

# Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 General Subcommittee

## Contents

[2025.002G.Ac.v2.Monodnaviria\\_reorg\\_4nr](#)

[2025.G003.N.v1.Creation of ICTV Bioinformatics Study Group](#)

## 2025.002G.Ac.v2.Monodnaviria\_reorg\_4nr

**Title:** Reorganization of the realm *Monodnaviria* by moving three of the four kingdoms to new realms and renaming the realm *Monodnaviria* to “*Floreoviria*”

**Authors:** Mart Krupovic, Arvind Varsani, Simon Roux, F. Murilo Zerbini, Jens H. Kuhn, Eugene V. Koonin

### Summary:

#### **Taxonomic rank(s) affected:**

Realm

#### **Description of current taxonomy:**

Realm *Monodnaviria* includes four kingdoms, *Loebvirae*, *Sangervirae*, *Shotokuvirae*, and *Trapavirae*, which comprise bacteria-infecting viruses that form filamentous virions, bacteria-infecting viruses that form small icosahedral capsid, eukaryote-infecting viruses that form icosahedral capsids, and archaea-infecting viruses that produce pleomorphic virions, respectively.

#### **Proposed taxonomic change(s):**

We propose moving three of the four monodnavirian kingdoms, namely, *Loebvirae*, *Sangervirae*, and *Trapavirae*, into three new realms and renaming the realm *Monodnaviria* to “*Floreoviria*”.

#### **Justification:**

Realm *Monodnaviria* was created to unify viruses with small single-stranded DNA (ssDNA) or double-stranded DNA (dsDNA) genomes that replicate using, in most cases, homologous rolling circle replication initiation endonucleases (Reps) of the HUH superfamily. However, recent comparative sequence and structural analyses showed that Reps encoded by viruses from these different kingdoms are not orthologous and, in some cases, not homologous (that is, some Reps do not belong to the HUH superfamily). Furthermore, the structural modules of these viruses are also unrelated. Thus, grouping of viruses from the four kingdoms within the same realm is unjustified.

*Submitted:* 07/02/2025; *Revised:* 25/08/2025

**TABLE 1** - *Monodnaviria*, 3 new taxa\*

Operation	Rank	New taxon name
New taxon	Realm	<i>Efunaviria</i>
New taxon	Realm	<i>Volvereviria</i>
New taxon	Realm	<i>Pleomoviria</i>

**TABLE 2** - *Monodnaviria*, 3 move taxa\*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Kingdom	<i>Loebvirae</i>	<i>Efunaviria</i>	<i>Monodnaviria</i>
Move taxon	Kingdom	<i>Sangervirae</i>	<i>Volvereviria</i>	<i>Monodnaviria</i>
Move taxon	Kingdom	<i>Trapavirae</i>	<i>Pleomoviria</i>	<i>Monodnaviria</i>

**TABLE 3 - *Monodnaviria*, 1 rename taxon\***

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Realm	<i>Floreoviria</i>	<i>Monodnaviria</i>

### **2025.G003.N.v1.Creation\_of ICTV\_Bioinformatics\_Study\_Group**

**Title:** Creation of ICTV Virus Bioinformatics Study Group and its remit

**Authors:** Alejandro Reyes, Evelien Adriaenssens, Elliot Lefkowitz, Simon Roux

**Summary:**

***Brief description of current situation:***

The Virus Bioinformatics Expert Group was an unofficial group within the ICTV that discussed bioinformatics problems and was working towards streamlining and automating taxonomic processes. There never was an official remit or position within the ICTV.

***Proposed changes:***

We propose a new name and remit for the Virus Bioinformatics Study Group. This group will be placed as a Study Group with affiliation to all subcommittees and will consist of subcommittee chairs and invited virus bioinformatics experts.

***Justification:***

Having a Virus Bioinformatics Study Group will facilitate taxonomic endeavors and coordination across Study Groups, in support of the long-term goal of automated and scalable virus taxonomic processes.

*Submitted: —; Revised: —*