



This Word module should be used for all taxonomic proposals. Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic_Proposals_Help_2019.

Part 1: TITLE, AUTHORS, etc

Code assigned:	to be completed by ICTV officers
<p>Short title: Modify the International Code of Virus Classification and Nomenclature (ICVCN) to prospectively mandate a uniform Linnaean-style virus species naming format and to retrospectively mandate changing of existing species names to the same format within 2 years (with an exception provision for prokaryotic virus species names)</p>	

Author(s) and email address(es):

List authors in a single line <i>Archives of Virology</i> citation format (e.g. Smith AB, Huang C-L, Santos, F)	Provide email address for each author in a single line separated by semi-colons
Dutilh BE, Junglen S, Kropinski AM, Krupovic M, Adriaenssens EM, Kuhn JH, Postler TS, Rubino L, Sabanadzovic S, Simmonds P, Varsani A, Zerbini M	bedutilh@gmail.com; sandra.junglen@charite.de; phage.canada@gmail.com; evelien.adriaenssens@quadram.ac.uk; mart.krupovic@pasteur.fr; kuhnjens@mail.nih.gov; tp2405@cumc.columbia.edu; luisa.rubino@ipspp.cnr.it; SSabanadzovic@entomology.msstate.edu; peter.simmonds@ndm.ox.ac.uk; Arvind.Varsani@asu.edu; zerbini@ufv.br

Corresponding author

Kuhn, Jens H.; kuhnjens@mail.nih.gov

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal)	N/A – Direct submission to ICTV Executive Committee
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:

June 6, 2018

Date of this revision (if different to above):

July 8, 2019

ICTV-EC comments and response of the proposer:**Part 2: NON-STANDARD****Text of proposal:****INTRODUCTION**

Virus taxon names above the rank of species reflect names of similarly ranked taxa in other biological taxonomies by consisting of highly standardized single words. In virus taxonomy, these names end in rank-specific suffixes and follow certain requirements (i.e., all these names are mandated by the International Code of Virus Classification and Nomenclature [ICVCN; “Code”] to begin with a capitalized first letter, be italicized in their entirety, and to end in suffixes such as *-virus* [genera], *-viridae* [families], *-virales* [orders], or *-viricetes* [classes]). Examples are *Morbillivirus*, *Tombusviridae*, *Picornavirales*, and *Ellioviricetes*, respectively.

In botanical, mycological, prokaryotic, and zoological taxonomies, that is in *all non-virologic organismal taxonomies, species names are also highly standardized.* In these taxonomies, species names, with rare exceptions, follow a binomial format spearheaded by Carl Linnaeus in 1753 [7]. This format consists of two (→“binomial”) italicized and Latinized words with the first capitalized word being the name of the genus to which the species belongs (“genus name”) and the second lower case word denoting the species (“species epithet”) [3-5]:

- botany: *Arabidopsis thaliana* (L.) Heynh. (the species for thale cress, genus *Arabidopsis*); *Verticillium albo-atrum* Reinke & Berthold, 1879 (the species for an ascomycote, and an example for the rare case of Linnaean names being pseudobinomials due to a hyphen inserted in the species epithet);
- mycology: *Pleurotus ostreatus* (Jacq.) P. Kumm., 1871 (the species for pearl oyster mushrooms, genus *Pleurotus*);
- bacteriology: *Escherichia coli* Migula 1895 (genus *Escherichia*); and
- zoology: *Pan troglodytes* Blumenbach, 1775 (the species for common chimpanzees, genus *Pan*).

In virus taxonomy, species names are not yet standardized and, hence, follow a plethora of different formats, among others:

1. non-Latinized species-genus binomials, e.g., *Lassa mammarenavirus* (included in the genus *Mammarenavirus*);
2. non-Latinized species-genus trinomials and multinomials using words, e.g., *Tai Forest ebolavirus*, *Calla lily chlorotic spot orthospovirus* (included in genera *Ebolavirus* and *Orthospovirus*, respectively);
3. non-Latinized species-genus trinomials containing numbers or letters at different positions, e.g., *Mammalian 1 orthobornavirus*, *Avian orthoavulavirus 1* (included in genus *Orthobornavirus* and *Orthoavulavirus*, respectively);
4. non-Latinized genus-species binomials (e.g., *Alphaarterivirus equid*) or multinomials including numbers (e.g., *Etaarterivirus ugarco 1*);
5. non-Latinized genus-species binomials with species epithets being numbers or letters (e.g., *Aalivirus A*, *Sanfarnavirus 1*);

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6. non-Latinized binomials with identical suffixes in both word components (e.g., *Senegalvirus marseillevirus*);
7. single-word species names that on first glance appear to be genus names, e.g., *Lausannevirus*;
8. species names that are identical in spelling to the names of their member viruses and are only differentiated from them via italics and, sometimes, capitalization, e.g., *Cafeteria roenbergensis virus* as the species for Cafeteria roenbergensis virus or *West Nile virus* as the species for West Nile virus; and
9. species names that mimic virus names but are more or less distinct from the names of their member viruses, e.g., the species *Seneca virus A* for Seneca Valley virus; *Severe acute respiratory syndrome-related coronavirus* for severe acute respiratory syndrome coronavirus; *Pseudomonas virus D3112* for Pseudomonas phage D3112; *Salmonella virus P22* for Salmonella phage P22.

This inconsistency in species name formats and styles makes it difficult to impossible for virologists, let alone non-virologists like educators, policy-makers, students, or copy editors to identify a given name as a species name or to differentiate it from a virus name. In addition, search engines, in particular those embedded in commonly used electronic scientific databases, cannot easily be programmed to recognize species names because of the lack of a species name-defining format.

PROPOSAL**PART A: mandate a uniform virus species naming format**

The potential need for a uniform, standardized virus species naming format to decrease confusion in the literature, databases, and during oral proceedings has been discussed at the level of the ICTV Executive Committee (EC) over several years during the annual EC meetings. During the EC48 meeting in 2016, after emphasizing that “*most EC members indicated that they were in favour of moving to a binomial system in which the genus name was followed by a single word as the specific epithet*” [1], the EC tasked a subgroup to describe the current variety of species name formats and to describe potential pitfalls of a move to a uniform standard, which ultimately would require the renaming of most currently established species. This internal document [1] focused on various species naming formats, including the pros and cons of a Linnaean-style binomial format reminiscent of that used in all other biological taxonomies. Around the same time, a larger group of virologists together with several ICTV EC members authored a manuscript evaluating the feasibility and ease of switching existing virus species names to the Linnaean format using all then-official names of species in the order *Mononegavirales* and the family *Arenaviridae* [11].

Based on both documents, the EC discussed the issue of a standardized virus species naming format again during the most recent EC meeting, EC50, in 2018. A poll among all present EC members at the time resulted in unanimous support of establishing a **uniform** species naming format due to the advantages such a format would bring to proper species name/virus name differentiation and database programming. This TaxoProp formalizes the outcome of the EC poll by officially proposing to change the Code to mandate a uniform species naming format.

Importantly, because virus species names are currently not formalized and because numerous formats are in use, any move towards any standardized naming format would require changing the majority of virus species names independently of the chosen uniform

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format. Arguments for or against a particular naming format can therefore not be based on concerns regarding the need to memorize novel species names or the need to create novel names.

PART B: mandate a uniform binomial virus species naming format

The need to differentiate properly between virus species names and virus names and the obvious difficulty of the virologic community to do so correctly, which is evident in the published literature and has been pointed out by numerous experts [2, 6, 12]; the long-standing history of genus-species epithet-style binomial species names in all non-virologic subspecialties of biology; and the immediate conveyance of genus affiliation of a particular species in a traditional biological (Linnaean) species name also resulted in a unanimous EC50 vote to model the uniform virus species format accordingly, i.e., to mandate a binomial virus species naming format that is characterized by:

- two single word components only, separated by a space (true binomial akin to the prokaryotic species name *Escherichia coli*);
- the first word being the genus name (identifiable by the already mandated genus name suffix *-virus*) and the second name being the species epithet as in other biological taxonomies;
- the first word having its first letter capitalized and the second word never being capitalized again akin to other biological taxonomies;
- both word components being italicized; and
- both word components consisting only of letters of the standard Latin-script English alphabet containing 26 letters without diacritical marks.

This TaxoProp formalizes the outcome of the EC poll by officially proposing to change the Code to mandate a uniform binomial “genus-species epithet” virus species naming format with the stipulations outlined above.

Importantly, currently only a handful among the ≈5,000 established virus species names comply with the proposed format (namely those of the nidoviral family Arteriviridae). Consequently, acceptance of this TaxoProp would require almost all current virus species names to be changed independently of whether the chosen uniform format is to be Linnaean (“Latinized”) or not. Arguments for or against a truly Linnaean naming format therefore cannot be based on concerns regarding the need to memorize novel species names or the need to create novel names.

The EC also discussed community-derived suggestions to replace taxon names and/or virus names altogether with numerical codes. However, although assigning numerical codes to taxon names was considered potentially useful for database and other bioinformatic purposes, replacing taxon names with numerical codes was unanimously seen as unhelpful. Scientists need to be able to communicate in written and oral form about their viruses and affiliated taxa, and numerical codes are notoriously difficult to remember for audiences even for extremely short periods of time. Furthermore, a single-digit error in a numerical code (e.g., 0765.07.978 instead of 0765.08.878) may have disastrous consequences in a numerical system whereas a single typographical error in an otherwise recognizable taxon name may be identified right away and database confusion is much less likely to occur (e.g., *Escherikhia coli* instead of *Escherichia coli*).

Text of proposal:**PART C: mandate a uniform Linnaean virus species naming format**

Whether a mandated genus-species epithet virus species naming format should also require Latinization to result in truly Linnaean species names was deemed to require additional debate during the EC50 discussion. In early 2019, an informal poll was performed by one of the authors (Kuhn) among all ICTV negative-sense RNA virus Study Groups to inform the debate on this question. Within 2 weeks, one of us (Thomas Postler) was able to devise Linnaean-style names for all currently recognized (≈ 800) negative-sense RNA virus species. The poll was sent out to Study Groups to evaluate a) whether these names were objectionable in principle and b) whether the Study Groups saw any downsides to Linnaeanization if genus-species binomial virus species names were required by the ICTV. Whereas some virus species name changes were suggested, the Study Groups did not object in principle to most of the proposed names. Whereas several general objections were made to the implementation of Linnaean names, objectors typically did not provide suggestions for alternative naming schemes and objected primarily on grounds of change (e.g., the perceived notion of having to learn many new names), or concerns about having to learn Latin to be able to devise novel names. Based on these responses, we assume here that objectors to Linnaean species names favor devising non-Latinized genus-species-style virus species names. Importantly, during the debate, several ardent objectors changed their views and, after having considered all arguments that had been brought forward by others, began to support Linnaean virus species names.

This TaxoProp officially proposes to change the Code to mandate a uniform Linnaean binomial “genus-species epithet” virus species naming format, albeit without the “authority” appendages used in, for instance, zoological taxonomy.

As was pointed out by numerous discussants, Linnaean virus species names would bring the following major advantage over non-Linnaean names:

Linnaean species would be internationally recognizable as they do not change in typography (alphabet or language) even in texts using non-Latin alphabets or other scripts (Appendix A). A Linnaean species name, precisely because it looks foreign due to the unfamiliar Latin suffixes, typically remains untouched by copy editors or journalists, whereas a non-Latinized virus species name would automatically appear “English-looking,” thereby be easily confused with virus names, and thereby bring the temptation for translation. For instance, the current species name *Tai Forest ebolavirus* appears to be written in English and hence could easily be, but should not be, translated into Ukrainian (“еболавірус лісу Таї”) when only the name of the species-associated virus (Tai Forest virus) should undergo translation (“вірус лісу Таї”). Such illicit transliteration of species names is much less likely to occur when the species name has a distinct non-English/non-“living” language appearance (e.g., *Ebolavirus silvataiense*). Untranslated and untransliterated species names also bring the advantage of serving as a connection point for species members, which are written and translated in any language of relevance. That is, even a reader not familiar with Chinese script can identify a Chinese article as of possible relevance to his/her field due to the interspersed Latin species names of an organism of interest (Appendix A).

Several concerns are frequently brought up in context of Linnaeanization of virus species names, all of which we think need to be carefully reconsidered:

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Concern #1: “Latinization would require the new memorization of several thousand species names by virologists” [12]

- as pointed out above, no matter how virus species names are standardized, most current species names would have to be changed to adopt a uniform nomenclature. If memorization of species names is indeed a goal of individuals, new names will have to be memorized whether species names are Latinized or not;
- however, why individuals would have the need to memorize species names is unclear. Most virologists work with viruses and, hence, possibly have the need to remember certain virus names and their abbreviations—but not their affiliated species names. Whereas virus names are supposed to be as stable as possible over time, species names will likely change on a constant basis until virus taxonomy has been developed to cover the majority of the global virus diversity. Hence, new species names would have to be memorized constantly no matter their naming format. This situation is not different from other biological taxonomies, which, despite being much more developed/advanced than virus taxonomy, are still in major flux, with taxa being changed continuously;
- we also consider any attempts to memorize species names to be futile. A single entomologist is unlikely to be able to list even a fraction of the 400,000 currently established beetle species names (or even the actual beetles), let alone a scientist who has even a rough overview of animal species. Recent studies estimate that virus diversity by far exceeds those of prokaryotes [8-10], which are estimated to number in the billions to a trillion. Thereby any virologist’s attempt to memorize the species composition of even smaller taxa will likely be unsuccessful in the future.

Concern #2: “English is the language of science and hence virus species names ought to be written in English”

- English is demonstrably not *the* language of science and also not *the* language of virology. Large numbers of manuscripts are continuously being published in languages other than English, and the proportion of English to non-English languages is highly dependent on research subspecialty and virus. For instance, *the* language, if such an assignment can even be considered valid, of Omsk hemorrhagic fever virus (*Flaviviridae: Flavivirus*) research is Russian, with 1,133 of 1,283 publications being written in Cyrillic Russian rather than English (Kuhn, unpublished). Likewise, every other article on Crimean-Congo hemorrhagic fever virus (*Nairoviridae: Orthonairovirus*) research is written either in Farsi, French, Russian, Serbian/Croatian/Bosnian/Montenegrin, and Turkish rather than English. These proportions become even more dramatic in particular virologic subspecialties, such as epidemiology, clinic, or policy, most of which are dominated by articles in languages spoken in the regions where particular viruses are a massive problem for a local population (explaining, for instance, the Russian-language article numbers regarding Omsk hemorrhagic fever virus, which is endemic only in one part of Russia). We do not think that it is justified or wise for the ICTV to judge whether non-English science is “good” science and we, therefore, dismiss the argument that English is *the* language of science out of hand;
- virus taxonomy is already largely based on non-English languages, and, in fact, uses Latin and Greek quite frequently. For instance, the taxon-specific suffixes *-virus* - *viridae* - *virales*, *-viricetes* and so on are clearly Latin in origin. Common taxon names,

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such as *Rhabdoviridae*, are non-English mixtures of Greek (ῥάβδος [rhábdos] meaning “rod, wand”) and Latin (-*viridae*). In essence, the names of all virus taxon ranks, with the exception of species, are already Latinized, and we have seen no call to change these names to English equivalents;

Concern #3: “Using Latin for species names is Euro-centric”

- the use of any language is “centric” to a particular area. The use of English could also be considered “Euro-” or at least “western-centric.” However, Latin is a “dead” (more appropriately, historic) language and, in our view, will hence be less associated with imperialism than the use of any contemporary language, in particular because the use of Latinized species names is globally accepted already for species nomenclature in all non-virologic disciplines;
- it is also important to remember that this proposal does not propose to translate current species names into Latin, but rather only to create species names that are Latinized (a crucial difference that is elaborated below).

Concern #4: “Latinizing species names is hard to do and requires experts”

- as previous exercises have demonstrated, devising Linnaean species names for virus species is not remotely as complicated or time-consuming as is often assumed. A single person took only 2 weeks to devise novel, Linnaean-style species names for almost 800 established species—most of which were deemed acceptable by polled Study Groups [11]; Kuhn thought exercise of 2019). At the moment, the ICTV recognizes only ≈5,000 species; all current species could be renamed to fit Linnaean style within 3 months;
- first, all virus genus names end with the mandated Latinized suffix *-virus*. Hence, genus names within Linnaean species names can be derived from any language and be coined without any knowledge of Latin and yet be correctly Latinized. Second, this mandated suffix ascribes a single gender to all virus genus names (the Latin word “virus,” meaning slime or poison, is a noun of the neuter gender), thereby massively simplifying the declension of species epithets. The rules for species epithet declension are easily summarized or taught. Third, numerous current species names are coined based on geographical locations. Such species names can very easily be transformed into Linnaean names by following simple rules (“use geographic name and add Latin suffix -ense: *Zaire ebolavirus* → *Ebolavirus zairense*). A rule set could easily be established by Latin-knowledgeable members of the ICTV EC to support the establishment of Linnaean virus species names by ICTV Study Groups;
- most importantly, **Latinization does not mean Latin translation** and hence true knowledge of Latin is not required by individuals who would be involved with coining Linnaean species name. For instance, the Latin name for the English “apple” is “malum”. Apple→malum is a Latin *translation*. Both apple and malum are two distinct names for the same *thing* that one can eat, which is a member of the species *Malus pumila*. *Malus pumila* is therefore *not* the Latin name for apple (because that is malum). Instead *Malus pumila* is a category for things, in this case for apples. In English, one will always eat apples even if a scientist decided to change the species name *Malus pumila* to *Humpa dumpa*. One cannot eat categories. The Latin name for apple would still be malum even if the associated species name had changed, just like any current virus name would be untouched by changing associated species names. Furthermore,

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numerous species names in non-virologic taxonomies contain word stems from numerous, non-Latin/Greek languages, i.e. have nothing to with Latin except for their Latin suffixes. Examples are:

- Prokaryotes: *Afipia clevelandensis*, named after the US Armed Forces Institute of Pathology and the US city of Cleveland. The only Latin in this species name is *-a* and *-ensis*
- Zoology: *Wunderpus photogenicus*, named using German Wunder (miracle), Greek πούς [πούς] (foot) and English “photogenic”. The only Latin in this species name is *-us*.

There is also no need to model any new Linnaean virus species names after an existing one. For instance, the current species names *Adelaide River ephemerovirus* (for Adelaide River virus) and *Merino Walk mammarenavirus* (for Merino Walk virus) do not, as recently suggested [12], have to be translated into Linnaean species names such as *Ephemerovirus flumenadelaidense* and *Mammarenavirus viamerinense*, respectively. Instead, the first Linnaean species name could simply be *Ephemerovirus adalaidense* (referring only to Adelaide) and the second could be *Mammarenavirus lipkinii* (after one of the discoverers of Merino Walk virus). In fact, creating species names that are not reminiscent of the names of affiliated viruses may aid greatly in decreasing the confusion of species and virus names in general.

SUMMARY

A Linnaean species name system is used almost universally in biology. Linnaean virus species names would, therefore, be immediately obvious to virologists and non-virologists alike and extend the consistency of an already existing species naming system that will be understood and appreciated by scientists, governmental and international policy makers, editors, authors, and readers. In such a system, existing virus names would be clearly identifiable as (vernacular) names and could continue to exist in any language, whereas the scientific species names could serve as internationally-agreed points of reference spelled exactly the same way worldwide. Latinization of species names is favorable compared to the use of other languages because Latin is a “dead” language with a minimal character set that does not require diacritics and that will not change in its syntax (in part phrased based on [1]). Non-Latinized binomial species names, on the other hand, would not only bring about the likely confusion with virus names, but also require the insertion of diacritical marks for correct spelling, or, as is currently the case, the mandatory misspelling of words to avoid diacritics.

We propose that the new species format be formalized in an ICVCN change such as

“3.20

A species name shall consist of as few words as practicable but be distinct from names of other taxa. Species names shall not consist only of a host name and the word "virus.””

↓

“3.20

A species name shall consist of only two distinct word components separated by a space. The first word shall begin with a capital letter and be identical in spelling to the name of the genus

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to which the species belongs. The second word shall begin with a lower-case letter, shall not be a single letter or number, shall be a distinct species marker, and shall be Latinized. The entire species name shall be written in italicized letters.”

IMPLEMENTATION

We propose that newly proposed species names follow the Linnaean naming format immediately/in parallel to EC acceptance and International Union of Microbiological Societies’ ratification of this TaxoProp. We further propose that all recognized virus species names be renamed to follow the new ICVCN Rule within 2 years past ratification of this proposal via TaxoProps prepared and submitted by the respective ICTV Study Groups. In case of failure of certain Study Groups to adhere to this timeline, the responsible ICTV Subcommittee Chair(s) shall create the species names for ICTV Executive Committee review and voting.

We propose that an exception be granted to the prokaryotic virus community to allow non-Latinized genus-species epithet species names for a maximum of 5 years post-ratification of this TaxoProp for the community to devise an acceptable path forward for conversion of current species names. We propose this exception due to the recent massive taxonomic changes that this community already had to endure. In recent years the taxonomy of prokaryotic viruses has evolved significantly with e.g., the genus “P22-like viruses” sequentially changing to *P22likevirus*, *P22virus*, and lastly to *Lederbergvirus*. This development allows, for instance, for the species name *Salmonella virus P22* to become the genus-species binomial *Lederbergvirus P22*. Bacteriologists are not used to distinguish between taxonomic species and species members (they use the name *Escherichia coli* indiscriminately for both), and because bacteriology and phage research are strongly intertwined, rapid establishment of virus species names that are not reminiscent of virus names will likely cause greater confusion than in other virologic subspecialties. All classical phages have short alphanumeric names (such as “P22”), thereby making this issue primarily historic in nature. Promisingly, as a result of the influence of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science Programs (see: <https://phagesdb.org/>), species name epithet components such as *Bactobuster*, *Rosebush*, *Corncob*, *ChipMonk*, or *FrodoSwaggins* have appeared for newly discovered phages and phage species names. Since Streptomyces phage FrodoSwaggins is a representative of the Rima-like viruses, the Linnaean species name *Rimavirus frodoswagginsii* could be easily constructed. The Bacterial and Archaeal Viruses Subcommittee of ICTV will be encouraging the global phage community to seriously consider coining “trivial” rather than alphanumeric names for their viruses, thereby allowing the prospective implementation of Linnaean species names.

The ICTV shall establish and maintain a community-accessible and -searchable repository or database, which clarifies the history and relationship of old/outdated and new/Linnaean species names, including the names of the viruses assigned to them. The ICTV shall also discourage the creation of virus names that appear to be Linnaean species names to decrease confusion.

APPENDIX A: EXAMPLES OF (NON-VIRAL) LINNAEAN SPECIES NAMES IN NON-ENGLISH LITERATURE. Because Linnaean species names are clearly identifiable due to their “foreign-looking” Latinization, they remain unchanged in alphabet or language independently of the language of a given article.

Example 1: Turkish (extended Latin alphabet), taken from Türk tabipleri birliđi. 2010. Kırım kongo kanamalı ateş bilimsel deđerlendirme raporu. Ankara, Turkey.

ORIGINAL (with Linnaean tick species names bolded for emphasis and virus names highlighted in green)

Bölgemizde Kırım-Kongo kanamalı ateş virüsünün ana taşıyıcısı olan *Hyalomma marginatum* (Şekil 4) yaban hayatı ile çok yakından ilişkili olup, bozkır ikliminin diđer iklim kuşakları ile keşiştiđi bölgelerde, özellikle de kuru taban örtüsüne sahip bodur ormanlık (meşelikler, çalılıklar) alanlarda yayılış gösterir. *Hyalomma marginatum* iki konutlu bir yaşam döngüsüne sahiptir.

Note that this text contains a virus name, properly translated from the English “Crimean-Congo hemorrhagic fever virus” into the Turkish “Kırım-Kongo kanamalı ateş virüsünün”. Introduction of Linnaean virus species names would not change the text above except for a single insertion, leaving the virus name untouched:

MODIFIED ORIGINAL

Bölgemizde Kırım-Kongo kanamalı ateş (*Orthonairovirus haemorrhagiae*) virüsünün ana taşıyıcısı olan *Hyalomma marginatum* (Şekil 4) yaban hayatı ile çok yakından ilişkili olup, bozkır ikliminin diđer iklim kuşakları ile keşiştiđi bölgelerde, özellikle de kuru taban örtüsüne sahip bodur ormanlık (meşelikler, çalılıklar) alanlarda yayılış gösterir. *Hyalomma marginatum* iki konutlu bir yaşam döngüsüne sahiptir.

Example 2: Russian (Cyrillic alphabet), taken from Г. Г. Онищенко *et al.* 2014. Анализ эпидемиологической ситуации по геморрагической лихорадке с почечным синдромом в хабаровском крае и еврейской автономной области, прогноз ее развития на послепаводковый период 2013–2014 гг. Пробл особо опасн инфекц (1): 56-59.

ORIGINAL (with Linnaean rodent species names bolded for emphasis, vernacular rodent names highlighted in blue and virus names highlighted in green)

К настоящему времени здесь идентифицированы 5 серологически и/или генотипически различающихся хантавирусов: **Хантаан** (дальневосточный вариант FE), **Амур**, **Хабаровск**, **Владивосток** и **Пуумала** (дальневосточный вариант), каждый из которых взаимосвязан в своей эволюции с определенным грызуном-носителем. Однако только 2 из них – **вирусы Амур** и **Хантаан** (FE) доказаны в качестве этиологического агента при ГЛПС. Резервуарным хозяином генотипа **Амур** является **восточноазиатская лесная мышь** (***Apodemus peninsulae***) и генотипа **Хантаан** FE – **полевая мышь** (***Apodemus agrarius***).

Note that this text contains several virus names, properly translated from the English “Hantaan virus”, “Amur virus”, “Khabarovsk virus”, “Vladivostok virus”, and “Puumala virus” into the Russian “**вирус Хантаан**”, “**вирус Амур**”, “**вирус Хабаровск**”, “**вирус Владивосток**”, and “**вирус Пуумала**”, respectively. The text also contains two Russian rodent names, “**восточноазиатская лесная мышь**” and “**полевая мышь**”, which in English would be called “Korean field mouse” and “striped field mouse”, respectively, whereas their associated species names would be identical in spelling and Latin alphabet in both Russian and English texts.

Example 3: Chinese (Chinese non-alphabetic script), taken from 高海女, 李兰娟. 2014. 埃博拉病毒病研究的现状和思考. 中华临床感染病杂志 7(6): 481-485.

ORIGINAL (with Linnaean bat species names bolded for emphasis and virus names highlighted in green)

1976年发现埃博拉病毒后，科学家认定这是一种人兽共患传染病，在自然界中存在不发病的贮存宿主。然而，研究人员多次在流行区的各种动物中均未能检测到该病毒，直至2005年才第一次在锤头果蝠(*Hypsignathus monstrosus*)、无尾肩章果蝠(*Epomops franqueti*)、小领果蝠(*Myonycteris torquata*)中同时发现埃博拉病毒的RNA及抗体。

Note that this text contains a virus name, properly translated from the English “Ebola virus” into the Chinese “埃博拉病毒”. Introduction of Linnaean species names would not change the text above except for a single insertion, leaving the virus name untouched:

MODIFIED ORIGINAL

1976年发现埃博拉病毒(*Ebolavirus johnsonii*)后，科学家认定这是一种人兽共患传染病，在自然界中存在不发病的贮存宿主。然而，研究人员多次在流行区的各种动物中均未能检测到该病毒，直至2005年才第一次在锤头果蝠(*Hypsignathus monstrosus*)、无尾肩章果蝠(*Epomops franqueti*)、小领果蝠(*Myonycteris torquata*)中同时发现埃博拉病毒的RNA及抗体。

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