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Binomial nomenclature for virus species: a long view

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Abstract:	<p>On several occasions over the past century it has been proposed that Latinized (Linnaean) binomial names (LBs) should be used for the formal names of virus species, and the opinions expressed in the early debates are still valid. The use of LBs would be sensible for the current Taxonomy if confined to the names of the specific and generic taxa of viruses of which some basic biological properties are known (e.g. ecology, hosts and virions); there is no advantage filling the literature with formal names for partly described viruses or virus-like gene sequences. The ICTV should support the time-honoured convention that LBs are only used with biological (phylogenetic) classifications. Recent changes have left the ICTV Taxonomy and its Code uncoordinated, and its aims and audience uncertain.</p>
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4 1 **Binomial nomenclature for virus species: a long view**

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14 11 **Abstract**

15 12 On several occasions over the past century it has been proposed that Latinized (Linnaean)
16 13 binomial names (LBs) should be used for the formal names of virus species, and the opinions
17 14 expressed in the early debates are still valid. The use of LBs would be sensible for the current
18 15 Taxonomy if confined to the names of the specific and generic taxa of viruses of which some
19 16 basic biological properties are known (e.g. ecology, hosts and virions); there is no advantage
20 17 filling the literature with formal names for partly described viruses or virus-like gene sequences.
21 18 The ICTV should support the time-honoured convention that LBs are only used with biological
22 19 (phylogenetic) classifications. Recent changes have left the ICTV Taxonomy and its Code
23 20 uncoordinated, and its aims and audience uncertain.

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26 23 **Introduction**

27 24 The Executive Committee of the International Committee on Taxonomy of Viruses (ICTV-EC)
28 25 recently invited comments on a proposal to approve a standard binomial system of formal virus
29 26 names [25] How best to name and classify viruses have been constantly aired topics for
30 27 discussion since viruses were first discovered at the end of the 19th Century, and particularly
31 28 when the number and diversity of viruses was realized early in the 20th. It was clear that an
32 29 orderly system of nomenclature was required. So why has it taken so long to resolve the issues?
33 30 Can anything be learned from earlier discussion. I believe they can as opinions expressed early
34 31 in this debate are still valid, and indicate why it has taken so long, and also indicate how it can be
35 32 resolved.

36 33 The earliest attempts to name and classify viruses were mostly individual efforts [4, 20],
37 34 and the viruses of animals, bacteria and plants were discussed separately, but a watershed was
38 35 reached when Holmes [14] published "The Filterable Viruses" as Supplement 2 to the 6th
39 36 Edition of Bergey's 'Manual of Determinative Bacteriology'. It was an attempt to establish
40 37 parallel systems of nomenclature for the viruses of bacteria, plants and animals using Latinized
41 38 (Linnaean) binomials (LBs). One result was a meeting of the Society of General Microbiology
42 39 (UK) to discuss the issues, and as Christopher Andrewes noted in his contribution "The
43 40 organizers of this discussion have very sensibly placed me, as representing sound common sense,
44 41 between the two extremists, Drs Holmes and Bawden. Dr Holmes wants to start classifying and

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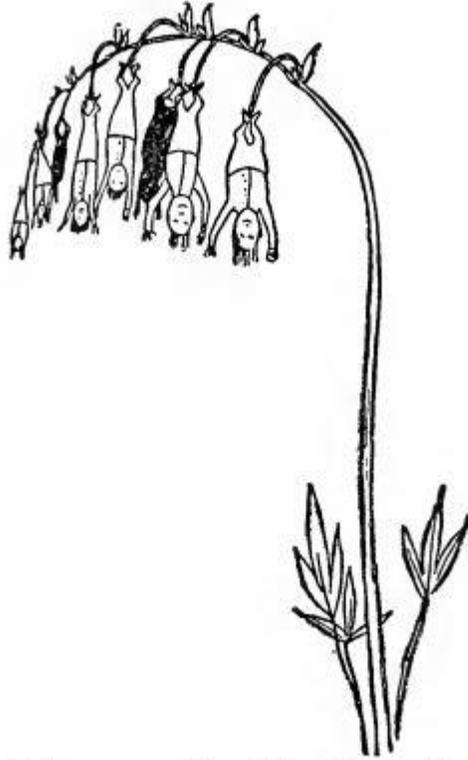
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4 42 naming viruses on Linnaean lines right away. Dr Bawden is almost certain to advise you to have
5 43 nothing to do with any such proceeding"; Holmes [15] pressed the need for nomenclatural
6 44 continuity which, he claimed, would be provided by LBs, Andrewes [2] mostly criticized the
7 45 details of the Holmes/Zhdanov groupings of animal viruses, but Bawden [5] first explained how
8 46 important it is for a classification to have a clear purpose, citing the different classifications of
9 47 plants by botanists or farmers:

10 48 *" The main concern of the farmer or gardener is not whether a plant is graminaceous or*
11 49 *cruciferous, but whether it is a useful plant for him to grow or a pernicious weed. To the*
12 50 *botanist, couch grass may be a near relative of wheat, and charlock of turnips, but to the farmer*
13 51 *one of each pair means a profit and the other a loss, two categories that, to his mind, could not*
14 52 *be more unrelated."*

15 53 Bawden then discussed the characters available at that time for distinguishing between
16 54 different viruses and concluded that they were inadequate to support a system of LB names
17 55 because they did not reveal the phylogenetic relationships of viruses:

18 56 *" The fact that we cannot group our 'collective species' by inferred phylogeny is one of*
19 57 *the reasons that makes me strongly oppose the use of Linnaean binomial names for plant viruses.*
20 58 *These names not only demand identification at the species level, which I hope I have shown can*
21 59 *be done, but the arrangement of species into genera, and the word genus to a modern taxonomist*
22 60 *suggests a group of phylogenetically related species that is clearly separated from other*
23 61 *genera."* Thus Bawden linked the use of Linnaean binomial names firmly with biological
24 62 (phylogenetic) relationships at both the species level and the genus.

25 63 The original attempts to classify viruses were based on details of their host ranges and
26 64 symptoms, but advances in biochemistry provided increasing amounts of information on the
27 65 composition of virions, and, using these, Cooper [7] classified the known viruses of animals on
28 66 whether their genome was RNA or DNA, whether or not there was lipid in the virions, and on
29 67 the size of their virions. Lwoff, Horne and Tournier [19] expanded this classification to apply to
30 68 viruses from all types of host by involving the structure of the virions, which they described as
31 69 either "cubical" or "helical". Lwoff presented the LHT system to a Cold Spring Harbor
32 70 Symposium in 1962 and stated that their classification was "rational" and "an attempt at a
33 71 coherent classification based on essential characters" but not "a natural phylogenetic
34 72 classification". The Symposium synopsis (<http://library.cshl.edu/symposia/1962/index.html>)
35 73 records that Peter Wildy, who was present, "responded rather strongly to what he saw as an
36 74 arbitrary scheme that was not meaningful.", and when he subsequently reported on the
37 75 Symposium to a meeting of microbiologists in the U.K., he summarized his views using a figure
38 76 from Edward Lear's 'Nonsense Botany' (1871):
39 77



Manypeeplia Upsidownia.

Bawden and Wildy were of the same opinion, both considered the adoption of a LB system to be premature, unless the viruses could be grouped in a ‘biological’ or ‘natural’ classification, rather than a system based on arbitrarily chosen characters.

The Cooper and LHT classifications were further developed by Baltimore [3], who separated all viruses into seven non-hierarchical categories based on the type and strandedness of their genomes, and the way in which their mRNAs were produced. There was again no evidence that this classification was biological (i.e. phylogenetic), but it is simple to understand and, perhaps as a result, continues to be widely taught.

In the latter half of the 20th century the amount of taxonomically informative data for viruses increased greatly as viruses were often chosen for research into new techniques during the early decades of development of molecular biology. More recently, methods for, first, protein sequencing and then nucleotide sequencing were developed, and these quickly confirmed that most of the virus groupings devised using phenotypic data [21] were congruent with the phylogenetic relationships calculated from their gene sequences [26], so they were, in essence, the basis for a biological classification.

Further advances in sequencing methods resulted in the discovery that virus-like gene sequences (metagenomes) could be obtained from a wide range of living materials; the extant virosphere was found to be very much larger than expected, and furthermore most of the metagenomes were found to be from outside the phylogenetic boundaries of known virus groupings. The ICTV responded very promptly to this exciting discovery, and a workshop of

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4 99 “invited experts in the field of virus discovery and environmental surveillance, and members of
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6 100 the ICTV Executive Committee” was held in June 2016 to discuss how best to include
7 101 metagenomic sequences into the official taxonomy of the ICTV. Proposals were developed
8 102 during the workshop, and were presented and approved at a meeting of the ICTV-EC just two
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10 103 months later and reported to the world as a ‘Consensus Statement’ of the ICTV-EC [27]! The
11 104 experts had decided to accept virus-like metagenomes as being those of viruses, and to
12 105 incorporate them into the ICTV Taxonomy, even though nothing was known of their phenotypic
13 106 properties, and degraded the precision of meaning of the word "virus". As a consequence, two
14 107 major changes were made to the content and appearance of the ICTV Taxonomy. First the
15 108 available ranks in its hierarchy were increased from five to 15 [24], from Species to Realms, and
16 109 secondly a start was made to include metagenomes in the ICTV Taxonomy [29]. Why this was
17 110 considered useful was not revealed, as those working with metagenomes only require the
18 111 existing vernacular locality-based names for their work.

22 112 So, now the ICTV Taxonomy has Realms at the base of its classification, and the Realms
23 113 are similar to the original LHT/Baltimore categories. The details of the first Realm, the
24 114 *Riboviria*; have been published on the ICTV website, and its name has already become widely
25 115 used on the Internet. Walker et al. [29] stated that:

28 116 *“Perhaps the most notable taxonomic change approved in this ratification is the establishment of*
29 117 *the realm Riboviria, a likely monophyletic clade of viruses with positive strand, double-strand or*
30 118 *negative-strand genomic RNA that use cognate RNA-directed RNA polymerases (RdRPs) for*
31 119 *replication. The realm Riboviria is placed at the highest taxonomic rank permitted by the ICTV*
32 120 *Code”.*

35 121 Although the word “likely” is included, the announcement concludes by stating that:
36 122 *“The evidence for monophyly of RNA viruses and for various clades within Riboviria has been*
37 123 *accumulating over the years from phylogenetic analyses of the universal marker, RdRP,*
38 124 *supplemented by comparison of additional molecular traits shared by subsets of RNA viruses”.*

41 125 This may surprise those who have already read one or other of a large number of
42 126 publications including, for example, Dolja and Koonin [8] who stated that:
43 127 *“Comparison of the genome architectures of RNA viruses discovered by metagenomics and by*
44 128 *traditional methods reveals an extent of gene module shuffling among diverse virus genomes that*
45 129 *far exceeds the previous appreciation of this evolutionary phenomenon.”!*

48 130 So are all the research papers stating that many, if not most, viruses with RNA genomes,
49 131 are polyphyletic in origin, wrong? No. The authors of the ICTV-EC paper have made the
50 132 fundamental mistake of mixing and confusing virus phylogenies and gene phylogenies. The
51 133 twigs of the *Riboviria* tree are mostly of different species and genera of viruses, but at various
52 134 points within the tree, they become the taxonomy of their RdRp genes alone! The *Riboviria* is
53 135 not a monophyly, but a chimaera (i.e. "something made up of parts of things that are very
54 136 different from each other"; Cambridge English Dictionary). It is possible to argue, as one referee
55 137 of this paper has, that the RdRp gene provides, for the *Riboviria*, the equivalent of "*the set of*
56 138 *core genes that are considered to reproduce the replicating lineages of bacteria through time* ,

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4 139 *even though they might acquire and discard various accessory modules related more to shorter*
5 *term environmental adaptation.*" (Anon). This is true but, rather than degrading the precision of
6 140 the words "monophyly" and "polyphyly", it would be better to devise a new word to describe this
7 141 newly discovered evolutionary strategem - perhaps "hyperphyly" is word it needs!
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10 143 The RdRp phylogeny used for the *Riboviria* is that of Wolf et al. [30] and its use implies
11 144 that the ICTV accepts as proven that all RNA-dependent RNA polymerase (RdRp) genes are
12 145 monophyletically related and with a particular topology. This result was obtained using rounds of
13 146 heroic "*semi-manual curation*" with the "*the boundaries of the RdRp domain expanded or*
14 147 *trimmed to improve their compatibility with each other*" resulting in aligned sequences of, for
15 148 example, in Branch 3, up to 89% indels (Y.I. Wolf; personal communication)! It should be noted
16 149 that an early and more direct phylogenetic analysis of the RdRps [31] found "*no support for the*
17 150 *common ancestry of RNA-dependent RNA polymerases and reverse transcriptases*" then known.
18 151 Even if the monophyly of the RdRps is confirmed, it may be difficult to distinguish whether it
19 152 has resulted from divergent evolution from a single ancestor or convergent evolution from more
20 153 than one ancestor [6, 16, 17]; there are probably few molecular structures able to fulfill the key
21 154 roles of an RdRp, and convergence by selection is known to be potent [(e.g. Hill et al., 2019).
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28 156 So what should the ICTV-EC decide apropos Latinized binomials? First, as advised by
29 157 Fred Bawden all those years ago, they should decide the purpose of the ICTV Taxonomy. It is
30 158 my opinion that it has become so complex that only specialists understand how it was derived
31 159 and hence what it can tell them, whereas its primary role, like the other international biological
32 160 Codes, is to best help the broader community, not just specialist viral phylogeneticists. It would
33 161 have been better perhaps to have separated the two roles by maintaining data on the basic
34 162 taxonomy of viruses, perhaps to the level of the ICTV Virus Taxonomy Profiles
35 163 (<https://www.microbiologyresearch.org/content/ictv-virus-taxonomy-profiles>), separate, for the
36 164 present, from attempts to present best the 'black box' of viruses past; there must be many better
37 165 ways than 2D spreadsheets! The ICTV Taxonomy should be a simple biological classification of
38 166 viruses, aligned, where possible, with the other biological Codes, so that users can easily move
39 167 between them. This could be accomplished by several important and concurrent changes.
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45 168 1) The ICTV Taxonomy should be solely and completely 'biological' and 'phylogenetic' at
46 169 all levels, not just species as at present. It would then qualify for the use of Latinized binomials
47 170 for approved species. The classification of viral genes, including metagenomes, is a separate,
48 171 intensely interesting topic, but at the moment it is very much in its early research phase;

49 172 2) The ICTV Taxonomy should be a taxonomy of viruses, not virions, not gene
50 173 sequences, but viruses. The ICTV should promote the view that most viruses are sub-cellular
51 174 organisms with a two-part life cycle (i.e. virions and virus infected host cells) as proposed by
52 175 Forterre [10], not just virions or metagenomes.

53 176 3) The definition of virus species must be clarified, and this is most easily accomplished
54 177 by aligning it with the logical principles used by the other biological Codes. The virus species is
55 178 currently defined as "*a monophyletic group of viruses whose properties can be distinguished*
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4 179 *from those of other species by multiple criteria*". This definition helps no-one, even though it is
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6 180 accompanied in the Code by a long explanation of the characters that may be useful for
7 181 distinguishing one species from others. Instead of trying (and failing) to define the characters
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9 182 that may be used to define a species, it is much simpler (and in line with the other biological
10 183 Codes) for the definition to state how, in practice, species have been defined and why. Thus,
11 184 minimally, a virus species is "*an isolate or group of virus isolates that is considered by experts*
12 185 *using multiple criteria to be so distinct that it is/they are most conveniently known by a single*
13 186 *name*" [12]. There is no need to enumerate those "multiple criteria", the reader only needs to
14 187 know that it has been done by experts who have used the most appropriate criteria, which differ
15 188 for different groups of viruses. However the ICTV should, like the other biological
16
17 188 nomenclatural Codes, use a system of 'types' [11] where "*a type is a particular specimen...of an*
18 189 *organism...to which the scientific name of that organism is formally attached*"
19 190
20 190 ([https://en.wikipedia.org/wiki/Type_\(biology\)](https://en.wikipedia.org/wiki/Type_(biology)) – 15 June 2019). The Codes of cellular organisms
21 191 nominate a single type for each species, and each name is permanently attached to its type. Thus
22 192 the species is the group of individual isolates that are so similar to the type that they are most
23 193 conveniently given the same name (NB for pairwise comparisons, one of the pair is always the
24 194 type). The nomenclatural Codes of cellular organisms have traditionally used dried specimens in
25 195 museums, viable cultures in collections, etc as their types. Existential types are now no longer
26 196 needed as genomic sequences provide ideal surrogates for types; each genomic sequence
27 197 provides a 'datum' for each virus in evolutionary space and time to which a name can be
28 198 attached. The ICTV now lists the Accession Codes of around 90% of the "Exemplar Isolates" in
29 199 its full ICTV Reports (https://talk.ictvonline.org/ictv-reports/ictv_online_report/). To help all
30 200 users, the Accession Codes of Exemplar Isolates should be formally adopted in the Virus Code to
31 201 define the types of approved virus species, and only viruses with a genomic type should be
32 202 recognised as species and given an ICTV approved name. Thus, a renovated Virus Code should
33 203 state, in full, that "*a virus species is an isolate or a group of virus isolates that is considered by*
34 204 *experts using multiple criteria to be so distinct that they are most conveniently known by a single*
35 205 *name, and with one isolate, for which there is a complete genomic sequence, specified as its*
36 206 *'genomic type'*. Each virus species, like the species of cellular organisms, would cease to be
37 207 merely a 'construct of the human mind', but it would be a group of isolates, related by common
38 208 ancestry, that are so similar that the experts who study them know them by a single name, and
39 209 the genomic type would ensure that one of those individuals, once upon a time, had a genomic
40 210 sequence that is now stored in the Genbank database - its parent virus population will move on,
41 211 but its type is stored for ever, we trust, in Genbank.
42 212

43 213 4) Users. The ICTV needs to be more active in its in its interaction with all users, even
44 214 though all understand that the ICTV depends on much selfless *pro bono* work. Its website is a
45 215 rather opaque collection of documents, and needs to have the most useful ICTV products in more
46 216 accessible formats, these should include the ICTV Taxonomy, the ICTV Profiles. Working
47 217 virologists most often require access to the approved name of "their current virus" to embellish
48 218 the Introduction to the next report/paper. Students will perhaps be more interested in the Virus
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Code, which should be revamped with clearly stated principles so that anyone with a grounding in science, especially biology, can understand it and thereby understand the ICTV Taxonomy. The ICTV should also use the social media for announcements, discussions, and so that the occasional ICTV ballots might have more validity.

If such changes are made:

1) The ICTV will be seen to support the long-term convention that LBs are only used for biological classifications;

2) Non-specialists will benefit and, when using the ICTV website, will not be fooled by a 'pseudophyly' into believing that the evolution of viruses has followed the same 'tree of life' plan as cellular organisms, but will discover that the pattern of evolution of viruses and of simple cellular organisms is profoundly different from that of cellular organisms with completely different ratios of horizontal and vertical gene flow;

3) The use of names of cellular organisms will benefit from exposure to the ICTV Code with its stricter separation of formal LBs and vernacular names;

4) The ICTV website must help promote the exciting opportunities for research revealed by metagenomes, not only using the latest mega-data computational techniques [e.g. 1, 9, 18, 22, 23, 26, 28] to explore the 'black hole' of virus pre-history, but also as clues for finding and describing the myriad of undescribed viruses that have provided metagenomes.

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Declarations

This work was funded by me; I have no 'conflicts of interest' or 'competing interests'

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