



Discussions > Taxonomic Opinions

Binomial Species Names



Offline [admin](#) 138.26.21.102 [over 2 years ago](#)

A place for discussion of the potential adoption of a binomial nomenclature system for virus species names.



Offline [admin](#) 138.26.21.102 [over 2 years ago](#)

The article, "Binomial nomenclature for virus species: a consultation" has now been published in Archives of Virology:

<http://link.springer.com/article/10.1007/s00705-019-04477-6>

Comments and further discussion on the topics raised in the article can be discussed in this forum. To participate, please be sure you are signed to the web site using your ICTV user name and password. (Click on the little silhouette in the upper-right of this page). If you need to register for an ID, please navigate to <https://talk.ictvonline.org/login?ReturnUrl=%2Flogin>.

Files pertinent to this discussion can be found at <https://ictv.global/files/binomial>.

Offline [edrybicki](#) 197.86.144.209 [over 2 years ago](#) *in reply to* [admin](#)



Colleagues: as a sometime Study Group Chair (two different groups of plant viruses; Bromoviridae and Geminiviridae) and longtime member of and contributor to the ICTV, I am frankly aghast that we are revisiting territory that we left behind more than fifty years ago. It was recognised then that viruses are not like cell-based organisms, and that we had a chance to get away from the straitjacket of Latin binomials imposed on us several hundred years ago. And now - we are to return to binomials, and to Latin, yet??

No! Please, no!

The problems with virus taxonomy and nomenclature, such as they are, are largely the making of folk who ignore established and customary rules, and establish names like "Marseillevirus": what is this? The name gives absolutely no idea; neither does "mimivirus", which I still think was named after someone's dog.

Bean golden mosaic begomovirus, on the other hand, very aptly describes the type member of the genus Begomovirus, as does Panicum streak mastrevirus - both geminiviruses (family Geminiviridae) in good standing. Plant virologists seem to have been the most law-abiding of ICTV members, and it was from their ranks that the idea of using generic names as identifiers first came from, as in the usage shown above.

Now what could possibly be wrong with yellow fever flavivirus, or its relative hepatitis C hepacivirus? Very descriptive of exactly which virus you mean, rather than calling them flavivirus YF35 or hepacivirus H1, or some such gobbledegook.

I realise that virology has a problem with the enormous number of sequences that appear to be whole virus genomes, that no-one knows what to do with. The answer is that a sequence is NOT a virus, until it is shown to be one - at which point it can get a name, based on its phylogenetic relationships.

Jumbling up names that have been in common usage for many years is going to be resisted; having a taxonomic scheme that reverses the order by which virologists have known things, more so. Why bother?? What is so wrong with our present naming system, that we have to so drastically change it - and moreover, have species names that may be completely different to the common names of actual viruses?

I see no good reason to get in line with the rest of biology: viruses are, after all, the most numerous lifeforms on the planet; cramming them into an archaic straitjacket devised for organism with legs or leaves, and grudgingly extended to microbes, is simply retrograde.

So let's not do it.



Offline [Gary Foster](#) 137.222.114.246 [over 2 years ago in reply to edrybicki](#)

it is deja vu all over again..... it is like the flat earth society popping up their heads every now and again.



Offline [nicobejerman](#) 190.216.64.214 [over 2 years ago in reply to admin](#)

I strongly agree with Ed Rybicki comments. I think that the simple binomial nomenclature should be used instead of the suggested Linnean binomial nomenclature



Offline [kropinsk](#) 99.225.181.159 [over 2 years ago in reply to nicobejerman](#)

I will start by stating that I'm in favour of a binomial system. Please note that with bacterial viruses (bacteriophages, phages) unlike many/most(?) plant and animal viruses, the symptoms of infection are simply cell death, so the taxon *Escherichia kill virus 1* would be almost totally useless. Before you continue reading please consider what you would do if your plant or animal virus only killed cells i.e. didn't produce interesting symptoms like tobacco mosaic virus, cowpea chlorotic mottle virus, tomato bushy stunt virus, yellow fever virus, monkey pox virus, deformed wing virus etc. Now imagine that you don't even have a host. That is what we face with viromic data.

Under our current system for taxonomy of isolatable bacterial viruses we create taxa such as *Escherichia virus Tweedledum* (Host + virus + common name) in the genus *Tweedledumvirus*. This system worked very well when GenBank contained relatively few complete phage genomes. BUT today (December 16, 2019) there are 233 *Bacillus*, 299 *Salmonella*, 309 *Pseudomonas*, 453 *Escherichia*, and 1540 *Mycobacterium* phage complete genomes in NCBI. And, these belong to a wide spectrum of ICTV recognized taxa.

The consequence is that other than providing information on the host the current classification system does provide one with any other information. If we employed a binomial naming system employing "genus name + common name" e.g., *Tweedledumvirus tweedledee* I personally believe that this would considerably simplify things.

A couple of decades ago, when phage taxonomy was younger, one phage isolate was equivalent to one phage species. With the rise in numbers, and sequencing efforts from multiple evolution experiments, we have come to a point where one phage species can be representative for any number of isolates. A binomial system would be better placed to make the distinction between the taxon (the abstract box we are putting the isolates in) and the phages themselves. For example, today *Escherichia* phage T1 belongs to the species *Escherichia virus T1*. Wouldn't it be more informative to know that *Escherichia* phage T1 belongs to the species *Tunavirus T1*?

Please note that speaking as a prokaryotic virologist with some 70 years

publishing experience on phages I believe that I have never mentioned a taxon such as *Escherichia virus T1*, where similarity exists I state that the new isolate is similar to *Escherichia* phage T1 or should be considered a new member of the *Tunavirus*.



Offline [Eric Delwart](#) 12.124.114.18 [over 2 years ago](#)

My preference would be to use #3 with a freeform name following the genus name. Using longer, more complex, species name such as *Panicum streak mastrevirus* was fine when only a "few" viral genomes were characterized (typically from cell-cultured isolates) and their cellular host and symptoms/disease signs were well known (and most often the reason they were studied). Now what we know of the biology of most viral genomes characterized using metagenomics is often extremely limited or non-existent (particularly for genomes from environmental rather than biological samples). The actual host and whether the virus is pathogenic is information often acquired later or for many viruses not at all. Indeed some information would be lost by changing name of species like *Panicum streak mastrevirus* to *Mastrevirus panicum* or *Mastrevirus streak* or *Mastrevirus panicumstreak* but the phylogenetic information that it belong to the *Mastrevirus* genus would remain and an epithet can carry a lot of information. Those who study this or other viruses whose name would change would likely rapidly find out what the new binomial name of their favorite virus is.

The objection that information held within current virus species name would be lost using a binomial name is correct only for the shrinking proportion of viral species whose current name include more biological information that can be contained in a binomial name with a freeform epithet. A freeform epithet would have the advantage that species like *Carnivore protoparvovirus 2* could become *Protoparvovirus carnivore2*. Species names like *Cardiovirus A* or *Enterovirus B* could stay the same. Another advantage of binomial classification is its simplicity for naming the torrent of "new" viral species currently being characterized. Assuming the genome can be classified into an existing genus the first name would be obvious and only an epithet needed to identify the species which could be any word even a made up word like tylcND1 which provide a lot of room for expected future expansion.

One issue would be for genomes that do not fall into an existing genus. In these cases a new genus name would have to be proposed followed by an epithet. Of course changing some well-established names could be disturbing, For example *Human immunodeficiency virus 1* could become *Lentivirus HIV1*. Likely the resistance will be strong.



Offline [edrybicki](#) 197.88.57.89 [over 2 years ago in reply to Eric Delwart](#)

You see, I don't mind that sort of thing - as in, reclassifying ALL lentiviruses so as to get away from the notion that human-infecting viruses are somehow special, because they are demonstrably NOT. It worked with papillomaviruses - although they adopted that

GODAWFUL Greek alphabet orthography - and lentiviruses are overdue some attention. It's the LATIN I object to: there is NO good reason for it, at all. And we should resist its use.



Offline [Gary Foster](#) 137.222.114.249 [over 2 years ago in reply to edrybicki](#)

I'm with ED



Offline [jkreuze](#) 179.6.212.225 [over 2 years ago in reply to Gary Foster](#)

So am I, no need to go completely renaming all things into some extinct language



Offline [Henri Agut](#) 86.238.27.7 [over 2 years ago](#)

Dear All,

I am glad that my proposal published in 2002 has gained a novel visibility and is now widely open to discussion under the auspices of ICTV [1, 2]. It is now recognized by colleagues that the official binomial name of virus species, albeit of limited use in papers or talks, will constitute a unique unambiguous reference in scientific exchanges whatever the vernacular (common) language used for these exchanges. This is simply the application of the principles used in all other domains of biology to the nomenclature of viruses. The robustness of the Latin binomial nomenclature proposed is based on the use of the genus name with a capital initial as the first term of the official name. I would like to make an additional comment concerning the species epithet following the first term of name. In my opinion, the epithet has to follow several rules : (i) to be unique for a given species (of course !) ; (ii) to be written in italics like the first term of the name ; (iii) to provide a valuable scientific information about the considered species (host tropism, circumstances of discovery, induced syndrome,...) ; iv) to avoid, as much as possible, conflicting interference with the common name of virus ; (v) to consist of, when possible, a single Latinized word written without any capital initial BUT, when necessary, to include more than one Latinized word and/or arabic numbers so as to respect the rules above. In short, we should be flexible and accept the free form of the epithet whenever specialists in this viral species deem it necessary.

As examples, herpes simplex viruses 1 and 2 (HSV-1, HSV-2), also named human herpesviruses 1 and 2 (HHV-1, HHV-2), might be officially designated as *Simplexvirus labialis* and *Simplexvirus genitalis* respectively in reference to the prototypic expression of their pathogenic role in humans. However, the names *Simplexvirus hominis 1* and *Simplexvirus hominis 2* might be preferred because the question of host related to co-speciation process is central for herpesviruses and the spectrum of diseases induced by these viruses far exceeds oral and genital herpes. Concerning the three species of human roseoloviruses identified so far, human herpesviruses 6A, 6B, and 7

(HHV-6A, HHV-6B, HHV-7), they might be named *Roseolovirus hominis 1, 2 and 3* respectively in accordance with the chronology of their discovery but the names *Roseolovirus hominis 6A, 6B, and 7* would require less adaptive efforts for exhausted searchers (including myself) who spent three decades in their study.

I am fully confident that the community of currently active virologists will find the expected consensus solutions for an official binomial Latin nomenclature without any civil war.

Best regards

Henri Agut

1. Agut H (2002). Back to Latin tradition: a proposal for an official nomenclature of virus species. Arch Virol 147:1465–1470
2. Siddell SG, Walker PJ, Lefkowitz EJ et al (2019). Binomial nomenclature for virus species: a consultation. Arch Virol [doi.org/.../s00705-019-04477-6](https://doi.org/10.1007/s00705-019-04477-6)



Offline [Gary Foster](#) 137.222.114.246 [over 2 years ago in reply to Henri Agut](#)

war is pretty much inevitable I'm afraid.



Offline [Gary Foster](#) 137.222.114.246 [over 2 years ago](#)

"Latin is the path to the dark side. Latin leads to anger. Anger leads to binomial. Binomial leads to suffering."

ICTV proposal for binomial Latin nomenclature for plant viruses . Don't, just DON'T

This has come around on a regular cycle during my 35 career, it soaks up a huge amount of our time and effort, but eventually it get kick away, until the next time.



Offline [Gary Foster](#) 137.222.114.246 [over 2 years ago](#)

can I just say that this has to be one of the stupidest ways to get the opinion of the virology community....there are 8, yes a lowly 8 subscribers on here



Offline [Elliot Lefkowitz](#) 138.26.21.102 [over 2 years ago in reply to Gary Foster](#)

But also note that there have been 1,991 views. Subscribing simply means that you get an email when a new post appears. You can view this page, or even post a new reply without being a subscriber.

Offline [Gary Foster](#) 137.222.114.249 [over 2 years ago in reply to Elliot Lefkowitz](#)



you cant post unless you subscribe



Offline [Elliot Lefkowitz](#) 138.26.21.102 *over 2 years ago in reply to [Gary Foster](#)*

All you need to do to post is register on the site and login. (New registrations are accepted immediately, and anyone can register.) You do not need to subscribe to post. Subscribing only enables email notification of new posts.



Offline [Gary Foster](#) 137.222.114.249 *over 2 years ago in reply to [Elliot Lefkowitz](#)*

ooooops that what I meant, you have to register



Offline [Gary Foster](#) 137.222.114.249 *over 2 years ago in reply to [Gary Foster](#)*

either way, this isn't the best way to engage with the community



Offline [Elliot Lefkowitz](#) 138.26.21.102 *over 2 years ago in reply to [Gary Foster](#)*

I am not sure there is a best way to engage the community. The best we can do is encourage communication in as many ways that makes sense and that provides an opportunity for feedback, and keeps a history of all posts. In that manner, members of the ICTV Executive Committee become aware of the ongoing discussions, can comment as desired, and most importantly, use the community's opinions in determining the final outcome.



Offline [Gary Foster](#) 137.222.114.249 *over 2 years ago in reply to [Elliot Lefkowitz](#)*

an email could be sent out by the major virus journals, with simple poll questions, results gathered and collated, it is what we did for this type of thing, see here <https://bsppjournals.onlinelibrary.wiley.com/doi/full/10.1111/j.1364-3703.2011.00752.x>



Offline [Elliot Lefkowitz](#) 138.26.21.102 *over 2 years ago in reply to [Gary Foster](#)*

Registration is something that we unfortunately have found necessary. Otherwise, you either receive an overwhelming number of spam posts, or you have to have all discussions moderated. Registration seems preferable to moderation.



Offline [Gary Foster](#) 137.222.114.249 *over 2 years ago in reply to [Gary Foster](#)*

The poll I've set up as to whether we should use Latin stand at

YES 27.9 %

No 72.1 %

262 votes, 4 days left for poll



Offline [Gary Foster](#) 137.222.114.249 *over 2 years ago in reply to [Elliot Lefkowitz](#)*
true



Offline [DigitalNeuroma](#) 71.228.199.138 *8 months ago in reply to [Elliot Lefkowitz](#)*
Nope, you need to be a subscriber to post.



[losterbaan](#) 132.236.192.57 *over 2 years ago*

I originally wrote the following as an email directly to the ICTV Executive Committee. Upon further reflection, I've decided to also publish it here publically.

To whom it may concern,

I would like to voice my opinion in favor of the "freeform text" option for virus species epithets, as outlined in Siddel et al. 2019 (Archives of Virology). My reasoning is outlined below.

I am a newly minted PhD and am just getting started in my career as a virologist. I recognize that I'll likely be on the younger end of the distribution of virologists that offer up an opinion on this topic.

While my older colleagues may have years of experience to add weight to their opinions, I have *stakes*.

Whatever the ICTV decides on this issue, I will have to *live* and *work* with the consequences for the remaining decades of my career. Thus I do not offer the above opinion lightly or frivolously.

My support for converting virus species names to Latinized binomials (regardless of the final form chosen for the species epithets) is largely practical. As Postler et al. 2017 (Syst Biol, 66(3):463-473) point out, the lack of standardized binomials for virus species makes it difficult, if not impossible, to incorporate virus taxonomy into many standardized bioinformatics tools. Some colleagues may argue that the reason NOT to use binomials is that, in the age of big data, there are simply too many virus species to uniquely name using binomials and that the current system gives the necessary flexibility needed to make virus species names unique and memorable. You know what computer programmers hate? Flexibility. You know who we need on our side in the age of big data? Computer programmers. Let's do ourselves a favor and try not to alienate and frustrate our bioinformatics allies by clinging to "the way things have always been."

My support for the "freeform text" option for virus species names epithets comes from a pragmatic understanding of the virological community. We're weird. I don't know about you, but I love trying to explain to non-virologist colleagues why viruses are so cool. They're not living, but they do so much! But they're not just chemicals! And they evolve. And they're tricky: they do so much with so little. And

they shred the "central dogma" of biology to pieces: RNA to DNA? No problem! Double stranded RNA genome? Single stranded RNA genome? Circular genomes, linear genomes: you've got it! And I think many of my virologist colleagues share that glee and joy in being just a bit "outside the box" of traditional biology.

You're going to get pushback on the binomial convention no matter what. People are really attached to their favorite viruses and their names. So why force them into the overly rigid and bloodless options of "Latinized epithets" or "alphanumeric characters in a logical series"? Why not let them have a little fun and retain that "weirdness" that sets virology apart from other biological sciences? **Let us be weird, but with rules.**



Offline [James K. Douch](#) 128.250.0.116 *over 2 years ago*

I find the advantages of latinised epithets to be most compelling. I think disadvantage 2 of alphanumeric epithets is prohibitive, unless someone can suggest a tenable solution.



Offline [Gary Foster](#) 137.222.114.243 *over 2 years ago*

Do you agree with a possible move to a binomial Latin names of plant viruses

Yes

25.2%

No

74.8%

365 votes



Offline [DianaGR](#) 181.10.25.2 *over 2 years ago*

In general terms, I believe that a binomial nomenclature for viruses and of the Latin or Latinized type is favorable, considering several aspects of those presented here. Leaving aside all the biological and technical considerations that exist until now, in the knowledge and study of these particular entities, such as viruses, I believe that a change towards the binomial form can lead mainly to benefits in various ways of considered in the proposal (beyond the own and logical difficulties of its gradual implementation). And I lean preferentially, towards the Latin or Latinized form, because I strongly agree (according to my work experience), on the importance of simplicity, representativeness and ease of reproduction the names of the virus species, when considering exchanges formal information, among Agencies involved, which are direct and necessary users, of the taxonomic definitions in question.

That is, as mentioned for example in the disadvantage n °3 of the "Free form text", with respect to which some epithets may be directly unpronounceable, I believe in my personal opinion, and according to my experience as an agent of an official phytosanitary organism and continuous user of nomenclatures and taxonomies, that this may eventually hinder its use and transcription, which may have no minor consequences in the field of bilateral exchanges between Agencies, negotiations and phytosanitary releases, as is our case, etc.

I also agree with those who consider the other advantages of the Latin / Latinized system, that such a system would be consistent with all other biological taxonomies and that biologists are accustomed to applying latinized binomials to taxa.

In addition to the fact that since Latin is a historical language (which does not require diacritics, etc.), it can still be considered universal, stable and translatable (and elementary affordable) by the entire international scientific community (considering all the disciplines involved).



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago

Some preliminary thoughts (other comments regarding specific questions in the following thread)

Taxonomy is about the organized designation of whatever we are talking about. For viruses, it does make sense to establish a proper manner to designate species names, relying on genera previously established by ICTV, but not necessarily on higher-rank groupings (families, orders etc.). This principle is indeed similar in essence to the use of binomials for other life forms. Before Carl von Linné, species were designated using vernacular names and, in the scientific community, using short diagnostic phrases: quite like viruses today, except that these phrases were not unified for a given species (this unification has been one of ICTV's achievements in the last decades). This system was almost satisfactory and although Linné did see a urge in listing all godly creatures, there was no consensus about a real need to change their designation. It is merely for the sake of convenience that Linné introduced the binomial nomenclature, first informally as "trivial" names in scientific conversations with his students. Only later did he actually introduced the binomial nomenclature as mere synonymies to more official diagnostic phrases in the first editions of his *Species plantarum* ([Linnaeus, 1753](#)), and finally as full entries in the last ones. The convenience began to spread and lasted until today.

By the way, it should be noticed that, in other life forms, there is no contradiction but a complementarity between the use of (Latinized) binomials and of vernacular names. For instance, everyone is OK with "Bird" being the English vernacular name for Aves (and e.g. "Oiseau" the French one, "Vogel" the German one, etc.) while within Aves, "Nightingale" is the English vernacular name for "*Luscinia megarhynchos*" (and e.g. "Rossignol" the French one, "Ruiseñor" the Spanish one, etc.). In the virological community, there is currently a plain confusion between vernacular and scientific names, even in English ([Van Regenmortel et al., 2010](#)): the *status quo* is not fully satisfactory.

Any attempt at designing a uniform manner to name virus species should cross existing Taxonomy, biological features, and a clear prospect for adoption in every community of virologists (phages, plant viruses, animal viruses, human viruses, etc.). Earlier attempts have failed, for a number of reasons related to one or more of these dimensions. Indeed, there has already been attempts to

introduce Latinized binomials but these did not necessarily rely on genera and species, or other sensible properties, and they were not adopted. See for instance the result of one of these early attempts, in the title of this article from the 1st half of the 20th century ([Best, 1940](#)): "Methods for the preparation of pure tobacco mosaic virus nucleoprotein (*Marmor tabaci* var. *vulgare*, Holmes)". *Marmor tabaci* (*Tobacco mosaic virus*) and *Marmor cucumis* (*Cucumber mosaic virus*) never belonged to the same genus –nor even to the same family– and in any case no such thing as a genus or a family of plant viruses was identified back then; therefore genus names like *Marmor* did not make any sense and were soon duly forgotten. More recently, two types of proposals for binomials were made: Latinized ones ([Agut, 2002](#)) or Anglicized ones ([Van Regenmortel et al., 2010](#)).

ICTV ([Siddell et al., 2019](#)) proposes three options for the current consultation. These options differ in the so-called "specific epithet", used to designate the species within the given genus, but all three rely on the already established list of virus genera. This this shared feature does make a lot of sense and I won't discuss it further.

--> **Except maybe to suggest that some distinctive "first name" should be given in the case of species not yet assigned to a genus, in a manner more or less inspired of how "Candidatus" is used to designate non-cultured procaryotes whatever their actual genus ([Murray and Stackebrandt, 1995](#)): why not "Unassignedvirus" or an even simpler "Virus"?**



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago in reply to [OlivierLG](#)

Option #1: Latinized binomials

Option #1 of [Siddell et al. \(2019\)](#) is similar to an early proposal with Latinized binomials made by [Agut \(2002\)](#).

Although it would rely on established genera, it has not been adopted so far, perhaps because it has not been considered very practical. Indeed it is not.

Indeed, while this proposal is apparently rational, establishing it would imply a huge piece of work by ICTV experts to design and propose 1000s of new names "out of the blue". I am afraid I was not convinced by the attempt made by [Postler et al. \(2016\)](#) to demonstrate the feasibility of such an endeavor, nor by its result on the bases of the use cases proposed (the family *Arenaviridae* and the order *Mononegavirales*).

If this however succeeds, the inevitably poor connection to already established species names would mean another thick layer of discussions in every community to reach a multitude of agreements regarding each of the Latinized epithets.

When saliva is exhausted and these agreements have finally become widely consensual (if they do), another even thicker layer of efforts can be expected for the entire

community to recall and use them. In this respect, quoting [Postler et al. \(2016\)](#), I can hardly consider it to be "*an additional advantage*" that "*Latinized species names will appear foreign to most readers*": I would definitely prefer a naming system that would instead appear familiar to everyone in order for it to be adopted! Just the way the binomial system was adopted some centuries ago for other life forms because it was actually simpler than the already established system of species designation. "No, please no!" is likely to be the only consensus the Latinized binomial nomenclature of viruses will ever reach.

To say it otherwise, more "ICTVwise", I cannot foresee any good adoption prospect for an option that is so bluntly opposed of the ICTV Code (Rule #3.8 "*Existing names of taxa shall be retained whenever feasible*" [1]), however smart the name proposals would actually be.

--> **Inevitably, this must rule out Option #1.**

[1] <https://talk.ictvonline.org/information/w/ictv-information/383/ictv-code>



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago in reply to [OlivierLG](#)

An unproposed option: Anglicized binomials

Although it is mentioned but not proposed by [Siddell et al. \(2019\)](#), the more recent proposal with Anglicized rather than Latinized binomials, made by [Van Regenmortel et al. \(2010\)](#), bears the clear advantage of a good alignment with the current Anglicized taxonomy of species established by ICTV. However it also has some drawbacks, and serious ones I believe.

In most cases it would simply not be practical, and/or not actually binomial. For instance, HIV1 would not easily become *Human immunodeficiency 1 Lentivirus* on a daily basis in the medical communities. Even if it would, it would not really be a binomial nomenclature would it? In the case of HIV1 it would actually be a trinomial-plus-one-figure name, while other species would be attributed quadrinomial names (e.g. *African horse sickness Orbivirus*), or even worse. Hum.

In addition –and in fact, just like the current system–, this proposal would lead to the elaboration of complicated expressions in non-English languages (yes, there is a virology literature in vernacular languages!). For instance, in French, the sentence "the plant is infected by CMV" would become "la plante est infectée par le virus de la mosaïque du concombre (*Cucumber mosaic Cucumovirus*)". This rather complicated combination of the vernacular and the Anglicized scientific names would inevitably become the doubly incorrect –yet currently

quite frequent– “la plante est infectée par le *Cucumber mosaic cucumovirus*”, where the vernacular name is erased/crashed by the Anglicized scientific name that is used, instead of as a proper noun, as a common name (see the presence of a definite article) however in italics. What a (cucumber) soup.

--> For these reasons at least, I would not favor such a proposal either.



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago in reply to [OlivierLG](#)

Option #2: alphabetical characters in a logical series

I do not think Option #2 of [Siddell et al. \(2019\)](#) is practical enough, despite its apparent extreme rationality. Namely, I do not see which kind of “logic” would be able to lead a “logical” series of alphanumeric characters. An alphabetical order for the already described species, then the chronological order of the discovery/description of a future virus species, most probably? But then, as the ICTV proposers list as the 2nd disadvantage, how could subsequent taxonomical reorganizations be made, when necessary, without disordering such series?

--> No: Option #2 has to be ruled out as well because it lacks flexibility. It is too rational, in a way.



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago in reply to [OlivierLG](#)

Option #3: freeform text

Having disliked the status quo and excluded Options #1 and #2 of [Siddell et al. \(2019\)](#) as well as the unproposed option of Anglicized not-really-binomials of [Van Regenmortel et al. \(2010\)](#), what else remains? Let us consider Option #3. Although I first thought it was a strange proposal, I may be able to imagine some forms of Option #3, “freeform text”, that could probably be workable.

There is currently an existing and already adopted alphanumeric string attached unequivocally to each virus species: its acronym (or if there is no acronym, one can probably be created from full the species name in an easy and non-controversial manner). Each community of virologists and/or stakeholders is familiar with the use of these acronyms, which are sometimes even more easily remembered than the full species names (scientific as well as vernacular ones). Therefore, using the current acronym as an epithet could be an easy, efficient and straightforward way to proceed: *Lentivirus HIV1*, *Cucumovirus CMV*, *Potyvirus LMV*, *Mammarenavirus Lassa*, etc. This would:

- * Require a relatively limited effort for ICTV to establish the list of epithets, because most often the acronyms are already in use;
- * Not trigger lengthy discussions about the choices of one epithet vs. another, because most often these choices have already been made;
- * Be as pronounceable as the current acronyms, the broad use of which is an indication that they are practicable (even if, I admit, usually not very elegant);
- * Be adopted quite rapidly by all communities, since they have actually already been adopted.

Furthermore, coming back to the above example in a vernacular language (e.g. French), I could even imagine how sentences like "La plante est infectée par le virus de la mosaïque du concombre (*Cucumovirus CMV*)" could promote the proper difference between the vernacular and the scientific names, and therefore improve the current practice of naming virus species in every language and every community, not only academic ones. Note that better distinguishing between the vernacular and the scientific names, while it is an issue probably more easily perceived by a non-native English speaker, would actually also benefit the English speaker ([Van Regenmortel et al., 2010](#)).

--> Option #3 might be workable.



Offline [OlivierLG](#) 87.89.0.50 over 2 years ago in reply to [OlivierLG](#)

To summarize

1. If a binomial system were to be finally proposed for adoption I would therefore suggest it to be in the form: italicized [*Genus + Acronym*] for already established species, and [*Genus + whatever but in most cases the acronym*] for species yet to be described.

2. For species not yet assigned to a genus, "*Unassignedvirus*" or more simply "*Virus*" could be used as the first term (italicized to distinguish it from the object "a virus").

It is of course uneasy to imagine how such a practice would turn out in a few years' time, when new virus species are created for bona-fide viruses as well as, perhaps, for OTUs (the biological significance of which is uncertain, and will probably remain so for some time), or for any other type of entities future virus taxonomists would like to name. It is however easy to imagine how such a "freeform" system would bear enough flexibility to accommodate all foreseen as

well as unforeseen evolutions of virus taxonomy.



Offline [Gary Foster](#) 137.222.114.243 [over 2 years ago in reply to OlivierLG](#)

ah, some sense at last from the great Olivier



Offline [OlivierLG](#) 147.100.110.48 [over 2 years ago in reply to Gary Foster](#)

Triggered by your initiative on Twitter, Prof ;o)



Offline [Gary Foster](#) 137.222.114.243 [over 2 years ago in reply to OlivierLG](#)

I'm doing my very best to stimulate the discussion, in my own little way . ;-)



Offline [OlivierLG](#) 87.89.0.50 [over 2 years ago in reply to OlivierLG](#)

In some cases, the acronym of the species name already contains information about higher taxonomic levels. this is the case of the infamous *Betacoronavirus SARSr-CoV*. These rare situations, effectively redundant, would be easily examined by the relevant ICTV study groups, perhaps to reduce the redundancy and propose binomials such as (e.g. in the particular case above) *Betacoronavirus SARSr*. Or not!



Offline [jkreuze](#) 179.6.212.225 [over 2 years ago in reply to OlivierLG](#)

how about OTU



Offline [OlivierLG](#) 82.102.27.134 [over 2 years ago in reply to jkreuze](#)

I would say there must be (there is, I understand) a separate discussion about whether OTUs should be named at all. If the answer to this separate discussion is YES then easy. If it is NO then easy as well. But recognizing and naming this or that sort of stuff, including OTUs, are probably two distinct issues.



Offline [kay scheets](#) 74.195.242.170 [over 2 years ago](#)

I'm not fond of the idea of changing the taxonomy again. I will say that I don't see any information about what name to call a virus that has been recognized as a family member, but currently not placed in a genus (Trailing lespedeza virus 1 in family Tombusviridae). This species, like many species found in environmental surveys, showed no symptoms when collected. What will be the new name of this virus and any others that have been accepted with similar uniqueness? Will any

new species that definitely has characteristics that place it in a family automatically require the simultaneous proposal to make a genus for the species?



Offline [OlivierLG](#) 82.102.27.134 [over 2 years ago in reply to kay sheets](#)

"*Unassignedvirus TLV1*, family *Tombusviridae*", maybe? (awaiting genus clarification and then "*Whatever-new-genus-virus TLV1*")



Offline [F. Murilo Zerbini](#) 200.235.185.78 [over 2 years ago in reply to OlivierLG](#)

Actually, the ICTV Code was amended in 2019 and "unassigned" species are no longer acceptable. Every new species must be assigned to a genus (Rule 3.24). For the currently unassigned species (approx. 140), they will either be assigned to an existing genus or a new genus will have to be created for them.



Offline [OlivierLG](#) 87.89.0.50 [over 2 years ago in reply to F. Murilo Zerbini](#)

Fantastic. Therefore, the bullet #2 of my summary above does not apply. Besides the design of species criteria, in the last decades the ICTV has done a great job at naming and organizing the higher taxonomic ranks (of which an unassigned genus is actually a particular form).



Offline [admin](#) 67.9.18.208 [over 2 years ago in reply to F. Murilo Zerbini](#)

The new 2019 Taxonomy release (MSL#35) now contains 100 species unassigned to a genus.



Offline [Z. Hubalek](#) 81.200.57.168 [9 months ago](#)

I am very glad that taxonomy in virology is starting to accept standard binomial nomenclature valid in other disciplines of biology. The paper "**Binomial nomenclature for virus species: a consultation**" (Arch. Virol., 2020) is very appropriate and helpful.

I am attaching a copy my old comment (2008) on this topic together with the answer of the ICTV President:

International Committee on Taxonomy of Viruses (ICTV) - Collaboration, Information, Files, and Discussion

ICTV Collaboration

- Date [Zdenek Hubalek](#)
- Date Tue, Jul 15 2008 1:48 PM
- Replies 1 reply

- Subscribers 3 subscribers
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Virus nomenclature: Three steps forward, a half step back

Two contrasting opinions about virus taxonomy or, more precisely, about virus nomenclature, appeared in the first 2004 issue of Emerging Infectious Diseases (1,2). These differing ideas about scientific (vs. common) names of viruses are the part of a long disagreement among virologists that can be tracked to the early 1950s (3,4).

The three really major progressive steps of virus nomenclature achieved in the last decades have involved the acceptance of: 1) the taxa "**family**" and "**genus**" (the names are written in italics, the initial letter being capitalized); 2) the taxon "**species**" (5,6); 3) the **binomial nomenclature**. However, the last, recent step has been carried out in an inappropriate way, contradicting the rules of general biological (i.e. Linnean) nomenclature as Mark Eberhard (2) points out absolutely correctly. Linnean binomial nomenclature does namely use latinized (Latin, Greek) but not English common names for specific epitheta, and the specific epitheton (written in italics with the first letter noncapitalized) must always be situated after the generic name (written with the first letter capitalized), not in the reverse order as it has been lately suggested by the International Committee on Taxonomy of Viruses (ICTV). It is a pity that the standard latinized binomial nomenclature has not yet been generally adopted by the ICTV for viruses although it does work well in all other areas of life science. Because virologists have already accepted the fact that viruses belong to the field of biology, they have to follow the rules of general, i.e. Linnean biological nomenclature instead of constructing another system that is incompatible with other biological specialties. It is incorrect to object that it might be very difficult to coin latinized names for an estimated 1,600 (7) virus species. For instance, such binomials have been proposed without great difficulties for 50 or so arboviruses that occurred in Europe in the 20th century (8): the names have been based on generic names accepted by ICTV (9) and on the concept of virus species (4-6,10). The examples of the proposed arbovirus names have included, e.g., in the *Togaviridae* family: Sindbis virus - *Alphavirus sindbis* (but not *Sindbis Alphavirus*); in the *Flaviviridae*: West Nile virus - *Flavivirus nili* (but not *West Nile Flavivirus*); dengue virus - *Flavivirus dengue* (but not *Dengue Flavivirus*); tick-borne encephalitis virus - *Flavivirus ixodetis*; in the *Bunyaviridae*: Batai virus - *Bunyavirus batai*; sandfly fever Naples virus - *Phlebovirus neapolis*; sandfly fever Sicilian virus - *Phlebovirus siciliensis*; Toscana virus - *Phlebovirus toscanae*; Crimean-Congo hemorrhagic fever virus - *Nairovirus congocrimae*; in the *Reoviridae*: Eyach virus - *Coltivirus eiach*; Tribeč virus - *Orbivirus tribeci*; bluetongue virus - *Orbivirus linguaceyanei*.

It is obvious that the "latinized" specific epitheta can be coined easily from the commonly used names, largely with only minor changes (at least in arboviruses whose names are usually formed according to the geographic site of original isolation). These scientific labels of viruses of course

do not exclude at all the usage of the common English, German, French, Spanish, Russian, Czech etc. names of viruses. However, a sort of hybridization of Latin (generic) and English (specific) names in the binomes as suggested by the ICTV is controversial and hardly acceptable from the bionomenclature point of view.

Zdenek Hubalek

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[Reply: Jul 28 2008 6:00 PM](#)

(Posted for Andy Ball, ICTV President)

Dr Hubalek,

Thank you for posting your opinion on this issue, and for the taxonomic proposal you submitted to the ICTV Executive Committee proposing Latinized binomial names for a large number of 'arbovirus' species. Your proposal (2007.136G.01: Proposal of latinized binomial nomenclature for arboviruses) was discussed at the last Executive Committee meeting, but it was rejected on the grounds that it massively violated the first principle of virus nomenclature: that of stability. If it is

any comfort, another proposal to change the names of all virus species in the family Geminiviridae to conform to the 'Non-Latinized Binomial System' (NLBS) was also rejected by a vote of 15 to 1 at the same meeting and for the same reason.

The members of the ICTV Executive Committee overwhelmingly ascribe to the view that the disadvantages of renaming virus species on a large scale to conform to the NLBS or any other nomenclatural system greatly outweigh the potential advantages. While your proposal would have the merit of bringing virus species names into line with standard biological taxonomy, the disadvantages of changing the names of all arbovirus species (and, by extension, ALL virus species) far outweigh the benefit of uniformity.

With regards,

Andrew Ball
ICTV President

[Previewing Staged Changes](#)