Arch Virol (2003) 148: 1645–1653
DOI 10.1007/s00705-003-0150-5

VDN Virology Division News

Viral nomenclature, where next?

A. J. Gibbs

School of Botany and Zoology, Australian National University, Canberra, Australia

Received April 10, 2003; accepted May 5, 2003

The International Committee for Taxonomy of Viruses (ICTV), which was formed over 30 years ago, aims to develop a single, universal taxonomic scheme for all viruses or, in other words, "the classification of viruses and the assignment of names to taxa" [24]. The ICTV has been most successfully pursuing that aim and its mammoth 'Seventh Report' [34] records details of the names it has collated and approved, and of the classification, it has devised. Modern society however requires a single comprehensible system of virus naming and names, and so far the ICTV has failed to provide this. Here I will outline some of the current problems, how and why they may have arisen and suggest changes of emphasis for future work of the ICTV.

Who uses virus names?

Viruses must be properly identified and clearly named not only for the work of virologists but also, and perhaps more importantly, for the use of people working in medical and veterinary science, agriculture and horticulture, commerce and in the expanding areas of quarantine, biotechnology, patenting, bioterrorism preparedness, etc. Correct naming is crucial where international agreements are involved. Drebot et al. [12] discussed this issue and gave, as an example, the 'Select Agent Rule' which will control the "possession, use and transfer of select viral and microbial agents" to, from and within the U.S.A. In a similar vein, signatories to the "Agreement on Sanitary and Phytosanitary Measures" resulting from the Uruguay Round of the General Agreement on Tariff and Trade have accepted that any phytosanitary measure (e.g. quarantine) which acts as a non-tariff barrier to trade must be technically justified. This requires the National Plant Protection Organizations of all signatories to maintain records of the disease status of traded plants and, of course, this requires records of accurately named viruses and other pathogens.

It is likely that most users of virus names are not virologists, probably not English speakers, and I believe Van Regenmortel and Fauquet [33] misunderstand the role of virus nomenclature in modern global society when, in arguing against latinized binomial for the formal names of viruses, they state that "The use of English instead of Latin names for species is in line with the fact that English has replaced Latin as the language of communication used by scientists"; Latin never was the language of communication between scientists, English may not now be the primary language of most of those communicating about viruses, and virologists are probably not the principal day-to-day users of virus names.

Most users of common virus names are not interested in virus classification and merely want to know that a name they are using is correct; they want to know that it unequivocally identifies to others the virus they are discussing. Implicitly, they need to know that the name is linked, directly or indirectly, to a description of the virus, which shows that it is clearly distinct from related viruses. A smaller but nonetheless significant group of users around the world are those involved in virus identification. These are interested in virus classification but, even more importantly, need to have access to concise descriptions, diagnostic data and materials for their work. However neither of these groups has been significantly helped by the work of the ICTV. Although its regular Reports contain the collated and approved names of several thousand virus species, these names are unattached; they are not linked descriptions, specimens or materials or, in many instances, the original common names. Although the ICTV's present International Code of Virus Classification and Nomenclature (ICVCN; 24) Rule 3.5 states that taxa "*will be established only when representative member viruses are sufficiently well characterized and described in the published literature so as to allow them to be identified unambiguously and the taxon to be distinguished from other similar taxa*", the Report provides no record of which data in the published literature led the relevant ICTV Study Group to recommend that the taxon and its name be approved; one presumably must read all the published literature for a viral species and decide for oneself which parts the Study Group considered to be correct and acceptable. This and other problems have arisen because the ICTV has developed its own idiosyncratic nomenclatural code, which differs in several fundamental ways from all the other Biological Codes of Nomenclature.

Viruses; unusual or unique

When viruses were first studied about a century ago, they were mostly known by 'negative properties', they did not grow in microbial media, they could not be seen using microscopes and they were not removed by ultra-filtration. Therefore the earliest virologists named these enigmatic pathogens after the diseases they caused.

The committee that later became the International Committee on Taxonomy of Viruses (ICTV) was established in 1966, to introduce order into the naming of viruses. Its first rules reflected the concerns of the time, but some have persisted and are found in one form or another in the present International Code of Virus Classification and Nomenclature (ICVCN). In particular the mid 20th century was a time when the nature of viruses was being discussed – were viruses living or dead and, in the absence of sex, could they form species? The essence of the early debates is still to be seen in such recent statements as "Although viruses are pathogens, they are not genuine pathogenic microorganisms" and "Viruses are not living organisms and they occupy a unique position in biology. Since they are not functionally active outside of their host cells, they lead only a kind of borrowed life" [29].

These uncertainties, together with a lack of confidence in whether the early classifications were based on characters that truly reflected relatedness, led early virologists to cling to traditional common names, usually English, and to reject several attempts to introduce latinized binomial names in the style of Linnaeus [14, 30]. They also resulted in the ICVCN Rule 2.2 which states that: "*Nomenclature of viruses and sub-viral agents is independent of other biological nomenclature. Virus and virus taxon nomenclature are recognised to have the status of exceptions in the proposed International Code of Bionomenclature (BioCode)*", "*Because names of virus species do not have the binominal form required under this Code . . .*".

Many biologists, if not most, now accept that viruses are organisms in that they evolve and form definable species, even though they are sub-cellular. They are probably polyphyletic in origin, not so much a family, more a way of life. They pass the metabolic phase of their life cycle in cellular hosts upon which they totally depend for some metabolic processes, however they represent in their dependency on cellular hosts just one extreme of a range of inter-organismal dependencies. No one questions whether the bacteria or protozoa, which digest the cellulose that termites eat, are organisms. Yet they depend totally on one another. Likewise the totally obligate relationships of insects and *Buchnera* or *Wolbachia* do not stop them all being considered organisms. The dependency of viral genes on their cellular hosts is no more "a kind of borrowed life" than that of any sub-genomic set of genes. Viruses overlap cellular organisms in all their characters; some have genomes bigger than those of bacteria [21], they lack mitochondria but so too do some protozoa, some viral genomes encode tRNAs [27], etc. Thus viruses are part of nucleic acid-based life on earth, and there is no longer any scientific reason for their nomenclatural code to be grossly different from the other three Codes of Biological Nomenclature.

Biological codes of nomenclature; the cellular and viral models

Three Codes of Nomenclature cover all cellular organisms; that of animals (*http://www.iczn.org/code.htm*), plants and fungi (*http://www.bgbm.fu-berlin.de/iapt/nomenclature/code/*) and bacteria (*http://www.dsmz.de/bactnom/bactname.htm*), and the BioCode project (*http://www.biosis.org.uk/zrdocs/codes/biocode.htm*) is attempting to amalgamate them. This is an attainable objective as all are based on a few shared principles. The core tenet of all, as stated for example in the draft BioCode (Principle III), is that "*The application of names of taxa is determined by means of name-bearing types*", each a specimen "*conserved permanently as a single curatorial unit*" (BioCode 15.1), the details of which have been published named, established and registered (BioCode 5–13) in a designated way. Thus for these Codes each name is tied to a particular described specimen. That name becomes the name of the species (i.e. the population of specimens) of which it is a representative. This rule stabilizes the names and enables specimens to be re-examined and taxonomic revisions made, whenever new evidence, new methods, new specimens or a new revision, require it to be done. The name of the type specimen is normally a latinized binomial and thus is very readily distinguished from common names because of its language, its distinctive form and italicisation. It is the crucial link between the described type specimen (concrete object), the species (a conceptual class) in a classification, and all the common names (Fig. 1A). By contrast each ICTV-approved name is attached directly to a species (Fig. 1B), in essence a population of isolates, and this may include a range of slightly different isolates and strains. As a consequence the ICTV Report lists, for some species, the Accession Codes of gene sequences of more than one isolate, and these sequences are often different!

Virus names; common and *ICTV-approved*

The study of viruses is just over 100 years old. During the first half of that period most were named after the diseases they caused, and attempts to introduce latinized binomial names tied to seemingly artificial classifications [22] were rejected because "Latinized binomial names, if they are to be of value, must be linked to a stable classification system, based on intrinsic characteristics of the viruses, so that they are a joint information retrieval and storage system" [17]. It was not until the properties of the structure and composition of viral molecules were revealed by the developing science of molecular biology during the second half century that attempts were made to determine their relationships. However for everyday discourse virologists have continued to use obscure and sometimes quaint common names, most of them

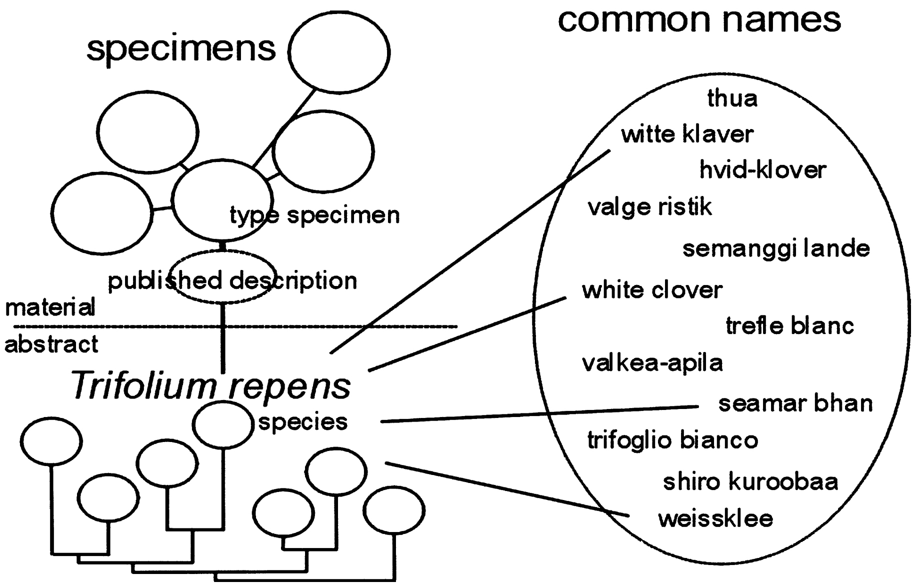

Fig. 1A. A diagram showing the nomenclatural components that link the name *Trifolium repens* L. with "white clover" and other common names, and with its 'lectotype', which was collected by Linnaeus from the garden of George Clifford in Hartekamp, The Netherlands. The specimen is now held in the Clifford Herbarium of the Natural History Museum, London, U.K., and can be viewed on their website at http://internt.nhm.ac.uk/cgi-bin/botany/clifford/detail.dsml?B=BM000646755

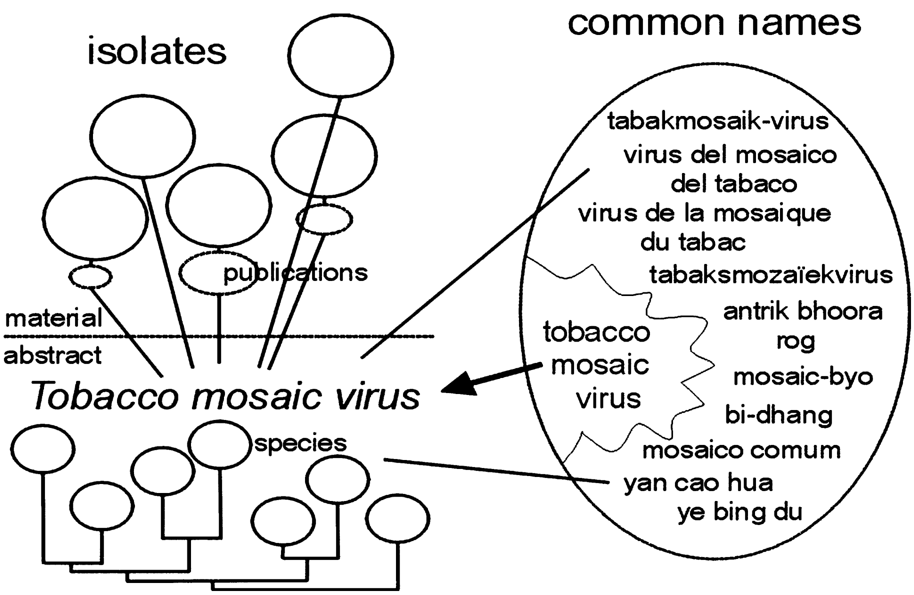

Fig. 1B. A diagram showing the nomenclatural components associated with the name *Tobacco mosaic virus*. The properties of different isolates of tobacco mosaic virus have been described to various extents in publications, and consideration of that published data led a Study group of the ICTV to suggest that a species be approved, but which data they considered to be relevant or correct is not known. The official name now given to the virus was obtained by italicising the common English name memorable, and most used everyday by non-virologists. Most virologists wish to continue to use such names, unaltered, as they provide a direct link with the original literature and are part of the tradition of their branch of virology.

During the early stages of development of virus classification Gibbs et al. [16, 18] proposed the use of a 'cryptogram' when mononomial common names were being used in a taxonomic sense; it added some potentially phylogenetic information. However when the first stable genera (groups) were recognised and named Fenner, in his 1976 ICTV Report [13], informally used non-latinized binomials of the form, "myxoma leporipoxvirus" and "West Nile flavivirus", and names of this form have been used widely, especially by plant virologists [5]. In a separate development, descriptions of the best known plant viruses (http://www.dpvweb.net/) became a database of all plant viruses (9; http://image.fs.uidaho.edu/vide/) and this is now being developed and expanded into the encyclopaedic ICTV database [10, 11]; *http://www.ncbi.nlm.nih.gov/ICTVdb/*).

During the early years of its existence the ICTV merely checked that proposed names conformed to simple Rules, such as that "No person's name shall be used . .", "Names for taxa shall be easy to use and easy to remember . . .", "Subscripts, superscripts may not be used". However increasingly the ICTV modified the common names before approving them, for example mouse and pig viruses became murine or murid and suid viruses, but there is no authoritative database linking the original common names and the approved ICTV names, and so often the relationships between these names must be guessed. For example, there are many publications recording research on "mouse hepatitis virus", which is possibly the same as the *Murine hepatitis virus* in the ICTV databases but this is not stated, and similarly although *Suid herpesvirus 1* and pseudorabies virus are linked in the databases, Aujeszky's disease virus is not mentioned!

In 1998 the Executive Committee of the ICTV decided that all the monomial names of viral species it had approved were to be italicised with the first letter of the name capitalized, and the resulting names were to be the "approved International Names" [23, 25], and hence equivalent in status to the latinized binomial names of cellular organisms. The likely confusion that this wholesale take-over of English common names would cause became clear when Officers of the ICTV and presumably speaking on its behalf, stated that this rule only "applies when the species name is used to refer to a taxonomic entity, i.e. an abstraction corresponding to a taxon in the virus classification" [28], whereas the same name without italics refers, as before, to "concrete viral objects that cause disease" [33]!! This is not the only way the decision to italicise creates problems [2, 4, 6, 7, 15] and recent clarifications and explanations of these rules [30, 33, 35] have merely increased the confusion [8].

Thus the present ICTV-approved virus names differ in three significant ways from those of other organisms; they are mononomial in content, they name taxonomic abstractions and are not associated with type specimens, they are usually English and are confusingly similar to the common names from which they were derived, whereas formal names of cellular organisms are binomial, of described type specimens, Latinized and completely distinctive.

The confusion may soon increase further as, at a recent ICTV meeting in Paris, there was much support "for the idea of non-latinized *binomial* nomenclature", and ICTV Study Groups and Subcommittees have been asked "to consider the implications" [23]. So there is now the possibility of further change, and current literature may soon have four variants of each common English virus name, each with a subtly different meaning. For example one of the oldest virus names, tobacco mosaic virus, is the common English name of a virus and has been in use for the past century, but the 1998 ruling decided that *Tobacco mosaic virus* would be the approved name of the 'species'. This name, together with tobacco mosaic tobamovirus, the non-latinized binomial form of the name, may soon be joined by *Tobacco mosaic tobamovirus*, the ICTV-approved non-latinized binomial name [31]!

The ICTV recently added a further layer of confusion [8] by producing a list of "ICTV approved acronyms"; originally for plant virus names [20], but now for all virus names. TMV is the approved acronym for one or other of the variant names above, but which, is uncertain. In order for each approved acronym to be unique some are very complex and the component letters are 'case-sensitive', for example TToMoV, ToLCV-BanII and TYLCV-Ch are three out of 25 begomovirus acronyms starting with "T". The notion of an approved acronym destroys the purpose of an acronym which is to be a brief representation of a polynomial that is being used repetitively on one occasion. As could have been predicted, one recently published text book [19] has used approved virus acronyms throughout as surrogate names, and the same objective is behind the suggestion that "it is simpler, in texts written in various languages, to use acronyms and abbreviations taken from English virus names rather than to coin new abbreviations derived from the different virus names in each national language" [33]!

Finally, one should note that the ICTV database now includes 'Virus Codes' [10], which designate tobacco mosaic virus, for example, as "00.071.0.01.001", but although these codes are actually database locators, their prominence in the database might make some believe that they are part of each name.

Viral species – philosophical or pragmatic?

Throughout its existence the ICTV has spent an inordinate amount of time trying to define the concept of a virus species, and its latest effort ([32]; ICVCN Rule 3.21), states: "*A virus species is defined as a polythetic class of viruses that constitute a replicating lineage and occupies a particular ecological niche*". This definition mostly accords with the principles used to define cellular organisms (i.e. plants, animals, bacteria and fungi), however the use of the "polythetic" principle does not. A polythetic class of individuals is one that is defined by a set of properties, many of which are possessed by every individual, but none of which is possessed by all individuals [3]. The polythetic principle, in its usual sense, has been successfully used in procedures to identify and classify organisms using phenotypic characters (e.g. leaf shape, coat colour, beak shape, etc); Adanson [1] used it, for example, to identify and describe plants when he visited West Africa for the first time in the 18th century. It was also used correctly as the principle behind the cryptograms proposed by Gibbs et al. [18] to add meaning to common names of all viruses. However nowadays, species, especially those for which gene sequence data is available are defined monothetically, that is, by a set of properties shared by all individuals in the taxon. ICVCN Rule 3.21 is self-contradictory because to be sure that the individuals "constitute a replicating lineage", they must share characters they have inherited from a common ancestor, and therefore that lineage can be defined by some or all of that monothetic set of shared characters.

It is said that "proof of the pudding is in the eating", and thus it is noteworthy that although Marc van Regenmortel, when President of the ICTV, refined his advocacy of the principle of 'polythetic virus species' in many publications, no virus species has, in practice, been described by the ICTV using the concept; the latest ICTV Report includes no descriptions of viral species. Drebot et al. [12], while lauding the development of the polythetic species concept, note however that "The principal responsibility for taxonomic placement lies with the individual ICTV Study Groups, committees made up of individuals with extensive experience and expertise regarding the viruses in a particular taxon . . . Thus the primary level of taxonomic authority, quite reasonably, lies with experts." So it is clear that, in practice, the viral species officially recognised by the ICTV are not defined by the philosophically elegant polythetic principle but, more pragmatically perhaps, as "strains whose properties are so similar that there seems little value in giving them separate names" [17].

Where next?

It is important to realize that taxonomy is a triptych; data, names and classification. Formal approved names are the crucial links, the linchpins, of the informational network of that triptych. Formal virus names should not, and are not intended to, replace or change common names in everyday use by virologists and other users of virus names. The recent decision of the ICTV to generate formal names by italicizing the currently approved virus names, most of which are minor variants of common English names, is a sure recipe for confusion and for producing error. The best way to minimize confusion and error is for the formal names to be distinctly different from the common names, and for a public database to link the formal name of each taxon both with its associated data and classification, and with all the known common names of that taxon.

The simplest way to produce distinctive formal names is for them to have the same style and form as those of the other biological nomenclatures – latinized binomials; their form and style ensures that they are instantly recognized as such world-wide, whereas italicized English names do not carry the same message. The reasons why latinized binomials should be used have been convincingly argued by Agut [2]. Half the names required (i.e. the generic half of each binomial) are already devised, and if stricter criteria are applied to candidate species during the collation of the 'type' for the ICTVdB (see below), then perhaps a third of the viruses currently given ICTV approved names will continue to be known by their common names until they are better characterized.

In summary, a relatively stable classification of all known viruses has emerged over the past three decades, largely as a result of the efforts of the ICTV, the primary aim of the Committee should now be to work on the names and data associated with that classification. The ICTV should:

1) abandon its attempt to build a system of formal virus names from selected and modified common names. The ICTV database (ICTVdB) should include all the common name(s) of all viruses in all languages, and the ICTV might, as suggested by Bos [8], coordinate advice on the design of common names in all major languages;
2) assemble and record within the ICTVdB a properly curated 'type' description for each ICTV-approved and named taxon. This 'type' should include key data, important references, sequence Accession Codes, and details of the locality of stored infective materials (i.e. the 'type specimen' of an approved species), cloned genes, photographs, antisera, etc. Minimally each ICTVdB 'type' description should consist of the monothetic set of characters, that distinguishes the taxon from related taxa or those with which it might be confused, and this minimal description should be distinctively displayed in the ICTVdB;
3) provide for each approved species a latinized binomial name to link its common name(s), the 'type' description and the classification;
4) modify the ICVCN to become congruent with the other Codes of Nomenclature, not only so that all biological names conform, more or less, to one set of principles, but also so that virologists can become fully involved in discussions about the BioCode and Phylocode (*http://www.ohiou.edu/phylocode/index.html*).

Viruses are master explorers of evolutionary space, and thus the ICTV has not always successfully 'shoe-horned' them into the five hierarchically-arranged categories it has used; orders, families, genera, species, and a sub-species 'too-hard basket'. However moving the prime focus of the efforts of the ICTV from biochemical classification to the provision of useful names, and to helping those involved in identification, will shift emphasis to the two taxonomic levels, that are most important in a binomial name, the genus and species [17]. My proposals would eliminate significant irritating anomalies, like that of poliovirus discussed by Drebot et al. [12]. The elevation of useful names (e.g. furovirus) to family and above so that their nomenclatural value is lost at the species level should be avoided, and the regrouping of taxa that have been separated using biochemical criteria of unknown biological significance (e.g. genomic map differences) should be encouraged.

The changes that my suggestions will require to the ICVCN are minor, and suggestions for these, together with examples of 'type' descriptions and fuller details of the changes

I propose, will be lodged at *http://www.danforthcenter.org/iltab/ictvnet/asp/_MainPage.asp*. The International Code of Nomenclature of Bacteria was completely revised in the 1970's to accommodate the new knowledge of the relationships of bacteria, and it now operates with the starting date of 1980 [26]. The ICTV must seriously also consider making a similar cathartic change.

Acknowledgements

Thanks to members of Coopers and Cladistics of Canberra for providing the initial stimulus for this paper, and also for the very helpful and trenchant criticisms of its various drafts by Lute Bos, Cornelia Büchen-Osmond, Charles Calisher, Mike Crisp, James Dale, Frank Fenner, Bryan Harrison, Mark Gibbs, David Gordon, Laurence Mound, Fred Murphy, Peter Scott and John Trueman, and for help from Steve Cafferty, Shou Wei Ding, Elliot Kitajima and Kazusato Ohshima in preparing the Figures.

References

1. Adanson M (1763) Familles des plantes, vol 1. Vincent, Paris
2. Agut H (2002) Back to Latin and tradition: a proposal for an official nomenclature of virus species. Arch Virol 147: 1465–1470
3. Beckner M (1959) The biological way of thought. Columbia University Press, New York
4. Bos L (1999a) The naming of viruses: an urgent call to order. Arch Virol 144: 631–636
5. Bos L (1999b) Plant viruses, unique and intriguing pathogenesis – a textbook of plant virology. Backhuys, Leiden
6. Bos L (2000) Structure and typography of virus names. Arch Virol 145: 429–432
7. Bos L (2002) International naming of viruses – a digest of recent developments. Arch Virol 147: 1471–1477
8. Bos L (2003) Virus nomenclature; continuing topicality. Arch Virol 148: 1235–1246
9. Brunt A, Crabtree K, Dallwitz M, Gibbs A, Watson L (1996) Viruses of plants. C.A.B.International, U.K., 1484 pp
10. Büchen-Osmond C, Dallwitz MJ (1996) Towards a universal virus database – progress in the ICTVdB. Arch Virol 141: 392–393
11. Büchen-Osmond C, Blaine L, Horzinek MC (2000) The universal virus database of the ICTV (ICTVdB). in: Virus Taxonomy. Classification and Nomenclature of Viruses, Seventh Report of the International Committee on Taxonomy. Van Regenmortel MHV, Fauquet CM, Bishop DHL, Carstens EB, Estes MK, Lemon SM, Maniloff J, Mayo MA, McGeoch DJ, Pringle CR, Wickner RB (eds) Academic Press, San Diego
12. Drebot MA, Henchal E, Hjelle B, LeDuc JW, Repik PM, Roehrig JT, Schmaljohn CS, Shope RE, Tesh RB, Weaver SC, Calisher CH (2002) Improved clarity of meaning from the use of both formal species names and common (vernacular) virus names in virological literature. Arch Virol 147: 2465–2471
13. Fenner F (1976). The classification and nomenclature of viruses. Second Report of the International Committee of Taxonomy of Viruses. Intervirology 7: 1–115
14. Gibbs A (1969). Plant virus classification. Adv Virus Res 14: 263–328
15. Gibbs AJ (2000). Virus nomenclature descending into chaos. Arch Virol 145: 1505–1507
16. Gibbs AJ, Harrison BD (1968) Realistic approach to virus classifcation and nomenclature. Nature, Lond. 218: 927–929
17. Gibbs AJ, Harrison BD (1976) Plant Virology: the principles. Edward Arnold, London, 292 pp
18. Gibbs AJ, Harrison BD, Watson DH, Wildy P (1966) What's in a virus name? Nature 209: 450–454
19. Hull R (2002) Matthews' Plant virology. Academic Press, San Diego, 1001 pp
20. Hull R, Milne RG, Van Regenmortel MHV (1991). A list of proposed standard acronyms for plant viruses and viroids. Arch Virol 120: 151–164
21. La Scola B, Audic S, Robert C, Jungang L, De Lamballerie X, Drancourt M, Birtles R, Claverie J-M, Raoult D (2003) A giant virus in amoebae. Science 299: 2033

22. Lwoff A, Horne R, Tournier P (1963) Cold Spring Harbor Symp Quant Biol 27: 51
23. Mayo MA (2002) ICTV at the Paris ICV: Results of the Plenary Session and the Binomial Ballot. Arch Virol 147: 2254–2260
24. Mayo MA, Horzinek MC (1998) A revised version of the International Code of Virus Classification and Nomenclature. Arch Virol 143: 1645–1654
25. Pringle CR (1998) The universal system of virus taxonomy of the International Committee on Taxonomy of Viruses (ICTV), including new proposals ratified since publication of the sixth report in 1995. Arch Virol 143: 203–210
26. Sneath PHA (Ed.) (1992) International Code of Nomenclature of Bacteria, 1980 Revision. American Society for Microbiology, Washington, DC
27. Van Etten JL, Graves MV, Müller DG, Boland W, Delaroque N (2002) *Phycodnaviridae* – large DNA algal viruses. Arch Virol 147: 1479–1516
28. Van Regenmortel MHV (1999). How to write the names of virus species. Arch Virol 144: 1041–1042
29. Van Regenmortel MHV (2000a) Introduction to the species concept in virus taxonomy. In: Van Regenmortel MHV, Fauquet CM, Bishop DHL, Carstens EB, Estes MK, Lemon SM, Maniloff J, Mayo MA, McGeoch DJ, Pringle CR, Wickner RB (eds) Virus Taxonomy. Seventh Report of the International Committee on Taxonomy of Viruses. Academic Press, San Diego, 3–16
30. Van Regenmortel MHV (2000b) On the relative merits of italics, Latin and binomial nomenclature in viral taxonomy. Arch Virol 145: 433–441
31. Van Regenmortel MHV (2003) http://www.danforthcenter.org/iltab/ICTVnet/asp/iMessageDisplayPost.asp?PID=51
32. Van Regenmortel MHV, Bishop DHL, Fauquet CM, Mayo MA, Maniloff J, Calisher CH (1997) Guidelines to the demarcation of virus species. Arch Virol 142: 1505–1518
33. Van Regenmortel MHV, Fauquet CM (2002). Only italicised species names of viruses have a taxonomic meaning. Arch Virol 147: 2247–2250
34. Van Regenmortel MHV, Fauquet CM, Bishop DHL, Carstens EB, Estes MK, Lemon SM, Maniloff J, Mayo MA, McGeoch DJ, Pringle CR, Wickner RB (eds) (2000). Virus Taxonomy. Seventh Report of the International Committee on Taxonomy of Viruses. Academic Press, San Diego
35. Van Regenmortel MHV, Mayo MA, Fauquet CM, Maniloff J (2000) Virus Nomenclature: Consensus versus chaos. Arch Virol 145: 2227–2232

Author's address: Prof. Adrian Gibbs, School of Botany and Zoology, Faculty of Science, Australian National University, Canberra, 0200, Australia; e-mail: adrian.gibbs@anu.edu.au