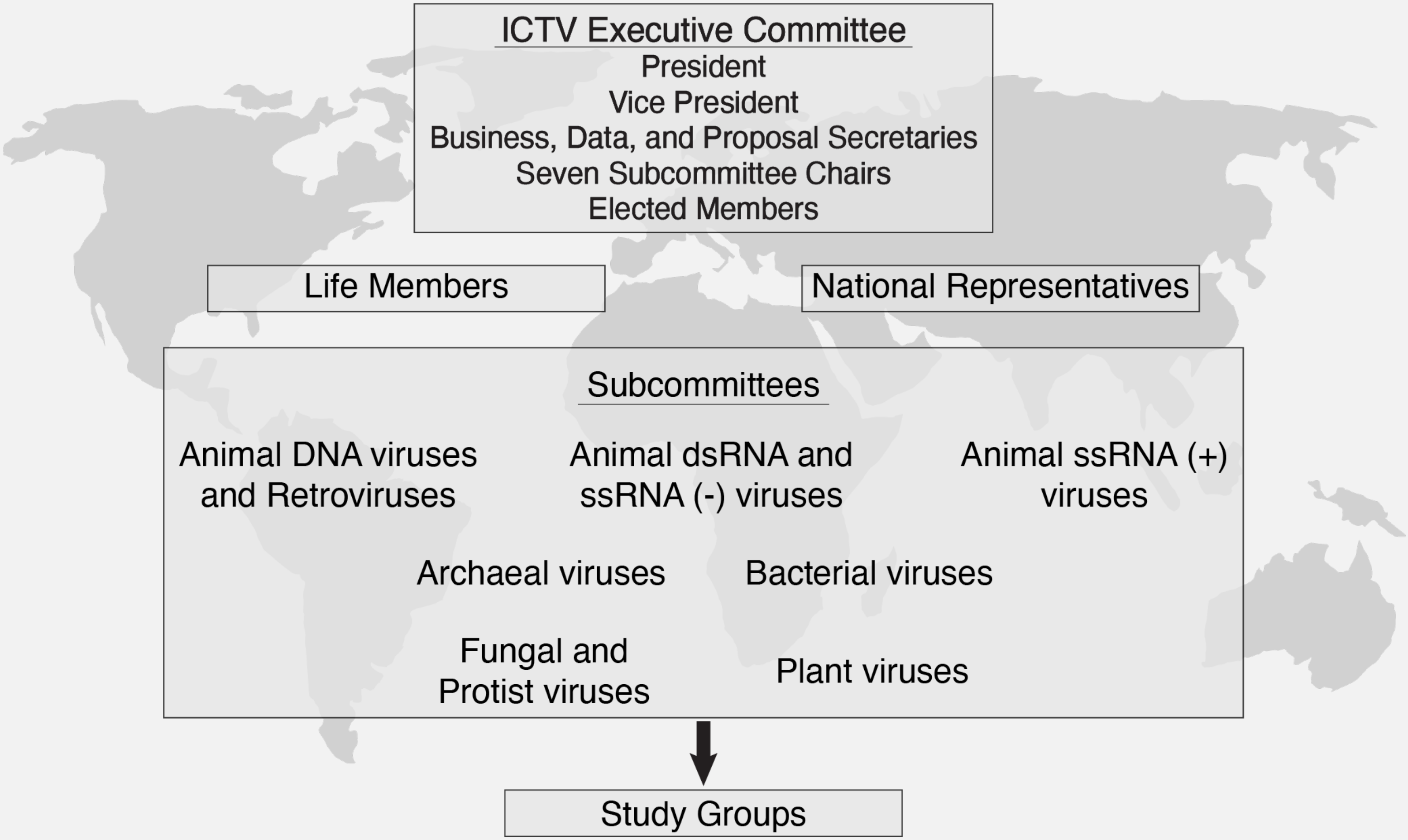
1995: 6th Report

# HISTORY OF VIRUS TAXONOMY

| MSL # | Year | Release / ratification record |
|---|---|---|
| - | **1966** | First meeting of the International Committee on Nomenclature of Viruses (ICNV) |
| 1 | **1971** | ICNV 1st Report (MSL #01) |
| 2 | **1974** | Postal vote April-May 1974 (MSL #02) |
| 3 | **1975** | ICTV Plenary session vote 12/16 September 1975 in Madrid (MSL #03) |
| 4 | **1976** | ICTV 2nd Report (MSL #04) |
| 5 | **1978** | Plenary session vote 30 August 1978 in The Hague (MSL #05) |
| 6 | **1979** | ICTV 3rd Report (MSL #06) |
| 7 | **1981** | Plenary session vote 4 August 1981 in Strasbourg (MSL #07) |
| 8 | **1982** | ICTV 4th Report (MSL #08) |
| 9 | **1984** | Plenary session vote 5 September 1984 in Sendai (MSL #09) |
| 10 | **1987** | Plenary session vote 12 August 1987 in Edmonton (MSL #10) |
| 11 | **1990** | Plenary session vote 29 August 1990 in Berlin (MSL #11) |
| 12 | **1991** | ICTV 5th Report (MSL #12) |
| 13 | **1993** | Plenary session vote 10 August 1993 in Glasgow (MSL #13) |
| 14 | **1995** | ICTV 6th Report (MSL #14) |
| 15 | **1996** | Plenary session vote August 1996 in Jerusalem (MSL #15) |
| 16 | **1997** | Postal vote autumn 1997 (MSL #16) |
| 17 | **1998** | Postal vote autumn 1998 (MSL #17) |
| 18 | **1999a** | ICTV 7th Report (MSL #18) |
| 19 | **1999b** | Plenary session vote August 1999 in Sydney (MSL #19) |
| 20 | **2002a** | Postal vote spring 2002 (MSL #20) |
| 21 | **2002b** | Plenary session vote 30 July 2002 in Paris (MSL #21) |
| 22 | **2004** | Postal vote 2004 (MSL #22) |
| 23 | **2005** | ICTV 8th Report (MSL #23) |
| 24 | **2008** | EC 39: Kingston, June, 2007; EC 40: Istanbul, August 2008; Email ratification 2008 (MSL #24) |
| 25 | **2009** | ICTV 9th Report; EC41: Leiden, June 2009; Email ratification 2009 (MSL #25) |
| 26 | **2011** | EC 42: Paris, June, 2010; EC43: Sapporo, September 2011; Email ratification 2012 (MSL #26) |
| 27 | **2012** | EC 44, Leuven, July 2012; Email ratification 2013 (MSL #27) |
| 28 | **2013** | EC 45, Edinburgh, July 2013; Email ratification 2014 (MSL #28) |
| 29 | **2014** | EC 46, Kingston and Montreal, Canada, July 2014, Email ratification 2015 (MSL #29) |
| 30 | **2015** | EC 47, London, UK, July 2015; Email ratification 2016 (MSL #30) |
| 31 | **2016** | EC 48, Budapest, Hungary, August 2016; Email ratification 2017 (MSL #31) |
| 32 | **2017** | EC 49, Singapore, July 2017; Email ratification 2018 (MSL #32) |
| 33 | **2018a** | EC 50, Washington, DC, July 2018; Email ratification October 2018 (MSL #33) |
| 34 | **2018b** | EC 50, Washington, DC, July 2018; Email ratification February 2019 (MSL #34) |
| 35 | **2019** | EC 51, Berlin, Germany, July 2019; Email ratification March 2020 (MSL #35) |
| 36 | **2020** | EC 52, Online meeting, October 2020; Email ratification March 2021 (MSL #36) |
| 37 | **2021** | EC 53, Online, July 2021; Email ratification March 2022 (MSL #37) |
| 38 | **2022** | EC 54, Online meeting, July 2022; Email ratification March 2023 (MSL #38) |
| 39 | **2023** | EC 55, Jena, Germany, August 2023; Email ratification April 2024 (MSL #39) release v4, October 30, 2024 |
| 40 | **2024** | EC 56, Bari, Italy, August 2024; Email ratification February 2025 (MSL #40) release v2, August 22, 2025 |
| 41 | **2025** | EC 57, Birmingham, Alabama, USA, August 2025; Email ratification February 2026 (MSL #41) release v1, March 20, |

# THE ICTV ORGANIZATION

## International Committee on Taxonomy of Viruses
## Organizational Chart



**ICTV Executive Committee**
President
Vice President
Business, Data, and Proposal Secretaries
Seven Subcommittee Chairs
Elected Members

Life Members

National Representatives

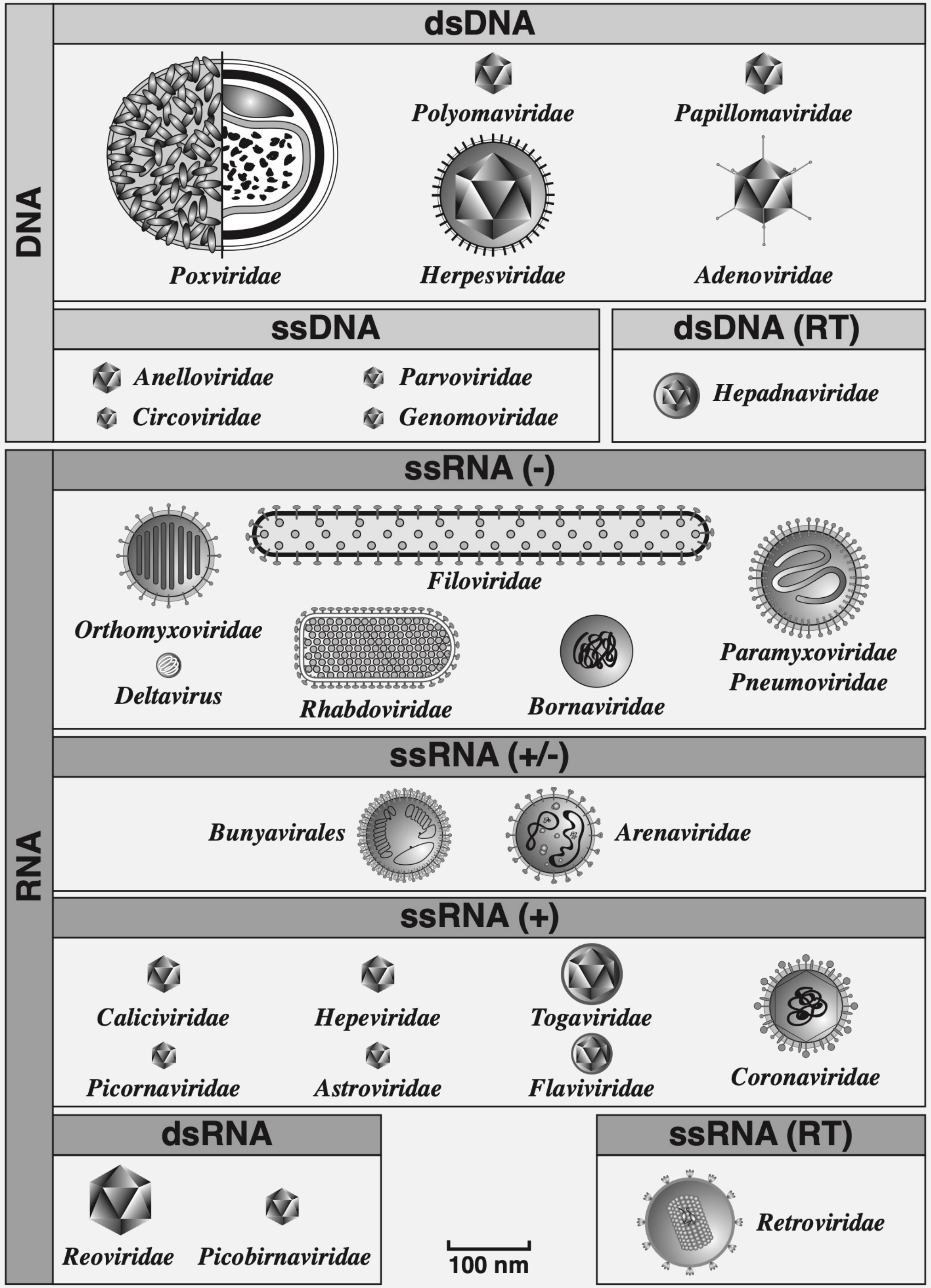
**Subcommittees**

- Animal DNA viruses and Retroviruses
- Animal dsRNA and ssRNA (-) viruses
- Animal ssRNA (+) viruses
- Archaeal viruses
- Bacterial viruses
- Fungal and Protist viruses
- Plant viruses

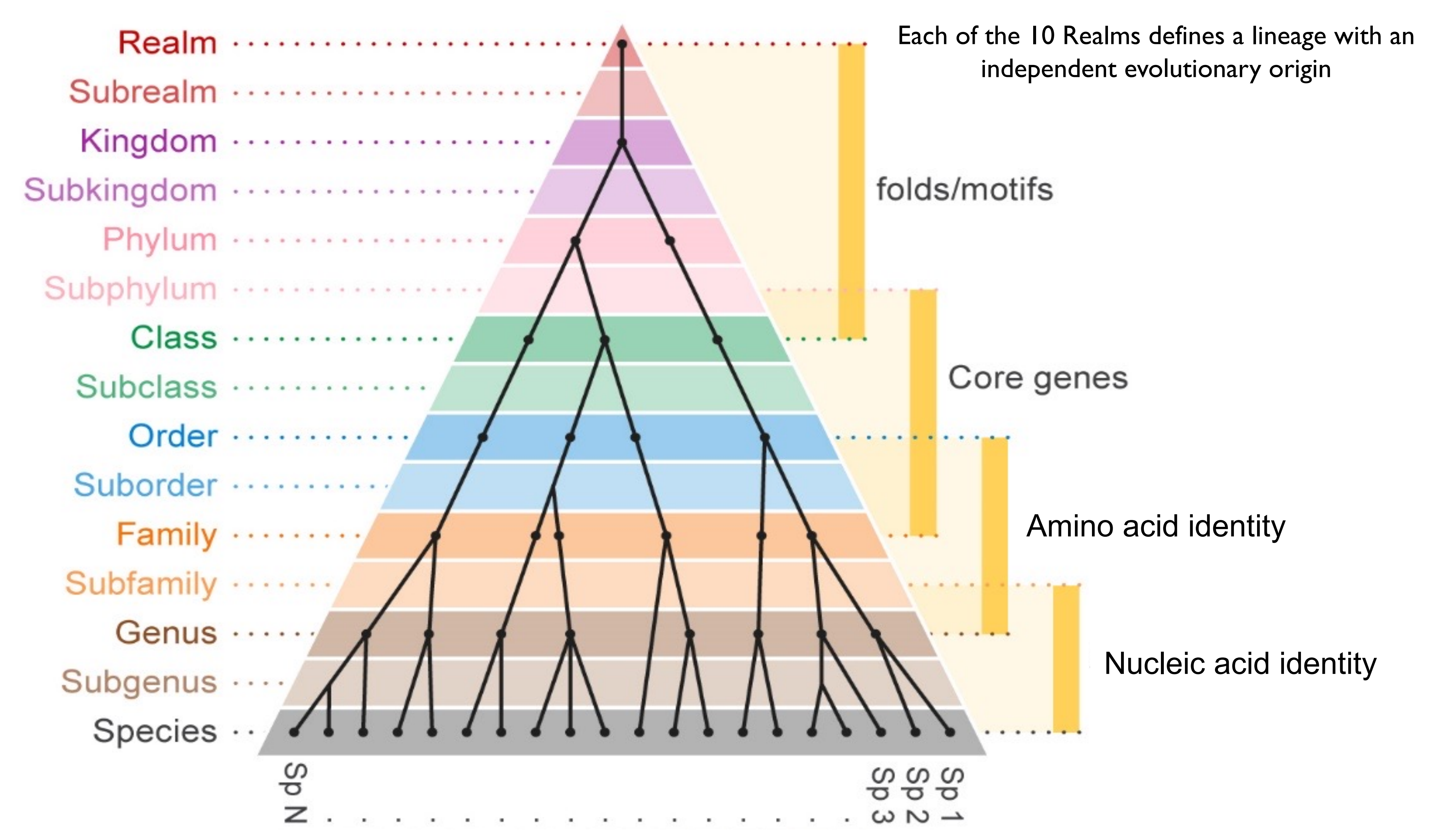
Study Groups

# CLASSIFICATION

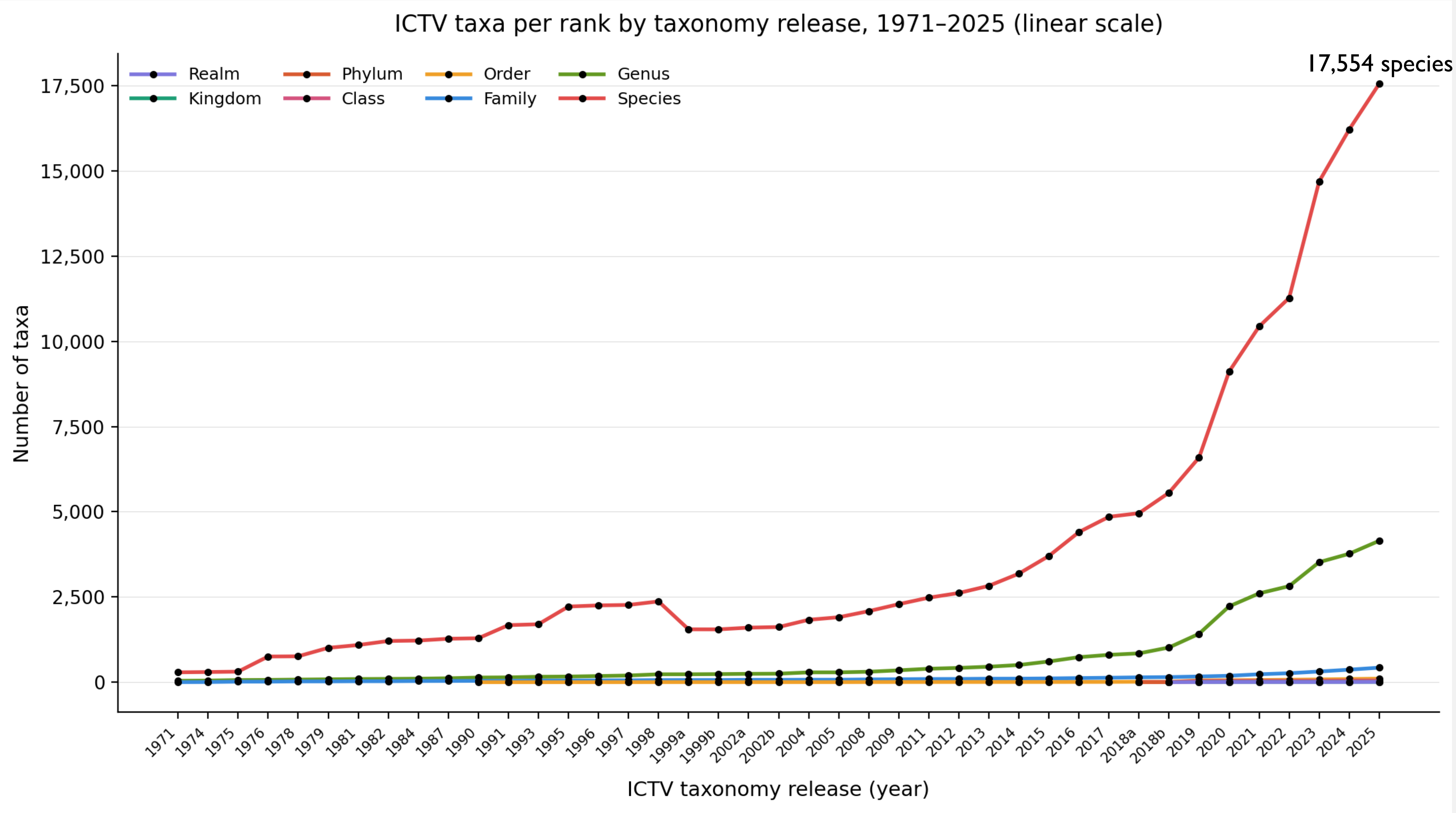
- The identification and comparison of characters that distinguish one virus from another.
- Phenotypic
  - Host range
  - Pathogenicity
  - Virion/capsid structure
  - Presence of an envelop
  - Molecular composition of the genome
- Genotypic
  - Sequence
  - Gene content
  - Gene synteny
  - Gene expression program
  - Phylogenetic relationships



# VIRUS TAXONOMIC RANKS

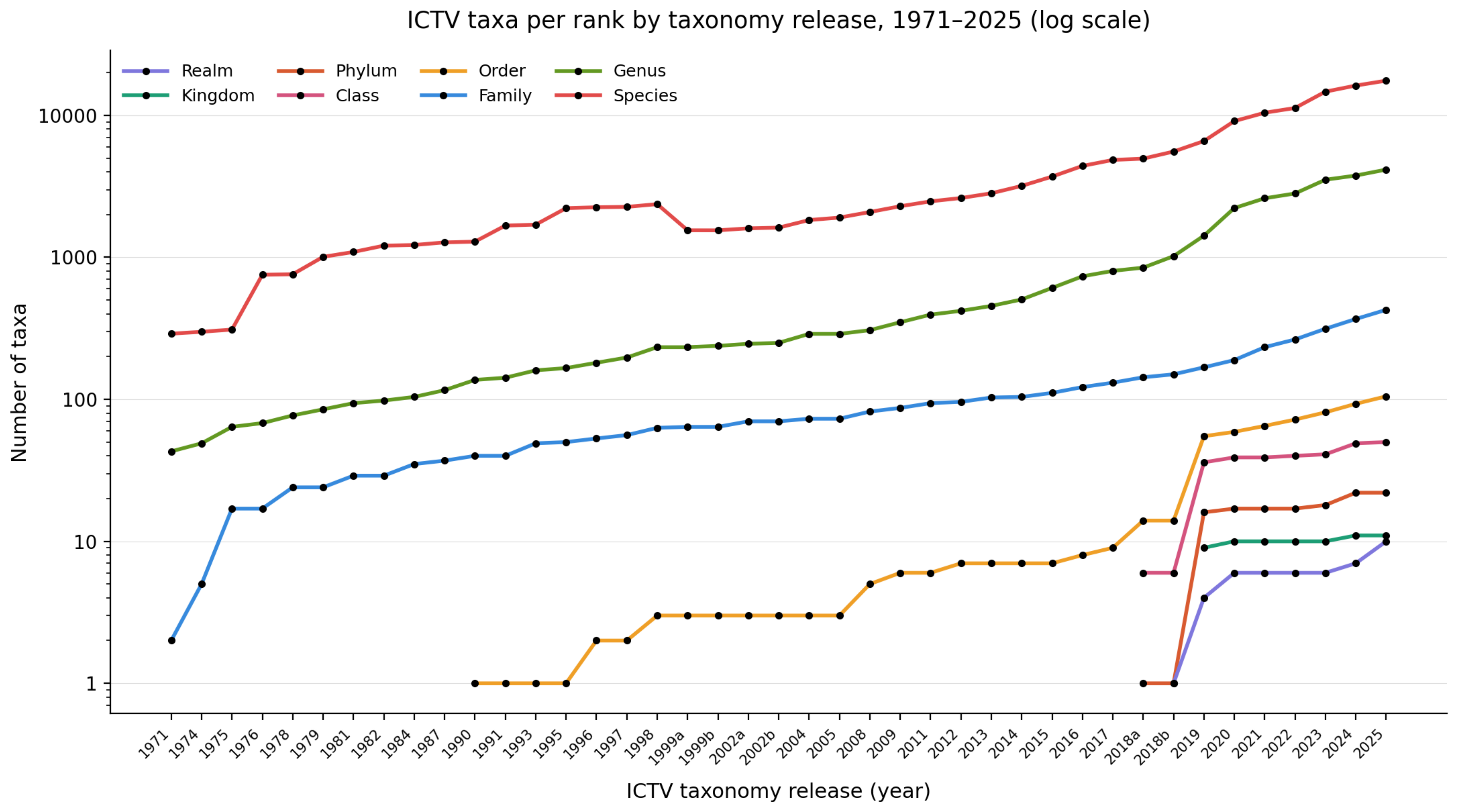


Each of the 10 Realms defines a lineage with an independent evolutionary origin



ICTV taxa per rank by taxonomy release, 1971–2025 (linear scale)

17,554 species


ICTV taxa per rank by taxonomy release, 1971–2025 (log scale)
Realm
Kingdom
Phylum
Class
Order
Family
Genus
Species
Number of taxa
10000
1000
100
10
1
ICTV taxonomy release (year)
1971
1974
1975
1976
1978
1979
1981
1982
1984
1987
1990
1991
1993
1995
1996
1997
1998
1999a
1999b
2002a
2002b
2004
2005
2008
2009
2011
2012
2013
2014
2015
2016
2017
2018a
2018b
2019
2020
2021
2022
2023
2024
2025

# NOMENCLATURE

- Realm: *Riboviria*
- Kingdom: *Orthornavirae*
- Phylum: *Pisuviricota*
- Class: *Pisoniviricetes*
- Order: *Picornavirales*
- Family: *Picornaviridae*
- Genus: *Enterovirus*
- Species: *Enterovirus coxsackiepol*
  - Binomial name
    - Genus name + species epithet

# WHAT'S IN A NAME?

| Name | Poxvirus Example | Coronavirus Example | Who Creates? | Who Updates? |
|---|---|---|---|---|
| Virus | **Monkeypox virus** | **SARS-CoV-2** | Discoverer | Scientific community |
| Species | • *Monkeypox virus*<br>• ***Orthopoxvirus monkeypox*** | • *Severe acute respiratory syndrome-related coronavirus*<br>• ***Betacoronavirus pandemicum*** | ICTV | ICTV |
| Disease | • Monkeypox virus<br>• **MPOX** | • 2019-nCoV<br>• hCoV-19<br>• **COVID-19** | WHO | WHO |
| Sub-species | • West African; DRC, Congo Basin<br>• 1, 2, 3<br>• **I, IIa, IIb** | **Alpha, Beta, Gamma, Delta, Omicron…** | Scientific community (WHO-consulted) | Scientific community (WHO-consulted) |

# COMMUNICATING WITH THE WORLD

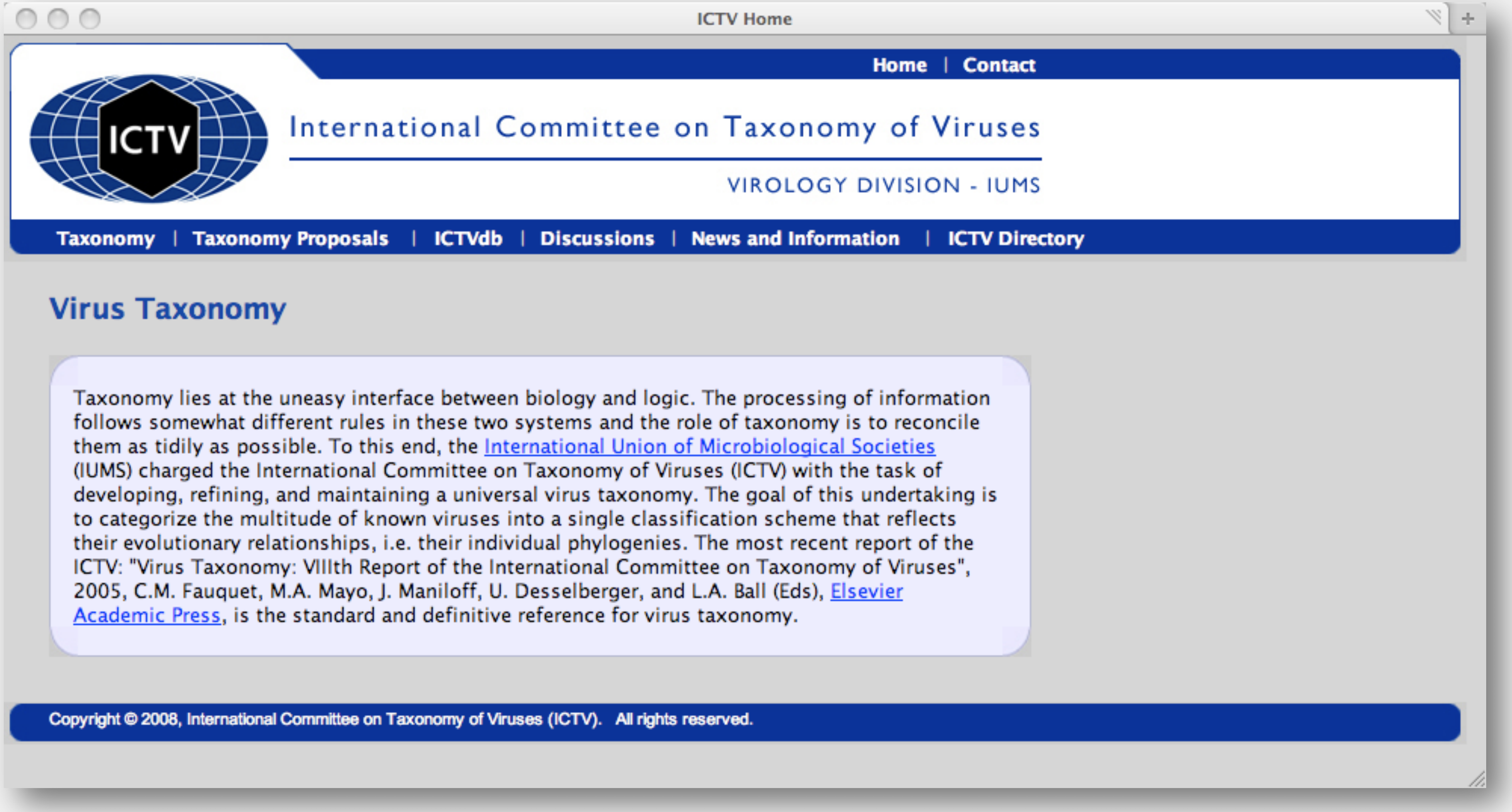
What if someone created a comprehensive virus taxonomy and no one knew it existed?

# VIRUS TAXONOMY:
# A COMMUNITY KNOWLEDGEBASE SUPPORTING VIRUS RESEARCH

U24 AI162625

08/03/2021 – 05/31/2026

# ICTV circa 2007-2008

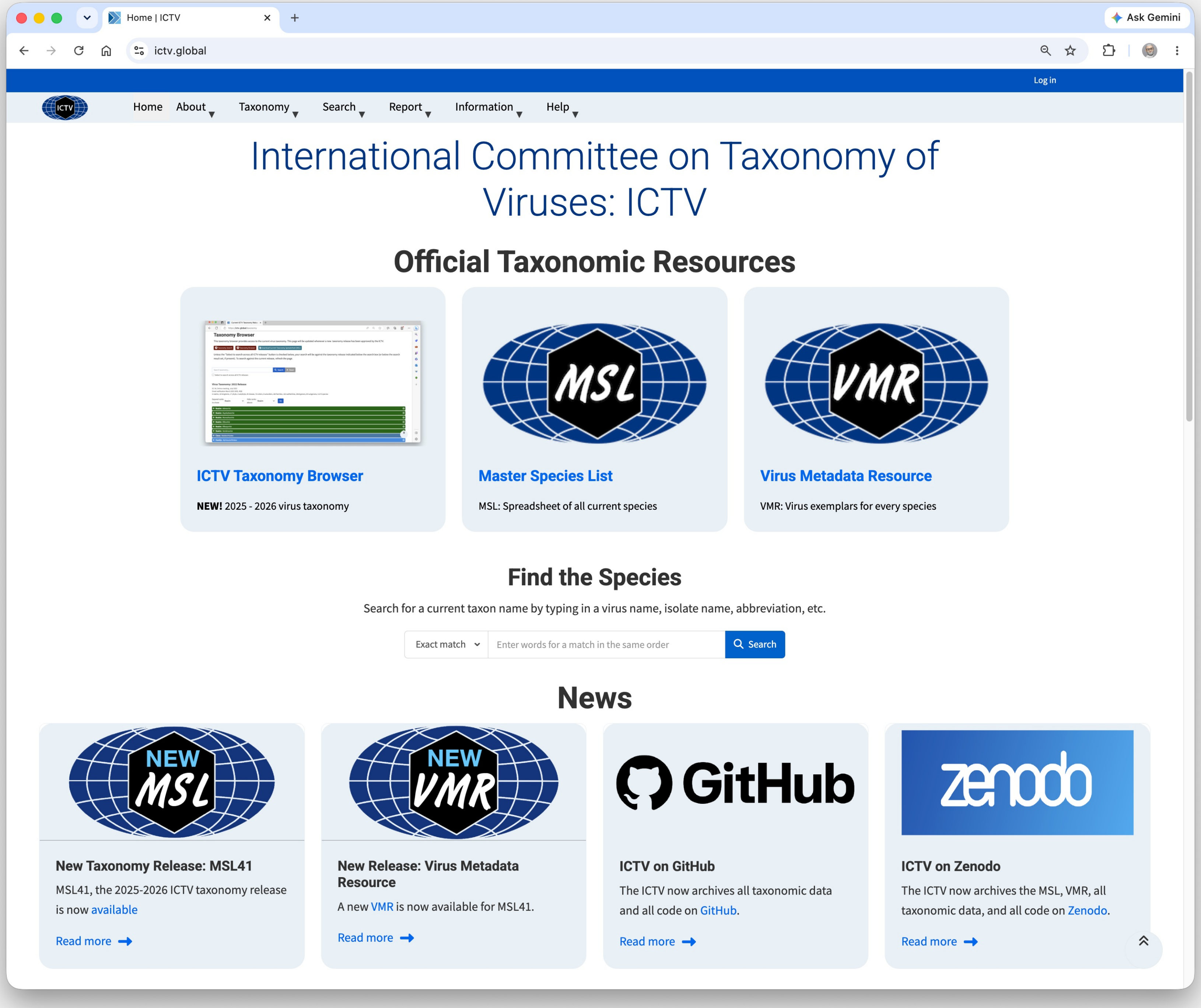


## Virus Taxonomy

Taxonomy lies at the uneasy interface between biology and logic. The processing of information follows somewhat different rules in these two systems and the role of taxonomy is to reconcile them as tidily as possible. To this end, the International Union of Microbiological Societies (IUMS) charged the International Committee on Taxonomy of Viruses (ICTV) with the task of developing, refining, and maintaining a universal virus taxonomy. The goal of this undertaking is to categorize the multitude of known viruses into a single classification scheme that reflects their evolutionary relationships, i.e. their individual phylogenies. The most recent report of the ICTV: "Virus Taxonomy: VIIIth Report of the International Committee on Taxonomy of Viruses", 2005, C.M. Fauquet, M.A. Mayo, J. Maniloff, U. Desselberger, and L.A. Ball (Eds), Elsevier Academic Press, is the standard and definitive reference for virus taxonomy.

# VIRUS KNOWLEDGEBASE AIMS

- Infrastructure
  - Provide a stable, responsive, scalable information technology platform
- Information
  - Enrich the virus taxonomy by expanding the available information on virus properties
- Tools
  - Develop and deploy analytical tools that support the creation, expansion, and management of virus taxonomy
- Accessibility
  - Provide flexible, interoperable access to taxonomic data
- Outreach and Training
  - Establish programs that introduce these resources to current and potential users and provide training in their use
- Sustainability



International Committee on Taxonomy of Viruses: ICTV

Official Taxonomic Resources

**ICTV Taxonomy Browser**

**NEW!** 2025 - 2026 virus taxonomy

**Master Species List**

MSL: Spreadsheet of all current species

**Virus Metadata Resource**

VMR: Virus exemplars for every species

Find the Species

Search for a current taxon name by typing in a virus name, isolate name, abbreviation, etc.

News

**New Taxonomy Release: MSL41**

MSL41, the 2025-2026 ICTV taxonomy release is now available

Read more

**New Release: Virus Metadata Resource**

A new VMR is now available for MSL41.

Read more

**ICTV on GitHub**

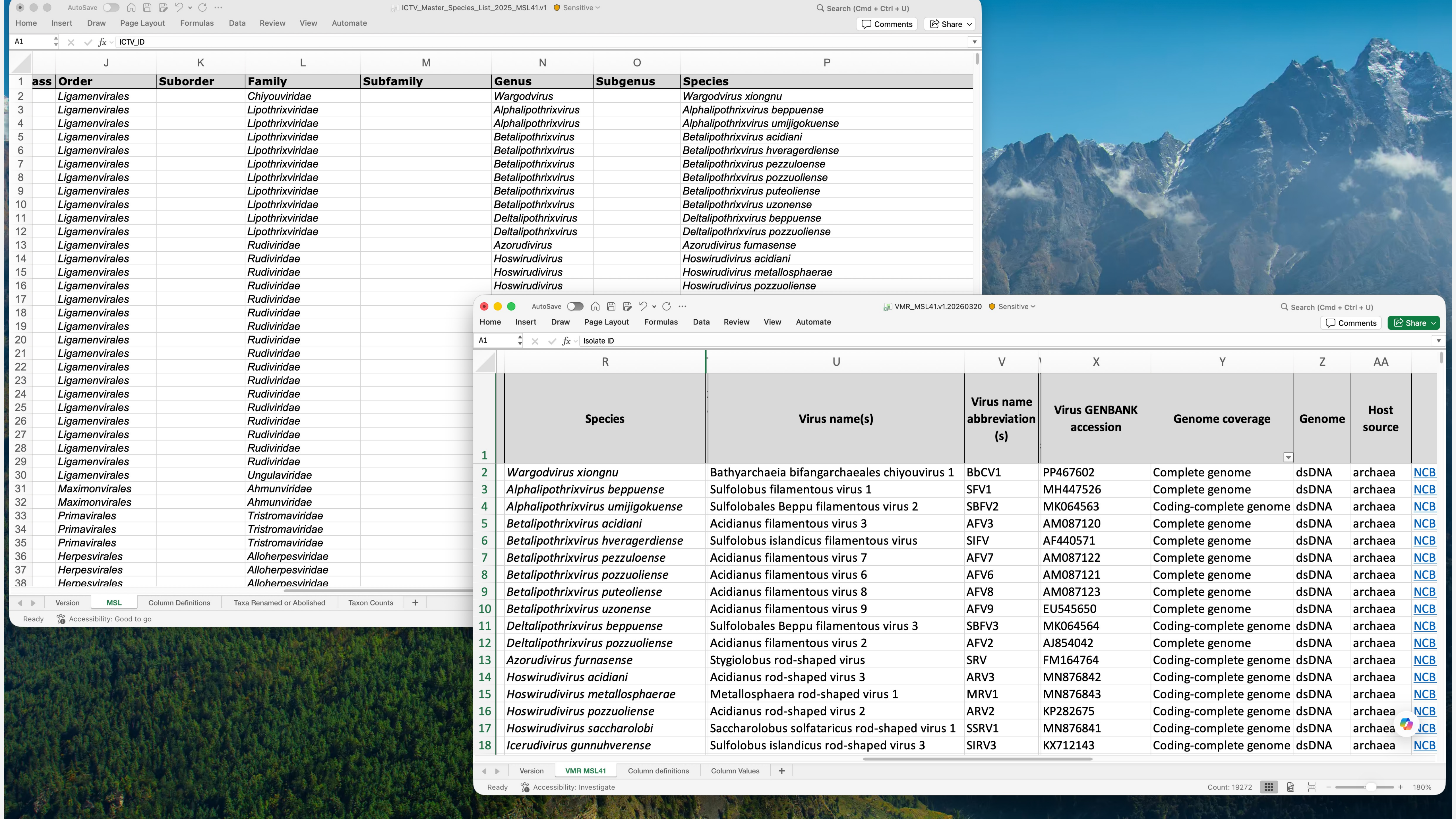
The ICTV now archives all taxonomic data and all code on GitHub.

Read more

**ICTV on Zenodo**

The ICTV now archives the MSL, VMR, all taxonomic data, and all code on Zenodo.

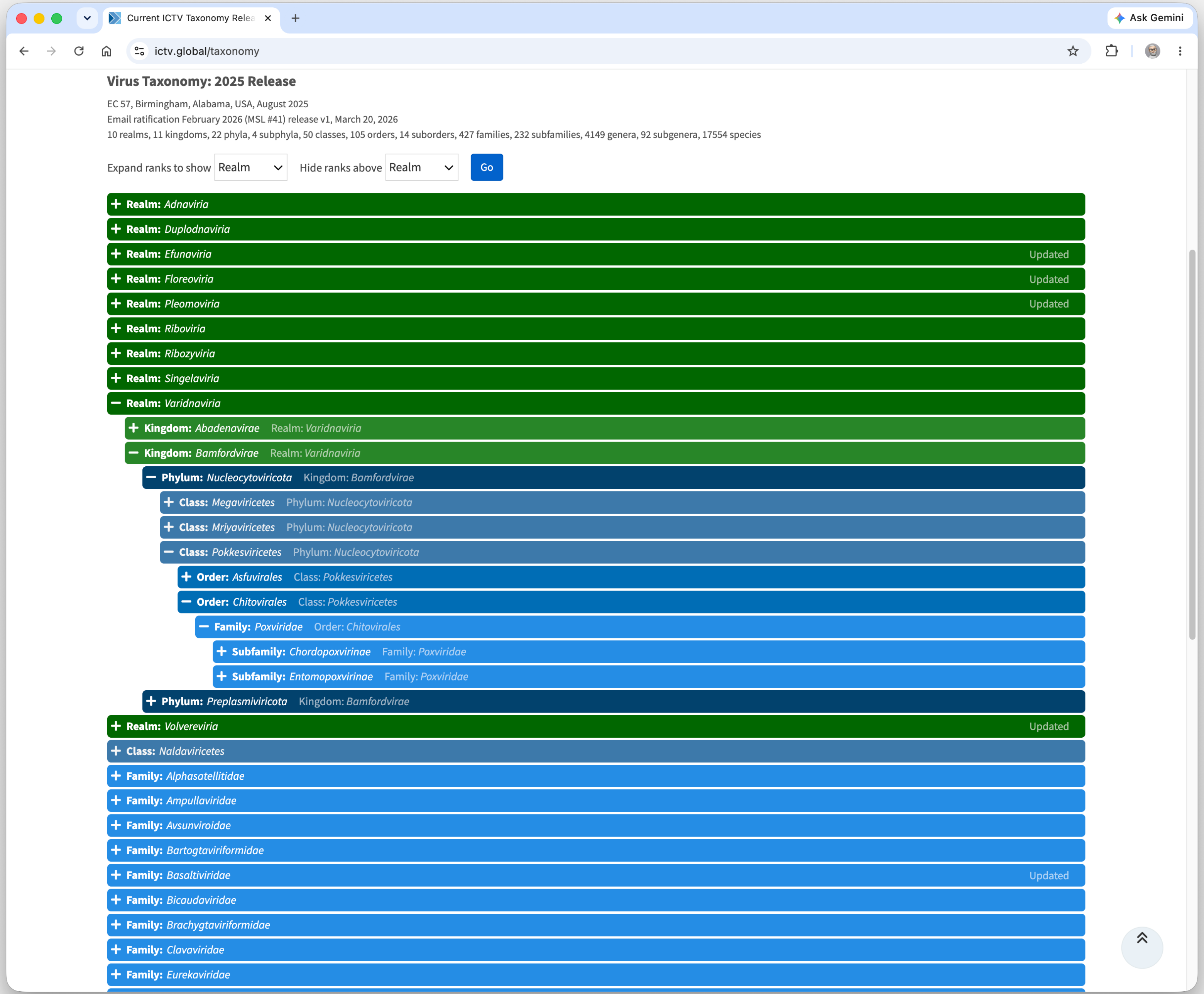
Read more



| | J | K | L | M | N | O | P |
|---|---|---|---|---|---|---|---|
| 1 | Order | Suborder | Family | Subfamily | Genus | Subgenus | Species |
| 2 | *Ligamenvirales* | | *Chiyouviridae* | | *Wargodvirus* | | *Wargodvirus xiongnu* |
| 3 | *Ligamenvirales* | | *Lipothrixviridae* | | *Alphalipothrixvirus* | | *Alphalipothrixvirus beppuense* |
| 4 | *Ligamenvirales* | | *Lipothrixviridae* | | *Alphalipothrixvirus* | | *Alphalipothrixvirus umijigokuense* |
| 5 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus acidiani* |
| 6 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus hveragerdiense* |
| 7 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus pezzuloense* |
| 8 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus pozzuoliense* |
| 9 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus puteoliense* |
| 10 | *Ligamenvirales* | | *Lipothrixviridae* | | *Betalipothrixvirus* | | *Betalipothrixvirus uzonense* |
| 11 | *Ligamenvirales* | | *Lipothrixviridae* | | *Deltalipothrixvirus* | | *Deltalipothrixvirus beppuense* |
| 12 | *Ligamenvirales* | | *Lipothrixviridae* | | *Deltalipothrixvirus* | | *Deltalipothrixvirus pozzuoliense* |
| 13 | *Ligamenvirales* | | *Rudiviridae* | | *Azorudivirus* | | *Azorudivirus furnasense* |
| 14 | *Ligamenvirales* | | *Rudiviridae* | | *Hoswirudivirus* | | *Hoswirudivirus acidiani* |
| 15 | *Ligamenvirales* | | *Rudiviridae* | | *Hoswirudivirus* | | *Hoswirudivirus metallosphaerae* |
| 16 | *Ligamenvirales* | | *Rudiviridae* | | *Hoswirudivirus* | | *Hoswirudivirus pozzuoliense* |
| 17 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 18 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 19 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 20 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 21 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 22 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 23 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 24 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 25 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 26 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 27 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 28 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 29 | *Ligamenvirales* | | *Rudiviridae* | | | | |
| 30 | *Ligamenvirales* | | *Ungulaviridae* | | | | |
| 31 | *Maximonvirales* | | *Ahmunviridae* | | | | |
| 32 | *Maximonvirales* | | *Ahmunviridae* | | | | |
| 33 | *Primavirales* | | *Tristromaviridae* | | | | |
| 34 | *Primavirales* | | *Tristromaviridae* | | | | |
| 35 | *Primavirales* | | *Tristromaviridae* | | | | |
| 36 | *Herpesvirales* | | *Alloherpesviridae* | | | | |
| 37 | *Herpesvirales* | | *Alloherpesviridae* | | | | |
| 38 | *Herpesvirales* | | *Alloherpesviridae* | | | | |

| | R | U | V | X | Y | Z | AA | |
|---|---|---|---|---|---|---|---|---|
| 1 | Species | Virus name(s) | Virus name abbreviation (s) | Virus GENBANK accession | Genome coverage | Genome | Host source | |
| 2 | *Wargodvirus xiongnu* | Bathyarchaeia bifangarchaeales chiyouvirus 1 | BbCV1 | PP467602 | Complete genome | dsDNA | archaea | NCB |
| 3 | *Alphalipothrixvirus beppuense* | Sulfolobus filamentous virus 1 | SFV1 | MH447526 | Complete genome | dsDNA | archaea | NCB |
| 4 | *Alphalipothrixvirus umijigokuense* | Sulfolobales Beppu filamentous virus 2 | SBFV2 | MK064563 | Coding-complete genome | dsDNA | archaea | NCB |
| 5 | *Betalipothrixvirus acidiani* | Acidianus filamentous virus 3 | AFV3 | AM087120 | Complete genome | dsDNA | archaea | NCB |
| 6 | *Betalipothrixvirus hveragerdiense* | Sulfolobus islandicus filamentous virus | SIFV | AF440571 | Complete genome | dsDNA | archaea | NCB |
| 7 | *Betalipothrixvirus pezzuloense* | Acidianus filamentous virus 7 | AFV7 | AM087122 | Complete genome | dsDNA | archaea | NCB |
| 8 | *Betalipothrixvirus pozzuoliense* | Acidianus filamentous virus 6 | AFV6 | AM087121 | Complete genome | dsDNA | archaea | NCB |
| 9 | *Betalipothrixvirus puteoliense* | Acidianus filamentous virus 8 | AFV8 | AM087123 | Complete genome | dsDNA | archaea | NCB |
| 10 | *Betalipothrixvirus uzonense* | Acidianus filamentous virus 9 | AFV9 | EU545650 | Complete genome | dsDNA | archaea | NCB |
| 11 | *Deltalipothrixvirus beppuense* | Sulfolobales Beppu filamentous virus 3 | SBFV3 | MK064564 | Coding-complete genome | dsDNA | archaea | NCB |
| 12 | *Deltalipothrixvirus pozzuoliense* | Acidianus filamentous virus 2 | AFV2 | AJ854042 | Complete genome | dsDNA | archaea | NCB |
| 13 | *Azorudivirus furnasense* | Stygiolobus rod-shaped virus | SRV | FM164764 | Coding-complete genome | dsDNA | archaea | NCB |
| 14 | *Hoswirudivirus acidiani* | Acidianus rod-shaped virus 3 | ARV3 | MN876842 | Coding-complete genome | dsDNA | archaea | NCB |
| 15 | *Hoswirudivirus metallosphaerae* | Metallosphaera rod-shaped virus 1 | MRV1 | MN876843 | Coding-complete genome | dsDNA | archaea | NCB |
| 16 | *Hoswirudivirus pozzuoliense* | Acidianus rod-shaped virus 2 | ARV2 | KP282675 | Coding-complete genome | dsDNA | archaea | NCB |
| 17 | *Hoswirudivirus saccharolobi* | Saccharolobus solfataricus rod-shaped virus 1 | SSRV1 | MN876841 | Coding-complete genome | dsDNA | archaea | NCB |
| 18 | *Icerudivirus gunnuhverense* | Sulfolobus islandicus rod-shaped virus 3 | SIRV3 | KX712143 | Coding-complete genome | dsDNA | archaea | NCB |

# TAXONOMY BROWSER



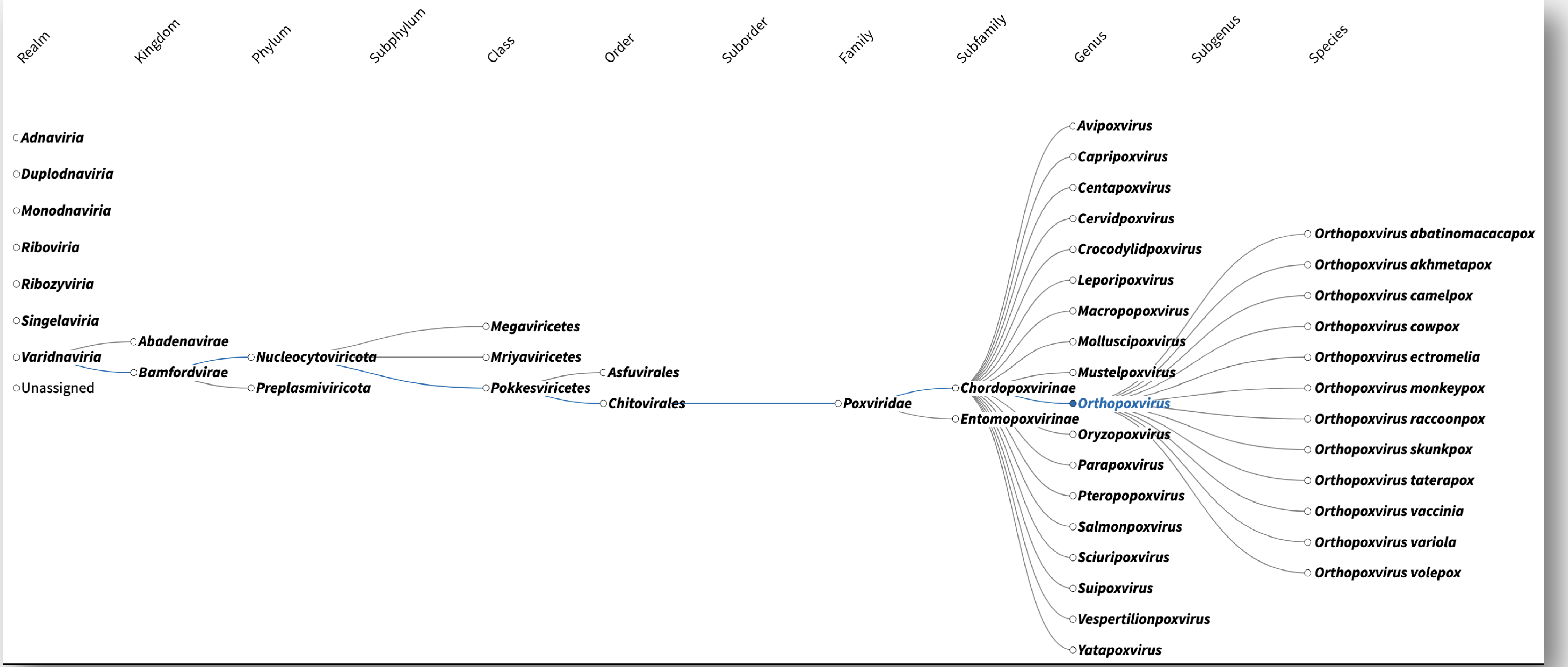
**Virus Taxonomy: 2025 Release**

EC 57, Birmingham, Alabama, USA, August 2025
Email ratification February 2026 (MSL #41) release v1, March 20, 2026
10 realms, 11 kingdoms, 22 phyla, 4 subphyla, 50 classes, 105 orders, 14 suborders, 427 families, 232 subfamilies, 4149 genera, 92 subgenera, 17554 species

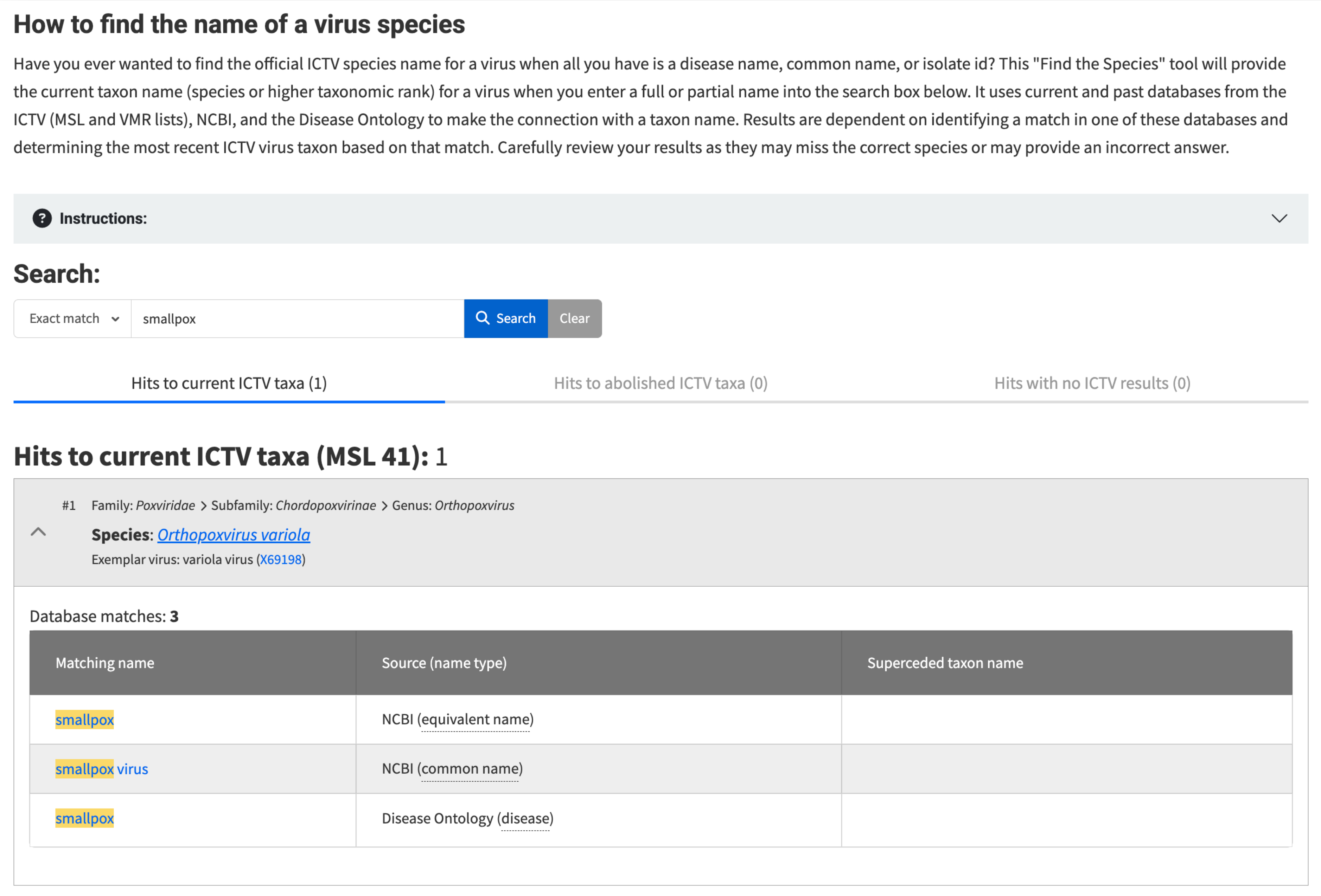
Expand ranks to show: Realm  Hide ranks above: Realm  Go

- + **Realm:** *Adnaviria*
- + **Realm:** *Duplodnaviria*
- + **Realm:** *Efunaviria* Updated
- + **Realm:** *Floreoviria* Updated
- + **Realm:** *Pleomoviria* Updated
- + **Realm:** *Riboviria*
- + **Realm:** *Ribozyviria*
- + **Realm:** *Singelaviria*
- − **Realm:** *Varidnaviria*
  - + **Kingdom:** *Abadenavirae* Realm: *Varidnaviria*
  - − **Kingdom:** *Bamfordvirae* Realm: *Varidnaviria*
    - − **Phylum:** *Nucleocytoviricota* Kingdom: *Bamfordvirae*
      - + **Class:** *Megaviricetes* Phylum: *Nucleocytoviricota*
      - + **Class:** *Mriyaviricetes* Phylum: *Nucleocytoviricota*
      - − **Class:** *Pokkesviricetes* Phylum: *Nucleocytoviricota*
        - + **Order:** *Asfuvirales* Class: *Pokkesviricetes*
        - − **Order:** *Chitovirales* Class: *Pokkesviricetes*
          - − **Family:** *Poxviridae* Order: *Chitovirales*
            - + **Subfamily:** *Chordopoxvirinae* Family: *Poxviridae*
            - + **Subfamily:** *Entomopoxvirinae* Family: *Poxviridae*
    - + **Phylum:** *Preplasmiviricota* Kingdom: *Bamfordvirae*
- + **Realm:** *Volvereviria* Updated
- + **Class:** *Naldaviricetes*
- + **Family:** *Alphasatellitidae*
- + **Family:** *Ampullaviridae*
- + **Family:** *Avsunviroidae*
- + **Family:** *Bartogtaviriformidae*
- + **Family:** *Basaltiviridae* Updated
- + **Family:** *Bicaudaviridae*
- + **Family:** *Brachygtaviriformidae*
- + **Family:** *Clavaviridae*
- + **Family:** *Eurekaviridae*

# VISUAL TAXONOMY BROWSER



# FIND THE SPECIES



## How to find the name of a virus species

Have you ever wanted to find the official ICTV species name for a virus when all you have is a disease name, common name, or isolate id? This "Find the Species" tool will provide the current taxon name (species or higher taxonomic rank) for a virus when you enter a full or partial name into the search box below. It uses current and past databases from the ICTV (MSL and VMR lists), NCBI, and the Disease Ontology to make the connection with a taxon name. Results are dependent on identifying a match in one of these databases and determining the most recent ICTV virus taxon based on that match. Carefully review your results as they may miss the correct species or may provide an incorrect answer.

**Instructions:**

## Search:

Exact match
smallpox

## Hits to current ICTV taxa (MSL 41): 1

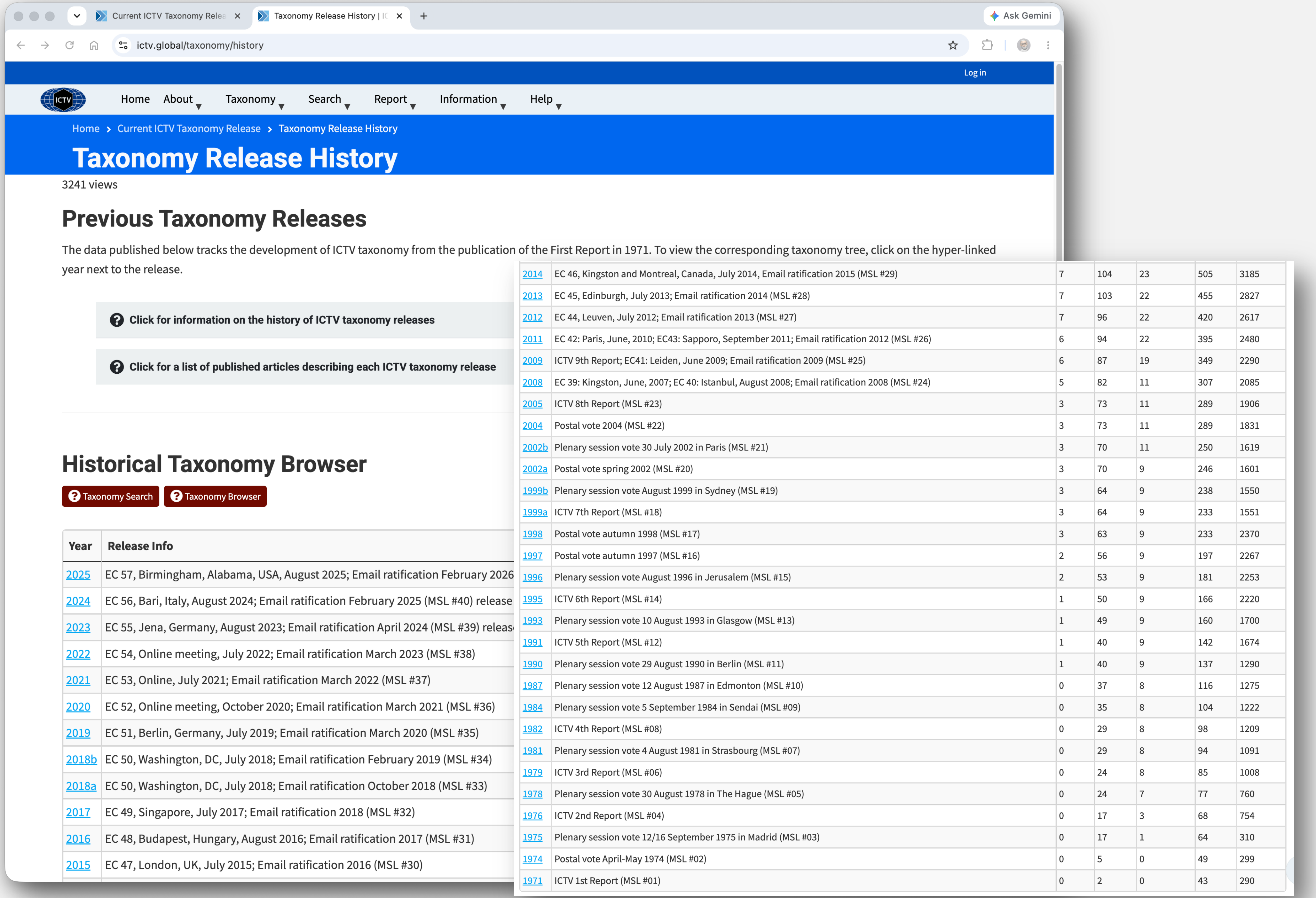
#1 Family: *Poxviridae* > Subfamily: *Chordopoxvirinae* > Genus: *Orthopoxvirus*

**Species:** *Orthopoxvirus variola*

Exemplar virus: variola virus (X69198)

Database matches: **3**

| Matching name | Source (name type) | Superceded taxon name |
|---|---|---|
| smallpox | NCBI (equivalent name) | |
| smallpox virus | NCBI (common name) | |
| smallpox | Disease Ontology (disease) | |



# Taxonomy Release History

3241 views

## Previous Taxonomy Releases

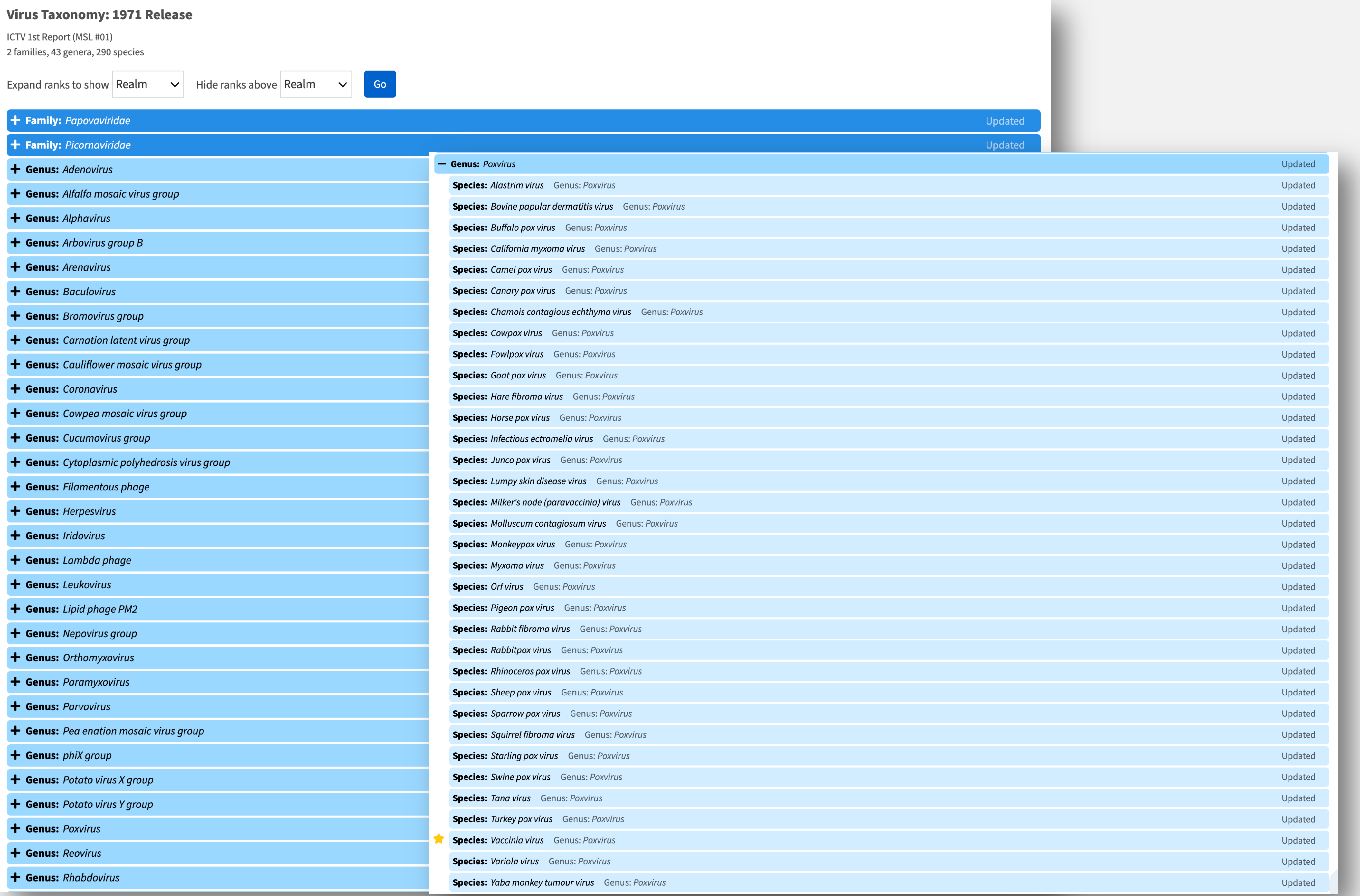
The data published below tracks the development of ICTV taxonomy from the publication of the First Report in 1971. To view the corresponding taxonomy tree, click on the hyper-linked year next to the release.

Click for information on the history of ICTV taxonomy releases

Click for a list of published articles describing each ICTV taxonomy release

## Historical Taxonomy Browser

| Year | Release Info | | | | | |
|---|---|---|---|---|---|---|
| 2025 | EC 57, Birmingham, Alabama, USA, August 2025; Email ratification February 2026 | | | | | |
| 2024 | EC 56, Bari, Italy, August 2024; Email ratification February 2025 (MSL #40) release | | | | | |
| 2023 | EC 55, Jena, Germany, August 2023; Email ratification April 2024 (MSL #39) releas | | | | | |
| 2022 | EC 54, Online meeting, July 2022; Email ratification March 2023 (MSL #38) | | | | | |
| 2021 | EC 53, Online, July 2021; Email ratification March 2022 (MSL #37) | | | | | |
| 2020 | EC 52, Online meeting, October 2020; Email ratification March 2021 (MSL #36) | | | | | |
| 2019 | EC 51, Berlin, Germany, July 2019; Email ratification March 2020 (MSL #35) | | | | | |
| 2018b | EC 50, Washington, DC, July 2018; Email ratification February 2019 (MSL #34) | | | | | |
| 2018a | EC 50, Washington, DC, July 2018; Email ratification October 2018 (MSL #33) | | | | | |
| 2017 | EC 49, Singapore, July 2017; Email ratification 2018 (MSL #32) | | | | | |
| 2016 | EC 48, Budapest, Hungary, August 2016; Email ratification 2017 (MSL #31) | | | | | |
| 2015 | EC 47, London, UK, July 2015; Email ratification 2016 (MSL #30) | | | | | |
| 2014 | EC 46, Kingston and Montreal, Canada, July 2014, Email ratification 2015 (MSL #29) | 7 | 104 | 23 | 505 | 3185 |
| 2013 | EC 45, Edinburgh, July 2013; Email ratification 2014 (MSL #28) | 7 | 103 | 22 | 455 | 2827 |
| 2012 | EC 44, Leuven, July 2012; Email ratification 2013 (MSL #27) | 7 | 96 | 22 | 420 | 2617 |
| 2011 | EC 42: Paris, June, 2010; EC43: Sapporo, September 2011; Email ratification 2012 (MSL #26) | 6 | 94 | 22 | 395 | 2480 |
| 2009 | ICTV 9th Report; EC41: Leiden, June 2009; Email ratification 2009 (MSL #25) | 6 | 87 | 19 | 349 | 2290 |
| 2008 | EC 39: Kingston, June, 2007; EC 40: Istanbul, August 2008; Email ratification 2008 (MSL #24) | 5 | 82 | 11 | 307 | 2085 |
| 2005 | ICTV 8th Report (MSL #23) | 3 | 73 | 11 | 289 | 1906 |
| 2004 | Postal vote 2004 (MSL #22) | 3 | 73 | 11 | 289 | 1831 |
| 2002b | Plenary session vote 30 July 2002 in Paris (MSL #21) | 3 | 70 | 11 | 250 | 1619 |
| 2002a | Postal vote spring 2002 (MSL #20) | 3 | 70 | 9 | 246 | 1601 |
| 1999b | Plenary session vote August 1999 in Sydney (MSL #19) | 3 | 64 | 9 | 238 | 1550 |
| 1999a | ICTV 7th Report (MSL #18) | 3 | 64 | 9 | 233 | 1551 |
| 1998 | Postal vote autumn 1998 (MSL #17) | 3 | 63 | 9 | 233 | 2370 |
| 1997 | Postal vote autumn 1997 (MSL #16) | 2 | 56 | 9 | 197 | 2267 |
| 1996 | Plenary session vote August 1996 in Jerusalem (MSL #15) | 2 | 53 | 9 | 181 | 2253 |
| 1995 | ICTV 6th Report (MSL #14) | 1 | 50 | 9 | 166 | 2220 |
| 1993 | Plenary session vote 10 August 1993 in Glasgow (MSL #13) | 1 | 49 | 9 | 160 | 1700 |
| 1991 | ICTV 5th Report (MSL #12) | 1 | 40 | 9 | 142 | 1674 |
| 1990 | Plenary session vote 29 August 1990 in Berlin (MSL #11) | 1 | 40 | 9 | 137 | 1290 |
| 1987 | Plenary session vote 12 August 1987 in Edmonton (MSL #10) | 0 | 37 | 8 | 116 | 1275 |
| 1984 | Plenary session vote 5 September 1984 in Sendai (MSL #09) | 0 | 35 | 8 | 104 | 1222 |
| 1982 | ICTV 4th Report (MSL #08) | 0 | 29 | 8 | 98 | 1209 |
| 1981 | Plenary session vote 4 August 1981 in Strasbourg (MSL #07) | 0 | 29 | 8 | 94 | 1091 |
| 1979 | ICTV 3rd Report (MSL #06) | 0 | 24 | 8 | 85 | 1008 |
| 1978 | Plenary session vote 30 August 1978 in The Hague (MSL #05) | 0 | 24 | 7 | 77 | 760 |
| 1976 | ICTV 2nd Report (MSL #04) | 0 | 17 | 3 | 68 | 754 |
| 1975 | Plenary session vote 12/16 September 1975 in Madrid (MSL #03) | 0 | 17 | 1 | 64 | 310 |
| 1974 | Postal vote April-May 1974 (MSL #02) | 0 | 5 | 0 | 49 | 299 |
| 1971 | ICTV 1st Report (MSL #01) | 0 | 2 | 0 | 43 | 290 |



**Virus Taxonomy: 1971 Release**

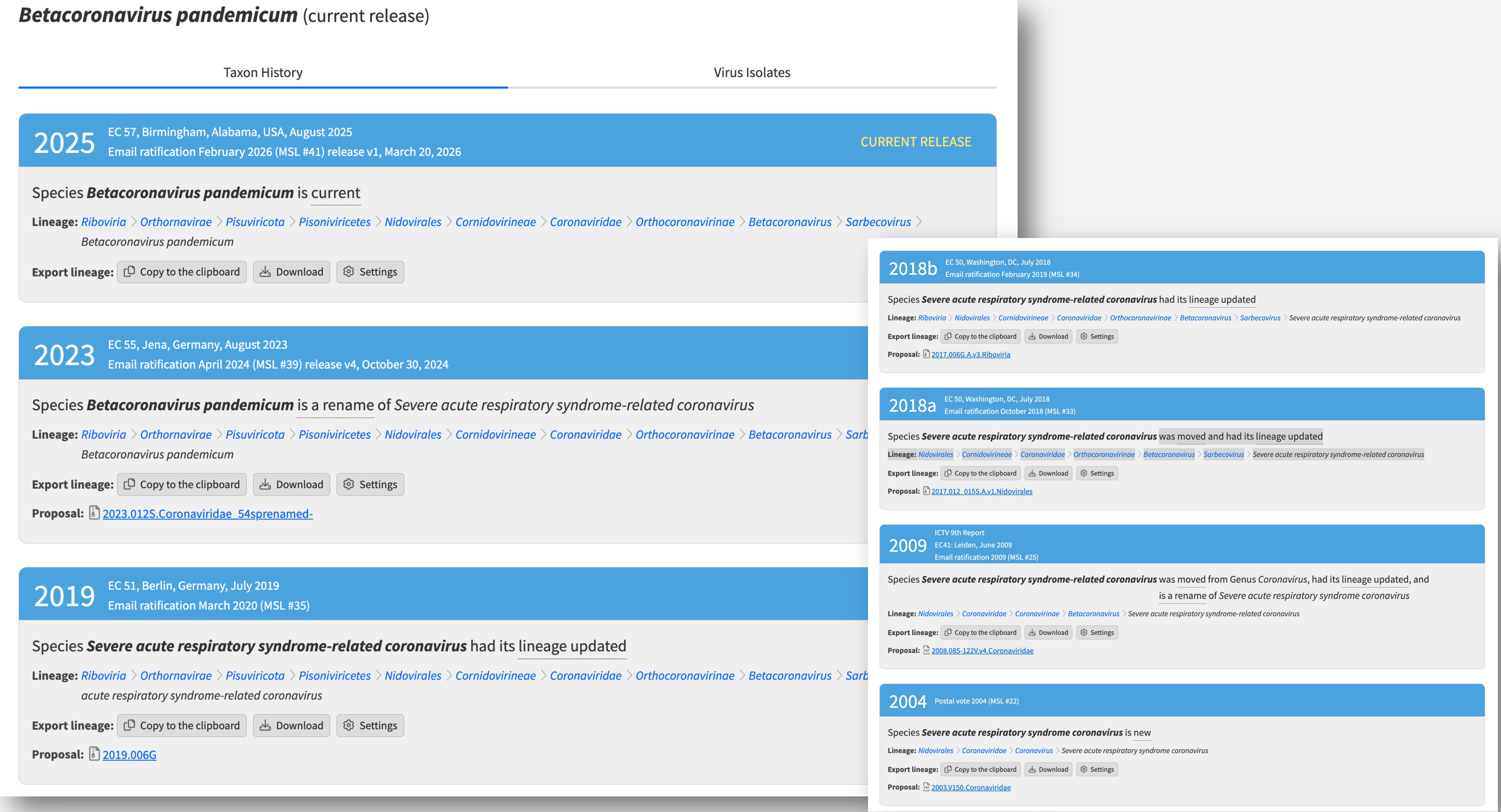
ICTV 1st Report (MSL #01)
2 families, 43 genera, 290 species

+ **Family:** *Papovaviridae* Updated
+ **Family:** *Picornaviridae* Updated
+ **Genus:** *Adenovirus*
+ **Genus:** *Alfalfa mosaic virus group*
+ **Genus:** *Alphavirus*
+ **Genus:** *Arbovirus group B*
+ **Genus:** *Arenavirus*
+ **Genus:** *Baculovirus*
+ **Genus:** *Bromovirus group*
+ **Genus:** *Carnation latent virus group*
+ **Genus:** *Cauliflower mosaic virus group*
+ **Genus:** *Coronavirus*
+ **Genus:** *Cowpea mosaic virus group*
+ **Genus:** *Cucumovirus group*
+ **Genus:** *Cytoplasmic polyhedrosis virus group*
+ **Genus:** *Filamentous phage*
+ **Genus:** *Herpesvirus*
+ **Genus:** *Iridovirus*
+ **Genus:** *Lambda phage*
+ **Genus:** *Leukovirus*
+ **Genus:** *Lipid phage PM2*
+ **Genus:** *Nepovirus group*
+ **Genus:** *Orthomyxovirus*
+ **Genus:** *Paramyxovirus*
+ **Genus:** *Parvovirus*
+ **Genus:** *Pea enation mosaic virus group*
+ **Genus:** *phiX group*
+ **Genus:** *Potato virus X group*
+ **Genus:** *Potato virus Y group*
+ **Genus:** *Poxvirus*
+ **Genus:** *Reovirus*
+ **Genus:** *Rhabdovirus*

− **Genus:** *Poxvirus* Updated

**Species:** *Alastrim virus* Genus: *Poxvirus* Updated
**Species:** *Bovine papular dermatitis virus* Genus: *Poxvirus* Updated
**Species:** *Buffalo pox virus* Genus: *Poxvirus* Updated
**Species:** *California myxoma virus* Genus: *Poxvirus* Updated
**Species:** *Camel pox virus* Genus: *Poxvirus* Updated
**Species:** *Canary pox virus* Genus: *Poxvirus* Updated
**Species:** *Chamois contagious echthyma virus* Genus: *Poxvirus* Updated
**Species:** *Cowpox virus* Genus: *Poxvirus* Updated
**Species:** *Fowlpox virus* Genus: *Poxvirus* Updated
**Species:** *Goat pox virus* Genus: *Poxvirus* Updated
**Species:** *Hare fibroma virus* Genus: *Poxvirus* Updated
**Species:** *Horse pox virus* Genus: *Poxvirus* Updated
**Species:** *Infectious ectromelia virus* Genus: *Poxvirus* Updated
**Species:** *Junco pox virus* Genus: *Poxvirus* Updated
**Species:** *Lumpy skin disease virus* Genus: *Poxvirus* Updated
**Species:** *Milker's node (paravaccinia) virus* Genus: *Poxvirus* Updated
**Species:** *Molluscum contagiosum virus* Genus: *Poxvirus* Updated
**Species:** *Monkeypox virus* Genus: *Poxvirus* Updated
**Species:** *Myxoma virus* Genus: *Poxvirus* Updated
**Species:** *Orf virus* Genus: *Poxvirus* Updated
**Species:** *Pigeon pox virus* Genus: *Poxvirus* Updated
**Species:** *Rabbit fibroma virus* Genus: *Poxvirus* Updated
**Species:** *Rabbitpox virus* Genus: *Poxvirus* Updated
**Species:** *Rhinoceros pox virus* Genus: *Poxvirus* Updated
**Species:** *Sheep pox virus* Genus: *Poxvirus* Updated
**Species:** *Sparrow pox virus* Genus: *Poxvirus* Updated
**Species:** *Squirrel fibroma virus* Genus: *Poxvirus* Updated
**Species:** *Starling pox virus* Genus: *Poxvirus* Updated
**Species:** *Swine pox virus* Genus: *Poxvirus* Updated
**Species:** *Tana virus* Genus: *Poxvirus* Updated
**Species:** *Turkey pox virus* Genus: *Poxvirus* Updated
★ **Species:** *Vaccinia virus* Genus: *Poxvirus* Updated
**Species:** *Variola virus* Genus: *Poxvirus* Updated
**Species:** *Yaba monkey tumour virus* Genus: *Poxvirus* Updated

# TAXONOMY HISTORY



***Betacoronavirus pandemicum*** (current release)

**2025** EC 57, Birmingham, Alabama, USA, August 2025
Email ratification February 2026 (MSL #41) release v1, March 20, 2026
CURRENT RELEASE

Species ***Betacoronavirus pandemicum*** is current

**Lineage:** *Riboviria* > *Orthornavirae* > *Pisuviricota* > *Pisoniviricetes* > *Nidovirales* > *Cornidovirineae* > *Coronaviridae* > *Orthocoronavirinae* > *Betacoronavirus* > *Sarbecovirus* > *Betacoronavirus pandemicum*

**Export lineage:** Copy to the clipboard | Download | Settings

**2023** EC 55, Jena, Germany, August 2023
Email ratification April 2024 (MSL #39) release v4, October 30, 2024

Species ***Betacoronavirus pandemicum*** is a rename of *Severe acute respiratory syndrome-related coronavirus*

**Lineage:** *Riboviria* > *Orthornavirae* > *Pisuviricota* > *Pisoniviricetes* > *Nidovirales* > *Cornidovirineae* > *Coronaviridae* > *Orthocoronavirinae* > *Betacoronavirus* > *Sarb*
*Betacoronavirus pandemicum*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2023.012S.Coronaviridae_54sprenamed-

**2019** EC 51, Berlin, Germany, July 2019
Email ratification March 2020 (MSL #35)

Species ***Severe acute respiratory syndrome-related coronavirus*** had its lineage updated

**Lineage:** *Riboviria* > *Orthornavirae* > *Pisuviricota* > *Pisoniviricetes* > *Nidovirales* > *Cornidovirineae* > *Coronaviridae* > *Orthocoronavirinae* > *Betacoronavirus* > *Sarb*
*acute respiratory syndrome-related coronavirus*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2019.006G

**2018b** EC 50, Washington, DC, July 2018
Email ratification February 2019 (MSL #34)

Species ***Severe acute respiratory syndrome-related coronavirus*** had its lineage updated

**Lineage:** *Riboviria* > *Nidovirales* > *Cornidovirineae* > *Coronaviridae* > *Orthocoronavirinae* > *Betacoronavirus* > *Sarbecovirus* > *Severe acute respiratory syndrome-related coronavirus*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2017.006G.A.v3.Riboviria

**2018a** EC 50, Washington, DC, July 2018
Email ratification October 2018 (MSL #33)

Species ***Severe acute respiratory syndrome-related coronavirus*** was moved and had its lineage updated

**Lineage:** *Nidovirales* > *Cornidovirineae* > *Coronaviridae* > *Orthocoronavirinae* > *Betacoronavirus* > *Sarbecovirus* > *Severe acute respiratory syndrome-related coronavirus*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2017.012_015S.A.v1.Nidovirales

**2009** ICTV 9th Report
EC41: Leiden, June 2009
Email ratification 2009 (MSL #25)

Species ***Severe acute respiratory syndrome-related coronavirus*** was moved from Genus *Coronavirus*, had its lineage updated, and is a rename of *Severe acute respiratory syndrome coronavirus*

**Lineage:** *Nidovirales* > *Coronaviridae* > *Coronavirinae* > *Betacoronavirus* > *Severe acute respiratory syndrome-related coronavirus*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2008.085-122V.v4.Coronaviridae

**2004** Postal vote 2004 (MSL #22)

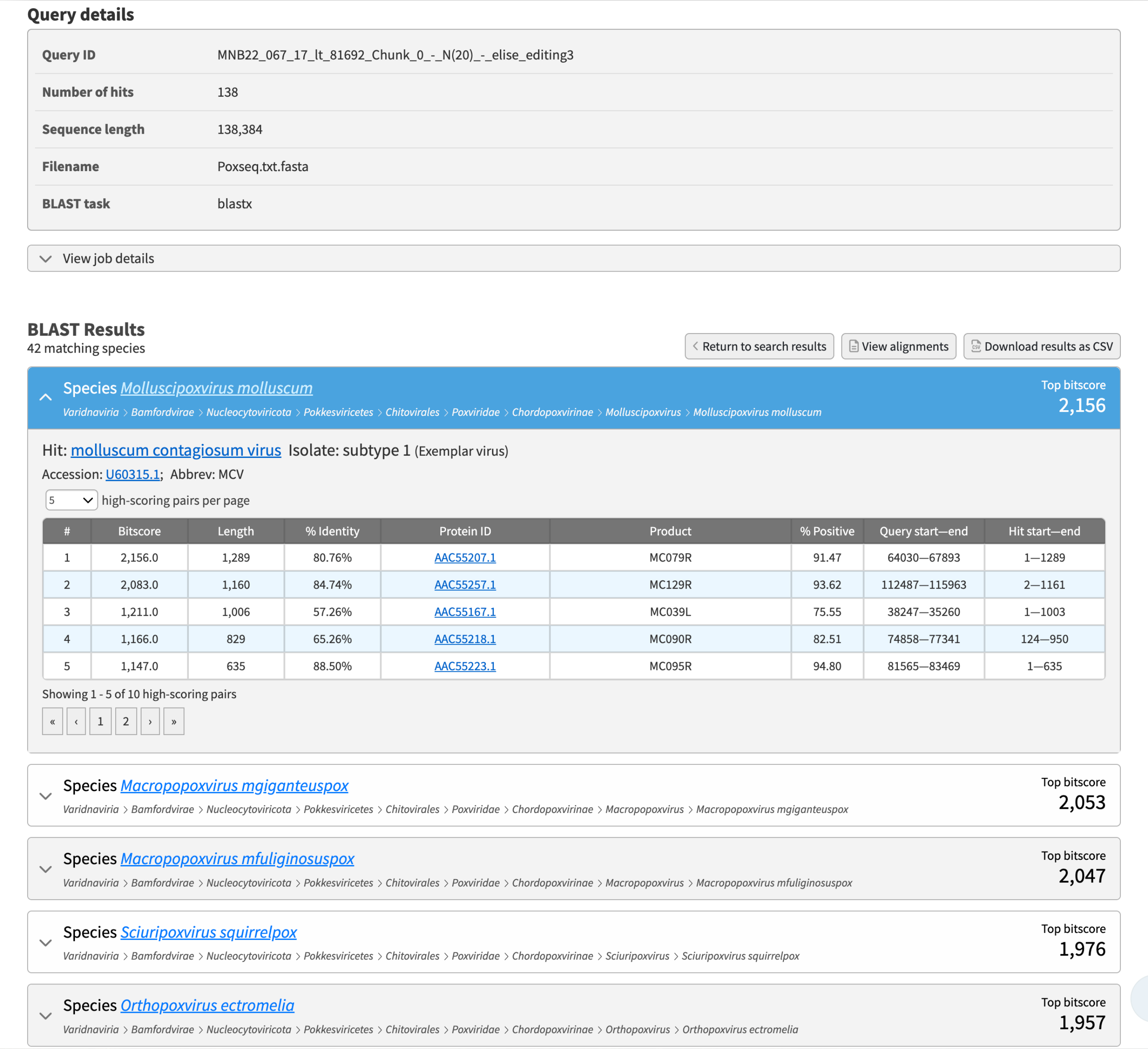
Species ***Severe acute respiratory syndrome coronavirus*** is new

**Lineage:** *Nidovirales* > *Coronaviridae* > *Coronavirus* > *Severe acute respiratory syndrome coronavirus*

**Export lineage:** Copy to the clipboard | Download | Settings

**Proposal:** 2003.V150.Coronaviridae

# TAXABLAST



**Query details**

| | |
|---|---|
| **Query ID** | MNB22_067_17_lt_81692_Chunk_0_-_N(20)_-_elise_editing3 |
| **Number of hits** | 138 |
| **Sequence length** | 138,384 |
| **Filename** | Poxseq.txt.fasta |
| **BLAST task** | blastx |

**BLAST Results**

42 matching species

Species *Molluscipoxvirus molluscum* — Top bitscore 2,156

*Varidnaviria › Bamfordvirae › Nucleocytoviricota › Pokkesviricetes › Chitovirales › Poxviridae › Chordopoxvirinae › Molluscipoxvirus › Molluscipoxvirus molluscum*

Hit: molluscum contagiosum virus Isolate: subtype 1 (Exemplar virus)

Accession: U60315.1; Abbrev: MCV

5 high-scoring pairs per page

| # | Bitscore | Length | % Identity | Protein ID | Product | % Positive | Query start—end | Hit start—end |
|---|---|---|---|---|---|---|---|---|
| 1 | 2,156.0 | 1,289 | 80.76% | AAC55207.1 | MC079R | 91.47 | 64030—67893 | 1—1289 |
| 2 | 2,083.0 | 1,160 | 84.74% | AAC55257.1 | MC129R | 93.62 | 112487—115963 | 2—1161 |
| 3 | 1,211.0 | 1,006 | 57.26% | AAC55167.1 | MC039L | 75.55 | 38247—35260 | 1—1003 |
| 4 | 1,166.0 | 829 | 65.26% | AAC55218.1 | MC090R | 82.51 | 74858—77341 | 124—950 |
| 5 | 1,147.0 | 635 | 88.50% | AAC55223.1 | MC095R | 94.80 | 81565—83469 | 1—635 |

Showing 1 - 5 of 10 high-scoring pairs

Species *Macropopoxvirus mgiganteuspox* — Top bitscore 2,053

*Varidnaviria › Bamfordvirae › Nucleocytoviricota › Pokkesviricetes › Chitovirales › Poxviridae › Chordopoxvirinae › Macropopoxvirus › Macropopoxvirus mgiganteuspox*

Species *Macropopoxvirus mfuliginosuspox* — Top bitscore 2,047

*Varidnaviria › Bamfordvirae › Nucleocytoviricota › Pokkesviricetes › Chitovirales › Poxviridae › Chordopoxvirinae › Macropopoxvirus › Macropopoxvirus mfuliginosuspox*

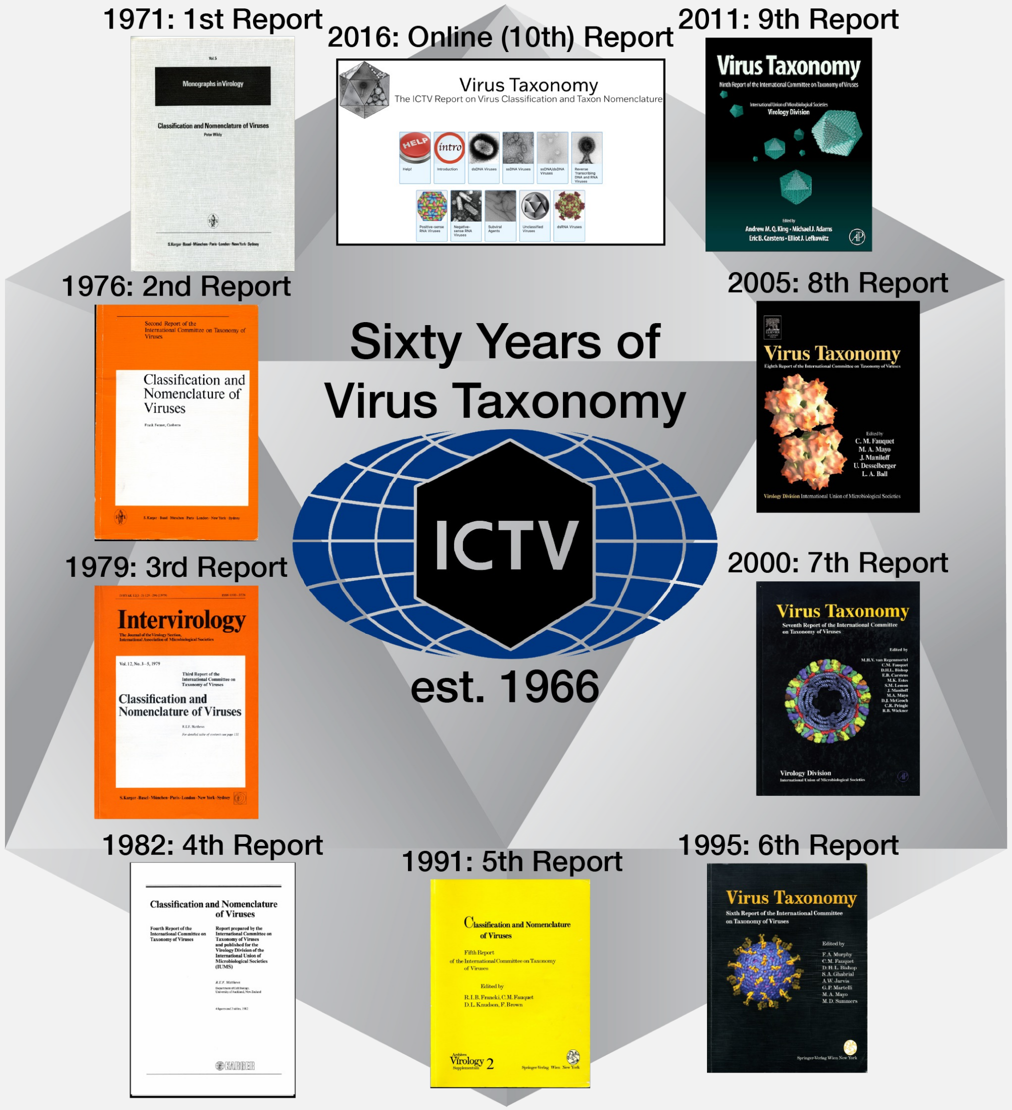
Species *Sciuripoxvirus squirrelpox* — Top bitscore 1,976

*Varidnaviria › Bamfordvirae › Nucleocytoviricota › Pokkesviricetes › Chitovirales › Poxviridae › Chordopoxvirinae › Sciuripoxvirus › Sciuripoxvirus squirrelpox*

Species *Orthopoxvirus ectromelia* — Top bitscore 1,957

*Varidnaviria › Bamfordvirae › Nucleocytoviricota › Pokkesviricetes › Chitovirales › Poxviridae › Chordopoxvirinae › Orthopoxvirus › Orthopoxvirus ectromelia*

# ICTV REPORT



1971: 1st Report

2016: Online (10th) Report

2011: 9th Report

1976: 2nd Report

2005: 8th Report

1979: 3rd Report

2000: 7th Report

1982: 4th Report

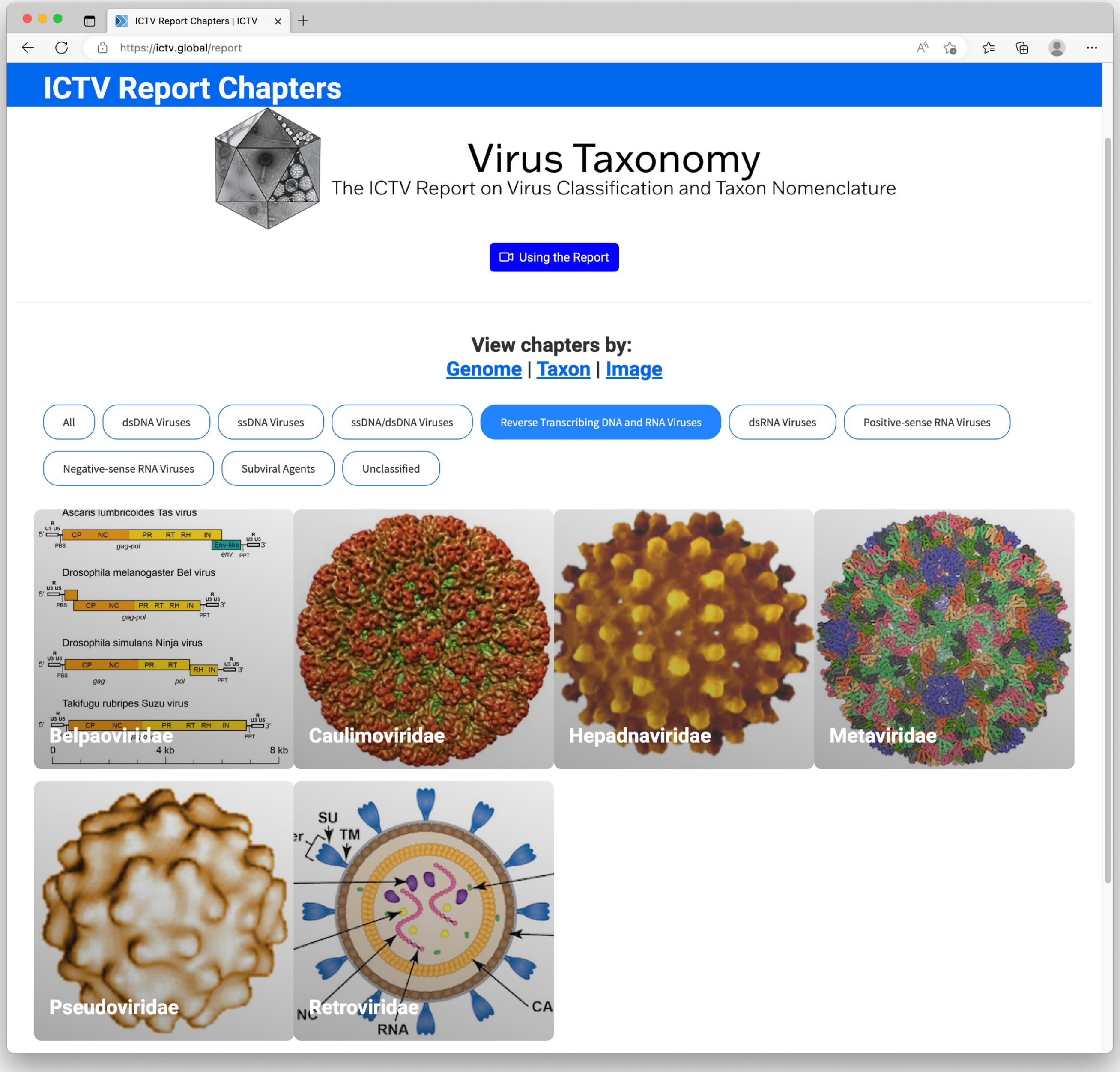
1991: 5th Report

1995: 6th Report

Sixty Years of Virus Taxonomy

ICTV

est. 1966



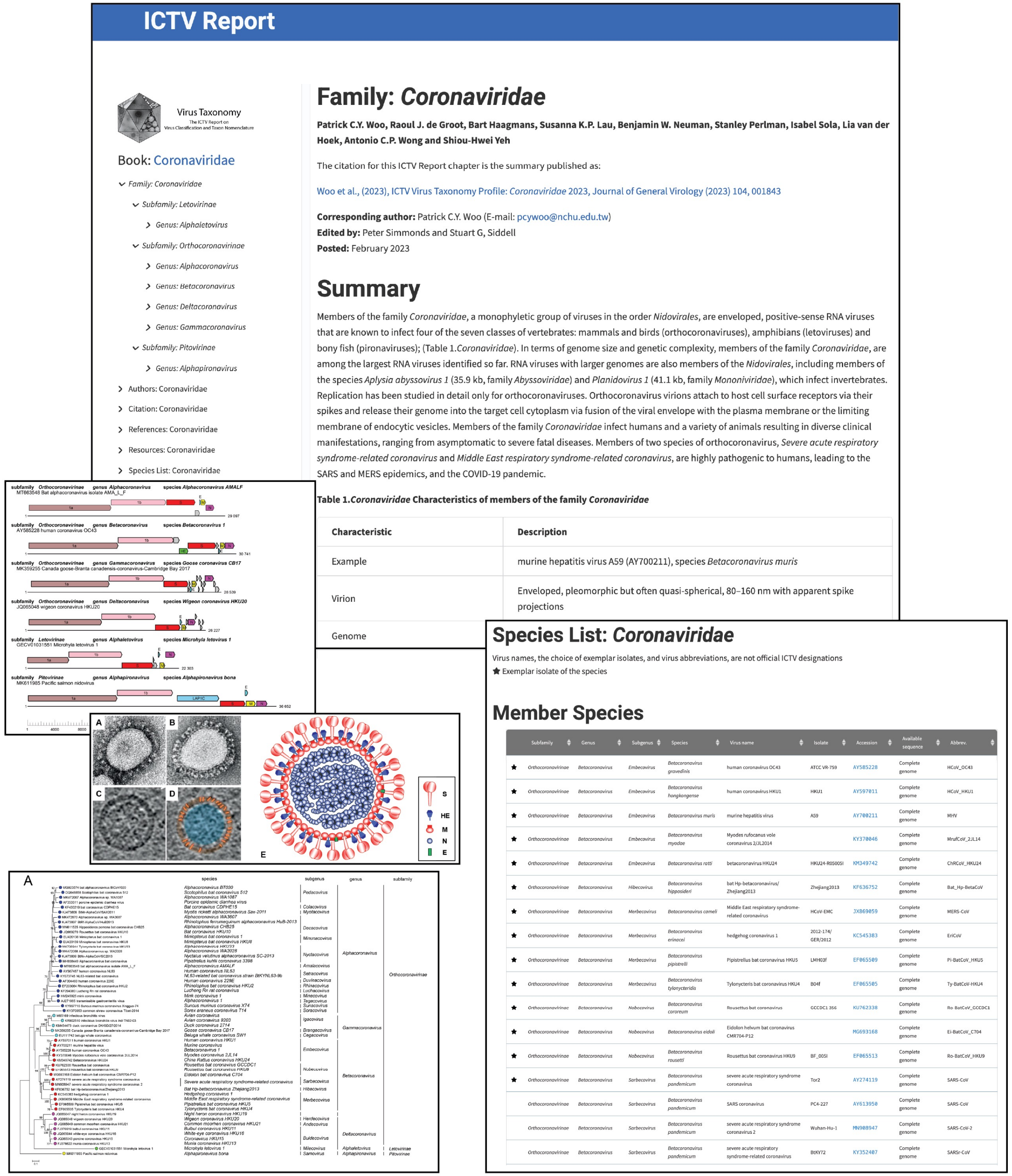
ICTV Report Chapters

Virus Taxonomy

The ICTV Report on Virus Classification and Taxon Nomenclature

View chapters by:

Genome | Taxon | Image



# ICTV Report

Virus Taxonomy
The ICTV Report on Virus Classification and Taxon Nomenclature

Book: Coronaviridae

- Family: Coronaviridae
  - Subfamily: Letovirinae
    - Genus: Alphaletovirus
  - Subfamily: Orthocoronavirinae
    - Genus: Alphacoronavirus
    - Genus: Betacoronavirus
    - Genus: Deltacoronavirus
    - Genus: Gammacoronavirus
  - Subfamily: Pitovirinae
    - Genus: Alphapironavirus
- Authors: Coronaviridae
- Citation: Coronaviridae
- References: Coronaviridae
- Resources: Coronaviridae
- Species List: Coronaviridae

## Family: *Coronaviridae*

**Patrick C.Y. Woo, Raoul J. de Groot, Bart Haagmans, Susanna K.P. Lau, Benjamin W. Neuman, Stanley Perlman, Isabel Sola, Lia van der Hoek, Antonio C.P. Wong and Shiou-Hwei Yeh**

The citation for this ICTV Report chapter is the summary published as:

Woo et al., (2023), ICTV Virus Taxonomy Profile: *Coronaviridae* 2023, Journal of General Virology (2023) 104, 001843

**Corresponding author:** Patrick C.Y. Woo (E-mail: pcywoo@nchu.edu.tw)
**Edited by:** Peter Simmonds and Stuart G, Siddell
**Posted:** February 2023

## Summary

Members of the family *Coronaviridae*, a monophyletic group of viruses in the order *Nidovirales*, are enveloped, positive-sense RNA viruses that are known to infect four of the seven classes of vertebrates: mammals and birds (orthocoronaviruses), amphibians (letoviruses) and bony fish (pironaviruses); (Table 1.*Coronaviridae*). In terms of genome size and genetic complexity, members of the family *Coronaviridae*, are among the largest RNA viruses identified so far. RNA viruses with larger genomes are also members of the *Nidovirales*, including members of the species *Aplysia abyssovirus 1* (35.9 kb, family *Abyssoviridae*) and *Planidovirus 1* (41.1 kb, family *Mononiviridae*), which infect invertebrates. Replication has been studied in detail only for orthocoronaviruses. Orthocoronavirus virions attach to host cell surface receptors via their spikes and release their genome into the target cell cytoplasm via fusion of the viral envelope with the plasma membrane or the limiting membrane of endocytic vesicles. Members of the family *Coronaviridae* infect humans and a variety of animals resulting in diverse clinical manifestations, ranging from asymptomatic to severe fatal diseases. Members of two species of orthocoronavirus, *Severe acute respiratory syndrome-related coronavirus* and *Middle East respiratory syndrome-related coronavirus*, are highly pathogenic to humans, leading to the SARS and MERS epidemics, and the COVID-19 pandemic.

**Table 1.*Coronaviridae* Characteristics of members of the family *Coronaviridae***

| Characteristic | Description |
|---|---|
| Example | murine hepatitis virus A59 (AY700211), species *Betacoronavirus muris* |
| Virion | Enveloped, pleomorphic but often quasi-spherical, 80–160 nm with apparent spike projections |
| Genome | |

## Species List: *Coronaviridae*

Virus names, the choice of exemplar isolates, and virus abbreviations, are not official ICTV designations

★ Exemplar isolate of the species

## Member Species

| | Subfamily | Genus | Subgenus | Species | Virus name | Isolate | Accession | Available sequence | Abbrev. |
|---|---|---|---|---|---|---|---|---|---|
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Embecovirus* | *Betacoronavirus gravedinis* | human coronavirus OC43 | ATCC VR-759 | AY585228 | Complete genome | HCoV_OC43 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Embecovirus* | *Betacoronavirus hongkongense* | human coronavirus HKU1 | HKU1 | AY597011 | Complete genome | HCoV_HKU1 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Embecovirus* | *Betacoronavirus muris* | murine hepatitis virus | A59 | AY700211 | Complete genome | MHV |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Embecovirus* | *Betacoronavirus myodae* | Myodes rufocanus vole coronavirus 2/JL2014 | | KY370046 | Complete genome | MrufCoV_2JL14 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Embecovirus* | *Betacoronavirus ratti* | betacoronavirus HKU24 | HKU24-R05005I | KM349742 | Complete genome | ChRCoV_HKU24 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Hibecovirus* | *Betacoronavirus hipposideri* | bat Hp-betacoronavirus/ Zhejiang2013 | Zhejiang2013 | KF636752 | Complete genome | Bat_Hp-BetaCoV |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Merbecovirus* | *Betacoronavirus cameli* | Middle East respiratory syndrome-related coronavirus | HCoV-EMC | JX869059 | Complete genome | MERS-CoV |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Merbecovirus* | *Betacoronavirus erinacei* | hedgehog coronavirus 1 | 2012-174/ GER/2012 | KC545383 | Complete genome | EriCoV |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Merbecovirus* | *Betacoronavirus pipistrelli* | Pipistrellus bat coronavirus HKU5 | LMH03f | EF065509 | Complete genome | Pi-BatCoV_HKU5 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Merbecovirus* | *Betacoronavirus tylonycteridis* | Tylonycteris bat coronavirus HKU4 | B04f | EF065505 | Complete genome | Ty-BatCoV-HKU4 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Nobecovirus* | *Betacoronavirus cororeum* | Rousettus bat coronavirus | GCCDC1 356 | KU762338 | Complete genome | Ro-BatCoV_GCCDC1 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Nobecovirus* | *Betacoronavirus eidoli* | Eidolon helvum bat coronavirus CMR704-P12 | | MG693168 | Complete genome | Ei-BatCoV_C704 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Nobecovirus* | *Betacoronavirus rousetti* | Rousettus bat coronavirus HKU9 | BF_005I | EF065513 | Complete genome | Ro-BatCoV_HKU9 |
| ★ | *Orthocoronavirinae* | *Betacoronavirus* | *Sarbecovirus* | *Betacoronavirus pandemicum* | severe acute respiratory syndrome coronavirus | Tor2 | AY274119 | Complete genome | SARS-CoV |
| | *Orthocoronavirinae* | *Betacoronavirus* | *Sarbecovirus* | *Betacoronavirus pandemicum* | SARS coronavirus | PC4-227 | AY613950 | Complete genome | SARS-CoV |
| | *Orthocoronavirinae* | *Betacoronavirus* | *Sarbecovirus* | *Betacoronavirus pandemicum* | severe acute respiratory syndrome coronavirus 2 | Wuhan-Hu-1 | MN908947 | Complete genome | SARS-CoV-2 |
| | *Orthocoronavirinae* | *Betacoronavirus* | *Sarbecovirus* | *Betacoronavirus pandemicum* | severe acute respiratory syndrome-related coronavirus | BtKY72 | KY352407 | Complete genome | SARSr-CoV |

# WHAT DISTINGUISHES ONE TAXON FROM ANOTHER: DEMARCATION CRITERIA

What are the distinguishing characteristics between two viruses that support their separation into distinct species, genera, families, orders...

# TAXON DEMARCATION CRITERIA

Demarcation Criteria (DC) define the specific properties and methods that are used to determine if a virus belongs to an existing taxon or will require the creation of a new taxon (or taxonomic hierarchy) for its classification.

- DC are currently available in ICTV Report chapters, taxonomy proposals, and the published literature.
- DC are defined for every virus rank from realm to species.
- Individual ICTV Study Groups are responsible for defining and updating the DC for each virus family.

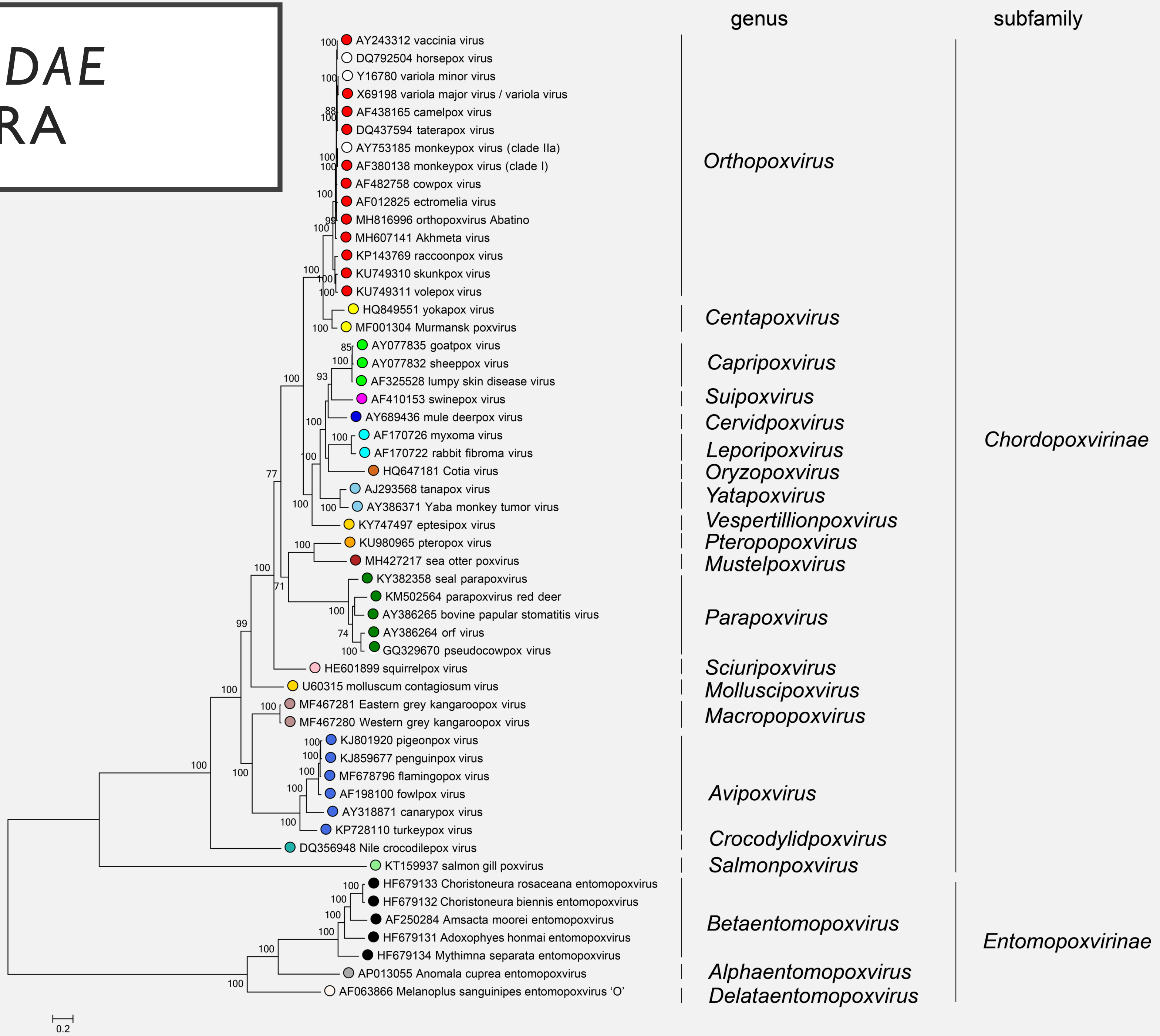
# DEMARCATION CRITERIA

- Realm: *Varidnaviria*
  - Vertical jelly-roll major capsid protein
- Kingdom: *Bamfordvirae*
  - Double jelly-roll major capsid protein
- Phylum: *Nucleocytoviricota*
  - Nucleocytoplasmic large DNA viruses
- Class: *Pokkesviricetes*
  - Middle English for "pox"
- Order: *Chitovirales*
  - Reference to poxvirus virion morphology (Greek)

# DEMARCATION CRITERIA *POXVIRIDAE:* SUBFAMILY:GENERA:SPECIES

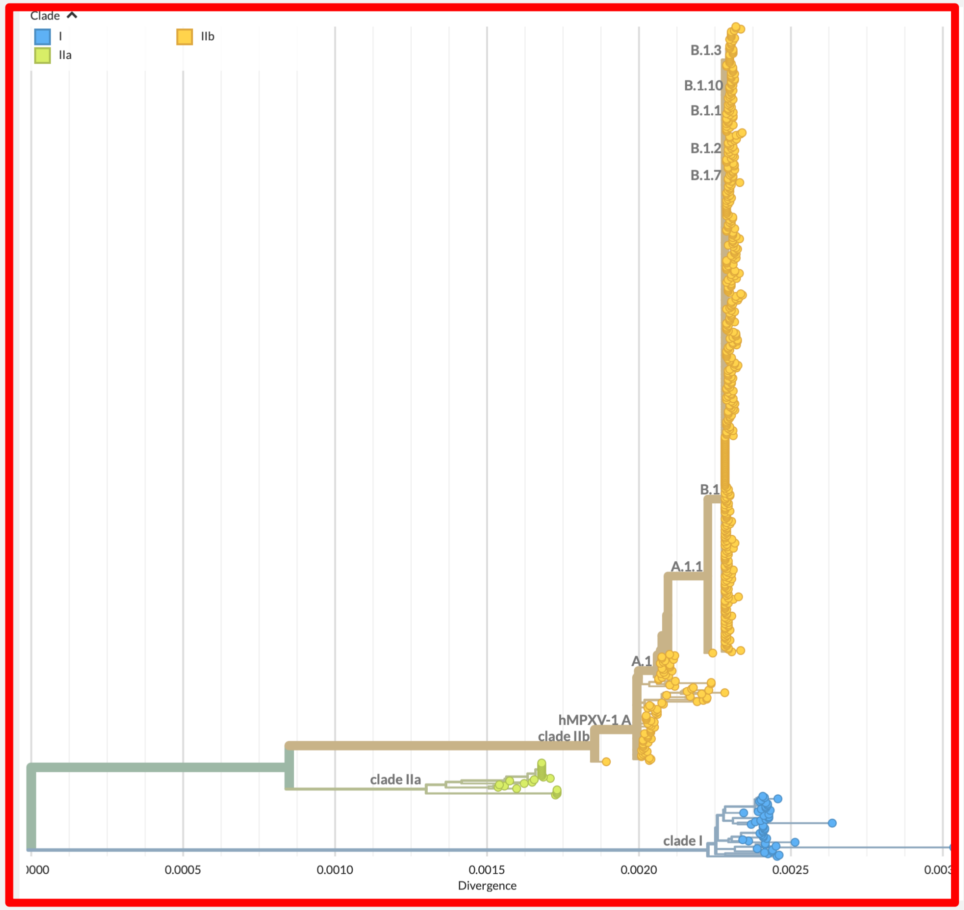
- Phenotypic
  - Natural host range (Subfamily)
  - Growth characteristics and host range in cell culture
    - Morphology of pocks; Plaque characteristics
  - Disease characteristics.
    - Morbidity, mortality, etc.
  - Serological criteria
    - Plaque neutralization tests, cross-protection in animals
- Genotypic
  - Gene content
  - Genome organization
  - Amino acid sequence identity of commonly shared genes.
    - hemagglutinin or A-type inclusion protein
  - Nucleotide sequence identity, conserved, core region of orthopoxvirus genomes
      - Different species <96% - 98%
      - Isolate >98%
  - Phylogenetic analysis

# *POXVIRIDAE*
# GENERA



# *ORTHOPOXVIRUS* SPECIES + CLADES

## Clade Designations: WHO Committee

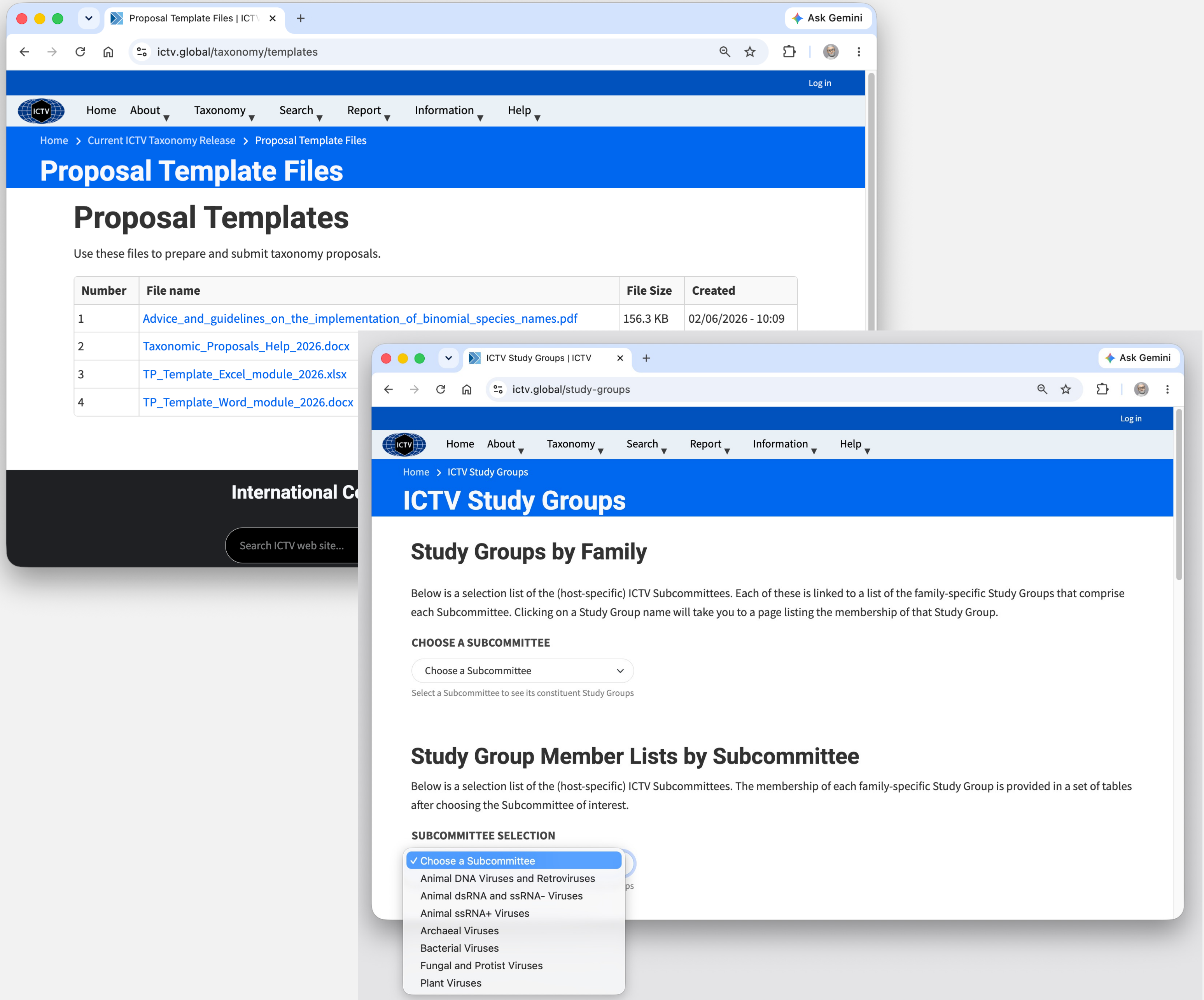


nextstrain.org

# HOW TO CREATE A TAXONOMY PROPOSAL

# TAXONOMY PROPOSALS

- New Taxonomy
  - Isolate a virus
  - Apply demarcation criteria
  - Prepare proposal and submit
  - Subcommittee/Study Group review
  - Executive Committee (EC) review
  - Ratification
  - Publication



## Proposal Template Files

### Proposal Templates

Use these files to prepare and submit taxonomy proposals.

| Number | File name | File Size | Created |
|---|---|---|---|
| 1 | Advice_and_guidelines_on_the_implementation_of_binomial_species_names.pdf | 156.3 KB | 02/06/2026 - 10:09 |
| 2 | Taxonomic_Proposals_Help_2026.docx | | |
| 3 | TP_Template_Excel_module_2026.xlsx | | |
| 4 | TP_Template_Word_module_2026.docx | | |

## ICTV Study Groups

### Study Groups by Family

Below is a selection list of the (host-specific) ICTV Subcommittees. Each of these is linked to a list of the family-specific Study Groups that comprise each Subcommittee. Clicking on a Study Group name will take you to a page listing the membership of that Study Group.

CHOOSE A SUBCOMMITTEE

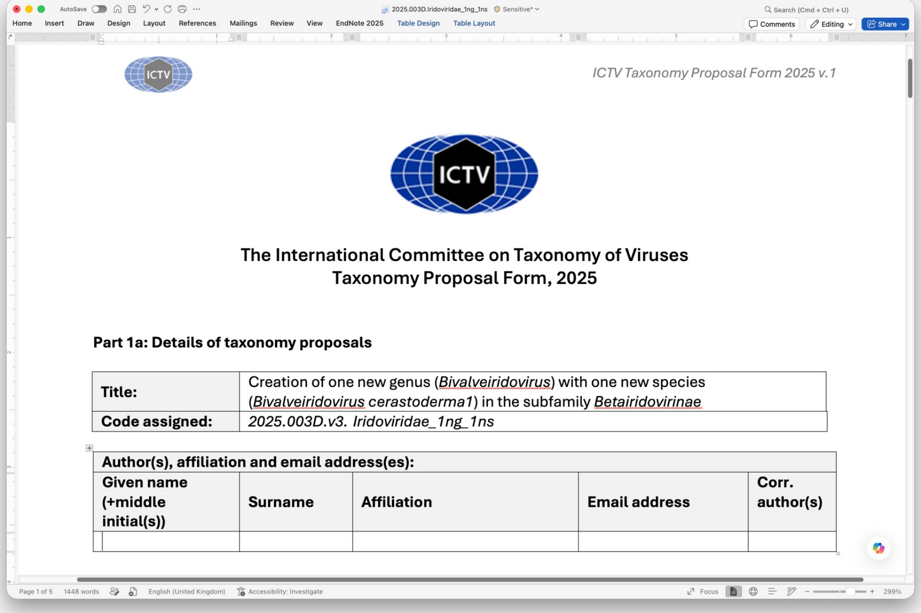
Select a Subcommittee to see its constituent Study Groups

### Study Group Member Lists by Subcommittee

Below is a selection list of the (host-specific) ICTV Subcommittees. The membership of each family-specific Study Group is provided in a set of tables after choosing the Subcommittee of interest.

SUBCOMMITTEE SELECTION

# TAXONOMY PROPOSAL



ICTV Taxonomy Proposal Form 2025 v.1

The International Committee on Taxonomy of Viruses
Taxonomy Proposal Form, 2025

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

| | |
|---|---|
| **Title:** | Creation of one new genus (*Bivalveiridovirus*) with one new species (*Bivalveiridovirus cerastoderma1*) in the subfamily *Betairidovirinae* |
| **Code assigned:** | *2025.003D.v3. Iridoviridae_1ng_1ns* |

**Author(s), affiliation and email address(es):**

| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
|---|---|---|---|---|
| | | | | |

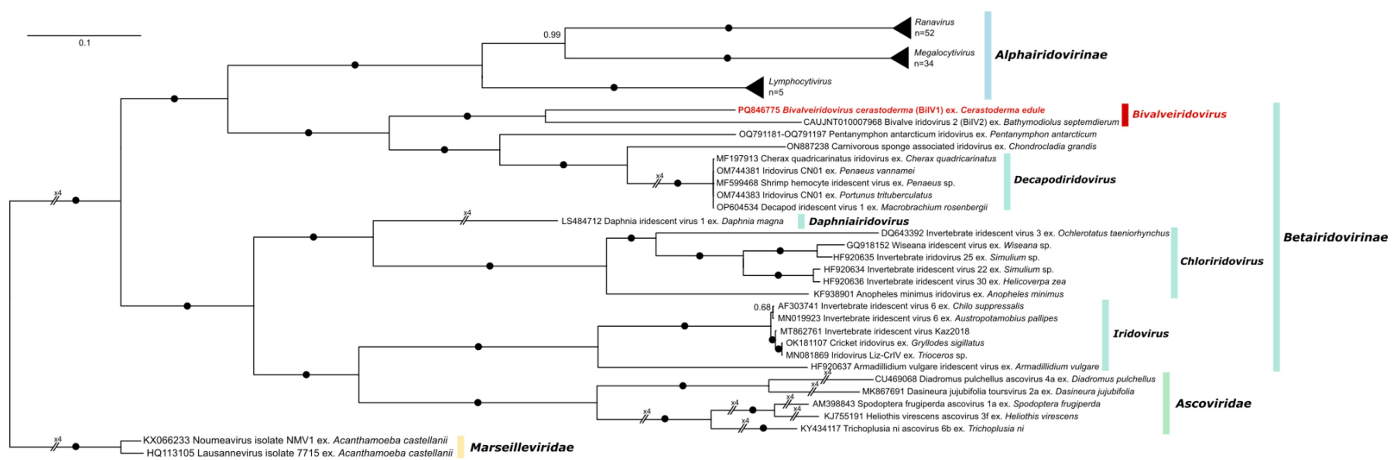
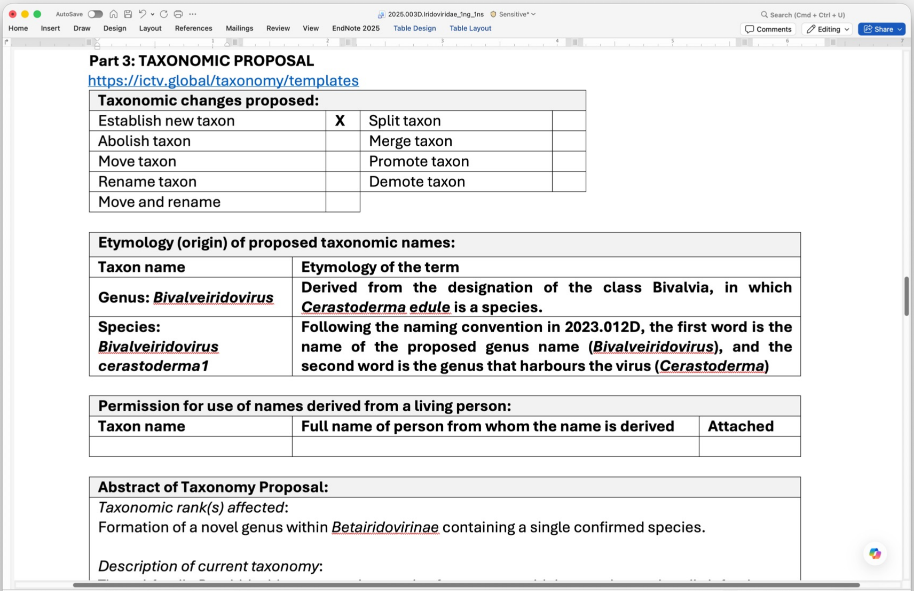


Figure 2. Bayesian consensus tree constructed from a concatenated multiple amino acid alignment of major capsid protein, DNA-directed RNA polymerase II subunit Rpb2, putative A32-like packaging ATPase, putative CTD phosphatase-like protein, putative helicase protein, and putative transcription elongation factor S-II-like protein from BilV1, 113 other *Iridoviridae*, five *Ascoviridae* and two *Marseilleviridae*. The tree is rooted to the *Marseilleviridae* clade. Branch labels denote posterior probabilities, with black circles used when posterior probability = 1.



**Part 3: TAXONOMIC PROPOSAL**

https://ictv.global/taxonomy/templates

| **Taxonomic changes proposed:** | | | |
|---|---|---|---|
| Establish new taxon | X | Split taxon | |
| Abolish taxon | | Merge taxon | |
| Move taxon | | Promote taxon | |
| Rename taxon | | Demote taxon | |
| Move and rename | | | |

**Etymology (origin) of proposed taxonomic names:**

| **Taxon name** | **Etymology of the term** |
|---|---|
| **Genus: *Bivalveiridovirus*** | **Derived from the designation of the class Bivalvia, in which *Cerastoderma edule* is a species.** |
| **Species: *Bivalveiridovirus cerastoderma1*** | **Following the naming convention in 2023.012D, the first word is the name of the proposed genus name (*Bivalveiridovirus*), and the second word is the genus that harbours the virus (*Cerastoderma*)** |

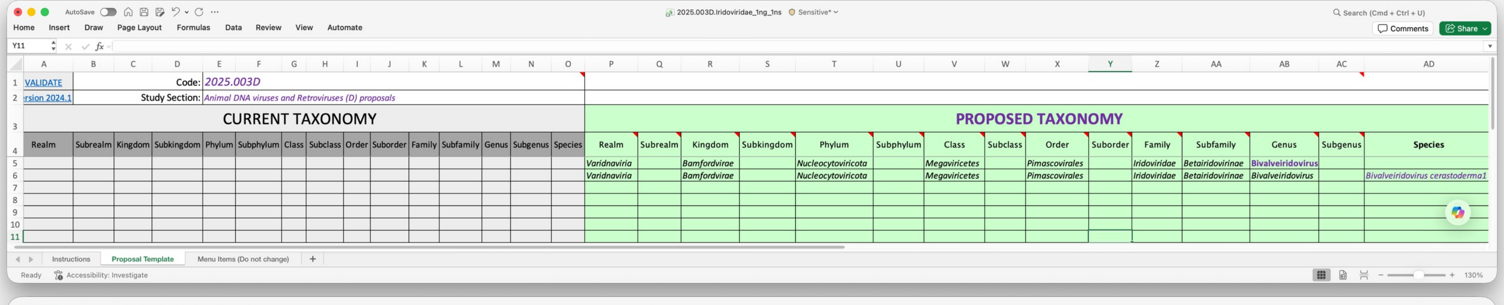
**Permission for use of names derived from a living person:**

| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
|---|---|---|
| | | |

**Abstract of Taxonomy Proposal:**

*Taxonomic rank(s) affected*:
Formation of a novel genus within *Betairidovirinae* containing a single confirmed species.

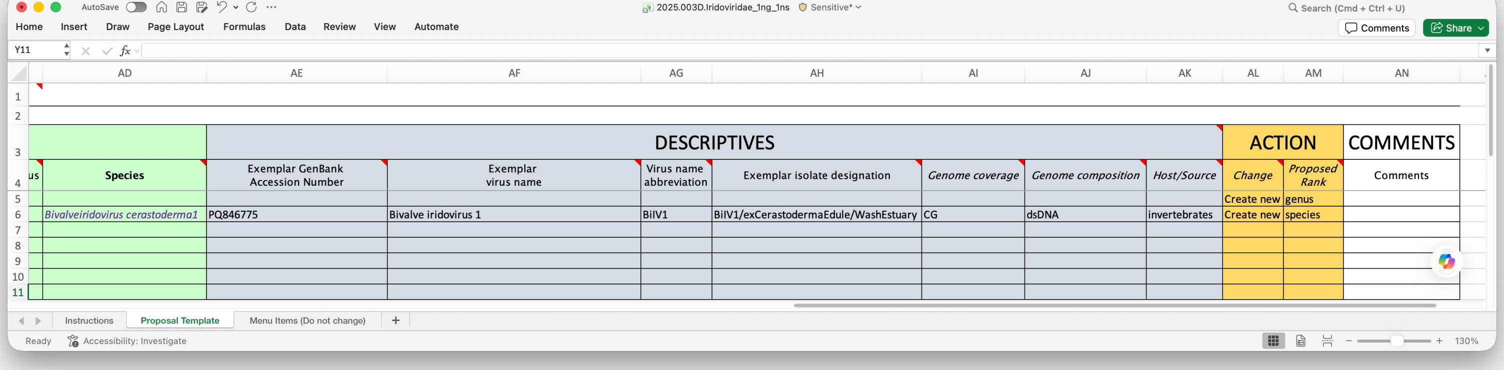
*Description of current taxonomy*:



VALIDATE
rsion 2024.1

Code: *2025.003D*
Study Section: *Animal DNA viruses and Retroviruses (D) proposals*

| | CURRENT TAXONOMY | | | | | | | | | | | | | | PROPOSED TAXONOMY | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 4 | Realm | Subrealm | Kingdom | Subkingdom | Phylum | Subphylum | Class | Subclass | Order | Suborder | Family | Subfamily | Genus | Subgenus | Species | Realm | Subrealm | Kingdom | Subkingdom | Phylum | Subphylum | Class | Subclass | Order | Suborder | Family | Subfamily | Genus | Subgenus | Species |
| 5 | | | | | | | | | | | | | | | | *Varidnaviria* | | *Bamfordvirae* | | *Nucleocytoviricota* | | *Megaviricetes* | | *Pimascovirales* | | *Iridoviridae* | *Betairidovirinae* | ***Bivalveiridovirus*** | | |
| 6 | | | | | | | | | | | | | | | | *Varidnaviria* | | *Bamfordvirae* | | *Nucleocytoviricota* | | *Megaviricetes* | | *Pimascovirales* | | *Iridoviridae* | *Betairidovirinae* | *Bivalveiridovirus* | | *Bivalveiridovirus cerastoderma1* |



| | | DESCRIPTIVES | | | | | | | ACTION | | COMMENTS |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 4 | Species | Exemplar GenBank Accession Number | Exemplar virus name | Virus name abbreviation | Exemplar isolate designation | *Genome coverage* | *Genome composition* | *Host/Source* | *Change* | *Proposed Rank* | Comments |
| 5 | | | | | | | | | Create new | genus | |
| 6 | *Bivalveiridovirus cerastoderma1* | PQ846775 | Bivalve iridovirus 1 | BiIV1 | BiIV1/exCerastodermaEdule/WashEstuary | CG | dsDNA | invertebrates | Create new | species | |

# VIRUS TAXONOMY AND THE ICTV LOOKING TOWARDS THE FUTURE

# CHALLENGES

- Newly emerging viruses
  - How fast can we classify?
- Analysis and management of extremely large datasets
  - The human virome and its impact on the microbiome and disease
  - 100 Million new species?!
- Dealing with "disobedient" mechanisms of variation
  - Recombination; segment exchange
- Satisfying the needs of all stakeholders
  - Virologists, Other Scientists, Health Care, Government, Policy Makers, Biodefense, Biotech, Pharmaceutical, Agricultural, Public

# PRINCIPLES TO GUIDE VIRUS TAXONOMY IN THE FUTURE

ICTV Workshop: Virus Classification in a Metagenomic Age
April 2022, Oxford UK
To be published 2/13/23 PLoS Biology

- Virus taxonomy should reflect the evolutionary history of viruses
- Virus properties may guide assignment of ranks to maximize their utility
- Taxonomy based on evolution is but one of many possible means to classify viruses
- Taxonomic assignments of viruses derived from metagenomic studies require strict sequence quality control

# AI-GUIDED TAXONOMY

- **Demarcation Criteria (DC) Ontology**: Organized database of DC extracted from ICTV text.
- **Large Language Models (LLMs)**: LLM trained on the taxon DC ontology to support virus classification and preparation of taxonomy proposals.
- **Model Context Protocol (MCP)**: Provide MCP server-based connections to ICTV data and tools.
- **TaxonAgents:** Automated taxonomic classification through a collection of AI Agents that will extract the appropriate DC and apply those criteria to classify newly isolated viruses.
- **TaxaChat:** A helpdesk based on the Retrieval-Augmented Generation (RAG) framework, providing guided use of the ICTV website, its data, and search/analytical tools.

# ICTV EXECUTIVE COMMITTEE 2026

- President: F. Murilo Zerbini
- Vice-President: Evelien Adriaenssens
- Business Secretary: Hanna Oksanen
- Proposals Secretary: Peter Simmonds
- Data Secretary: Elliot Lefkowitz
- Subcommittee Chairs:
  - Arvind Varsani
  - Holly Hughes
  - Jens Kuhn
  - Mart Krupovic
  - Dann Turner
  - Sejo Sabanadzovic
  - Luisa Rubino

- Elected members:
  - Poliane Alfenas-Zerbini
  - Frank Aylward
  - Juliana Freitas-Astúa
  - Małgorzata Łobocka,
  - Arcady Mushegian
  - Judit Pénzes
  - Alejandro Reyes
  - David Robertson
  - Simon Roux
  - Nobuhiro Suzuki
  - Koenraad Van Doorslaer

# THOSE WHO DO THE WORK

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- **Curtis Hendrickson**
- **Logan Mims**
- Liam Van Der Pol
- Travis Ptacek

- **Eden Black**
- **Steve Powell**
- **Don Dempsey**