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# Comment on "50 years of the International Committee on Taxonomy of Viruses - progress and prospects" submitted by Marc Van Regenmortel 14/02/2017



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The comment below has been posted at the request of Marc Van Regenmortel. The comment is in reference to the article "50 years of the International Committee on Taxonomy of Viruses - progress and prospects" published in Archives of Virology: [Adams, M.J., Lefkowitz, E.J., King, A.M.Q. et al. Arch Virol \(2017\). doi:10.1007/s00705-016-3215-y.](#)

This welcome history of ICTV activities during the last 50 years is a useful document that gives virologists access to an enormous amount of information and data currently available on virus classification and taxonomy . However, it is a pity that the authors did not describe in more detail the current controversy surrounding the questionable definition of virus species that the ICTV introduced in 2013. This definition suffers from three major shortcomings that are bound to severely impede the creation of new virus species in the future .

1) The new species definition does not accept that all biological classifications are conceptual constructions of the mind that use abstract species classes as the fundamental units of classification. A species class is a conceptual construct that is defined by listing certain properties of its members that are the concrete viral objects studied by virologists. Since a species is an abstract concept , it does not have the physical properties that only viruses possess . The 2013 ICTV definition unfortunately defines a viral species not as a class but as a group of physical viral objects , where each virus is part of the species group in the same way that a soldier is part of a battalion. As a result , the definition is incompatible with the logic of classes based on the relations of class membership and class inclusion that are central to all hierarchical biological classifications [1,2] . The 2013 definition confounds mental concepts with real objects which , incidentally, has been a problem prevalent in the whole of biology [3.4].

2) The earlier definition of virus species endorsed by the ICTV in 1991 stated that virus species are polythetic classes ( also known as cluster classes) defined by a combination of statistically covariant and easily mutated properties of the viruses that are the members of each class [2]. Properties useful for

defining virus species are ,for instance, the natural host range , cell and tissue tropism, pathogenicity , mode of transmission, immunological characteristics , small genome differences etc which are all properties that tend to vary considerably among different members of the same species . This is the very reason species are defined polythetically by a combination of changeable , phenotypic and biological properties that are rarely predictable from genome sequences . Since none of these properties is a species- defining property necessarily present in every member of the class ( and absent in the members of other classes ), it is not possible to establish or define such a species class on the basis of a single , stable property. The situation is entirely different with higher taxa such as virus families that can be defined using only one or very few stable properties such as replication strategy or virion structure that can often be predicted from the genome sequence. . Higher taxa always have more members than do lower species taxa ,which require more properties to meet the qualification for membership. The logical principle that decreasing the number of required qualifications always increases membership invalidates the odd claim that a single property could be sufficient for defining a species [1,2]. The new 2013 definition of virus species unfortunately makes virologists believe that a new species can be established on the basis of a single property ,for instance a certain characteristic feature the viral genome , even in the absence of any knowledge of the biological properties of the viruses themselves. One of the reasons for this erroneous expectation is that a single diagnostic marker that allows a virus to be identified as a member of a previously established species is mistaken for a species-defining property that would be sufficient for a taxonomist to use to establish a completely new species [2].

3) It is often believed that a part of an object is a property of that object , although a part of a thing is a thing and not a property [5]. Since a viral genome is a part of a virus , one could indeed use one or other property of viral genomes such as its composition or presence of certain nucleotide motifs for producing a classification of viral nucleotide sequences, although this would not be a classification of viruses. Similarly , one could classify the various types of engines found in motor cars, but this would produce a classification of engines ( i.e. a part of a car ) and not a classification of motor cars. The claim made by the Metagenomic Working Group (6) that it must be feasible to create new species and incorporate them in the current ICTV system of virus classification simply on the basis of metagenomic viral genome sequences , even if there is no information whatsoever on the biological properties of the viruses themselves , seems utterly unrealistic. It contradicts the well-established principle that multiple biological criteria that may differ in the individual members of a species are nevertheless collectively needed for defining a species ; it also overlooks the fact that one cannot rely on bioinformatics for predicting from nucleotide sequences the fairly unstable and changeable biological properties of the members of a species [2,7].

The current ICTV definition of a virus species as a monophyletic group of viruses does not make it possible to distinguish species from monophyletic genera simply by examining nucleotide sequences . Since the definition disregards the relation of class inclusion essential in any hierarchical classification , it also cannot create taxa compatible with the current ICTV system of virus classification that relies heavily on biological properties of viruses . A more complete analysis of the problems that will be encountered if

attempts are made to incorporate metagenomically derived hypothetical species taxa in the current ICTV system of virus classification is available in a recent review [7].

- [1] Buck R.C.,Hull D.L. (1966).The logical structure of the Linnaean hierarchy. *Systematic Zoology* ,**15**:97-111  
<http://dx.doi.org/10.1007/s00705-013-1846-9>
- [2] Van Regenmortel M.H.V. ( 2016). Classes, taxa and categories in hierarchical virus classification: a review of current debates on definitions and names of virus species. *Bionomina* **10** :1-10
- [3] Calisher C.H. ( 2010) What is the difference between a virus species and a virus? The same as the difference between *Homo sapiens* and you .*Rev Pan-Amaz Saude* **1**: 137-139. doi:10.5123/ s2176-62232010000300019.
- [4] Ereshefsky M. ( 2011) Mystery of mysteries: Darwin and the species problem. *Cladistics* **27**:67-79
- [5] Mahner M., Bunge M. ( 1997) Foundations of Biophilosophy. Berlin, Springer - Verlag ; p 11
- (6) Simmonds P. et al ( 2017) *Nat Rev Microbiol*, doi:10:1038/nrmicro.2016.177
- [7] Van Regenmortel M.H.V. ( 2016) Only viruses , but not their genome sequences , can be classified into hierarchical species and genus classes . *Current Topics in Virology* , 13 :59-68



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The article by Adams et al. (2017) was written as a brief factual account of the history of the ICTV over 50 years and to highlight recent developments facilitated by a grant from the Wellcome Trust. We acknowledged the different views on the species definition, but it was never our intention to use the article to debate this issue.



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## Response to Marc Van Regenmortel, posted for Adrian Gibbs on May 9, 2017

Comment on Marc van Regenmortel's comments submitted to ICTV online on St Valentine's Day 2017 discussing the ICTV's review of progress and prospects over the past 50 years.

Marc continues his promotion of epistemological purity in virus taxonomy, and sees three "major shortcomings" in the recent changes to the virus species definition adopted by the ICTV.

The first, a classical 'straw man' objection, is based on notions of 'conceptual' and 'concrete'

objects. Even if real, this shortcoming is of little consequence in practice as, when communicating, educated humans infer those differences intuitively by context.

The second and third shortcomings claimed by Marc reveal his misunderstanding of gene sequences and their role in modern biology. Marc's arguments are based on the belief that the viral genome is a single character. This is wrong. The possession of a genome may be treated as a single character with two states, it is either present or absent, but a genomic sequence is quite different. The genome of, say, tobacco mosaic virus (6395 nucleotides) could in theory have  $4^{6395}$  variants or states, thus it is a rich store of various types of information. In practice most of the potential variants of the TMV genome have never been found in the world population of TMV because the genomes of the present population have regions that have been inherited unchanged from the common ancestor. These regions, motifs, are found throughout the genomes of all organisms, and are the basis of modern molecular phylogenetics and all aspects of molecular biochemical research. Gene sequences are also used as surrogates for the 'type specimens' of classical biological taxonomies and, increasingly, in the modern taxonomy of viruses.

The lasting value of Marc's original publication of a virus species concept was that he stimulated virologists to discuss and understand what constituted virus species and how best to define them. However, in practice, no virus species was ever defined using his definition. This was because each virus species accepted by working virologists was inferred to be the progeny of a common ancestor. Such virus populations have genomes with sequences that are more or less homologous. The homologous regions form sequence motifs, which define monothetic not polythetic classes, and can be used to define taxa at all levels (Gibbs et al 2004)

Gibbs, A.J., Armstrong, J.S and Gibbs, M.J. (2004) A type of nucleotide motif that distinguishes tobamovirus species more efficiently than nucleotide signatures. Arch. Virol. 149, 1941-1954

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