PLANT VIRUS TAXONOMY: THE NEW BINOMIAL NOMENCLATURE FOR VIRUS SPECIES

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The principles of modern taxonomy were established in the 18th century by Carl Linnaeus, aiming at the hierarchical classification of biological organisms based of their different characters, by grouping organisms sharing similar features in taxa. These principles apply also to virus taxonomy. Recognized international organizations are in charge of the classification and nomenclature of taxa. The International Committee on Taxonomy of Viruses (ICTV), formerly the International Committee on Nomenclature of Viruses, founded in 1966, is responsible for developing and maintaining an internationally agreed system of hierarchical classification of viruses and naming of taxa. The ICTV oversees also the classification of other mobile genetic elements including satellite nucleic acids, viriforms and viroids.

The advancements in virus taxonomy are made available to the scientific community through a website (https://ictv.global/). Reports and papers are published to inform virologists about the decisions reached on virus classification and nomenclature and to engage the community in the ICTV activities. The core of the ICTV is represented by the Study Groups (https://ictv.global/sc), comprising experts in specific taxa, who take care of taxonomic proposals (TaxoProps) of new species. However, anyone can submit a proposal for consideration, without being part of the ICTV. Contrary to what could be commonly perceived, taxonomy is a very dynamic discipline since classification may change as far as new data are obtained.

Over time the ICTV has adapted its taxonomic framework to the current knowledge on the evolution of virosphere. In particular, the ICTV now allows the classification of viruses known only from genome sequences obtained by metagenomic analyses. Taxonomic ranks have been expanded beyond orders up to realms, to include eight primary ranks (realm, kingdom, phylum, class, order, family, genus and species) and seven secondary ranks (subrealm, subkingdom, subphylum, subclass, suborder, subfamily and subgenus), paving the way to comprehensive studies on evolutionary connections of viruses. Thus, taxa in the 15-rank taxonomy must be monophyletic.

An example is the realm *Riboviria*, the first established realm comprising all currently classified RNA viruses. The only mandatory taxa are genus and species, meaning that unassigned species in a family will be abolished unless they are assigned to a genus.

At present, virus taxonomy consists of 6 realms, 10 kingdoms, 17 phyla, 2 subphyla, 39 classes, 65 orders, 8 suborders, 233 families, 168 subfamilies, 2606 genera, 84 subgenera, 10434 species (https://ictv.global/taxonomy).

The expansion of taxonomic ranks brings virus taxonomy closer to other biological taxonomies. Species naming in all these taxonomies follow a Latinized binomial format (i.e., binomial nomenclature) first introduced by Carl Linnaeus in 1753, consisting of two italicized words

indicating the genus ("genus name") and the species ("specific name/species epithet"), respectively. Typical examples of binomial species names are *Arabidopsis thaliana*, *Saccharomyces cerevisiae*, *Homo sapiens*, and *Escherichia coli*. The adoption of the binomial nomenclature allow to clearly distinguish the species (*e.g.* *Homo sapiens, Saccharomyces cerevisiae*) from physical entities (a human, yeast).

In contrast, viral species names did not follow a uniform format, except for the requirement to be italicized and to have the first letter of the first word capitalized. The distinction between the virus species and the virus name based mainly on the font style has been for years cause of confusion between two substantially different concepts. In fact, "virus species" is a taxonomic category, whereas "virus" is referred to the physical entity, which is able to infect a host, or can be studied in laboratories. Taking cucumber mosaic virus as an example, the correct wording would have been: "The species *Cucumber mosaic virus* is a member of the genus *Cucumovirus* in the family *Bromoviridae*", but "Plants infected by cucumber mosaic virus (CMV) show symptoms". The difficulty in discriminating between virus and virus species is testified by the numerous mistakes contained in published scientific papers.

The ICTV recognized the need for a standardized nomenclature for virus species a long time ago and, after years of internal debates, in 2020 launched a call for public discussion and feedback on adopting a uniform binomial nomenclature. Following this, a binomial nomenclature for virus species was ratified by the ICTV in the 2021 vote. Thus, a virus species name will consist of two (and only two) italicized words, the first one being the genus name and the second one consisting of a "freeform" species epithet. In this framework, Linnaean-style, Latinized virus species are permitted, but not mandated. The species names can be composed using the standard Latin-script English alphabet containing 26 letters and/or Arabic numbers. Starting 2021, newly created virus species names adopted a binomial format.

The process of renaming all current species is underway and must be completed by the end of June 2023, to be ratified early in 2024. Very importantly, this process involves virus species names only. The common virus name will remain unchanged, and will be the same which has been always used. Plant virologists showed much concern about the adoption of binomials to name virus species. Indeed, plant viruses usually have nicely descriptive names, which are familiar to most of the plant virology community.

Once established that virus names will not be affected by the conversion of virus species names into binomials, an effort to reach a consensus among the plant virus Study Groups to find a shared binomial format is ongoing. For the time being, most of the Study Groups in the Plant Viruses Subcommittee adopted a Latinized, Linnaean-style binomial format. The species epithet recalls mainly the host, the geographic origin, or symptoms, and there is space for creativity (Table 1). It must be noted that "Latinized" does not mean "Latin", so there is no need to study this language to develop Latinized binomials. In any case, for those interested, a guide for creating Latinized binomial virus species names is available

(https://www.microbiologyresearch.org/content/journal/jgv/10.1099/jgv.0.001800).

A different approach was embraced by several Study Groups, who preferred to use the virus name abbreviation as epithet, either native or in lowercase letters, as in the case of *Foveavirus ChVB* for

cherry virus B (genus *Foveavirus*) and *Tepovirus ChVT* for cherry virus T (genus *Tepovirus*), or *Sobemovirus smamv* for snake melon asteroid mosaic virus (genus *Sobemovirus*). The advantage of Latinization stands in its stability, being derived from a historic language and represented in the same form in every language, while virus names can vary depending on the language. For instance, maize mosaic virus (English), vírus del mosaico de la maíz (Spanish), فيروس موزاييك الذرة (Arabic), 玉米花叶病毒 (Chinese) all belong to the species *Alphanucleorhabdovirus maydis*. However, the approval of a freeform epithet allows the Study Groups to make their own choice, so the debate among plant virologists is still open.

All the virus species currently approved by the ICTV are reported in two publicly available spreadsheets, the Master Species List (MSL) (https://ictv.global/msl) and the Virus Metadata Resource (VMR) (https://ictv.global/vmr). The VMR is particularly useful, since it reports both virus species and virus names, as well as the exemplar isolates and GenBank entries, making it easy to identify virus taxonomy.

Figure

The hierarchical virus taxonomy classification (reproduced from
https://ictv.global/taxonomy/about)
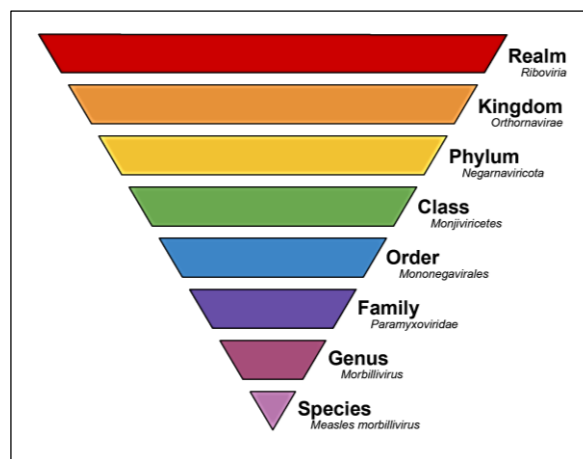
Table 1. Examples of binomial format adopted within the ICTV Plant Viruses Subcommittee

Virus name	Former virus species	Genus	Binomial format
citrus psorosis virus	*Citrus psorosis virus*	*Ophiovirus*	*Ophiovirus citri* (from the host genus *Citrus*)
grapevine Algerian latent virus	*Grapevine Algerian latent virus*	*Tombusvirus*	*Tombusvirus algeriaense* (from Algeria)
groundnut bud necrosis virus	*Groundnut bud necrosis virus*	*Orthotospovirus*	*Orthotospovirus arachinecrosis* (a combination of the host genus, *Arachis*, and the symptom *necrosis*)
strawberry latent ringspot virus	*Strawberry latent ringspot virus*	*Stralarivirus*	*Stralarivirus SLRSV* (from the abbreviation SLRSV)