

1 Commentary on the proposed Section 10 amendments to the International Code of Nomenclature of
2 Prokaryotes regarding *Candidatus* names
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11 Abstract:

12 Amendments were proposed to the International Code of Nomenclature of Prokaryotes (ICNP) in January
13 [Arahal et al. (2024) *Int. J. Syst. Evol. Microbiol.* **74**: 006188] that would cause major changes in the
14 treatment of *Candidatus* names. The amendments introduce Section 10 to name taxa whose names cannot
15 be validly published under the ICNP because of the absence of type strains. This section creates a parallel
16 'pro-nomenclature' and formalizes alternative material which could serve as nomenclatural types. When
17 conspecific isolates of taxa with *Candidatus* names are deposited in culture collections as type strains, the
18 names can be validly published, and it is required that the same *Candidatus* name be used. While the
19 amendments are promoted to provide stable names and rules of nomenclature for uncultivated taxa, the
20 system is deeply flawed. It removes the permanent association between names and types, which will make
21 the meaning of names imprecise and ambiguous. It creates 'pro-nomenclature', which is confusing and
22 unnecessary. Since many taxa which cannot be validly named under the ICNP can already be named under
23 the SeqCode, it duplicates and creates overlap with an established nomenclatural system without providing
24 tangible benefits. As the SeqCode recognizes names formed under the ICNP, the ICNP should recognize
25 names formed under the SeqCode as they have done for the Cyanobacteria named under the International
26 Code of Nomenclature for algae, fungi and plants (ICN). For these reasons, we urge the members of the
27 International Committee of Systematics of Prokaryotes (ICSP) to reject these amendments.

28 Main text:

29 In 2020, a proposal to amend the International Code of Nomenclature of Prokaryotes (ICNP) to allow DNA
30 sequences to serve as nomenclatural types was rejected by the International Committee on the Systematics
31 of Prokaryotes (ICSP) (Sutcliffe et al., 2020, Whitman, 2016). This proposal would have enabled creation
32 of stable names for taxa for which type strains cannot be deposited in two international culture collections,
33 a requirement of the current ICNP. Major kinds of taxa that would have been affected included the
34 uncultivated known from metagenome-assembled genomes (MAGs) and single-amplified genomes
35 (SAGs); fastidious prokaryotes that cannot be deposited because the collections lack the expertise,
36 resources, or desire to accession them; and cultures isolated from countries with legal barriers for their
37 distribution. Many of these taxa had *Candidatus* names, which are provisional names outside the legislative
38 portion of the ICNP that lack standing in nomenclature. Therefore, in response to the need for stable naming
39 of taxa that currently cannot be formally named under the ICNP, a committee under the auspices of the
40 International Society for Microbial Ecology developed the SeqCode, an alternative code of nomenclature in
41 which DNA sequences serve as types (Murray et al., 2020, Hedlund et al., 2022, Whitman et al., 2022).
42 The SeqCode was designed to complement the ICNP so that it would be possible to create unified
43 taxonomies of uncultivated and cultivated prokaryotes with a shared nomenclature.

44 The proposal of Arahal et al. (Arahal et al., 2024) is an alternative to the SeqCode and is currently open for
45 discussion on the ICSP Slack channel. After July 4 2024, it will be voted on by the ICSP. For the reasons
46 discussed below, we believe that this proposal will greatly hinder progress in prokaryotic systematics, and
47 we urge the ICSP to vote against it. This opinion is endorsed by the signatories listed below.

48 The amendments in the newly proposed Section 10 introduce *Candidatus* names into the code to name
49 taxa whose names cannot be validly published under the ICNP because of the absence of type strains

50 deposited in two or more international culture collections (Arahal et al., 2024). In contrast to the previous
51 informal nomenclature for *Candidatus* names, Section 10 creates a parallel 'pro-nomenclature' which
52 regulates the application of names amongst taxa with *Candidatus* names. However, the pro-validated
53 names will not have formal status in nomenclature and will not compete for priority with validly published
54 names. It also requires publication of *Candidatus* names in the IJSEM and designation of types, which were
55 not previously required. However, when isolates of taxa with *Candidatus* names are deposited in culture
56 collections to serve as type strains, the names can be validly published. The *Candidatus* designation must
57 be dropped and the species name used as the validly published name for the conspecific isolate. In this
58 way, the system provides stable names and rules of nomenclature for uncultured genera and species. Thus,
59 it addresses a major concern in prokaryotic biology by providing a system of stable naming for taxa that
60 cannot be deposited in culture collections.

61 There are very serious criticisms of the proposed Section 10. It accomplishes its goals by introducing a
62 number of novel devices into the ICNP, each of which are problematic as described below. 1) It creates
63 'pro-nomenclature'. 2) It requires changes in types for *Candidatus* names if they become validly published,
64 and it allows changes in the category of types for *Candidatus* names. 3) It introduces requirements to 'reuse'
65 names. Each of these are problematic, will be difficult to apply, and cause confusion. They also fail to solve
66 any important practical problems.

67 The purpose of nomenclature is to create names that will be used in scientific literature. While *Candidatus*
68 names have become widely used in the last twenty years, Section 10 changes the meaning of the term, a
69 distinction that may not be appreciated outside of the microbial systematics community. It also introduces
70 a complicated 'pro-nomenclature' where *Candidatus* names can be 'pro-legitimate', 'pro-correct', and 'pro-
71 validly published'. As a consequence, for the foreseeable future there will exist *Candidatus* names that are
72 'pro-illegitimate' and *Candidatus* names that are 'pro-validly published' without ready means to distinguish
73 them. Given the complexity, many scientists will ignore these distinctions.

74 While codes of nomenclature often allow multiple kinds of types, most do not permit changing the types of
75 names because it makes the names ambiguous and leads to confusion. For instance, Article 7.2 of the
76 International Code of Nomenclature for algae, fungi and plants (ICN) states: "A nomenclatural type (typus)
77 is that element to which the name of a taxon is permanently attached, whether as the correct name or as a
78 synonym" (Turland et al., 2018). For the same reason, reusing a name for a different type is usually avoided.
79 Although occasional changes in types, i.e. designation of neotypes, have been tolerated in prokaryotic
80 systematics for decades, these are not common. However, Section 10 is proposing changes in types for
81 thousands of *Candidatus* names, which will lead to intolerable confusion. Not only does it require the
82 change in nomenclatural type when a representative isolate becomes available, but Rule 70 also promotes
83 the replacement of nomenclatural types when a preferred type (discussed below) is obtained. The
84 permanent association of names to their types is the basis for their precise meanings. When types change,
85 the circumscription inevitably changes as well, and names become ambiguous (Figure 1). It has previously
86 been claimed that the ICNP is fully aligned with the other codes of nomenclature, but this will no longer be
87 true if rules to change type material are introduced. Most importantly, changing types is unnecessary and
88 serves no practical purpose.

89 Section 10 stabilizes the nomenclature of *Candidatus* names for genera and species but adds more
90 complexity for the names of the higher taxonomic ranks. Genera are the types of all higher taxonomic ranks.
91 Because 'pro-validly published' *Candidatus* genus names cannot be types for validly published names, they
92 cannot be types for validly published names of the higher taxonomic ranks under the ICNP. However, to
93 retain the *Candidatus* name of higher taxonomic ranks, Section 10 allows changing the type of the
94 *Candidatus* name to that of a different genus-level taxon whose name can be validly published, i.e. the type
95 can be deposited in culture collections. In this case, Section 10 requires that the original *Candidatus* taxon
96 must be renamed. As a consequence, the types of the higher taxonomic rank and one genus change, and
97 one type is given a new *Candidatus* name. Under Section 10, the valid publication of names of all the taxa
98 with *Candidatus* names is likely to occur over many years as taxa are brought into culture. Thus, the names

99 of higher taxa can be expected to remain in flux for the foreseeable future. Moreover, frequent database
100 curation will be required to keep the names current.

101 Section 10 also contains biases that are difficult to understand and will confound its implementation.

102 For example, Rule 69 establishes preferences for four different kinds of *Candidatus* type material. Types
103 with lower preferences can be replaced with types of higher preferences. Under Rule 69(1)a, non-pure
104 cultures are the preferred type and can only have *Candidatus* names. This rule seems to include obligate
105 symbionts. Currently, names of obligate symbionts can be validly published, and *Microcaldus* is a recent
106 example (Sakai et al., 2022). Presumably, this name would become illegitimate or 'pro-legitimate' if this
107 amendment is accepted. This rule also seems to be oblivious to recent discoveries of abundant obligate
108 symbionts, which are revising our views of prokaryotic biology (Brown et al., 2015, Gios et al., 2023, Hug
109 et al., 2016, Rinke et al., 2013). Under Rule 69(1)b, the next level of preferred types is preserved specimens,
110 but this rule requires that museums or other collections be established to house them. These collections
111 will need resources that do not currently exist. Rules 69(1)c and d allow genome and DNA sequences to
112 serve as types, but they are the least preferred. The rationale for preferring types of mixed cultures or
113 preserved specimens over genome sequences, which can precisely identify taxa and are widely used in
114 most current taxonomic studies, is not clear. The advantages of DNA sequences over these alternative
115 types are well-documented in the literature, particularly for uncultivated taxa. Nevertheless, if the original
116 type for a *Candidatus* name is a sequence of a gene, Section 10 will allow replacement of the type three
117 times, first with a genome sequence, then a preserved specimen, and then a mixed culture. Finally, if a
118 pure culture can be deposited, the type can be changed a fourth time upon valid publication. Importantly,
119 these changes in type fail to provide any practical benefits for the scientific community.

120 Lastly, Section 10 fails to provide criteria for quality of the types. When the SeqCode was developed, a
121 consensus prevailed that genome sequences had to meet high experimental standards to serve as types
122 (Hedlund et al., 2022). For instance, under normal circumstances a highly contaminated or incomplete MAG
123 or the sequence of a 16S rRNA gene cannot serve as a type under the SeqCode. Section 10 would allow
124 inferior data to serve as the experimental basis of *Candidatus* names. Only poor taxonomic decisions can
125 follow from poor data.

126 In summary, Section 10 introduces a complex system intended to incorporate *Candidatus* names into the
127 formal nomenclature of prokaryotes. This goal is accomplished by discarding the permanent association
128 of types to names, introducing ambiguity and instability. It sacrifices the clarity of ICNP and, if adopted,
129 represents a step backwards in prokaryotic systematics. It will also create overlap of names already
130 regulated under the SeqCode, promulgating further confusion.

131 In contrast, the SeqCode accomplishes all the goals of Section 10 more simply without sacrificing the
132 precision and unambiguity of the ICNP. It provides stable names for taxa that cannot be named under the
133 ICNP and means of designating the nature of the type. It ensures the quality of the DNA sequences that
134 can serve as types. It provides the SeqCode Registry, a convenient online resource to track names that is
135 compatible with databases and replaces the rather archaic system of published validation lists. This
136 important service can review nomenclature proposals before they are published and provide
137 comprehensive automatic as well as manual checks of both sequences and nomenclature. The SeqCode
138 also requires deposition and free availability of raw sequence data in INSDC databases, which allows
139 reanalysis of the raw data. Because it is a database, the SeqCode Registry can communicate with other
140 databases, which facilitates the wide dissemination of names and type genomes. Because genome
141 sequences are known for most type strains, the integration of SeqCode and ICNP names in stable
142 taxonomies is straightforward. The SeqCode currently recognizes names formed under the ICNP. The
143 ICSP should amend the ICNP to recognize names formed under the SeqCode just as it recognizes
144 names of Cyanobacteria formed under the ICN, which represents a precedent for recognition of names
145 from other codes.

146 Therefore, we request that the International Committee of Systematics of Prokaryotes (ICSP) reject the
147 proposal of Arahall et al. (2024). The microbiologists listed below have endorsed the opinions expressed in
148 this commentary.

149

150 Endorsements: The following have endorsed the contents of this paper. Ricardo Amils, Universidad
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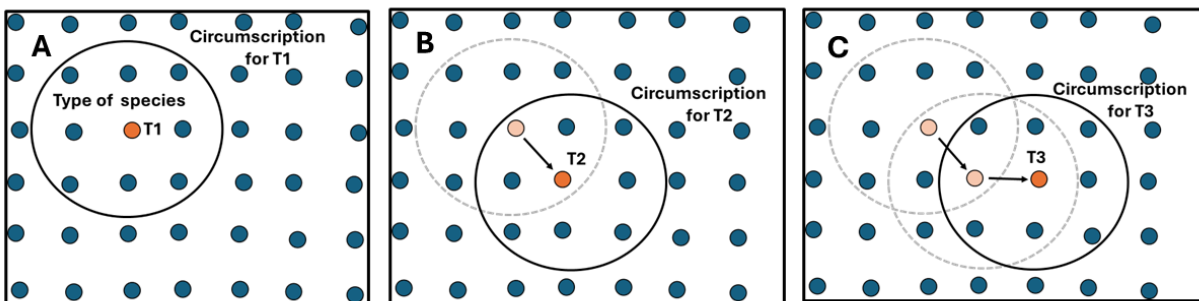
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192 Figure Legend

193 **Figure 1.** Why it is a bad idea to change nomenclatural types. Changes in type are accompanied by
194 changes in circumscription of the species, resulting in changes in the meaning of the name. **A.** Selection of
195 a nomenclature type implies that similar organisms will be included in the circumscription of the group. **B.**
196 Change in type from T1 to T2 also changes the circumscription because the species now includes those

197 organisms like T2. Some organisms in the circumscription of T1 are excluded from the circumscription of
198 T2. **C.** Change in type from T2 to T3 changes the circumscription again, and the type T1 is no longer
199 included in the circumscription of T3 even though the name has not changed.



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