

Comments posted 24th February

Dear Colleagues,

My specific comments (in red) on the wording of the proposed changes that for clarity has been inserted into the original text.

Proposal 1 (Whitman 2016). Extend the nature of the type acceptable for valid publication of a species or subspecies name to allow the use of complete or partial genome sequences as type (Whitman 2016). The new rules would be worded [new text is underlined]:

Rule 18a. The type of a species or subspecies must unambiguously identify the taxonomic group and is a designated strain or other material. Whenever possible, the type of a species or subspecies is a designated strain.

A) The Code is neutral on a number of points, including whether a nomenclatural type “must unambiguously identify the taxonomic group”. The “nomenclatural type if that element of a taxon with which a name is permanently attached”, but at the same time does not preclude that it may be considered later on that a name is a heterotypic synonym of another name. This wording should be deleted. It would be appropriate to substitute “nomenclatural type” in all instances in the Code where the term “type” is used alone.

B) The use of the term “material” implies a physical object. In the case of genome sequences there is a difference between the sequence chemically encoded on a piece of DNA and the digital sequence information that is obtained by experimental procedures and deposited in an electronic database as an electromagnetic signal in binary code.

(3) [first section] As from 1 April 2020*, sequences of genomic DNA may also serve as the type when it unambiguously identifies the species. When possible, it should be a high quality draft or better genome sequence.

C) For “sequences of genomic DNA” read “digital sequence information that is obtained by experimental procedures and deposited in an electronic database”. Remove “unambiguously identifies the species” since this is outside of the remit of the Code. In essence “digital sequence information” is the same as a description.

Rule 30.3.c. [new rule] When a sequence is the type, the accession number in a publically available database or the sequence must be given. It is recommended that, when possible, a sample of the DNA be deposited in at least two publically accessible service collections in different countries and the catalog numbers be indicated.

D) We are not talking about a physical sequence, but digital sequence information obtained by experimental procedures and deposited in an electronic database as an electromagnetic signal in binary code. This is essentially a description at the level of the genome.

E) The term “catalog” is incorrect and should be replaced by “accession”. DNA deposited in at least two publically accessible service collections constitutes as preserved specimen. It is also questionable what

purpose this would serve, since, In contrast to a written description, illustration or preserved specimen on a microscope slide of the organism the only way of examining the preserved DNA with regards its physical nature (i.e. by determining the nucleotide sequence by current methods) would be to destroy it. See also Sneath and Neimark:

<https://doi.org/10.1099/00207713-45-1-188>

<https://doi.org/10.1099/ijms.0.63718-0>

Proposal 2 (Whitman 2016). Articulates a general concept for what can serve as type for a species.

Rule 18a (3). [second section] As new methods are developed, they may serve as the type material so long as they unambiguously identify the species or subspecies and can be readily archived and compared.

F) This is already covered by Principle 1 (4), but also makes the mistake that a method cannot serve as a nomenclatural type. This can be deleted.

Proposal 3 (Whitman 2016). Allows valid publication of the name of a genus in the absence of a type species if the type is too ambiguous to circumscribe a species.

The rule would be:

"Rule 20a. The nomenclatural type (see Rule 15) of a genus or subgenus is the type species or the sequence of one or more genes that unambiguously identifies the genus or subgenus. The type species is the single species or one of the species included when the name was originally validly published. Only species whose names are legitimate may serve as types."

G) This links back to the issue of "unambiguously identifying" a taxon, which is not part of the remit of the Code. It also makes a claim that one or more genes may unambiguously identify the genus or subgenus. Since different authors may evaluate the same information differently this would not preclude the establishment of heterotypic synonyms, ie the two taxa were not unambiguously identified. "Or the sequence of one or more genes that unambiguously identifies the genus or subgenus" should be deleted.

Proposal 4 (Whitman et al. 2019). Upon acceptance of Proposal 1, the priority of the names of Candidatus taxa published before 1 April 2020* which are otherwise in accordance with the rules of the Code will have priority based upon their date of publication in the IJSEM unless a synonymous name already exists based upon deposition of type cultures.

Whitman et al. (2019) also provides a simple nomenclature for identifying the nature of the type material:

'When the type is a culture, the superscript "T" will be used immediately following the name or strain identifier. If the type is a sequence, the superscript "Ts" will be used. If the type is a description, preserved specimen or illustration, the superscript "Td" will be used. If a representative of a taxon is brought into culture, the type strain is then designated as described in Rule 18f. The name may be

emended by the new authors, and the superscript “Ts” or “Td” is replaced by the superscript “T”.’

H) As indicated previously, at the rank of species and subspecies this would apply to the nomenclatural type and not to the corresponding name.

*The original date of 1 January 2020 is changed to reflect the time necessary to bring this matter to a vote.

I) In the past all changes to the Code were documented in articles in the IJSEM, in the minutes of the appropriate committees/commissions and applied from their date of publication of the version of record.

Dr. Brian J. Tindall

No affiliation with an employer or organisation is intended or to be inferred