

Part 1: TITLE, AUTHORS, APPROVALS, etc

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Part 2: NON-TAXONOMIC PROPOSAL

Text of proposal

Most taxonomic systems invoke the principle of "nomenclatural types". For each named taxon there is a designated **nomenclatural type**. For example, a **type species** is the species in a genus whose members have the characters that define the genus. In other words, the type species includes the type specimens that serve to anchor or centralize the defining features of a particular genus.

Strictly speaking, the nomenclatural type should be permanently associated with the taxon name. For example, the genus *Bromovirus* has the type species *Brome mosaic virus*. If the genus needs to be split, the new genus that contains the species *Brome mosaic virus* would have to be named *Bromovirus* and a different name would be needed for the other new genus.

The type species is not necessarily the most typical or representative element of the taxon.

Currently Rule 3.25 of the ICTV Code states that:

Approval of a new genus must be accompanied by the approval of a type species

We propose that this rule is abolished for the following reasons.

1. The requirement for type species in virus taxonomy is historical. It was based upon the requirement in other codes when the inclusion of members in a species was generally based on (overt) phenotypic characters. It also led to a rule that was abolished in 2011, namely extinct Rule 2.4, which stated

The application of names of taxa is determined, explicitly or implicitly, by means of nomenclatural types.

In principle, this rule would have required that all taxa required a nomenclatural type. For example, each family would have a type genus and each order would have a type family. To our knowledge, this rule was never enforced, either explicitly (i.e. by designating nomeclatural types), or implicitly (i.e. by using an identical or related stem for the taxon name and its [putative] nomenclatural type). Indeed, when this was actually done (e.g. family *Flaviviridae* and genus *Flavivirus*), we believe that it led to considerable confusion.

- 2. The concept of nomenclatural types goes hand in hand with the deposition of physical specimens. Nowadays, even in the zoological and botanical communities, the deposition of a DNA sample or DNA sequences is considered as a sufficient specimen (note, however that this is not the case for prokaryotic cells¹). In the case of viruses, we have never required the deposition of a specimen (i.e. virus isolate) to create a new species, although we do require that an exemplar genome sequence has to be deposited (usually at GenBank). With the recognition of species that are defined by sequence data alone, particularly in metagenomic samples, this will be the only possible form of deposition going forwards.
- 3. There is a common misconception that members of the type species are typical of all members of the genus, or even higher ranks. As phylogeny becomes more important in the demarcation of species, this misconception becomes more apparent. In fact, part of the ICTV virus species definition "A species is a monophyletic group of viruses whose properties can be distinguished from those of

other species by multiple criteria" also fits uneasily with the idea that there is a type species that is "typical" of the genus. Rather, the feature that "defines" the genus is the relationship between the sequences of genus members, and not the sequence of any particular member.
If the type species no longer serves a clear and useful purpose, we think it should be abolished. We propose to remove the requirement for the designation of a type species when creating a new genus (i.e. abolish Rule 3.25), and to revoke the designation of type species that currently exist. Rules 3.26 to 3.31 should also be renumbered as Rules 3.25 to 3.30, respectively.

Part	3:	TAXO	DNOMIC	PROP	OSAL
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Name of accompanying Excel module					
Abstract					
Text of proposal					

Supporting evidence

References

Murray AE, Freudenstein J, Gribaldo S et al. Roadmap for naming uncultivated Archaea and Bacteria. Nat Microbiol (2020).

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