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Classes, taxa and categories in hierarchical virus classification: a review of current debates on definitions and names of virus species

MARC H.V. VAN REGENMORTEL

Abstract

The species taxon was introduced in virus classification as late as 1991 when it was endorsed by the International Committee on Taxonomy of Viruses (ICTV). The official definition of virus species was as follows: "A virus species is a polythetic class of viruses that constitute a replicating lineage and occupy a particular ecological niche". Its key feature was that it incorporated the notion of polythetic class also known as a cluster class. Whereas monothetic classes are defined by one or a few properties that are both necessary and sufficient for membership in the class, polythetic classes are defined by a variable set of statistically covariant properties, none of which is a defining property necessarily present in every member of the class. Since a virus species class is a conceptual construction, it cannot be described by its physical or material properties and can only be defined by listing certain properties of the viruses that are its members. Properties used for defining virus species are properties of viruses that can be altered by a few mutations, such as their natural host range, pathogenicity, mode of transmission and small differences in the viral genome. This means that these species-defining properties vary considerably in different members of the same virus species. Since higher taxa such as genera and families have more viruses as members than species taxa, they require fewer defining properties than species taxa which require more properties to meet the qualifications for membership. The logical principle that increasing the number of qualifications decreases membership invalidates the claim that a single property could be sufficient for defining a virus species.

The bionominalist school of thought which claims that species are individuals instead of classes is examined and it is concluded that bionominalism does not provide a useful framework for classifying viruses. Since large numbers of sequences of viral genomes have become available, many attempts are currently made to establish species solely on the basis of genome data obtained from putative members of a viral species. Since the nucleic acid sequence present in a virus particle is part of the phenotype of the virus, a virus classification based on nucleotide sequences is a phenotypic classification that relies on molecular sequences rather than on the morphological and biological properties of viruses. Since it is not possible to infer the phenotypic properties of a virus from its genome sequence, a genome-based classification which privileges phylogeny is actually a classification of viral genomes rather than a classification of viruses.

In recent years, it has been suggested that it should be possible to define a virus species monothetically by a single species-defining property such as a genome nucleotide motif and that the term 'polythetic' should therefore be removed from the official species definition. In 2013, the ICTV ratified the following new definition of virus species: "A virus species is a monophyletic group of viruses whose properties can be distinguished from those of other species by multiple criteria". Since every virus species, genus or family could be considered to be a monophyletic group, this was actually a definition of 'virus taxon' instead of virus species. Many objections were raised against this new species definition and these are available on the ICTV website. A major concern was that 'polythetic class' in the earlier definition had been replaced by 'group' of viruses, because a group is a collection of viruses that are linked by a part-whole relation, whereas the term class implies the logical relations of class membership and class inclusion used in all hierarchical classifications. The authors of the new definition actually claimed that the term class should be used only to denote a category in the classification hierarchy, above the category order and below the category phylum. Examples were also given of the pernicious consequences that followed from the fact that new species could now be established on the basis of a single criterion of nucleotide sequence similarity in viral genomes.

In 1998, the ICTV introduced species names that differed from virus names only by typography, with the result that measles virus became officially a member of the species Measles virus (italicized, with a capital initial). This led to considerable confusion and the ICTV subsequently agreed that its Study Groups in charge of the taxonomy and nomenclature of individual virus families could propose non-Latinized binomial names

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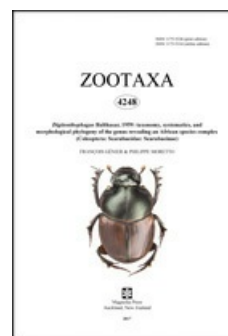
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(NLBNs) for species in certain virus genera. Such NLBNs, which had been used unofficially for 50 years, are obtained by replacing the terminal word 'virus' that occurs in all common English virus names with the name of the genus to which the virus belongs, which also ends in -virus. Measles virus thus became a member of the species Measles morbillivirus which was more easily recognized as a species name since binomial names in biology are associated with taxonomic species names. In the last four years, numerous species NLBNs have been introduced in several virus families.

Keywords

Virus taxonomy, Linnaean hierarchy, International Committee on Taxonomy of Viruses (ICTV), binominalism, polythetic class, virus identification, viral phenotype, DNA barcoding, viral genomes, species-defining properties, begomoviruses,

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