Discussion

Virus species and virus identification: Past and current controversies

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Abstract

The basic concepts used in virus classification are analyzed. A clear distinction is drawn between viruses that are real, concrete objects studied by virologists and virus species that are man-made taxonomic constructions that exist only in the mind. Classical views regarding the nature of biological species are reviewed and the concept of species used in virology is explained. The use of pair-wise sequence comparisons between the members of a virus family for delineating species and genera is reviewed.

The difference between the process of virus identification using one or a few diagnostic properties and the process of creating virus taxa using a combination of many properties is emphasized. The names of virus species in current use are discussed as well as a binomial system that may be introduced in the future.

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1. The nature of classification

Classifying objects is a human prerogative based on the capacity of the mind to conceptualize and recognize the presence of similar properties in individual objects. Properties and classes are related abstract entities: when a property is ascribed to an object, the object thereby becomes a member of a particular class defined by that property (Quine, 1987). If a virus has a positive strand RNA genome, it becomes automatically a member of the class of positive strand RNA viruses. Classifying viruses consists in inventing taxonomic classes like particular families or species and allocating individual viruses to these classes in order to achieve some order whereby similar viral agents are grouped together. It is important to realize that all taxonomic classes are abstract concepts, i.e. constructions fabricated by the mind and not real entities located in space and time. The failure to distinguish between real objects such as organisms and viruses and the mental constructions and abstractions needed to build up any classification system has been a fertile source of confusion in taxonomy (Van Regenmortel, 2003).

2. The nature of viruses

Viruses have been defined as molecular genetic parasites that use cellular systems for their own replication (Villarreal, 2005). Viruses are considered to be biological entities because they possess some of the properties of living systems like having a genome and being able to adapt to certain hosts and biological habitats. However, this does not mean that viruses should be regarded as microorganisms. Viruses do not possess some of the essential attributes of living organisms such as the ability to capture and store free energy and they lack the characteristic autonomy that arises from the presence of integrated, metabolic activities. A virus becomes part of a living system only after its genome has been integrated in an infected host cell. Most biologists accept that the simplest system that can be said to be alive is a cell (Mahner and Bunge, 1997). Only unicellular and multicellular organisms possess the property of being alive, while the organelles, macromolecules and genes found in cells are not themselves considered to be alive. The difference between viruses and various types of organisms is quite obvious when the functional roles of the proteins found in viruses and in organisms are compared. When

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proteins are divided in three functional categories corresponding to energy utilization, carriers of information and mediators of communication, the proportion of each protein class found in viruses is markedly different from that found in living organisms (Tamames et al., 1996; Patthy, 1999). Viruses have the highest proportion of proteins involved in information processes related to the control and expression of genetic information but have very few proteins of the energy and communication classes (Fig. 1). This distribution arises because viruses utilize the metabolic machinery of the host cell and rely entirely on the energy supply system of their hosts. In contrast, bacteria have the highest proportion of proteins of the energy class involved in small molecule transformations while animals have a high proportion of proteins involved in intra and intercellular communication (Patthy, 1999).

Some authors regard viruses as living microorganisms on the basis that they share with certain parasitic organisms the property of being obligate parasites. However, the dependency of viral genes on their cellular hosts is a totally different type of parasitism from the dependency shown, for instance, by bacteria that colonize the gut of certain animals. Obligate parasitism on its own is not a sufficient criterion for establishing that an entity is alive (Van Regenmortel, 2003).

Another important distinction is that between viruses and virus particles or virions. Only virions can be fully described by their intrinsic chemical and structural properties such as their mass, size, chemical composition, genome properties, etc. Viruses on the other hand, possess in addition so-called relational or emergent properties that are actualized only during transmission, infection and replication processes. These relational properties exist only by virtue of a relation with other entities like a host or a vector and they emerge only in the system as a whole. Confusing "virus" with "virion" is similar to confusing the entity "insect" which includes several different life stages, with a single one of these stages such as a pupa, a caterpillar or a butterfly.
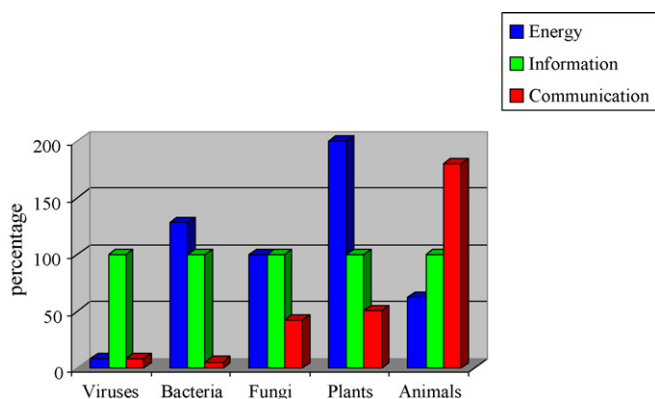

Fig. 1. The proteins of viruses and organisms have different functional roles. The vertical bars represent the proportion of proteins in the categories of energy utilization and carrier of information, relative to those in the category of mediator of information. Viruses have the highest proportion of proteins involved in information processes, i.e. in the control and expression of genetic information (from Patthy, 1999).

3. Classes and individuals

Distinguishing between real, tangible objects like viruses (i.e. concrete individuals) and mental constructs like virus species and genera (i.e. classes) that exist only in the mind is a basic requirement for clear thinking. Although a taxonomic class is defined by properties possessed by concrete objects, it is an abstract, conceptualized collection, i.e. a mental construct.

Classes used in biological classifications have a hierarchical structure, the main ranks being the species, genus, family, order and phylum. A class such as a particular species can only belong to one higher-rank class immediately above it, such as a particular genus and that genus in turn can only belong to one family. The logical relationship between two successive abstract classes in the hierarchy is known as class "inclusion", whereby the lower-rank class is "included" in the higher-rank one. Class inclusion must be distinguished from the relationship of "class membership" which is the relationship used to establish a link between the abstract class and its members which are concrete individuals. Class membership is thus able to bridge two different logical categories, the abstract and the concrete (Buck and Hull, 1966; Mahner and Bunge, 1997, p. 230).

In a biological classification scheme, an individual organism or a virus can be a member of several abstract classes like a species or a genus. Class membership must be distinguished from the so-called "part-whole" relationship which exists only between two concrete objects, one being a part of the other in the way, for instance, that cells and organs are parts of an organism. It is not possible for a concrete object like a virus to be "part" of an abstract entity like a species (similarly a thought cannot be part of an object). The mixing of logical categories has led to much debate in viral taxonomy (Bos, 2003; Van Regenmortel, 2003).

A universal class, also known as an Aristotelian class, is defined by properties that are constant and immutable. This allows members of such a class to be recognized with absolute certainty since one or more property is necessarily present in every member of the class. Virus families, for instance, are universal classes because they consist of members, all of which share a number of defining properties that are both necessary and sufficient for class membership. Allocating a virus to a family is thus an easy task since a few structural or chemical attributes will suffice to allocate the virus to a particular family. For instance, all the members of the family Adenoviridae are non-enveloped viruses that have an icosahedral particle and double-stranded DNA, with projecting fibers at the vertices of the protein shell. Additional universal classes such as subfamilies, superfamilies and orders are also used in virology and they are also defined by characters that are necessarily present and allow an unambiguous allocation of the members belonging to such classes (Fauquet et al., 2005).

Unfortunately, not all properties of members of classes correspond to unambiguous predicates like the presence or absence of a DNA genome or of a particular type of particle. Many qualitative properties of concrete objects are inherently vague and do not provide precise demarcation lines. For