Dear EC members

As a contribution to the agenda item in Section 7 on species names at the forthcoming EC meeting, I have drafted out some thoughts and discussion about the various issues about species names and the extent of their reference compared to the rest of biology. Some of this follows on from the nomenclature discussion on the Oxford meeting and subsequent publication (on the existence of parallel nomenclatures).

I appreciate that this is quite a complex document, although this is perhaps inevitable given the underlying issues. It also, despite the analysis, does not come to a definite conclusion, but I hope it appropriately formulates and summaries the issues in question in a more structured way, and it does put forward several possible options going forward.

For some, many of the ideas discussed are heretical, and have not really been addressed since the start of virus and virus species name reference distinctions made by Marc van Regenmortel three decades ago. I would therefore ask you to bring an open mind to the various discussion points, be aware of how species reference works elsewhere in biology and finally, consider the possibility that the introduction of species name binomials may not provide the clarity of reference that might have been originally hoped. As the introductory dialogue shows, quite the opposite in some cases.

Look forward to the discussions at the EC.

Best wishes

Peter

The nomenclature of viruses and virus species – options for change

The following is an approximate transcript of a conversation with an experienced principal investigator (PI) at an UK HCV workshop in May, 2023. It took place immediately after a presentation where I described the new species nomenclature for viruses, with examples from the *Flaviviridae* family:

- PI That was a great update on virus taxonomy and very interesting to hear about the changes to the name of HCV by the ICTV
- PS Many thanks, although as I presented and tried to emphasise, it's not the name of the virus that is being changed, it is a change to the name of its species to the new term *Hepacivirus hominis*
- PI Yes, it's very interesting to see these Latin names being used, but I wonder how long it will take clinicians to get used to using, what was it, Hepacivirus, er.... hominis?
- PS Well, the clinician would still refer to it as HCV
- PIbut we now know that its real scientific name is now going to be *Hepacivirus hominis*..... can we abbreviate it to HH possibly?
- PS <inwardly groans, deep breaths> I enjoyed your student's presentation too

The International Committee for the Taxonomy of viruses (ICTV) recently mandated a systematic change to the names of virus species to a regular (usually Latinised) binomial format (genus + species epithet) so that they match those of taxon names used elsewhere in biology. These are believed to be more distinctive and recognisable as species names than previously - many of which were just italicised versions of the names of the viruses assigned to them. Conversion of the over 10,000 currently assigned species names to a binomial format will be completed in the next ICTV ratification round in early 2024. Several short and longer summaries have been published by the ICTV to justify these changes and to explain the process (1-3).

Despite this step towards harmonisation of taxonomic terms, there still remain major differences in how the ICTV requires names of viruses and names of virus species names to be used from conventions followed in the rest of biology. Based on the original and highly influential treatise *"Viruses are real, virus species are man-made, taxonomic constructions"* and subsequent writings by Marc van Regenmortel (4, 5), virus taxonomic groupings are regarded as man-made categories with definitions. These are contrasted with organisms that can only be described (see Appendix 1). Taxa can therefore be regarded as typologically¹ distinct from the objects assigned to them. Viruses, as members of a species, whether as externally visualised virion particles, or as replication complexes within infected cells, are tangible objects with a physical existence, while the species to which a virus is assigned is an abstract man-made category. Although not the only way to conceptualise the nature of viruses (6, 7), the distinction between viruses as objects and species as categories has been explicit in the taxonomy of viruses since the beginnings of the ICTV (4, 5). This distinction has been reflected in the development of separate rules and conventions for writing names of viruses and for writing the names of the species to which they are assigned.

In this dichotomy, virus names are unregulated by the ICTV and simply follow whatever the virus community wishes to call them. Thus the virus name hepatitis C virus (HCV) was coined by the discoverers of this medically important virus when first described (8), while its species name (currently *Hepacivirus hominis*) was assigned by ICTV committees at a much later date. Virus names possess no standardised format and also may have local forms in different languages (*eg.* English: rabies virus; French: virus de la rage). In marked contrast, species names are formalised and regulated by the ICTV and are now mandated to be in a binomial format (genus + species epithet).

¹ The word "typology" can be used to describe the range of reference to objects or categories of a given term.

Species nomenclature is universal and invariant across languages. with names containing only letters of the Latin alphabet and numbers. In binomial names, the first word would be the name of the genus and the second a species epithet derived from a descriptive element for the viruses assigned to it.

While the typological distinction between names for viruses and virus species is logical and has been in use for over three decades, the typology of species as category and virus as object is inconsistent with the approach used for species nomenclature elsewhere in biology. Typically, while biologists implicitly differentiate between an instance of an organism and its classification to a species or other taxonomic rank, there appears to be no perceived requirement for different terminologies for them. Hence, the species term can equally refer to a taxonomic category (*eg.* "a border terrier is a member of the species *Canis familiaris*") or to physical objects, such as in statements "anatomically modern *Homo sapiens* spread out of Africa 150,000 years ago". Indeed, for the (vast majority of) species that lack common names, such as *Drosophila melanogaster* and *Streptococcus pneumoniae*, there is no other option.

Outside of virology, whether or not species names are used or not is more related to need for precision in communication; species binomial names are proposed and adopted through publication in approved journals describing its properties and creating a corresponding entry in the species list maintained by the relevant official body (ICZN, ICBN, ICPN) – there may additionally be a type specimen submitted to an international repository. Species names are universal terms in scientific discourse, in contrast to language-specific and often less precise terms in vernacular use. Indeed, references to organisms may not even map precisely with species categories (*eg.* Siamese cat, sea gull, horse, orchid, oak tree, plague). Rather than signifying a typological difference between an organism and the taxon to which it is assigned (as assumed in virology), binomial names are more commonly described as "scientific names" or "systematic names" in recognition of their formal definitions and universality.

Strikingly, common, language-specific names can be also used for both species and instances of a species outside of virology. The word "dog" as in "a dog bit me on the ankle" describes a concrete (hairy) entity, while "a border terrier is a type of dog" represents an (approximate) species term in a classification statement. In this and elsewhere where common names map onto species (*eg.* human being / *Homo sapiens*; cat / *Felis cattus*, polar bear / *Ursus maritimus* among a huge number of possible examples), the use of common names or binomial species names is very much a matter of convention and context, not typological necessity. Indeed, for the majority of assigned animal, plant, fungal and bacterial species, the lack of a common names forces binomial terms (*Escherichia coli, Drosophila melanogaster etc.*). The ease with which language can change its reference between objects and categories is intrinsic to the innate mapping of words to internal categories and instances of them (Appendix 2).

Virologists, particularly those involved in taxonomy, have codified the typological distinction between objects and containers as they refer to viruses and taxa. Nevertheless, when it comes to classification of viruses below the level of species, the distinction between categories such as serotype, strain or genotype and the viruses assigned to that genotype evaporates. In the specific example provided in Appendix 3 (from numerous occurrences of combined usage), a statement where a genotype of hepatitis C virus (HCV) is used as a category ("Variants infecting injecting drug users in the UK are largely of genotypes 1a and 3a") coexists happily with statements where genotypes refer to objects "the patient in the ward is infected with genotype 1a"). The latter usage is not allowed when a species term is used ("the patient in the ward is infected with *Hepacivirus hominis*").

Should the typology of virus and species names be changed to match usage in the rest of biology? The introduction of binomial names for virus species matching those used elsewhere in biology had the laudable intention of making species names more obviously recognisable. The change would, it was hoped, accentuate the difference between species names (as categories) and the names of viruses (as objects) assigned to them. However, as exemplified by the dialogue at the start of article, the use of binomial names for virus species may in some circumstances increase confusion. Those confronted with binomial species names for viruses may make an implicit assumption that they might take on the same dual reference to species and objects used elsewhere in biology. If the (presumed systematic) name of HCV is now *Hepacivirus hominis*, then surely patients can be infected with the species too.

Indeed, lit is safe to assume that all clinicians, veterinarians and crop scientists learn about taxonomy and species terms in biology and become accustomed to their nomenclature long before they learn about the atypical species name typology for viruses. For example, a clinician may declare that a patient is infected with *Streptococcus pneumoniae* but might be surprised to be told by an ICTV EC member that the patient cannot be infected with *Respirovirus pneumoniae*. In the latter case, the correct terminology according to ICTV rules would be that the patient was infected with a member of the species *Respirovirus pneumoniae* or to use the virus name, infected with human parainfluenza virus 4. With identical name formats but with different underlying references to categories and objects, confusion and incorrect usage of virus and virus species names becomes inevitable.

Another argument for widening species name reference is utilitarian. The ongoing expansion of the number of viruses characterised from metagenomic studies may lead to the assignment of 100,000 or more additional species in the next few years. Under current conventions, virologists would have to create both species and virus names, a dual inventory that is unnecessary in the classification of other organisms (such as the current 350,000 and still expanding number of beetle species). This could be avoided if species reference was expanded to include the viruses assigned to them.

Is a species assignment adequate as a description of a virus? Referring to viruses directly by their species names may have advantages in compatibility with biological usage and avoiding virus and species name duplication. However, a major concern is that species names may not always adequately describe and differentiate what might be quite different viruses assigned to the species. Indeed, there is substantial, and partly historical, variability in assignment principles that have created species terms that may not map directly to the names of viruses assigned to them.

Historically, and rather like the original classification of animals and plants, virus species were originally assigned as a lowest division of viruses with distinguishably different properties. Species assigned might be based upon characteristic descriptions of transmissible diseases, such as yellow fever, measles, or rubella in humans, plum pox, wheat yellow dwarf or banana bunchy top in crops, or disease location, such a virus haemorrhagic diseases in the Semliki forest or Crimean Congo haemorrhagic fever. The use of these disease descriptions to assign and name virus species were often made before their subsequent virological and genomic characterisation. Subsequent work generally showed that their genetic relationships generally, although not invariably, followed their phenotypic distinctiveness from each other. albeit with little consistency in degrees of genetic divergence from each other (see Appendix 1). In such cases, there is a one-to-one equation of virus and virus species assignment.

More recently, cases have arisen where multiple clinically distinct viruses are more consistently assigned to the same species on genetic grounds. These assignments often arose when genomic characterisation of virus isolates from geographically or phenotypically distinct clinical cases revealed the presence of closely related viruses. From a huge number of possible examples, this includes the

assignment of polioviruses and the markedly less pathogenic coxsackiviruses types (*eg.* serotypes C20, C22 and C24) to the same species, *Enterovirus coxsackiepol*. Multiple viruses, such as Bunyamwera virus, Germiston virus, Lokern virus, Mboké virus, Ngari virus, Santa Rosa virus, Stanfield virus and Xingu virus have all been assigned to the species, *Orthobunyavirus bunyamweraense* even though they were originally described as distinct viruses geographically and clinically. The human-infecting hepatitis E virus has been assigned to the same species, *Paslahepevirus balayani*, as a range of related viruses also infecting pigs, boars, rabbits and camels. In these and compatible cases, the virus name is actually the more useful label that than its species assignment. For example, a statement that a patient is infected with (a member of) *Enterovirus coxsackiepol* is inadequate as clinical description, when compared to one that identifies patients infected with poliovirus (international public health disaster) and those with CVA-22 or CVA-24 (no clear clinical relevance).

Similarly, the species to which SARS-CoV-2 is assigned includes quite different viruses, such as SARS-CoV and a range of related viruses infecting bats. These are all closely related to each other genetically but they possess quite distinct properties from the agent of the last global pandemic. Infection with *Betacoronavirus sarsi* in therefore an uninformative statement clinically, for public health and for the individual concerned. Indeed, the existence of intra-species variability in virus phenotypes is reflected in approximately 5% (460 / 11273) of the species entries in the ICTV Virus Metadata Resource listing additional viruses, generally to reflect the range of properties beyond that of the exemplar virus.

As a further problem, there are several very widely used virus names that do not map onto species assignments because they are polyphyletic. For example, the terms human immunodeficiency virus type 1 (HIV-1) and HIV type 2 (HIV-2) used to describe the causative agents of AIDS are fundamental in microbiology, infectious diseases and have wider societal use. Genetically, however, neither virus possesses a single common ancestor distinct from chimpanzee- (HIV-1) or sooty mangabey- (HIV-2) infecting viruses from which they derive (9), with subtypes (HIV-1 groups M, N and O; HIV-2 groups A, B, P and others) originating from separate zoonotic events. The two species to which they are current assigned therefore includes a wide range of primate viruses and illustrates the need for separate HIV-1 and HIV-2 terms to describe human infections and as causative agents of AIDS.

The comparison with bacterial species is stark - with some rare exceptions, such as *E. coli* that infects humans as a commensal, but which may exist in enteropathic or enterohaemorrhagic forms such as *E. coli* O157:H7, species assignment of bacteria generally provides an appropriate categorisation. There is thus little or no need for names of bacteria separate from their systematic names. In wider biology, the description of variants within a species possessing different characteristics is generally achieved through the creation of additional ranks below species, such as subspecies, variety or pathovar. These might be assigned using trinomials (*eg. H. sapiens sapiens* or *Pan troglodytes verus* as examples from zoology) although these remain taxonomic terms and possess its associated typology – they are not equivalent to the use of virus names to indicate a specific subgroup of viruses within a wider species definition.

Conclusions. This review of virus nomenclature during the period of transition to binomial species names raises a number of questions about the relationships between virus and species names, and their parallels elsewhere in in biology. As described, the issues under discussion are perhaps more nuanced than might have been initially assumed and there may not be a "one size fits all" solution.

There are several possible future options for species nomenclature change that the ICTV might consider – these include:

- a) Retain the current ICTV principles of nomenclature and typology. Viruses as objects would be named separately from ICTV mandated nomenclature of virus species that retain their typological reference to categories or containers. This would not resolve the tendency of the wider community to imbue virus species binomial names with the typological properties of species encountered elsewhere in biology.
- b) Re-cast virus species names as systematic names and extend their reference to viruses and their assigned species taxon. Under this approach, existing virus names would simply be colloquial terms used by the community and possess no taxonomic status (in the same way that "dog" is unrepresented in the ICZN species list). Where reference to specific subsets of viruses within a species, such as serovars or genotypes, is required, these could be formulated into a trinomial (*B. sarsi* subsp. SARS-CoV-2) and incorporated into the ICTV taxonomy.
- c) Transition to shared systematic names for viruses and their species assignments, but retain the current cataloguing of virus name terms where these are widely used or required. For example, virus names may be used more appropriately for general use ("measles virus" in preference to "Morbillivirus hominis") and where they are required to separately identify subsets of viruses within a species (eg. HIV-1, SARS-CoV-2, poliovirus). Species names and the names of viruses assigned to the species or a subset of the species would possess both object and category reference (and thus resolve the currently inconsistent shared typology in the HCV genotype example). Newly assigned species would not require virus names unless these were of value colloquially or were required to differentiate subsets.

The "do nothing", "change to biology" and "compromise" options each possess different advantages and disadvantages and it would be helpful if these could be evaluated by the ICTV and the wider community.

Wider compatibility with biology. Of course, making changes to the nomenclature and reference of virus species manes is only one step towards greater compatibility with conventions used elsewhere in biological taxonomy. For example, higher ranks of virus taxa above genus and species are written in italicised form (*eg. Flaviviridae, Ribovira*), whereas they are not italicised in other biological taxonomies. Is this a distinction that the ICTV wishes to maintain? Similarly, the ICTV does not provide clear guidance on whether genus names used in species epithets can be abbreviated after first mention (*Hepacivirus* hominis -> *H. hominis*). As with species reference, there will be an immediate tendency to do this when virus species names start to resemble those used elsewhere in biology.

As for species nomenclature and reference, it should be recognised that steps towards wider sharing of taxonomic conventions are self-amplifying in the community, and I believe that the change for binomial names for virus species may create pressures for wider changes in virus taxonomy in the future by the wider virology community and perhaps also the journals.

Peter Simmonds 27/07/2023

Appendix 1: What are species?

The classification of organisms into discrete species and higher taxa is a key organisational tool in biology and serves to catalogue and structure the vast diversity of life. It has historically provided the primary basis for taxonomy, starting from around the time of Linnaeus and Darwin in the 19th century (10, 11). The assignment of animals, plants and fungi into species is widely based upon their capacity to interbreed and consequent membership of a shared gene pool (12, 13), although there are many boundary exceptions and occasional asexual replication strategies of some larger multicellular organisms

The extent to which asexual eukaryotes, prokaryotes, archaea and viruses can be similarly assigned to discrete species has been extensively debated but is currently resolved in favour of creating parallel taxonomies of species, genera and higher rank assignments that are analogous to those of animals and plants, despite the inapplicability of biological species (sexual compatibility) criteria. However, in view of their microscopic size, until the second half of the 20th century, classification of bacteria and viruses and the species to which they were assigned primarily focussed on the characteristics of their associated diseases rather than of the causative organisms. Diseases have indeed guided their nomenclature – tuberculosis is caused by bacteria of the species *Mycobacterium tuberculosis*, cholera by *Vibrio cholerae*, measles caused by measles virus, similarly for the viruses casing rabies and influenza.

As sequence acquisition for viruses accelerated through the 1980s, there was a transition from classifications based on disease, or phenotypic properties of viruses to one largely based on genetic relationships. Methodological advances, such as large-scale nucleotide sequencing of virus genomes has provided a wealth of new information on the nature of viruses and their evolutionary relationships that was absent from their original phenotypically-based classification. However, to a large extent, the assignment of specific diseases to different virus species matched genetic relationships between causative viruses. Thus, the orthoflaviviruses responsible for distinct mosquito-borne diseases such as Japanese encephalitis virus, West Nile virus, Chikungunya viruses and Dengue fever virus were also genetically distinct from each other and from other orthoflaviviruses vectored by ticks. The existence of genetic correlates for earlier disease-based species assignments indeed frequently provided an initial framework with which to add newly discovered viruses to the classification whose disease phenotypes were less well characterised or unknown. However, for newly discovered viruses where information on disease associations or other phenotypic properties may be entirely lacking, nucleotide or amino acid sequence divergence and patterns of natural genetic clustering may represent the only metric available for species and higher rank taxonomic assignments.

Apart from the current requirement in the ICTV code that members of the same species have to be monophyletic, *ie*. consistently group together genetically to the exclusion of all other viruses (14), there are no pre-defined sequence divergence thresholds or other metrics of genetic relatedness to define virus species. Indeed, the degree of genetic divergence between virus species can be highly variable in different virus groups even within the same family; members of the same species in the genus *Hepacivirus* (family *Flaviviridae*) may show up to 35% nucleotide sequence divergence from each other, while members of different species in the genus *Orthoflavivirus* in the same family may differ by <2%. The intrinsic arbitrariness of these species assignment criteria contrasts with the frequent precision and biological relevance of those used for cellular organisms. Organisms with sexual reproduction can be assigned into species if they share gene pools and the profound evolutionary consequences for inter- and intraspecies competition and fitness selection Similarly, while classification of bacteria into species also had historic roots in the phenotypic properties of isolates, genomic methods such as multilocus sequence typing (MLST)(15) and metrics of genomic

sequence similarity are increasingly used for bacterial species assignments. Indeed, a relatively robust 94% average nucleotide sequence identity (ANI) threshold can be used to assign isolates to bacterial species in a way that is comparable to traditional and MLST methods (16, 17).

Appendix 2. Intrinsic categorisation.

In a wider cognitive and linguistic context, the distinction between a category and the entities assigned to that category are not generally differentiated conceptually or separately expressed in language. As described previously (18), and far more elegantly in (19), species are categories that possess a part/whole relationship between the individual and the species to which it is assigned. In the example provided, the Earth may be classified as an instance of the astronomical category "planet", as might Mars, Jupiter and others in our solar system, planets being defined as being typically large, round in shape and in a stable orbit around a star. This definition differentiates planets from other celestial entities, such as comets, asteroids and moons. However, it is also possible to create sentences such as "a meteorite crashed into the planet" where "planet" is used to mean a physical object.

There are of course alternative formulations of species conceptualisation where species are regarded a real biological entities (20-22) and these take us even further from the ICTV mandated conception of a species as a container or category. As an evolutionary group rather than a category, virus species comprise organic replicating lineages - the species term, *Orthoflavivirus zikaensis* would then refer to the physical collection of Zika virus particles and replicating entities within the cells and hosts they infect at any one instance as physical objects. In further distinction, a species as an evolutionary group can only be described, not defined, unlike a class with specific inclusion and exclusion criteria, Under this formulation *Orthoflavivirus zikaensis* can remain as a species even if that lineage of viruses evolves away from its original species assignment criteria, for example a change in geographical range following the recent emergence of the virus in South America.

Appendix 3. Internal inconsistency with nomenclature for virus strains and genotypes.

The virus species nomenclature for viruses as objects and taxa as containers is inconsistent with the way in which viruses are described at other taxonomic levels, particularly the terminology used for virus variants below the level of species. In this specific example (but widely encountered in other virus groups), hepatitis C virus (HCV) is assigned to the species *Hepacivirus hominis*, one of many species within the genus *Hepacivirus* in the family *Flaviviridae*. Species have been created for groups of viruses showing <50% nucleotide sequence divergence from each other, a division that corresponds closely to their differences in host range. However, viruses within the species *Hepacivirus hominis* are also genetically quite diverse with 8 genotypes of HCV currently assigned using a 32-33% nucleotide sequence divergence threshold. These below-species level assignments associate with serological and epidemiological differences and response to therapy, and are widely used in in the medical and scientific literature.

Thus hepacivirus species, genotypes and subtypes are all genetically determined categories, but there is no semantic distinction between genotypes and viruses assigned to genotypes. Classification statements where genotypes are a category, such as "Variants infecting injecting drug users in the UK are largely of genotypes 1a and 3a" use the same terminology as statements where genotypes are objects "the patient in the ward is infected with genotype 1a". This usage is more comparable to terminology used elsewhere in biology, where the context determines the typology of the terms, *ie.* whether a category (genotype) or an instance of a category (a physical virus) is being referred to. In contrast, the usage "the patient was infected with *Hepacivirus hominis*" is not allowed by the ICTV because, so it is argued, a patient cannot be infected with an abstract taxonomic category.

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