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# Requiring Binomial Names (Latinized or Non-Latinized) for ICTV Taxa



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The comment below was posted on behalf of Marc Van Regenmortel:

### **A comment on viral genome sequences, virus names and species names.**

On the occasion of Tim Skern taking over the editorship of Archives of Virology from Marc Van Regenmortel, Springer Nature and the Medical University of Vienna organized a timely symposium in Vienna on 29th June 2018 devoted to the acute problem of trying to incorporate in the current ICTV classification huge numbers of novel viral nucleotide sequences recently identified by high-throughput sequencing of metagenomic data [1]. In the last 50 years, viral taxonomy has been developed by relying almost exclusively on the phenotypic properties of viruses and 4853 virus species have so far been demarcated in this manner. This makes it in fact impractical to simply add to this current list, many thousands of new species in the form of virus-like nucleotide sequences on the assumption that these must represent new viruses with completely unknown phenotypic characteristics. The current 4853 virus species have been demarcated using viral characteristics such as the chemical and biological properties of the individual viruses that are members of each species. However, because of the error-prone process of nucleic acid replication, these phenotypic species-defining properties are not all necessarily present in every member of any species [2]. As a result, the nucleotide sequences that are hypothesized to represent different species may therefore also vary in individual viruses, making it impossible to demarcate different virus species solely on the basis of a hypothetical single genome common to all the members of the species. This simply means that species-level classification of viruses is currently not feasible if one must rely only on known viral nucleotide sequences.

The 1991 ICTV definition of virus species [ 3 ] stated that a virus species is a polythetic class of viruses. Since all taxonomic classes (species, genera and families) are conceptual constructions of the mind and not physically real objects, it is odd that many biologists nevertheless regard species as both a conceptual category and as a concrete, material object [ 4 ]. In biology, this logical confusion is facilitated because the vast majority of living organisms do not have individual names and are referred to by using the latinized

species name. In virology, however, this logical confusion could easily be avoided because every individual virus has a name that differs from the name of the species to which the virus belongs [4].

In 2013, the ICTV endorsed a new definition of virus species [ 5 ] which stated that a virus species is a material object composed of a monophyletic group of real viruses that are all physically part of the species. This new definition is reminiscent of the binomialist school of thought [ 6,7] and regards species as concrete individuals rather than as conceptual classes and it is therefore an example of the common logical fallacy of reification [ 8 ] which treats abstract classes as if they were concrete physical entities. The taxonomic implications of this new ontology of species have been discussed at length [9,10] and this has led to the conclusion that binomialism is not a suitable framework for biological classification since it does not accept that conceptual classes and taxa can correspond to evolving biological objects that exist on Earth for only limited amounts of time instead of being eternal and timeless [4]. What is crucial, however, is not to confuse real objects with their conceptual representation.

Several speakers at the Vienna symposium referred to the difficulties that were encountered when creating names for virus species that were clearly different from the names of the viruses that are members of each species. In 1998, the ICTV Executive Committee had to decide between two proposals for the official names of virus species. The first one was to introduce non-Latinized binomial names (NLBNs) formed by replacing the terminal word "virus" occurring in all English virus names with the genus name to which the virus belongs, which also ends in -virus. In the case of measles virus, the species name would be Measles morbillivirus, with a capital initial and in italics like all the names of taxonomic categories in virology. Such binomial names had been used in ICTV Reports (11,12,13,14) as well as in many plant virology papers and books [4] and are widely applicable to all viruses [15].

The second proposal was to use as species names the English names of viruses and simply italicizing them to indicate that they were official species names. Unfortunately, the ICTV EC opted for the second proposal which was soon found to create considerable confusion because virologists often did not know in their writing whether they wanted to refer to the virus or to the species [16,17]. Since binomial names are always associated with taxonomic entities in biology, the introduction of NLBNs for virus species would clearly indicate to virologists that they should use them for referring to taxonomic entities whereas they should use the virus names for referring to real, infectious viruses.

Since the report on the Vienna symposium mentioned that I had advocated the introduction of Latinized species binomial names already 20 years ago, I would like to clarify my position regarding the use of Latin in viral taxonomy. Opposition to the use of Latinized names in viral taxonomy has been widespread for at least 40 years [18] and was a major reason for the delayed adoption of the species concept in virology [4]. Many virologists had assumed that the introduction of virus species would inevitably entail the use of Latin virus names which they strongly opposed [19] and, indeed, the use of species in viral taxonomy was only introduced in 1991 when the initial ICTV rules regarding the possible use of Latin in taxonomy had been removed [14]. In fact, the ICTV and the virological community have always followed their own rules

regarding the names and typography of viral taxonomic entities and did not follow the traditions that exist in the rest of biology and are stipulated in the Biological Code of Nomenclature [4,20,].For instance the names of viral orders, families, genera and species are italicized, species names are not latinized and binomial species names use the order introduced in 1976 [11] of species first / genus second instead of the order genus name first / species identifier second, used by Linnaeus. There is, of course, no necessary connection between the use of binomials and of Latin and little justification for altering the taxonomic conventions used by virologists. Binomials are useful because the inclusion of the genus name gives additional information on viral characteristics and this advantage exists whether the genus name precedes the species or vice versa. A large number of NLBNs for virus species have been introduced in recent years [4,21,22,23] which have the advantage that they combine well-known genus names with known species names.

A few proposals had been made in the past to introduce Latin names in virology [24,25] but these were never implemented. Recently, a new proposal was published in the form of a tentative thought experiment [26] which tested the feasibility of converting all the species names in the family Arenaviridae and the order Mononegavirales into Linnaean binomials by using the format of the genus name followed by a latinized species epithet, which reverses the order of species name first, genus name second used in current NLBNs species names. Such a system would require the creation of 4853 new Latinized species epithets that follow the rules of Latin grammar. For instance Alfalfa dwarf cytorhabdovirus could become *Cytorhabdovirus medicagonis* and Measles morbillivirus could be replaced by *Morbillivirus hominis* [26]. Since thousands of novel species epithets would have to be coined and memorized, for instance when Adelaide River ephemerovirus is replaced by *Ephemerovirus fiumenadelaidense* or Merino Walk mammarenavirus by *Mammarenavirus viamerinense*, it seems unlikely that virologists would welcome having to learn thousands of complicated new species epithets instead of keeping for instance the easily memorized pairs Adelaide River virus - Adelaide River ephemerovirus and Merino Walk virus - Merino Walk mammarenavirus, for the viruses and species respectively. Creating thousands of Latinized binomial species names based only on nucleotide sequences would, of course, be even more fanciful.

It was claimed [26 ] that the current NLBNs are incompatible with many bioinformatic projects that use the Biocode because the software would assume that in the case of Lassa mammarenavirus, for instance, Lassa was the genus and mammarenavirus the species epithet. However, it seems certainly feasible to develop a software that includes the rule that in the case of viruses, genus names that end in -virus always appear after the preceding virus name in Roman.

In conclusion, replacing familiar viral NLBNs that are known to virologists because many have been in use for 40 years, by Linnaean latinized binomials could perhaps be considered to be a conceivable but complicated alternative. However, the rationale and advantages of introducing many thousands of new, unfamiliar Latinized epithets for virus species simply because they follow the historic Linnaean tradition in use with living organisms [27,28] are certainly not evident.

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