Virus species polemics: 14 senior virologists oppose a proposed change to the ICTV definition of virus species

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Abstract The Executive Committee of the International Committee on Taxonomy of Viruses (ICTV) has recently decided to modify the current definition of virus species (Code of Virus Classification and Nomenclature Rule 3.21) and will soon ask the full ICTV membership (189 voting members) to ratify the proposed controversial change. In this discussion paper, 14 senior virologists, including six Life members of the ICTV, compare the present and proposed new definition and recommend that the existing

definition of virus species should be retained. Since the pros and cons of the proposal posted on the ICTV website are not widely consulted, the arguments are summarized here in order to reach a wider audience.

Introduction

Viruses are considered to be biological entities because they possess genomes and are able to adapt to particular

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hosts and biological habitats. It was natural, therefore, for the International Committee on Taxonomy of Viruses (ICTV) to classify viruses using the hierarchical Linnaean category levels of order, family, subfamily, genus and species used in biological classification. Although the species taxon has always been regarded as the most important level in biological classification, it took many years before a definition of virus species was ratified by the ICTV.

Many virologists argued that the only legitimate species concept was that of biological species used for sexually reproducing organisms which clearly was not applicable to viruses that replicate by clonal means. Several other virus species definitions were proposed but none gained general acceptance until the following definition was finally endorsed by the ICTV in 1991 [1, 2]:

A virus species is a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche.

The members of a polythetic class always have several properties in common but it is not necessary that they share a single common defining property. A schematic representation of five members of a polythetic class characterized by five properties, 1-5, is shown in Fig. 1. Each member possesses several properties but no single property is present in all the members of the class. In Fig. 1 the missing property in each member is represented by the grey sector. This means that membership of a polythetic species class cannot be established on the basis that a single defining property is universally present in all the members of the species. It should be emphasized that the properties represented in Fig. 1 are species-defining properties that may vary in different members of a species and not genus-defining properties that are the same in all the species included in a given genus.

The advantage of defining species as polythetic classes is that this makes it possible to accommodate individual viruses that lack one or another character that would normally be considered typical of the species. This is important because the biological and other properties of viruses used for differentiating between species are easily altered by a few mutations with the result that these properties

often vary in different members of the same species which may then be considered strains or variants [3].

Proposals to remove the term polythetic from the species definition

Several proposals have been made in recent years to change the ICTV definition of virus species. In 2008, A.J. Gibbs and M.J. Gibbs posted on the ICTV website the following so-called “broader” species definition which was obtained by removing the term “polythetic” from the definition: “A virus species is a class of viruses that constitutes a replicating lineage and occupies a particular ecological niche”. This proposal was based on an erroneous interpretation of the term polythetic which the authors took to mean variable [4]. They regarded genome-based properties as monothetic characters useful for species demarcation because they assumed that there are such things as monothetic and polythetic properties. These terms actually describe two types of classes with different distributions of properties in their members and not two types of properties. In a polythetic class, no defining property is necessarily present in all the members of the class whereas in a monothetic class also called an universal class, each member shares one or more properties necessarily present in every member of the class. Gibbs and Gibbs believed that the presence of a particular nucleotide motif in all the members of a species was a species-defining property, which according to them made the species a monothetic class. They considered that a part of a virus corresponds to one of its properties, whereas in fact a part of a thing is a thing and not a property [5, page 11].

Considering a part of a virus as one of its properties is a common mistake which then leads to a nucleotide motif being regarded as a species-defining property [6]. In fact, a nucleotide motif is only a diagnostic marker [7] useful for identifying the members of a species once the species has been created by taxonomists beforehand. It is indeed not possible to establish in advance which nucleotide motif will be present in every member of a particular species or genus since these taxa must first be established before it

Fig. 1 Schematic representation of the distribution of defining properties (1 to 5) in five members of a polythetic class. Each member possesses several of these properties (4 out of 5) but no

single defining property is present in all the members of the class. The missing property in each case is represented by the grey sector

becomes possible to determine the sequences of all (or a very large number) of their members [8].

In 2009 and 2010, comments were posted on the ICTV website pointing out these errors in the Gibbs and Gibbs proposal, which subsequently was not approved by the ICTV. Unfortunately, the ICTV deleted such comments from the website and more proposals were later posted which once again removed the term polythetic from the species definition.

In 2011, the following species definition was proposed on the website: “A virus species should be defined on the basis of a range of criteria to ensure that the viruses assigned to it form a phylogenically distinctive lineage”. This definition was presented not as an abstract definition of the species category but as a rule explaining what is required in practice to establish a new species. The authors assumed that in order for viruses to constitute a lineage, all the members of the species must necessarily have inherited one or more common properties from a common ancestor, and this convinced them that a species must be a monothetic rather than a polythetic class. Once again, portions of conserved sequences were regarded as species-defining properties and no criteria were proposed that could be used to demarcate different species from each other or from different genera. This is needed, of course, since all species and genus taxa correspond to individual lineages.

The current proposal to define a virus species as a monophyletic group of viruses

On 27 July 2012, another proposal by A. King, M. Adams, E. Lefkowitz and E. Carstens appeared on the ICTV website which recommended several very useful changes to the ICTV Statutes and International Code. Unfortunately the proposal also included the following new definition of virus species (proposal 2011.002sG) which once more removed any reference to polythetic class: “A species is a monophyletic group of viruses whose properties can be distinguished from those of other species by multiple criteria”. The authors acknowledged that the criteria by which different species within a genus can be distinguished may include properties such as natural and experimental host range, cell and tissue tropism, pathogenicity, vector specificity, antigenicity and the degree of relatedness of their genomes and genes. However, they did not explicitly state that one or more of these properties had to be simultaneously different in all the individual members of a species before it could be considered a new species (see Fig. 1).

By rejecting the notion that a species is a polythetic class, King et al were able to argue, for instance, that if two anelloviruses possessed only 65 % nucleotide identity, this sole criterion was sufficient to allocate them to

different species even in the absence of differences in biological properties. Furthermore, by defining a species as a monophyletic group of viruses, the authors were unable to provide a practical criterion for distinguishing one monophyletic species from another since every species, genus and family can be considered to be a monophyletic class.

Another reason monophyly is not a generally applicable criterion for species demarcation is the common occurrence in many viruses of recombination and reassortment phenomena among parts of virus genomes and of exchanges of genes between viruses and their hosts. This produces chimeric viruses with polyphyletic genomes [9] and it is then logically impossible to accurately represent such multi-dimensional phylogeny in a monophyletic scheme [10]. For example, horizontal gene transfer is common in tailed phages. One striking example is *Pseudomonas* phage Φ KZ, a myovirus with a genome of 280 kbp. Its 306 ORFs include 38 genes with homologs in eukaryotes, vertebrate viruses, other phages, and over 20 bacteria [11].

When comments were posted on the website pointing out some deficiencies in their new species definition, the authors of the proposal responded on 23 October 2012 with a 4-page document, claiming that the official ICTV definition was actually based on specious reasoning and on meaningless terms such as polythetic class, replicating lineage and ecological niche.

This polemical document and a response to it are available on the website (<http://talk.ictvonline.org/discussions/ictv1/f/63/t/3930.aspx>) but since the proposal calls into question the definition that has been used for more than 20 years to establish new polythetic virus species, the main objections to it are presented below:

1. The authors of the proposal repeat the same mistake as Gibbs and Gibbs when they claim that because a species corresponds to a replicating lineage (which they claim is a meaningless term), it cannot possibly be a polythetic class because all its members allegedly share a common property. They fail to appreciate that a variable distribution of properties is not itself a single common property of all the members of a species since if this were the case, it would turn every polythetic class into a monothetic one, which is patently absurd. This error is related to the liar paradox which says that if the statement: “this sentence is false” is true, then it is actually false and vice versa. Baldwin and Lessmann, [12] further explained this paradox, known in the philosophical literature as Russell’s paradox, as follows. Consider a group of barbers who shave only those men who do not shave themselves. Suppose there is a barber in the collection who does not shave himself, then by the definition of the collection, he

must actually shave himself. However, no barber in the collection can shave himself since he would then be a man who does shave men who shave themselves. Such paradoxes arise in set theory if sets are not distinguished from classes. The set of all viruses is not itself a virus. A class cannot be a “member” of any other class although it can be “included” in another class in the way a virus species is included in a genus class [13].

2. In an attempt to defend their proposal, the authors erroneously claim that it is incorrect to refer to a virus species as a class of viruses because they seem to be unaware that the term class (which is the stem from which the word classification arises) is universally used in taxonomy. A class is not physically real and is only a concept of the mind defined by the properties of its members. A conceptual taxonomic construct such as a virus species should not be confused with its members, namely the viruses which are objects located in space and time studied by virologists. The term class is useful because it links two different logical categories, concrete objects (viruses) and abstract conceptual taxa (species, genera, families). This reminds us that taxonomy lies at the interface between biology and logic [6, 10]. King et al, however, claim that the term class can only be used to refer to a category in the classification hierarchy situated above the category order and below the category phylum (such as Mammalia between Carnivora and Chordata in zoology). The category rank “class” is in fact not used in viral taxonomy. King et al object to a virus species being called a polythetic class and they propose instead to define a species as a group of viruses. However, a group only refers to a collection of concrete viral objects and it lacks the taxonomic implications of class which has members and which is therefore the correct term to use.
3. The authors of the proposal also erroneously claim that the term “replicating lineage” has never been defined and is devoid of meaning. This does not prevent them from using the term lineage themselves and to write that: “a virus species comprises only members of its defining lineage”. The reference to replicating lineage in the ICTV species definition indicates that the members of a species share descent from a common ancestor and constitute an evolving lineage; this means that they are therefore not simply unrelated objects with similar properties classifiable by overall phenotypic similarity as is done in numerical taxonomy [14]. Lineages can be divided in a variety of ways, some of them corresponding to different species, genera or families. Including the concept of lineage in the species definition is not meant to indicate which parts of a genome sequence are retained in individual members of species. It is emphasized here that the definition of the abstract concept of virus species cannot provide practical guidelines to help virologists establish new species taxa. The ICTV species definition was originally devised because many virologists argued that the species concept could not be used in virology if an appropriate definition had not been approved by the ICTV. Unfortunately, it is commonly believed that such a general definition will clarify which virus properties must be used to demarcate individual species taxa. This is clearly not the case since it is the task of ICTV Study Groups to provide individual species demarcation criteria, namely a combination of virus properties which makes it possible to decide if a particular virus is a member of one or other polythetic species taxon. The task of creating new virus species is also not the same as the task of identifying members of an established species. For example, virus identification can sometimes be done by detecting a common nucleotide motif in a viral genome or a common amino acid sequence in a viral protein on the basis of its reactivity with a monoclonal antibody [6, 8].
4. The authors of the proposal also claim that the concept of ecological niche has never been defined although it has been abundantly discussed in the taxonomic literature [3, 14, 15]. The ecological niche refers to the biotic properties of members of a virus species such as host range and responses, tissue and vector tropism and pathogenesis. The fact that the ecological niche may be nonuniform and highly variable and is often poorly correlated with phylogeny is one reason King et al dismiss its importance for species demarcation.
5. A clear example of the undesirable consequence of ignoring the polythetic principle when creating new species is shown by the inordinate number of begomoviruses that were approved by the ICTV, using a single arbitrary criterion of less than 89 % pairwise sequence identity in the DNA-A genome of different viruses. This led to 178 different begomovirus species being created in the absence of any biological evidence that all these taxa correspond to distinguishable, stable pathogenic entities that would justify the label “species”. Most begomoviruses infect the same hosts and produce very similar disease symptoms. King et al maintain that the use of a cut-off point of 89 % pairwise nucleotide identity was not an arbitrary decision for establishing begomovirus species because it was based on quantified genome data. They seem to be unaware that such quantitative data do not speak for themselves but must be interpreted. The decision by the *Geminiviridae* Study Group to use the 89 %

identity figure as sole criterion for species demarcation was an arbitrary decision because it ignored the paucity of biological differences between the members of the 178 species as well as the frequent occurrence of recombination among begomoviruses [10, 16]. If some of the sequences in the pairwise sequence distribution of begomoviruses had been assigned to strains, a lower cut-off point could have been chosen, and this would have produced fewer begomovirus species. In the case of the mastreviruses in the same virus family, only 28 species were established because a lower and more cogently chosen cut-off of 78 % sequence identity was used to demarcate species.

Conclusion

Attempts to remove the polythetic principle from the ICTV definition of virus species originate partly from a dislike for the term polythetic which is considered by some as being obscure and has somewhat different meanings outside of taxonomy. In the context of viral taxonomy, however, there is no ambiguity at all, since the term has been defined in numerous publications [3, 13, 14, 17]. Recently it has been proposed that the term “polythetic class” in the species definition could be replaced by “cluster class” which is a more easily understood synonym widely used in taxonomy [18, 19]. However, judging from the comments of King et al. as well as some comments posted in response to their proposal, it seems unlikely that the objections to using the term polythetic class in the species definition would disappear if the term were replaced by “cluster class”.

In conclusion, the new definition proposed by King et al. is in no way superior, and in many ways inferior, to the existing ICTV definition of virus species and by removing the polythetic principle, it certainly does not provide practical guidelines to help virologists establish new species in the future.

The full text of the document posted on the ICTV website by King et al. as well as a number dissenting comments can be viewed at: <http://talk.ictvonline.org/discussions/ictv1/f/63/t/3930.aspx>.

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