

Proposal for changes in the International Code of Nomenclature of Prokaryotes: granting priority to *Candidatus* names

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Abstract

Currently, the description of taxa designated *Candidatus* requires gene sequences and other taxonomically relevant available information in the absence of an isolated pure culture, and *Candidatus* names are provisional, i.e. without formal standing in nomenclature. If gene sequences are accepted as suitable type material for the description of prokaryotic species, many taxa designated *Candidatus* would fulfil all the requirements in the International Code of Nomenclature of Prokaryotes for priority. Here we propose that upon acceptance of sequence data as type material, all *Candidatus* names published before 1 January 2020 which are otherwise in accordance with the rules of the Code will have their priority based upon their date of publication in the *International Journal of Systematic and Evolutionary Microbiology*, either within a paper, a list of names of *Candidatus* taxa, or a Validation List, unless a synonymous name already exists based upon deposition of type cultures. We further propose that modifications of the superscript 'T' be used to identify the nomenclatural types. If the type material is a culture, the superscript 'T' will continue to be used. If the type material is a sequence, the superscript 'Ts' will be used. If the type material is some other form of description, the superscript 'Td' will be used.

The International Code of Nomenclature for Prokaryotes (the Code) provides a system to uniquely name each prokaryotic taxon based upon rules of priority and the availability of type material [1]. Essential to this nomenclatural system, the type material must unambiguously identify the taxon. It is now widely recognized that sequence data provides an unambiguous identification of prokaryotic taxa comparable to, if not better than, phenotypic comparisons of cultures [2]. For instance, genome sequences have been proposed to replace DNA–DNA reassociation techniques to genomically delimit species [3–7]. Even the complete genome sequence is not necessary, and in many cases multilocus sequence analysis is sufficient to identify novel species [8, 9]. Consequently, a number of authors have proposed that the Code be revised to include sequence data as type material for cultured as well as uncultured prokaryotes [10–13].

If these proposals are accepted after consideration by the International Committee on Systematics of Prokaryotes (ICSP), many names currently designated as *Candidatus* will fulfil most of the requirements for valid publication. As described in Rule 27 [1], the requirements for valid publication include: publication of the name in the *International Journal of Systematic and Evolutionary Microbiology* (IJSEM), a clear statement of the name and its etymology, an accessible description of the properties of the taxon or diagnosis, and

designation of the type material [1]. The issue then arises as to how these names can become validly published and gain priority. For this reason, we propose that upon acceptance of sequence data as type material, all *Candidatus* names published before 1 January 2020 which are otherwise in accordance with the rules of the Code will have priority based upon their date of publication in the IJSEM, either within a paper, a list of names of *Candidatus* taxa, or a Validation List, unless a synonymous name already exists based upon deposition of type cultures. Not all *Candidatus* names that have been published fulfil the requirements of Rule 27 as described above or fully comply with the rules of the Code. These names will not gain priority with this proposal. While the compilation of a list of *Candidatus* names that meet the criteria of Rule 27 is strongly encouraged, priority will not depend upon publication of such a list.

In addition, there is also some concern that it will be difficult to distinguish between taxa whose descriptions are based upon cultures from those with sequences as type material. We propose that modifications of the conventionally used superscript 'T' be used to identify the nomenclatural types. If the type material is a culture, the superscript 'T' will continue to be attached to the name or strain identifier. If the type material is a sequence, the superscript 'Ts' will be used. For some taxa described before 1 January 2001, the type material is a description, preserved specimen or

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illustration. In these cases, 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 18 f [1]. The name is emended by the new authors, and the superscript ‘Ts’ or ‘Td’ is replaced by the superscript ‘T’.

To implement these proposals, the following revisions of the Code [1] are suggested. A new rule is proposed:

Rule 24b [3] [new rule]

‘All *Candidatus* names published before 1 January 2020 which are otherwise in accordance with the rules of the Code will have their priority based upon their date of publication in the *International Journal of Systematics and Evolutionary Microbiology* (IJSEM), either within a regular paper, a list of names of *Candidatus* taxa, or a Validation List, unless a synonymous name already exists based upon deposition of type cultures.’

To Chapter 4. Advisory notes, a new paragraph will be added to the end of Section A. Suggestions for Authors and Publishers:

‘When the type material is a culture, the superscript “T” will be used immediately following the name or strain identifier. If the type material is a sequence, the superscript “Ts” will be used. If the type material 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”.’

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Conflicts of interest

The authors declare that there are no conflicts of interest.

Ethical statement

Not applicable because animals and humans were not used.

References

1. Parker CT, Tindall BJ, Garrity GM. International Code of Nomenclature of Prokaryotes. *Int J Syst Evol Microbiol* 2019;1A:S1–S111.
2. Sutcliffe IC, Trujillo ME, Goodfellow M. A call to arms for systematists: revitalising the purpose and practises underpinning the description of novel microbial taxa. *Antonie van Leeuwenhoek* 2012;101:13–20.
3. Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. *BMC Bioinformatics* 2013;14:60.
4. Chun J, Rainey FA. Integrating genomics into the taxonomy and systematics of the bacteria and archaea. *Int J Syst Evol Microbiol* 2014;64:316–324.
5. Li X, Huang Y, Whitman WB. The relationship of the whole genome sequence identity to DNA hybridization varies between genera of prokaryotes. *Antonie van Leeuwenhoek* 2015;107:241–249.
6. Richter M, Rosselló-Móra R. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci USA* 2009;106:19126–19131.
7. Chun J, Oren A, Ventosa A, Christensen H, Arahall DR et al. Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. *Int J Syst Evol Microbiol* 2018;68:461–466.
8. Rosselló-Móra R, Amann R. Past and future species definitions for bacteria and archaea. *Syst Appl Microbiol* 2015;38:209–216.
9. Glaeser SP, Kämpfer P. Multilocus sequence analysis (MLSA) in prokaryotic taxonomy. *Syst Appl Microbiol* 2015;38:237–245.
10. Whitman WB. Genome sequences as the type material for taxonomic descriptions of prokaryotes. *Syst Appl Microbiol* 2015;38:217–222.
11. Whitman WB. Modest proposals to expand the type material for naming of prokaryotes. *Int J Syst Evol Microbiol* 2016;66:2108–2112.
12. Konstantinidis KT, Rosselló-Móra R, Amann R. Uncultivated microbes in need of their own taxonomy. *ISME J* 2017;11:2399–2406.
13. Konstantinidis KT, Rosselló-Móra R, Amann R. Reply to the commentary “Uncultivated microbes-in need of their own nomenclature?”. *ISME J* 2018;12:653–654.

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