

The best of both worlds: a proposal for further integration of *Candidatus* names into the International Code of Nomenclature of Prokaryotes

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Abstract

The naming of prokaryotes is governed by the International Code of Nomenclature of Prokaryotes (ICNP) and partially by the International Code of Nomenclature for Algae, Fungi and Plants (ICN). Such codes must be able to determine names of taxa in a universal and unambiguous manner, thus serving as a common language across different fields and activities. This unity is undermined when a new code of nomenclature emerges that overlaps in scope with an established, time-tested code and uses the same format of names but assigns different nomenclatural status values to the names. The resulting nomenclatural confusion is not beneficial to the wider scientific community. Such ambiguity is expected to result from the establishment of the 'Code of Nomenclature of Prokaryotes Described from DNA Sequence Data' ('SeqCode'), which is in general and specific conflict with the ICNP and the ICN. Shortcomings in the interpretation of the ICNP may have exacerbated the incompatibility between the codes. It is reiterated as to why proposals to accept sequences as nomenclatural types of species and subspecies with validly published names, now implemented in the SeqCode, have not been implemented by the International Committee on Systematics of Prokaryotes (ICSP), which oversees the ICNP. The absence of certain regulations from the ICNP for the naming of as yet uncultivated prokaryotes is an acceptable scientific argument, although it does not justify the establishment of a separate code. Moreover, the proposals rejected by the ICSP are unnecessary to adequately regulate the naming of uncultivated prokaryotes. To provide a better service to the wider scientific community, an alternative proposal to emend the ICNP is presented, which would result in *Candidatus* names being regulated analogously to validly published names. This proposal is fully consistent with previous ICSP decisions, preserves the essential unity of nomenclature and avoids the expected nomenclatural confusion.

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Abbreviations: ICN, International Code of Nomenclature for Algae, Fungi and Plants; ICNP, International Code of Nomenclature of Prokaryotes; ICSP, International Committee on Systematics of Prokaryotes; ICZN, International Code of Zoological Nomenclature; INSDC, International Nucleotide Sequence Database Collaboration; IUMS, International Union of Microbiological Societies; SeqCode, Code of Nomenclature of Prokaryotes Described from DNA Sequence Data.

INTRODUCTION

Codes of nomenclature have been available for more than a century for the major taxonomic disciplines: zoology, botany and microbiology [1–3]. Organisms covered by these disciplines are classified taxonomically, i.e., arranged together in groups that have names. How organisms are arranged into such groups (taxa) is not subject to any central control. In contrast, the naming of given taxa in microbiology, botany and zoology is subject to regulations implemented by the respective codes of nomenclature. For instance, the ‘International Code of Zoological Nomenclature ... has one fundamental aim, which is to provide the maximum universality and continuity in the scientific names of animals compatible with the freedom of scientists to classify animals according to taxonomic judgments’ [1]. Taxon names regulated by codes of nomenclature are, thus, only conditionally stable, as they may need to change in cases of changes in taxonomic classifications. However, the name assigned to a given taxon is intended to be stable, apart from the relatively rarely occurring need to replace a name that was formed contrary to a rule.

The central question that a code of nomenclature must be able to answer is, which name should be applied to a given taxon. The need to be universal and unambiguous, regarding the names of taxa, is also emphasized by the ICN, i.e., the International Code of Nomenclature for algae, fungi, and plants [2], in its Preamble 1, which states that ‘Biology requires a precise and simple system of nomenclature that is used in all countries, dealing on the one hand with the terms that denote the ranks of taxonomic groups or units, and on the other hand with the scientific names that are applied to the individual taxonomic groups ... This Code aims at the provision of a stable method of naming taxonomic groups, avoiding and rejecting the use of names that may cause error or ambiguity or throw science into confusion’ [2].

Unambiguous nomenclature of micro-organisms is of particular importance, given their wide and diverse roles as pathogens of humans, plants and animals, or biotransformation agents of foods, beverages and the environment. The nomenclature of all prokaryotes has been regulated for nearly a century by the International Code of Nomenclature of Prokaryotes (ICNP) and its predecessors [3]. The publication of the ICNP is now overseen by the International Committee on Systematics of Prokaryotes (ICSP), a committee of the International Union of Microbiological Societies (IUMS), composed of representatives of national microbiological societies. The *International Journal of Systematic and Evolutionary Microbiology* (IJSEM) is now the official journal of record of the ICSP [4]. The IJSEM is the leading forum for describing and naming novel microbial taxa, the designated journal for validly publishing new prokaryotic names, and plays a significant role in the practical function of the ICNP.

The ICNP [3] defines several nomenclatural status values, primarily whether a name is ‘validly published’ and, therefore, has ‘standing in nomenclature’, but also whether a name is legitimate (i.e., validly published and in accordance with the Rules of the ICNP), or whether a name has been placed on the list of rejected names [3]. The primary function of the ICNP is to codify the Rules that determine the status of a name [3]. Rule 30 of the ICNP stipulates that, as of 1 January 2001 the deposition of viable cultures of the type strain in two culture collections, in different countries, is a prerequisite for the valid publication of a name, although exceptions may be requested [3].

The ICNP assigns the status ‘not validly published’ to names that do not meet the given criteria. The ICNP recommends the *Candidatus* status for incompletely characterized prokaryotes [3]. This status can well be used for as yet uncultivated bacteria and archaea [5, 6], and several thousand *Candidatus* names have been proposed in the literature [7], even disregarding the huge number of automatically created names [8]. The previous version [9] and the 2022 revision [3] of the ICNP may be criticized for insufficiently regulating the *Candidatus* status. However, the IJSEM already publishes *Candidatus* Lists [10, 11], and emendations of the ICNP to provide more detailed regulations for *Candidatus* names may be made at any time through proper procedure [4].

Based on an earlier publication [12], alternative proposals were made in 2016 and 2019 to emend the ICNP to allow for DNA sequences (mainly, but not only, genome sequences) to serve as nomenclatural types of species or subspecies for the purpose of validly publishing their names, in addition to cultivable, pure and viable type strains [13, 14]. Although titled differently, these proposals were not ‘modest proposals’, but represented an extreme response to an insufficiency of the ICNP in regulating the names of as yet uncultivated prokaryotes, as the adoption of these proposals in the ICNP would have blurred the distinction between validly published names and *Candidatus* names. However, the proponents of the proposals promoted their views in further publications [15–17]. The proposals received criticism from some authors [18, 19]. After a vigorous debate in 2020, according to the ICSP Statutes, which define how the ICNP should be emended [4], the ICSP rejected the proposals [13, 14] with a clear majority [20]. The rejection of the proposals did not result in considerations for alternative proposals for modifying the ICNP, but, instead, instigated an initiative to create a separate code outside the ICSP.

Obviously, the naming of taxa cannot be universal and unambiguous if there are two codes of nomenclature which, on the one hand, have the same scope and use the same naming scheme, but which, on the other hand, result in different names being applied to the same taxa. The value of standardisation should therefore not be underestimated. The creation of a second code with overlapping scope and the same naming scheme is a recipe for nomenclatural confusion [21], to the detriment of the wider scientific community that practising taxonomists ultimately serve.

To avoid nomenclatural confusion, an alternative system for naming prokaryotes would have to use a naming scheme that makes it immediately clear that the resulting names belong to the alternative nomenclatural system. One way to generate unambiguously

separate names is, of course, to use the status *Candidatus*, accompanied by the prefix ‘*Candidatus*’ to Latin names, as envisaged by the ICNP [3]. Alternatively, it may be preferable not to use Latin names in the uncultivated system, as has been suggested [20]. For instance, alphanumeric designators, such as ‘SAR11’ [22], could be sanctioned by a separate code of nomenclature, with the added advantage that such designators are already widely used.

However, such options were not chosen and a separate code, i.e. the ‘SeqCode’, or ‘Code of Nomenclature of Prokaryotes Described from Sequence Data’, was proposed [23–26]. Critical comments were raised [6, 21, 27], as the development of a separate code, like the proposals by Whitman *et al.* for emending the ICNP, is an extreme measure that risks creating nomenclatural confusion. Although proposed to exist in parallel, conflicts between the ICNP and the SeqCode were noted immediately [28].

The 2020 rejection of the proposals by Whitman and others [13, 14] was based on various arguments [20]. These arguments remain valid, despite the development of the SeqCode outside the ICSP [26]. In fact, the SeqCode appears to be a mechanism to implement the rejected proposal of Whitman *et al.*, without the approval of the ICSP [28], in the hope that the SeqCode might unite with the ICNP in the future. Whether the ICNP would merge with the SeqCode or whether it would accept the nomenclatural status values designated by the SeqCode, as has been suggested in the literature [23, 24], does not matter in this respect. Either step would be tantamount to accepting a proposal [13, 14] that had been recently declined according to designated accepted principles and procedures.

Given the need for standardization in nomenclature, a proposal for an alternative code to the ICNP cannot be seen as a positive move for the wider scientific community, which relies on unambiguous nomenclature to describe essential factors in every aspect of microbiology. It is therefore logical that a unified code should be implemented, taking into account the arguments for and against the proposal by Whitman and colleagues. In particular, it is necessary to consider a neglected aspect of the debate [20], namely that the measures proposed by Whitman, or by the other proponents of the SeqCode, are not necessary to achieve the goals that actually serve the wider scientific community.

This paper is thus organized as follows. It begins with a detailed explanation of the conflict between the SeqCode, on the one hand, and the ICNP and ICN, on the other hand [28]. The additional ways in which a separate code with an overlapping scope can lead to confusion in nomenclature are also described. This section further covers aspects of the way in which publications favouring the proposal by Whitman and colleagues [13, 14] or the SeqCode [24–26] misrepresented the ICNP. Afterwards, it is reiterated why the proposal by Whitman and colleagues was rejected in 2020. This is followed by covering the goals of the proposal by Whitman *et al.* [13, 14], which remain relevant and important to the wider scientific community. Separating the goals from the rejected implementation paves the way for an alternative proposal to emend the ICNP. In particular, we agree with the SeqCode initiative that additional regulations for the names of not yet cultivated taxa are beneficial, although we maintain that it is not necessary to modify the requirements for the valid publication of the name of a prokaryote to achieve such regulations. Finally, we describe the reasoning behind our proposal and the resulting proposed emendation of the ICNP. The study aims to be a comprehensive treatment of the subject and, therefore, cannot be overtly concise. However, we have included informative headings and subheadings to enable the reader to gain an overview of content and structure of the paper.

THE PROPOSED SEQCODE CONTRAVENES THE ICNP

The development of an additional code, i.e., the SeqCode [26], is an unfortunate step that will lead to unnecessary nomenclatural ambiguity and confusion. Firstly, a potentially huge number of specific conflicts can be expected. Secondly, a general conflict between the two codes is already apparent [28]. Thirdly, the few publications in favour of the SeqCode have misrepresented some key aspects of the ICNP. Fourthly, the SeqCode has needlessly taken measures, independent of the use of DNA sequences as nomenclatural types, that make it incompatible with the ICNP as well as with the ICN [2], and the ICZN, i.e., the International Code of Zoological Nomenclature [1]. Of these, the conflicts with the ICNP and the ICN are of practical relevance for the nomenclature of prokaryotes. These issues are discussed in detail in this chapter.

General and specific disagreement creates a dilemma

Different ‘correct’ names would be obtained for the same taxon

The separation between cultivated and uncultivated bacteria and archaea is artificial, simply because it can be bridged by cultivation [29–34]. Mass cultivation of prokaryotes is possible, using an approach called ‘culturomics’ [35–39]. Even prior to this approach, recovery of prokaryotic taxa initially found to be recalcitrant to cultivation [40] was resolved by careful consideration of the properties of phylogenetically similar organisms [41]; one would surmise that the determination of nearly complete genome sequences would provide the essential clues about the metabolic traits required for their growth in culture media, as inferred recently [42]. Cultivation and subsequent valid publication of a name under the ICNP may also be triggered by the discovery of an organism using metagenomics [43]. As difficult as cultivation may be in any particular case, it also may be successful in many groups of prokaryotes. Thus, two separate codes of nomenclature may well lead to several different names for the same taxon: a name based on a DNA sequence and ‘validly published’ under the SeqCode and a name validly published under the ICNP after

cultivation. Both names would be regarded as the correct name under the respective code and referred to in the literature; more confusingly, it would not be guaranteed that they would be identical.

Different dates of valid publication would be obtained

Moreover, even if the names were the same and spelled identically, their dates of valid publication would be different under the two codes. This would lead to further confusion, since the effect on priority would differ between the ICNP and the SeqCode. The problems are aggravated by the ways in which names of taxa above the genus rank are formed. Since the higher-rank names are derived from the names of the type genera, under the ICNP [3] or, in the case of classes (and subclasses), from the names of the type genera of the type orders, a conflict of names can easily be triggered that ranges from the species rank up to the phylum level. Thus, many specific conflicts are likely to arise between the two codes.

Use of the proposed SeqCode would contravene the ICNP

Additionally, there is already a general disagreement between the SeqCode and the ICNP, as the SeqCode assigns a distinct nomenclatural status to many names that are not considered validly published by the ICNP. This means, of course, that authors, journals and databases adhering to the ICNP would not accept names proposed under the SeqCode [28]. In particular, the status ‘validly published under the SeqCode’ cannot be accepted as the status of any name of a prokaryotic taxon, whether cultivated or uncultivated, according to the ICNP [3]. The general disagreement between the two codes is easy to explain: both codes overlap in scope, since the ICNP applies to all prokaryotes [3], which would necessarily include those not yet cultivated [28]; General Consideration 5 of the ICNP [3] states that, ‘This Code of Nomenclature of Prokaryotes applies to all Prokaryotes’. The scope of the ICNP is also evident from its title and the title of its publisher, the ICSP.

The application of the SeqCode would create a situation to some extent comparable to that before 1 January 1980. Until then, many thousands of names had been given to bacteria independently over time upon their isolation [44]. Thanks to the revision of the Code in 1975 [45] a new start was made with the Approved Lists of Bacterial Names [46] with about 2400 names, thus eliminating thousands of names [47]. With the current speed of genome analysis and growth of databases, the existence of two nomenclatural systems would make the situation even more complicated than before 1980.

Misinterpretation of the ICNP increases divergence and deserves rectification

Several publications supporting the proposals by Whitman *et al.* [13, 14] or of the SeqCode [24–26] presented some key aspects of the ICNP, and of codes of nomenclature in general, in a rather inaccurate manner. As such particularly critical readings of the ICNP provide the basis for the implementation of the SeqCode, these shortcomings need to be considered when proposing an extension to the ICNP and an alternative to the SeqCode.

Determining the correct name should not be oversimplified

For instance, Murray *et al.* [23] claimed that priority ‘simply means that the first validly published legitimate name is the ‘correct’ name of a taxon’. Unfortunately, it is not that simple, even if one disregards the possibility of conserving or rejecting names or epithets. We agree that Principle 6 of the ICNP [3] stipulates that the ‘correct name of a taxon is based upon valid publication, legitimacy and priority of publication’. However, this phrasing does not imply that these are the only factors which determine the correct name [48]. Principle 6 further refers to Chapter 3, Section 5 (Priority, Effective and Valid Publication of Names) of the ICNP, wherein Rule 23a provides further clarification. Moreover, Principle 8 already states that any ‘phylum or taxon of a lower rank with a given circumscription, position, and rank can bear only one correct name, i.e., the earliest that is in accordance with the Rules of this Code’ [3]. (Principle IV of the ICN [2] makes exactly the same point.) Accordingly, changes in circumscription, position, or rank may well result in situations in which the first validly published and legitimate name among a set of synonymous names is not the correct name of a taxon [48].

While the omission of this aspect by Murray *et al.* [23] might seem as trivial at first sight, a key concept of any code of nomenclature is that the code regulates nomenclature but not taxonomy [1–3]. This key concept is, in turn, implemented in the ICNP and in the ICN by leaving circumscription and position and, thus, the decision on the correct name of a taxon, to taxonomic opinion, in any case where several validly published and legitimate names are available [48]. For instance, if one believes that *Bacillus alginolyticus* Nakamura 1987 [49] should be placed in the genus *Paenibacillus*, which is merely a matter of taxonomic opinion, then *Paenibacillus alginolyticus* [49, 50] is the correct name of the species, even though the first validly published and legitimate name for the bacterium is *Bacillus alginolyticus* Nakamura 1987. These considerations are related to an issue mentioned above, namely that each code of nomenclature [1–3] provides only for relative stability of naming, not absolute stability, because each code endorses taxonomic freedom.

The proposal rejected in 2020 implied a logical contradiction

In fact, General Consideration 4 of the ICNP states that, ‘Rules of nomenclature do not govern the delimitation of taxa nor determine their relations’, while Principle 1.4 states that nothing ‘in this Code may be construed to restrict the freedom of

taxonomic thought or action' [3]. For these reasons, a ratification of the proposal by Whitman [13] would have introduced a logical contradiction into the ICNP. A statement was proposed to be included into Rule 18a and Rule 20a, which indicated that a DNA sequence (or any other 'type material') must unambiguously identify the species or genus to be of use as a nomenclatural type. 'In this regard, the key issue is whether the species is unambiguously identified, which is an absolute and not quantitative distinction. Either the evidence is sufficient to identify the species or it is not' [13]. However, the ability to unambiguously identify a prokaryotic taxon depends on two factors; the fidelity of the DNA sequence or other data; and the circumscription, or extent, of the taxon, which is subject to taxonomic opinion [3].

From a fundamental nomenclatural perspective, if all organisms that show an identical DNA sequence are considered to belong to the same species, then that DNA sequence unambiguously identifies the species; but if not all such organisms are considered to belong to the same species, then that DNA sequence does not unambiguously identify any species. If this DNA sequence had been selected as the nomenclatural type of a species, it could suddenly cease to be the 'type material' in the event of a change in taxonomic opinion. As a result of this change, the taxon name would no longer be validly published. Thus, Whitman's proposal [13] would have made the status of being validly published dependent on taxonomic opinion. This would, of course, be in contradiction with the precept that the ICNP does not govern taxonomy, but governs only nomenclature [3]. For this reason, whether a name is validly published must not be dependent on taxonomic opinion.

A code of nomenclature cannot actually grant priority

The view that a code of nomenclature could grant 'priority' also occasionally occurs in publications which argue for DNA sequences as nomenclatural types [14, 24]. However, whether a taxon name has priority depends, apart from its nomenclatural status of being validly published and legitimate, also on the names with which it competes for priority. Unless names are regarded as synonyms with an identical rank, circumscription and position, which is (apart from the rank) a matter of taxonomic opinion and not regulated by a code of nomenclature, they do not compete for priority. A code of nomenclature must provide the basis for granting a taxon name a claim to recognition and a date of valid publication or equivalent. However, if, according to some taxonomic view, this taxon name competed with another validly published and legitimate name that had an earlier date of valid publication, the former name would not have priority [3, 48]. The only options for granting a name or epithet preference over another name or epithet are, conservation and rejection [3, 48], and these measures do not necessarily rule out that competition with yet another name might occur.

The proposed SeqCode determines the priority of names above genus rank differently from three other codes

As mentioned above, under the ICNP, any taxon with a given circumscription, position and rank can have only one correct name, namely the earliest validly published and legitimate one, with exceptions possible only by conservation or rejection [3, 48]. The ICN regulates the question of priority in the same way, described in Article 11 [2]. Under the ICZN [1], validly published names are called 'available names' while correct names are called 'valid names'. However, Article 23 of the ICZN regulates priority analogously to priority in the ICN and the ICNP. The SeqCode deliberately deviates from the practice of the three other codes of nomenclature by deriving the priority of a name above the genus rank from the date of 'valid publication' of its type genus [25]. Whitman *et al.* [25] justify this deliberate creation of conflict in higher classification by emphasizing that 'the priority of the names of higher taxa depends on the date of validation of the name. Since naming higher taxa was not a common practice prior to Garrity *et al.*, these rules created the potential for instability and confusion'. However, names of taxa above the genus rank that are now considered prokaryotes date back to the nineteenth century [51], with a significant number of such names included in the *Index Bergeyana* [44] and in the Approved Lists of Bacterial Names [46]. In addition, the ICZN and ICN have for decades regulated the priority of names above genus rank in essentially the same way as the ICNP [1, 2].

It remains unclear how the nomenclature of taxa above the genus rank should be stabilized by *increasing* its dependence on assumptions of synonymy between genera. In fact, one might reasonably expect the opposite effect. Moreover, as the dates of valid publication of names at the genus rank or below are used for determining their priority, it is inconsistent to do otherwise in the case of taxa above genus rank, thus *increasing* confusion. Apart from that, the mere deviation from other codes of nomenclature [1–3], particularly from the ICNP and the ICN, is a likely source of instability and confusion.

Whitman *et al.* [25] further claimed that, 'it has been argued that a validly published family name has priority even when its type genus is illegitimate'. However, among the two articles allegedly making that argument, the one by Tindall [52] made no such statement, while the other article [53] may have confused names that are considered synonyms (because they are not regarded as the correct name) with names that are illegitimate. Whitman *et al.* [53] claimed that 'the genus *Sinobacter* is considered a later heterotypic synonym of *Solimonas* and [thus] is illegitimate'. However, whether taxon names are considered to be heterotypic synonyms, is merely a matter of taxonomic opinion. A name that is considered a later synonym is not illegitimate for this reason. This was clarified by Tindall in 2015 [54] and reiterated in Judicial Opinion 111 [55] and in guidelines for interpreting the ICNP, issued by the Judicial Commission [48]. Although the wording of Rule 51a might, at first consideration, suggest otherwise, the Rule must not be interpreted so as to create logical contradictions with other Rules [48, 54]. The 2008 and 2022 revisions of the ICNP [3, 9] make explicit, in Rule 21a, that only genera with a validly published and legitimate name can serve as nomenclatural

types for taxa above the genus rank with a validly published and legitimate name. Accordingly, a family name cannot have priority when its type genus has an illegitimate name [48]. Thus, we conclude that conflicts between the SeqCode and the ICNP (as well as the ICN) regarding the nomenclature above the genus rank were created based on a misinterpretation of the ICNP [54].

Other codes more strongly agree with the ICNP than with the proposed SeqCode

Palmer *et al.* [24] listed examples of the kinds of nomenclatural types that are distinct from cultures but are accepted by other codes of nomenclature [1, 2], as an argument for accepting DNA sequences as nomenclatural types under the ICNP. While comparisons between codes of nomenclature can provide valuable insights, none of the other kinds of nomenclatural types listed are DNA sequences. Article 40.4 of the ICN [2] indicates that the nomenclatural type of a taxon at or below the species rank can be an illustration only prior to 1 January 2007. However, since that date, the type must be a specimen; exceptions need special justification. That is, the ICN moved from allowing data derived from a physical object as type to insisting on the physical object itself as type. This was a move in the opposite direction compared to the proposal to accept DNA sequences as types [13, 14]. A similar move has been made in the ICNP, as Rule 30 requires the deposition of viable cultures of the type strain in culture collections, in at least two different countries, for the valid publication of a name since 1 January 2001 [3]. One can use the examples from other codes as arguments for accepting certain kinds of physical objects as nomenclatural types, such as preserved specimens. However, it makes no sense to use these examples as arguments for accepting DNA sequences as types, because DNA sequences are not physical objects.

The scope of a code and the criteria for valid publication are different things

Palmer *et al.* [24] also claimed that ‘despite General Consideration 5 of the ICNP stating the code “applies to all prokaryotes,” since January 2001 only species with type strains available in pure culture can be validly named ..., meaning that the code itself would be more accurately named the “International Code of Nomenclature of Cultivated Prokaryotes”’. However, the scope of a code of nomenclature [28] must not be confused with its (deliberately chosen) criteria for valid publication or equivalent [1–3]. For instance, to the best of our knowledge, it has never been suggested to rename the ICN to ‘International Code of Nomenclature for visible algae, fungi, and plants’, although the ICN requires evidence such as drawings or specimens for the valid publication of a name [2]. The number of names falling within the scope of a code of nomenclature is always greater than the number of names that are recognized under that code.

In fact, at some point in the not too distant past, all bacteria and archaea that now have a name validly published under the ICNP were uncultivated [7]. While there are several phyla of prokaryotes that still lack cultivated representatives, this was once true of all phyla. In fact, descriptions of prokaryotic species or subspecies that result in a name validly published under the ICNP almost always begin with an *uncultivated* organism that is then isolated and cultivated. Whether a prokaryote is cultivated is not an intrinsic property of that prokaryote but only a relationship between that prokaryote and historically contingent human activities. On the other hand, objective differences between the organisms covered by two otherwise similar codes of nomenclature are required to separate the codes cleanly when this is of interest. For example, the ICN [2] covers plants, fungi and algae, while the ICZN covers animals [1]; their overlap is negligible. One cannot turn a stingray into a petunia, a colony of *Volvox* into a Colorado beetle, or a golden jackal into a powdery mildew. One can, however, turn an uncultivated prokaryote into a cultivated one by cultivating it, however difficult that may be in some cases; and one can even more easily turn a cultivated prokaryote into an uncultivated one.

THE ICSP CAN HAVE THE BEST OF BOTH WORLDS

A single code can meet all needs

The useful aspects of the proposed SeqCode can be incorporated into the ICNP

Among other things, the ICNP [3] must seek a balance between the particular interests of those who wish to propose names and the particular interests of those who should use such established names. Neither the aim of proposing as many taxon names as possible nor excessive taxonomic conservatism should be the aim of an ICNP emendation. One question, for example, is whether the possibility of obtaining standing for species names proposed solely on the basis of a genome sequence is primarily in the interest of the publishing author or of the microbiological community at large. As shown in Table 1, there is an interest in retaining the benefits of the stability and security of the ICNP and integrating aspects of the SeqCode that are compatible and help to provide a better service to the wider scientific community. The differences between the two codes and a proposal for an ICNP emendation are presented in Table 1 and detailed in the following sections.

The ICNP covers all prokaryotes [28] and, in order to achieve this coverage, delegates a limited amount of prokaryotic nomenclatural responsibility to the ICN [56, 57]. By recognizing names validly published under the ICNP, the SeqCode delegates a considerable amount of responsibility to the ICNP and, thus, also indirectly to the ICN, although the SeqCode does not attempt to achieve compatibility with these codes (Table 1). Although it has been portrayed otherwise [58], the ICNP does not hinder any assignation of names to micro-organisms or descriptions of prokaryotic taxa [59]. The ICNP simply regulates which names are validly published, legitimate, and correct [28, 48].

Table 1. Comparison between the 2022 revision of the ICNP, the emended ICNP as proposed here and the SeqCode

Advantage	ICNP (2022 revision)	Proposed emendation	SeqCode
Covers all prokaryotes	Yes	Yes	(Yes)*
Compatible with the ICNP (2022 revision)	–	Yes	No
Compatible with the ICN (Shenzhen Code)	Yes	Yes	No
Governed by representative body	Yes	Yes	No†
Implements the preference of cultures over sequences as types	Yes	Yes	No
Regulates names of uncultivated taxa in detail	No	Yes	Yes

*For coverage of all prokaryotes, the ICNP delegates a small part of the responsibility to the ICN, but reciprocally, whereas the SeqCode delegates a significant part of the responsibility to the ICNP (and thus indirectly to the ICN), but not reciprocally.

†See the main text below for details on representativeness.

Compatibility with the ICN is important

The scope of the ICNP and the necessary compatibility with the ICN [2] are crucial in this context. The incompatibility of the SeqCode with the ICNP has been addressed above, as well as the related issue that the ICNP covers all prokaryotes, i.e. not just the cultivated ones. The text below explains in detail why the changes proposed here to emend the ICNP are fully compatible with the 2022 revision of that Code [3]. It remains to be clarified that names of *Cyanobacteria* have been integrated into the ICNP by accepting names of *Cyanobacteria* validly published under the ICN [2] as validly published simultaneously under the ICNP [56, 57]. Thus, agreement between the ICNP and the ICN is of relevance and has been implemented [60] under the mutual regulation of the ICNP and the ICN. For recognizing another code for the nomenclature of prokaryotes, such recognition would also have to be explicitly regulated in the ICNP. This has been the case for the ICN (for *Cyanobacteria*) but not for the SeqCode [28]; recognition of the SeqCode would not be consistent with previous decisions of the ICSP [20].

The ICNP optionally delegates the clarification of the nomenclatural status of names of *Cyanobacteria* to the ICN [48]. It does so without contradicting the ICN. The ICN reciprocates this in Article 45.1 [2]. Conversely, the disagreement between the ICNP and the SeqCode extends to a corresponding disagreement between the ICN and the SeqCode. The SeqCode heavily relies on the ICNP but, as explained above, it specifically overrides nomenclatural status values assigned by the ICNP, thus also distorting the relative priority of names.

The ICSP is representative of microbiologists worldwide

The 2020 decision does not indicate that the ICSP is unrepresentative

The ICSP is, by construction, a representative body of microbiologists worldwide [4]. Membership within IUMS and the appointment of a delegate to the ICSP is the responsibility of each national microbiological society [4]. Microbiologists who disagree with ICSP decisions, such as the decision against the proposal of Whitman *et al.* [61] in 2020, may be tempted to portray the ICSP as unrepresentative of the field [61]. However, the composition of the voting members of the ICSP was not the only, and perhaps not even a significant, factor in the rejection of the proposal by Whitman *et al.* to allow for DNA sequences to be nomenclatural types of taxa with validly published names [20]. Most non-voting participants in the debate also opposed the proposal [13, 14], and several societies and other institutions outside the ICSP petitioned against its adoption. Microbiologists who were surprised by the 2020 ICSP decision should bear in mind that anyone could have participated in the open ICSP debate that was launched long before the decision was made, or been a member of a society represented in the ICSP at the time.

Lloyd and Tahon [61] critically emphasized that the ICSP at that time did not include delegates from ‘South or Central America or most of Africa or Asia’, although they did not specify how the, admittedly, European- and North American-centric composition of the ICSP might have affected the outcome of the ICSP debate on DNA sequences as nomenclatural types [20]. The criticism of Lloyd and Tahon [61] in this regard can best be seen as a *post hoc, ergo propter hoc* fallacy [62]. The variety of factual arguments against the proposals [13, 14] presented during the debate [20] and reiterated below indicate that there is no basis for relating the composition of the ICSP to the outcome of the ballot.

Another likely *post hoc, ergo propter hoc* fallacy [62] is the idea that the “heavy influence of employees of large culture collections on this ICSP decision may be a financial conflict of interest, as the decision could affect the number of strains deposited” [61]. This assertion is based on the assumptions that a significant proportion of the revenue of large culture collections is derived from the handling of strain deposits, and that the salaries of culture collection staff involved in the 2020 debate [20] would be affected by changes in the sales volume of the culture collection concerned. No evidence was provided to support these suggestions and other claims made in the same publication [61] were found to be inaccurate [63]. Many public culture collections are non-profit organizations supported by national authorities. For example, the DSMZ (German Collection of Microorganisms and Cell

Cultures) is supported by the state of Lower Saxony. The staff of culture collections consists of dedicated experts who not only collect and provide strains, but are often called upon by industry or governmental agencies for their knowledge and expertise. Culture collections are recognized as Biological Research Centres [64], as they are also involved in research on taxonomy, new methodologies, conservation methods and other scientific issues.

The ICSP is more representative than other committees

Interestingly, none of the measures taken to establish the SeqCode [24–26] appear to represent the range of views and interests of microbiologists worldwide, certainly not to the same extent as the ICSP (Table 1). Neither the number of participants in online conferences dedicated to the SeqCode nor the publication of SeqCode-related articles in journals are necessarily convincing counter-arguments. For example, papers on nomenclature published in journals with high impact factors [58, 61, 65] may still be inaccurate [59, 63, 66], and such publications suggest that the way in which codes of nomenclature actually operate is not as widely understood as it should be [48, 67], a topic to which we will return below. The ICNP nomenclature serves all fields of microbiology and is widely used.

Cultures are preferred to DNA sequences

The following interrelated arguments speak against treating genome or other DNA sequences as nomenclatural types of species and subspecies on the same level as cultivated strains [20]. According to these considerations, changing the ICNP to allow for prokaryotic names based solely on sequences as nomenclatural types to be treated as equivalent to names based on cultivated strains would, thus, be an extreme move, which the ICSP was not willing to accept [20].

A culture is more informative than a DNA sequence

First and foremost, a culture contains more information than a genome sequence. This can most easily be proven as follows: one can generate a genome sequence from a culture, but not *vice versa*. This is related to the difference between an organism and the characters derived from that organism, which leads to an epistemological problem when using sequences as nomenclatural types for organisms. In a critical discussion of a proposal to use sequences as nomenclatural types for fungi, more than 400 mycologists [68] noted:

‘Should the proposals be accepted, the meaning of nomenclatural types would change in a fundamental way from physical objects as sources of data to the data themselves. [...] Names of taxa are applied to organisms, not to characters of those organisms. Therefore, a physical object should preferably serve as the type of a name, rather than the characteristics of that object.’

This reasoning is independent of historical considerations, such as the unavailability of DNA sequencing when the nomenclature codes defined nomenclatural types, and of differences between the codes, such as the fact that eukaryotic sequencing is more challenging and one cannot expect the same level of accuracy and depth.

There are two ways to avoid this problem in microbiology. One way is to develop a separate system for naming prokaryotes, so that names are explicitly given for sequences, not for organisms. Such a system would, of course, have to avoid the possibility of the generated names being confused with the names of organisms [21]. As explained above, the SeqCode fails to do this, mainly because the format of the SeqCode has been copied from that of the ICNP. An alternative approach would be to emphasize that names are provisional whenever they are based on DNA sequence information alone. This is one of the principles behind the *Candidatus* status [5, 6].

Sequence-only approaches reduce reproducibility

The absence of the underlying organisms from which the characters were derived also raises serious questions about reproducibility. ‘Such changes [i.e., the permission of sequences as nomenclatural types] are conducive to irreproducible science [and] the potential typification on artefactual data, ... ultimately causing nomenclatural instability and unnecessary work for future researchers that would stall future explorations of fungal diversity’ [68]. Under an ICNP that allowed DNA sequences as nomenclatural types, sequence artefacts would cause many conflicts, leading to an overwhelming number of Requests for Opinion [48] to resolve these conflicts. Accession numbers in publicly available databases [69], as recommended by Whitman [13], are not necessarily stable, as the sequence information can be updated. Even the use of different state-of-the-art sequencing methods can lead to discrepancies [70]. It was pointed out several times during the 2020 debate [20] that the Whitman [13] proposal does not specify quality checks. Necessarily, such measures would require considerations outside the scope of the ICNP, since methods used for classification are pointedly not included within codes of nomenclature. Again, these issues can be avoided by considering names based solely on DNA sequences as provisional [5] and as hypotheses-generating, rather than confirmatory. It would then be easier to regulate the replacement of their nomenclatural types once improvements in quality are achieved, as detailed below.

Quality issues arise with sequence-only approaches

It is well known and accepted that the determination of DNA sequences and further bioinformatic processing is not error-free [71]. Thus, the subsequent usage of digital sequence information as type material is questionable, especially since the taxonomic

use of such data may be subject to variation, generated from the particular protocols used to determine nucleotide sequences and to assemble sequence reads, the algorithms used [72] and the taxa used for comparison when making conclusions about taxonomic positions [73]. Acceptance of genome sequence data as type material does not consider those prokaryotes exemplified by, e.g., *Vibrio* and *Burkholderia* species that contain multiple chromosomes, where guidance from the SeqCode is lacking [26].

Doubts regarding the quality and reproducibility of genome and other DNA sequences are particularly important when dealing with environmental samples rather than isolates. Using a pure culture is still the best guarantee for obtaining a high-quality genome sequence [74]. Hence, the importance of genome sequences for contemporary taxonomy [75, 76] should not be used as an argument for using DNA sequences, rather than cultures, as nomenclatural types. Although it was sometimes depicted otherwise [20], critics of the proposal by Whitman [13] do not deny the crucial role of genome sequencing in contemporary microbiology. However, one must keep in mind that microbiology would soon navigate towards a dead end if DNA sequencing was not accompanied by other methods that allow for making sense of the sequence information. To date, a large proportion of prokaryotic genome sequences have been annotated only as 'hypothetical proteins', or have been annotated incorrectly. This situation can only be improved by subsequent laboratory testing, including cultivation [19, 77]. Culture collections are key players in the archiving and maintenance of type material and thus contribute significantly to the implementation of the FAIR principles: i.e., Findability, Accessibility, Interoperability, and Reusability of biological data [64].

Sequence-only approaches do not support all methods of interest

The negative effects of a ratification of the proposal by Whitman [13] on clinical and veterinary microbiology were emphasized in the literature [18]. Type and other, e.g., reference strains remain essential for research, particularly in the medical context, e.g., for developing antibiotics, vaccines, and other antimicrobial strategies, and for conducting experimental research into pathogenicity. Besides clinical and veterinary microbiology, many other sectors, such as food industry, quality control, and other fields in which the routine identification of prokaryotes is carried out by using methodologies not based on genomic DNA methods could be affected by the proposal by Whitman [13]. Microbiology laboratories that are not using genomic-based identification methods would not be able to have access to the information related to species described solely on the basis of their genome sequence. In the case that sequences would be used as nomenclatural types, only sequence-related bioinformatic methods could be applied to them. Methods newly developed in the future for exploring the phenotype of an organism or, for that matter, for DNA sequencing, as well, could not be applied, since the organism, itself, might not be available. As noted by hundreds of mycologists in 2018, by 'allowing already extracted data, such as a DNA sequence, to serve as type instead of the source of the data, new information cannot be obtained when this is required' [68].

We tend to believe that the methods used today are much better than those used, say, 50 years ago. Comments suggesting such a belief were made during the 2020 debate [20]. But how will researchers 50 years from now judge the methods we use today? The proposal to emend the ICNP [13, 14] relied heavily on the perceived accuracy of DNA sequencing, assembly and downstream genome-based taxonomy methods. It did not sufficiently take into account that these methods may be substantially revised in the future. In contrast, the deposit of type strains in culture collections does not presuppose the reliability of any particular method of analysis and makes the nomenclatural types accessible to future methods of analysis. Moreover, as codes of nomenclature should guarantee taxonomic freedom [1–3], one wonders how far this could be guaranteed if only a genome sequence or other DNA sequence were available for each taxon. This would certainly limit the range of methods, and therefore the concept of taxonomic freedom, that could be applied to organisms.

In a review of integrative taxonomy, a group of zoologists emphasised that 'is an inevitable trade-off between using complex integrative approaches for delimiting species that may provide stable names, and the need to accelerate the pace of taxonomic descriptions' [78]. These authors made a clear distinction between candidate species, i.e., 'clusters of specimens identified through DNA barcoding', of which the best equivalent in microbiology is species delineation by DNA sequence similarity thresholds [75], and 'species hypotheses [with] stability to their names, which requires a careful and often painstaking and time-consuming labor of species delimitation' [78]. This distinction would be best implemented in codes of nomenclature by having different systems for candidate taxa, on the one hand, and for taxa which are as well characterised as those with validly published names under the ICNP [3], on the other hand. Environmental DNA sequences as types may be less well suited for better species delineation than isolates because, as a *supporter* of the proposals of Whitman and colleagues [13, 14] noted during the ICSP debate in 2020 [20], 'a MAG [metagenome-assembled genome] that represents an abundant population is *not* a single-strain description but the average genome of the population/many cells'. Hence, such a MAG would not represent the variation of a population, which could instead be achieved by sequencing different isolates.

A strong incentive for cultivation and deposition must be retained

For these reasons, a sufficient incentive to cultivate bacteria and archaea and to deposit strains in culture collections should be retained in the Code. If genome or other DNA sequences were to be accepted as nomenclatural types for names validly published under the ICNP, the likely outcome would be that pure cultures would eventually cease to be used as types, since cultivating and depositing strains in culture collections is considerably more tedious than depositing a sequence in the International Nucleotide

Sequence Database Collaboration (INSDC) [69], which usually has to be done anyway [75]. During the 2020 debate, it was argued that an incentive for cultivation and deposit remained, due to the possibility of publishing emended taxon descriptions [20]. However, emendations do not carry the same weight as validly published names and are relatively rare [68]. Authors may well have other incentives to isolate strains, but it remains important that the rules of nomenclature sufficiently support isolation, cultivation and deposition.

During the 2020 debate [20], it was argued that the use of DNA sequences as nomenclatural types could circumvent legal restrictions on strain deposit or access imposed by certain countries [79]; however, this view was disputed. In particular, it was pointed out that similar restrictions are likely to be imposed on digital sequence information in the near future. The argument based on legal restrictions on deposition, although put forward by supporters of the Whitman proposals [13], also nicely illustrates that deposition of type strains, a requirement for valid publication of species and subspecies names under the ICNP [3], can be challenging. This actually supports the need for a sufficient incentive in the Code to deposit, particularly because the Code needs to balance the needs of those who intend to propose names with the needs of those who would subsequently have to deal with the proposed names. The example further demonstrates that, although the SeqCode is usually advertised as being needed to better deal with the names of uncultivated prokaryotes [24–26], there are also other motives behind its creation. Names have already been proposed as *Candidatus* names in the literature for the sole reason that the authors did not want to wait for the deposition of strains to be finished [80]. This also suggests that a strong incentive for cultivation and deposition should remain in the ICNP.

Depth and breadth are different goals and require different measures

Furthermore, the possibility to cheaply generate many new names may lead to nomenclatural inflation. A separate naming system may still create many names that may be considered meaningless, particularly if they are based only on the core genome [20]. As noted by mycologists, such ‘changes [i.e. the permission of sequences as nomenclatural types] are conducive to ... massive creation of names with low information content, ultimately causing nomenclatural instability and unnecessary work for future researchers that would stall future explorations of fungal diversity’ [68]. Thus, the generation of a huge number of names with no or low metadata information content and the same status as more informative names should be avoided. This can be easily done [6] by differentiating between validly published names and *Candidatus* names, as envisaged by the ICNP [3]. In contrast, it would not be sufficient to indicate in the designation of the nomenclatural type whether it is a strain, a sequence, or something else, as proposed by Whitman [13], as most users of taxonomic classifications only consider taxon names. For instance, INSDC records [69] do not contain such designations. Moreover, such an indication was only a recommendation in the proposal by Whitman [13]. Under the ICNP [3], the nomenclatural status of being validly published acts as a ‘quality standard’ and almost always indicates that a culture of the type strain is available from culture collections. This quality standard would be abandoned if DNA sequences were also allowed to be nomenclature types.

Intriguingly, proponents of DNA sequences as nomenclatural types sometimes freely acknowledge that cultivation remains to be important and valuable. For instance, Palmer *et al.* [24] mention that, it ‘has been argued that a code of nomenclature accepting DNA sequence data as nomenclatural types would negatively impact the motivation to study and archive pure cultures We acknowledge this concern and take it seriously’. This is at least a valuable acknowledgement and a valuable starting point. However, other publications in favour of DNA sequences as nomenclatural types have emphasised the benefits of regularly omitting culture deposition [12]. Palmer *et al.* argued that ‘metagenomics and other systems approaches focused on uncultivated microorganisms can provide invaluable support to guide cultivation efforts’ [24]. And, importantly, the insistence of the ICNP on cultures as nomenclatural types of species and subspecies with validly published names does not diminish the motivation to apply ‘metagenomics and other systems approaches’ [24]. Conversely, Palmer *et al.* [24] did not provide an approach to motivate cultivation or even deposition of strains. Palmer *et al.* [24] also emphasized that working with cultures, let alone deposition, is usually more time-consuming than working with sequences. However, this trade-off between quality and quantity is well known [78] and suggests conflicting goals. In contrast to Palmer *et al.* [24], we conclude that such conflicting goals require different sets of measures to serve each goal, rather than conflating them by giving the resulting taxon names the same nomenclatural status.

There is a need to better regulate the naming of as yet uncultivated prokaryotes

Some perceived problems with names of the uncultivated cannot be solved by a code of nomenclature

Lloyd and Tahon [61] complained in 2022 that the ICSP did not prevent ‘*Lokiarchaeota*’ from being renamed ‘from Marine Benthic Group B (MBG-B) and Deep-Sea Archaeal Group (DSAG). They are now members of the Asgard super-phylum and their nearly pure enrichment is “*Candidatus* Prometheoarchaeum syntrophicum”’. However, the only *Candidatus* name for this phylum potentially in agreement with the Code was ‘*Lokiarchaeota*’, even according to the 2008 revision of the ICNP [9], and further clarified by the inclusion of the phylum category in the ICNP in 2021 [81]. Furthermore, neither the assignment of this group to the ‘Asgard superphylum’ nor the assignment of ‘*Candidatus* Prometheoarchaeum syntrophicum’ to this group is an example of nomenclatural instability. These are taxonomic actions involving names at different taxonomic ranks, rather than the creation of synonyms with unclear preferences. The example of ‘*Bathyarchaeota*’ given in the same publication [61] is also

misguided. Indeed, care must be taken not to misunderstand the aims and limitations of a code of nomenclature in general, and not to misunderstand the real advantages and disadvantages of establishing a separate nomenclature code in particular.

The ICNP provides insufficient regulations for names of uncultivated taxa

Despite these remarks and despite all these necessary criticisms of the proposals of Whitman and colleagues [13, 14] and of the SeqCode [26], it should not be overlooked that their proponents are right about one crucial point. There are indeed a large number of prokaryotic names of interest that cannot be validly published under the ICNP, but for which it would be beneficial to better regulate their nomenclature. The ICNP already regulates how *Candidatus* names are formed and, implicitly through their orthography, also regulates the nomenclatural types of *Candidatus* names above genus rank. These aspects are already implemented in the IJSEM *Candidatus* Lists [82], highlighting that the SeqCode is already redundant to some extent. In addition, Appendix 11 of the ICNP already indicates that ‘nucleic acid sequences apt to determine the phylogenetic position of the organism’ should be included in the descriptions of *Candidatus* taxa [3]. Although the IJSEM *Candidatus* Lists [82] do not yet refer to sequence information, the emphasis on such ‘nucleic acid sequences’ may indicate recognition of the need for nomenclatural types. Otherwise, however, the ICNP does not implicitly or explicitly regulate the assignment of nomenclatural types to *Candidatus* genera, species or subspecies.

Furthermore, the ICNP does not regulate which *Candidatus* name should be used in the event of competition. Furthermore, the ICNP does not regulate whether *Candidatus* names must be reused after cultivation and valid publication, although this would be considered beneficial and a scientific courtesy. Similarly, the ICNP does not currently prohibit homonyms of *Candidatus* names when names are proposed for valid publication. Analogous regulations currently exist only in the SeqCode [26], although the SeqCode mixes names that the ICNP would consider *Candidatus* names with names validly published under the ICNP, in violation of the ICNP [28].

Equal status for sequence-based names is not necessary to achieve this goal

An official naming system that better integrates as yet uncultivated micro-organisms creates a stronger incentive to name them. However, unlike the SeqCode, codes of nomenclature need to retain an incentive for isolation, cultivation and deposit in culture collections. Both goals can be achieved by nomenclatural rules that recognize names assigned to as yet uncultivated taxa in a certain way and under certain conditions, and yet allow for subsequent upgrading (valid publication) upon successful cultivation of these organisms.

These considerations call for a modification of the ICNP that takes into account both sets of arguments. The aim is to achieve a single code for the nomenclature of prokaryotes that meets all needs of the modern microbiology community. In accordance with the ICSP Statutes [4], proposals for the revision of the ICNP are presented below. The Statutes also specify the time allowed for discussion and voting on proposals. The natural and obvious choice for a revision is to expand the ICNP's *Candidatus* concept. The proposed new Rules to be included in the ICNP are given below, after explaining the consequences of their implementation, in general, and the rationale behind the details of the proposal, in particular.

The proposed emendation of the ICNP has well-defined beneficial consequences

Reuse of *Candidatus* names and avoidance of homonyms makes sense

The sole potentially negative consequence for taxonomists working with cultivated prokaryotes is that additional attention would be required in certain situations. This would only affect future taxonomic work, as the corresponding Rule is not intended to be retroactive. Moreover, the emended ICNP would remain being a code of nomenclature and not of taxonomy, as indicated in General Consideration 4 [3], and would thus continue to be consistent with Principle 1(4), which prohibits any restriction of taxonomic freedom, in thought or action. The 2022 revision of the ICNP [3] already stipulates in Rule 27(2)(b) that, when proposing a new combination, all homotypic and heterotypic synonyms shall be listed. When proposing the name of a taxon for valid publication, it would, if the proposed emendation of the ICNP was ratified, in many cases be necessary to consider whether a taxon is equivalent to a taxon with a *Candidatus* name, according to the taxonomic view of the authors. If so, the name would need to be reused in the proposal of a name for valid publication. The valid publication of a species name previously known under a *Candidatus* name has occurred several times in the past [29–32]. However, the name, or at least the epithet of the *Candidatus* name, has not necessarily been reused in such cases [33, 34], simply because such reuse is not yet enforced by the ICNP. If the current proposal was ratified, the reuse of *Candidatus* names would also be regulated for taxa above species rank.

In other situations, i.e. where synonymy is not postulated, it would not be necessary to reuse a *Candidatus* name. On the other hand, it would be necessary to ensure that the name proposed for valid publication is different from all registered *Candidatus* names. Again, this is good practice and is consistent with the objective of the ICNP to avoid homonyms, even homonyms of names proposed under the ICN [2] or ICZN [1], as implemented in Principle 2 [3]; validly published names that turn out to be homonyms of a botanical or zoological name are illegitimate and must be replaced [83–85]. Given the already established IJSEM *Candidatus* Lists [10, 11], it should be much easier for microbiologists to keep track of *Candidatus* names than to keep track of names proposed under the ICN or ICZN.

A central collection of all relevant names is essential

In fact, if the current proposal was ratified, it would ensure that all *Candidatus* names with a potential need for reuse, and the need to avoid the creation of a homonym, were registered in the IJSEM. The IJSEM *Candidatus* lists would become more similar in purpose to the Validation Lists. In addition to the orthographic corrections already provided and the associated nomenclatural types for taxa above the genus rank, the nomenclatural types of species and subspecies would also be recorded in the *Candidatus* Lists. Requesting the List Editors to include a name in such a list would become primarily the responsibility of its authors. Thus, the situation for taxonomists would not be significantly different from current practice. It is already necessary to consider whether a taxon for which a new name or combination could be proposed matches a taxon with a validly published and legitimate name. Like everyone else, microbiologists working with isolates would often benefit from the increased nomenclatural stability brought about by the enforced reuse of *Candidatus* names.

A backward-compatible approach can adequately regulate names of uncultivated taxa

The proposed emendation of the ICNP would have a variety of advantages for taxonomists working with as yet uncultivated prokaryotes. *Candidatus* names would receive certain privileges in nomenclature under the ICNP. For instance, the choice of which *Candidatus* name to use in case of competition would be regulated by the ICNP. As mentioned above, the reuse of *Candidatus* names when proposing names for valid publication would also be regulated by the ICNP. Furthermore, the ICNP would require authors of *Candidatus* names to be indicated in cases of reuse of such names. Avoidance of homonyms of *Candidatus* names would also be enforced. The already established IJSEM *Candidatus* Lists [82] would be expanded to include more information, thereby expanding the implementation of the principle of centrally collection of names for supporting prokaryotic nomenclature. Like everyone else, scientists who explore the not yet cultivated prokaryotes would benefit from a single code of nomenclature governing all names of interest, as opposed to the confusion created by a second, co-existing and competing code that overlaps in scope with the ICNP [28].

The changes envisaged for the ICNP would be fully backward-compatible. While this emendation of the ICNP would introduce new status values for taxon names, the established nomenclatural status values would not change. For this reason, microbiologists would still have a choice when compiling lists of names of interest. They could restrict the scope of these lists to the names with standing in nomenclature, or also include *Candidatus* names registered in the IJSEM. The former approach makes more sense when dealing with a group of prokaryotes that can be easily cultivated, while also considering *Candidatus* names is more appropriate when dealing with a group of prokaryotes which mostly do not yet meet the criteria for valid publication under the ICNP.

The proposed implementation is governed by a few key principles

Names of uncultivated taxa can be regulated in analogy to names of cultivated taxa

A new section for Chapter 3, Rules of Nomenclature with Recommendations, of the ICNP is proposed below, Section 10. The proposed text contains many references to other sections of the ICNP, in accordance with the intention to regulate matters analogously to how these matters are regulated for validly published names. This is done to guarantee high consistency and low redundancy. In the unlikely event that the analogy to already existing sections of the ICNP is not clear, it would be provided for the Judicial Commission to be consulted, as usual [4]. Section 10 would supersede Appendix 11 where applicable, although changes to the wording of Appendix 11 do not appear to be necessary. Table 2 provides an overview of the main consequences of the proposed emendation of the ICNP.

Table 2. Additional regulations proposed for *Candidatus* names under the ICNP

The table is a slightly simplified representation, as it omits some aspects of the status of names, such as legitimacy. The SeqCode implements many of the regulations for *Candidatus* names by granting 'validly published' status to names, even if they have only sequences as nomenclatural types. However, such extreme measures are not needed to achieve the desired outcome.

Regulation	2022 revision	Proposed emendation
Avoid homonyms	among validly published names	among validly published names; among <i>Candidatus</i> names; between validly published names and <i>Candidatus</i> names
Enforce reuse of name	–	upon valid publication of taxon with <i>Candidatus</i> name
Indicate further authors	of epithet of validly published name in case of new combination	of epithet of validly published name in case of new combination; of <i>Candidatus</i> name or epithet in case of new combination or upon reuse
Competition for priority	between validly published names	between validly published names; between <i>Candidatus</i> names
Nomenclatural type	of all validly published names; of <i>Candidatus</i> names above genus rank (implicit)	of all validly published names; of all <i>Candidatus</i> names (explicit)

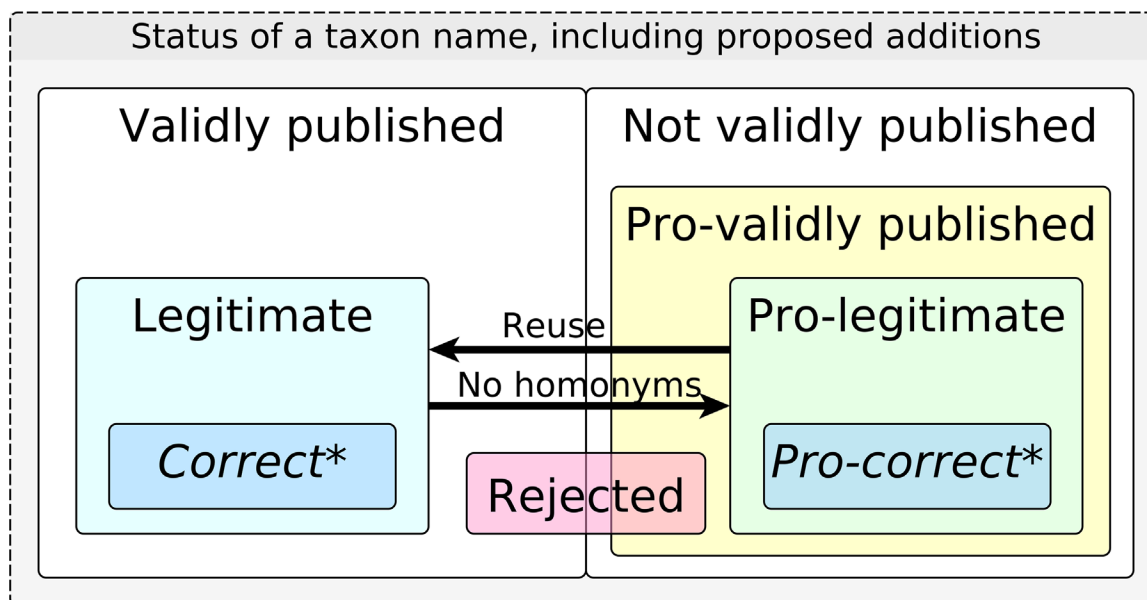


Fig. 1. Status values of names under the ICNP, including the proposed new status values (yellow background colour). Names that are not validly published would be able to obtain certain privileges, including their enforced reuse under defined conditions, as well as the avoidance of homonyms between validly published names and such names under specified circumstances. However, it is unnecessary to equate names based on cultures of type strains with names based on sequences alone. Status values affected by taxonomic opinion are italicized and marked with an asterisk. The list of rejected names already includes both validly published names and not validly published names. The picture is a modified and extended version of a picture published in guidelines issued by the Judicial Commission [48].

The key result of the 2020 rejection of the proposals by Whitman and colleagues [13, 14] by the ICSP is respected here, namely to retain the criteria for valid publication under the ICNP [20]. At the same time, the emendation of the ICNP proposed here would ensure that the name to be applied to a taxon can be determined even if in the absence of a validly published name, provided that a *Candidatus* name that meets a set of defined criteria is available. In this manner, the ICNP would become significantly more helpful in taxonomic areas covered by names whose valid publication is not yet likely. Providing regulations in these areas, analogously to how the correct name of a taxon is determined under the ICNP, is one of the main purposes of this emendation of the ICNP. The proposed Rule 66 defines all terms of interest in this context.

Proposed Rule 66(5) would generally require that matters relating to *Candidatus* names be dealt with by analogy with those relating to validly published names. An example of a more specific provision is found in proposed Rule 69, which states that the nomenclatural types of *Candidatus* names shall be regulated by analogy with Section 4 of the ICNP, followed by a list of exceptions, i.e., the additional provisions for *Candidatus* names. For example, when proposing the name of a *Candidatus* phylum, class, subclass, order or suborder for pro-valid publication, it would not be necessary to propose names at ranks between that rank and the genus rank. However, a type genus with a pro-validly published name would always be required.

New but easily understood status values will retain an informative code

In order to implement such regulations, it is necessary to distinguish between different kinds of names that are not validly published. To better express the analogy between the new rules and the regulations for validly published names, terms are reused where possible and modified by adding a prefix. We have chosen *pro-* as this prefix. It points to the terms 'prospective' and 'provisional', thus emphasizing that a *Candidatus* name does not meet all the requirements for a validly published name, but may well be a first step towards valid publication. For instance, each *Candidatus* name would obtain a nomenclatural pro-status and, depending on that pro-status, it would be subject to additional regulations and could obtain pro-standing in nomenclature. The proposed Rule 67 would be crucial in this respect. The use of neologisms such as 'pro-validly published' has the advantage over, for example, spelling out 'prospectively validly published' that it reduces the likelihood that users will be tempted to infer the meaning of the term from the words used, rather than looking up the definition in the emended ICNP. This helps to avoid misinterpretations such as those of the term 'nomenclatural type', often abbreviated to 'type', which does not refer to anything 'typical' [44]. Fig. 1 shows the status values of names under the ICNP and explains their relationships, including the proposed new status values.

The centralized collection of taxon names is a hallmark of the ICNP [3], i.e., their appearance in a single journal, the IJSEM, as prerequisite for valid publication. The same principle would, of course, apply to *Candidatus* names. The IJSEM List Editors already publish *Candidatus* Lists [82]. For this reason, inclusion in an IJSEM *Candidatus* List is the logical choice as a prerequisite for obtaining pro-standing in nomenclature if the effective publication of the name was not done in the IJSEM. Backward compatibility would equally be implemented by considering the already published *Candidatus* Lists. The date of publication, inclusion in an IJSEM list, and the possible need for augmenting previously included *Candidatus* names with information would be regulated in the proposed Rule 68.

A name supposed to be validly published may subsequently be found not to meet the requirements for nomenclatural types according to Rule 27(3) of the ICNP, usually because the requirements of Rule 30 have not been met [48]. The slight modification of the *Candidatus* concept [5, 6], in the proposed Rule 68(4), would allow such names to be relegated to pro-validly published status. Such a measure is more likely to ensure nomenclatural stability than simply removing such names from the set of validly published names.

Flexible requirements for nomenclatural types are useful

It was proposed that genome sequences or other DNA sequences should be used as nomenclatural types in the case of uncultivated prokaryotes [86]. Under the ICNP, more than 65 000 *Candidatus* taxa were described in this way [8]. However, not all *Candidatus* names proposed in the past are based on DNA sequences, let alone on genome sequences. In order to allow for backward compatibility, an implementation is of interest that yields a strong preference for genome sequences in taxonomic practice but also allows the use of non-pure cultures (such as enrichment cultures), preserved specimens, gene sequences, textual descriptions or illustrations. In this context, non-pure cultures and preserved specimens are preferable to genome or gene sequences because the latter can be obtained from the former but not *vice versa*. In any case, since all kinds of nomenclatural types need to be made available, in order to be of any use, this needs to be reflected in the proposal for Rule 69. The proposed wording would cause non-pure cultures and preserved specimens rarely to be used as nomenclatural types. Should they be used as nomenclatural types, a genome sequence derived from them could still be requested in minimal standards for the description of *Candidatus* taxa or in the instructions for authors of a journal that publishes such taxon descriptions.

Availability and quality of nomenclatural types are important

As for the required availability of genome sequences, it seems preferable to rely on INSDC deposits [69] but to focus on a single kind of INSDC accession number. Thus, it makes sense to rule out INSDC accession numbers for sequence reads, assemblies and protein sequences, as well as BioSample and BioProject accession numbers, and to rule out sequence identifiers in other databases, such as the Integrated Microbial Genomes and Microbiomes system [87] or the PathoSystems Resource Integration Center [88]. To request that every sequence to be used as nomenclatural type must, at least, yield a nucleotide accession number in INSDC (Rule 69) and, e.g., not only be placed in an archive for non-assembled sequence reads, also provides basic minimum requirements for sequence quality. Some flexibility should be implemented in this context by permitting authors to provide missing accession numbers when requesting the inclusion of a name in a *Candidatus* List, if these accession numbers were not included in the effective publication but sequence identifiers that can be mapped to INSDC nucleotide sequence accession numbers were included in that publication.

Gene sequences, textual descriptions and illustrations are not preferable as nomenclatural types. For this reason, the proposed Rule 69 would require a statement by the authors that they consider this kind of nomenclatural type to be sufficient in a particular case. However, since a code of nomenclature does not rule on taxonomy [1–3], and thus does not dictate to authors how to delineate taxa, a reference to the authors' own taxonomic judgment must be considered sufficient for this purpose.

Replacement of nomenclatural types should occur under defined conditions

Rule 70 would regulate the replacement of nomenclatural types of *Candidatus* names. This is necessary because, e.g., the later unavailability of a nomenclatural type may affect not only deposits in culture collections but also sequences in databases. Notably, Rule 70(2) refers to a specific taxonomic view for the sole purpose of defining conditions for replacing types; the Rule does not restrict taxonomic freedom. Rule 70 also allows for the replacement of a nomenclatural type in the case of an increase in sequence quality [89]. Regarding DNA sequencing, this does not directly affect non-pure cultures or preserved specimens used as nomenclatural types, as they can be sequenced again as technology improves, but it does affect nomenclatural types that are sequences themselves.

As explained above, the specificity of a DNA sequence depends on assumptions about the delimitation of taxa, which a code of nomenclature is not permitted to make. Under the reasonable assumption that sequence completeness is positively correlated with specificity, a code of nomenclature should not define requirements for completeness other than those implied by the requirement for inclusion in public sequence repositories [69]. Further details about the use of genome or other DNA sequences as nomenclatural types of *Candidatus* names should be delegated to minimal standards published by taxonomic committees or included in journals' instructions for authors; similar minimal standards were published in the past [75]. The ICSP-associated subcommittee [4] that would

oversee such standards could then respond more flexibly to technological developments than the ICNP itself, as emendations of the ICNP require proper legislation [4].

Sequence purity is addressed together with sequence completeness

Notably, the present proposal to emend the ICNP takes into account that names based on a sequence as nomenclatural type should remain provisional and prospective. One of the reasons for this requirement is sequence quality; the most promising (and reproducible) way to obtain a complete and uncontaminated DNA sequence is to derive it from a pure culture. Our proposal would make it relatively easy to replace a nomenclatural type in case of an improvement in sequence quality and in case of the removal of a sequence from INSDC (Rule 70). However, if a taxon name was based on a strongly contaminated sequence as nomenclatural type, this could call for the rejection of the name according to Rule 71, analogous to the application of Rule 56a(3) of the ICNP [3], in the case of an impure culture used as nomenclatural type of a taxon with a validly published name [48].

The proposed Rule 71 is designed to be compatible with Rule 66 [3, 4]. As for the rejection of names that are not validly published, some not validly published names are already included in the list of rejected names because these names had been proposed prior to 1980 but were not accepted into the Approved Lists of Bacterial Names [46]. These cases were recently summarized by the Judicial Commission [48]. The proposed Note to Rule 71 is added for the sake of completeness and for improving clarity.

Candidatus names can be retained upon valid publication and their authors be indicated

The proposal for Rule 72 is designed to enforce the retention of *Candidatus* names upon valid publication whenever possible, thereby implementing one of the ideas behind the proposals by Whitman and others [13, 14] and the deployment of the SeqCode [26]. Unfortunately, as explained above the proposal by Whitman [13] included a way of referring to taxonomic views that is incompatible with Principle 1(4) of the ICNP [3]. In contrast, the wording proposed here for Rule 72 avoids such a conflict. As with other codes of nomenclature [1–3], the ICNP does not rule on taxonomy and therefore cannot enforce a particular taxonomic opinion. However, taxonomists inevitably express some taxonomic opinion when proposing taxon names, and this opinion can be conditionally referred to. Views on synonymy held by the authors of taxon names are not enforced by the ICNP. However, if they are explicitly or implicitly expressed by the authors, regulations made by the ICNP can relate to them. The proposed Rule 72(1) deliberately makes no distinction between homotypic and heterotypic synonyms. The Rule also provides for some flexibility in the retention of *Candidatus* names, thus allowing a choice which, even in cases of conflict, results in the least number of name replacements overall or avoids the replacement of particularly frequently used names.

Finally, the proposed Rule 73 regulates how authors of a *Candidatus* name would be indicated if that name was reused in a valid publication. A citation in parentheses with the prefix ‘ex’ is proposed, because this seems to be the most compatible solution with the latest revision of the ICNP [3]. As specified in Rule 33c Note 2 and Rule 33d, this kind of citation is already used for the original authors of revived names; as specified in Rule 14b, it is used for the original authors of an infrasubspecific designation upon elevation to subspecies or species rank. In all three cases, the ‘ex’ authors are authors of a name that is not validly published, but from which a validly published name has been derived. Moreover, the two established usages cannot overlap with the additional usage proposed here, and the application of the prefix ‘ex’ will remain unambiguous.

Instability is acceptable only when caused by taxonomic freedom

The proposed emendation of the ICNP [3] only disallows the competition for priority between a *Candidatus* name and a validly published name. However, as long as a *Candidatus* name is not considered synonymous with a previously proposed validly published name, which is a matter of taxonomic opinion, such a competition would not even occur. As mentioned in the introduction, the stability of names provided by codes of nomenclature is only a conditional stability. For this reason, the instability caused by the adoption of changes in taxonomic opinion must already be accepted, and the proposed implementation does not cause any additional instability. On the other hand, if the validly published name was proposed later, the regulations for reuse would be applied if it is postulated that the names are synonymous, thus rescuing the *Candidatus* name anyway.

CONCLUSION: THE PROPOSED NEW SECTION OF THE ICNP

Section 10. *Candidatus* names

Rule 66

The *Candidatus* status should be used to propose names of prokaryotic taxa for which some information is available (Rules 67–68), but for which the requirements for valid publication of a name under Rule 27(3) are not met.

- (1) A *Candidatus* name consists of the word ‘*Candidatus*’, followed by a taxon name formed in accordance with Sections 2 and 3 of this Code.
- (2) *Candidatus* names are not validly published and cannot be the correct name of a taxon. However, *Candidatus* names are regulated by this Code analogously to validly published names. Unless otherwise indicated, terms specific to the regulation of *Candidatus* names are derived from the analogous terms used for the regulation of names in other sections of this Code

by adding the prefix *pro-*. *Candidatus* names have a nomenclatural pro-status and may have pro-standing in nomenclature (Rules 67–68), the main consequences of which are implemented by Rules 71–73.

- (3) *Candidatus* names may be: pro-validly published—the name is not validly published but is included in an effective publication (Rules 25a–25b) and meets certain other requirements (Rules 67–68); pro-legitimate—the name is pro-validly published and would be legitimate (Section 8) if it was validly published; pro-illegitimate—pro-validly published and not pro-legitimate; pro-correct—the name that must be adopted for a taxon under the Rules if the taxon does not have a correct name and it is of interest to assign a name to it (Rule 71).
- (4) A pro-validly published and pro-legitimate *Candidatus* name cannot compete with a validly published and legitimate name for priority (Rule 23a), but it can compete with another pro-validly published and pro-legitimate *Candidatus* name for pro-priority (Rule 71), by analogy with Rule 23a.
- (5) If a nomenclatural question arises in connection with a *Candidatus* name which is not expressly dealt with in Section 10, the solution to be chosen is in accordance with the Rules and has the most obvious analogy to a nomenclatural solution provided for in other Sections of this Code. Doubtful cases should be referred to the Judicial Commission (Appendix 8). The replacement of a pro-illegitimate name or epithet is conducted by analogy with Rules 54–55, but see also Rule 72(4)(b).

Note. For the history of the *Candidatus* status see Appendix 11. Section 10 supersedes Appendix 11 in the event of a conflict.

Pro-valid publication of a *Candidatus* name

Rule 67

A *Candidatus* name for a new taxon, or a new combination for an existing *Candidatus* taxon, is not pro-validly published unless the following criteria are met:

- (1) The name meets the requirements for publication in Rule 27(1).
- (2) The name meets the requirements for the formation of *Candidatus* names in Rule 66(1) in conjunction with the requirements for taxon descriptions in Rule 27(2).
- (3) The name meets the requirements for nomenclatural types in Rule 27(3), except for the following.
 - (a) In the case of the name of a species or subspecies, the name does not meet the requirements of Rule 30 but meets the requirements of Rule 69.
 - (b) In the case of the name of a taxon above the rank of species, the name of its nomenclatural type is not validly published, but it is pro-validly published and pro-legitimate.

Note. Possible exceptions to Rule 67 are defined in Rule 68(2), Rule 38(3) and Rule 68(4).

Rule 68

The date of pro-valid publication of a *Candidatus* name is the date of its publication in the IJSEM.

- (1) If the original proposal of the new *Candidatus* name or new *Candidatus* combination was not published in the IJSEM, pro-valid publication of the name may be achieved by its announcement in an IJSEM *Candidatus* List, by analogy with the announcement of a name in a Validation List for the purpose of its valid publication (Rule 27 Note 1).
- (2) If a *Candidatus* name does not meet the requirements of Rule 67, but has been included in an IJSEM *Candidatus* List that was published before 1 January 2025, the name is pro-validly published.
 - (a) If the nomenclatural type of such a name was not mentioned in the *Candidatus* List, a nomenclatural type will be provided in an addendum to the respective *Candidatus* List, published separately in the IJSEM by the List Editors. Such an addendum does not affect the date of pro-valid publication. If several possible nomenclatural types in accordance with Rule 67(3) have been provided in the effective publication, one shall be selected.
 - (b) If a nomenclatural type in accordance with Rule 67(3) cannot be determined for a name that is pro-validly published because of its inclusion in a *Candidatus* List, this shall also be announced in an addendum to a *Candidatus* List, and the name considered pro-illegitimate.
- (3) If a name meets the requirements given in Rule 67, with the exception of the use of the word '*Candidatus*' as stipulated by Rule 67(2), and the name is included in an IJSEM *Candidatus* List, then the name is pro-validly published and is considered to be a *Candidatus* name.
- (4) When a name that has been considered validly published is found to not meet the requirements for nomenclatural types in Rule 27(3), but is found to meet the requirements of Rule 67(3), the name should be given *Candidatus* status by announcement in an IJSEM *Candidatus* List, stating the reasons for not meeting the requirements of Rule 27(3) and including the information required by Rule 67(3). The presumed date of valid publication of the name shall then become its date of pro-valid publication.

- (5) A *Candidatus* name that has previously been pro-validly published in the IJSEM may be included in an IJSEM *Candidatus* List for the sole purpose of its orthographic or grammatical correction (Section 9). Such inclusion shall not affect the date of pro-valid publication.

Note. In order to determine the relative pro-priority of *Candidatus* names that were included in the same *Candidatus* List for the purpose of their pro-valid publication, each included name should be assigned a number reflecting the date of receipt of the request for inclusion in the *Candidatus* List, by analogy with Rule 24b(4). Within a *Candidatus* List which does not contain such numbers, relative pro-priority of each name is determined by the date of its original publication as indicated in the *Candidatus* List. *Candidatus* Lists published prior to 1 January 2025 may indicate more than one original publication per name. If so, the relative pro-priority of a name is determined by the date of the earliest indicated original publication of that name.

Nomenclatural type of a *Candidatus* name

Rule 69

The nomenclatural type of a pro-validly published *Candidatus* names is regulated by analogy with Section 4, except for the following.

- (1) The kind of nomenclatural type of a pro-validly published *Candidatus* name at the rank of species or subspecies is one of the following (in order of decreasing preference for the kind of nomenclatural type):
 - (a) A non-pure culture containing living cells of the species or subspecies from which characters of use in taxonomy can be obtained.
 - (b) A preserved specimen containing cells of the species or subspecies from which characters of use in taxonomy can be obtained.
 - (c) A genome sequence obtained from the species or subspecies, and deposited in one of the databases belonging to the International Nucleotide Sequence Database Collaboration (INSDC).
 - (d) A gene sequence obtained from the species or subspecies, and deposited in one of the databases belonging to the INSDC.
- (2) For the purpose of designating a nomenclatural type under Rule 69(1)(a) or Rule 69(1)(b), the culture or preserved specimen must be deposited in an appropriate collection. Evidence of its availability from that collection must be provided at the time of publication in the IJSEM.
- (3) For the purpose of designating a nomenclatural type according to Rule 69(1)(c) or according to Rule 69(1)(d), its INSDC nucleotide sequence accession numbers must be provided at the time of publication in the IJSEM, i.e., identifiers that can be used directly to obtain a nucleotide sequence from INSDC, without the need for an intermediate identifier. The INSDC nucleotide sequence accession numbers provided must specifically and completely cover the nucleotide sequence, and all associated sequence data must be available at the time of publication in the IJSEM. All sequence identifiers required to specifically and completely cover the sequence must be cited in the effective publication.
 - (a) If sequence identifiers other than INSDC nucleotide sequence accession numbers have been cited in the effective publication, INSDC nucleotide sequence accession numbers that can be unambiguously mapped to those identifiers must be provided when requesting the inclusion of the taxon name in an IJSEM *Candidatus* List.
 - (b) If INSDC nucleotide sequence accession numbers have been cited in the effective publication but not in the protologue (see Rule 27), these INSDC nucleotide sequence accession numbers must be provided when requesting the inclusion of the taxon name in an IJSEM *Candidatus* List.
- (4) For the purpose of designating a nomenclatural type under Rule 69(1)(d), the protologue must include a statement indicating that, in the taxonomic opinion of the authors, the gene sequence is sufficiently specific to distinguish the taxon from other taxa of the same rank. If such a statement has not been included in the protologue (see Rule 27), the statement must be provided when requesting the inclusion of the taxon name in an IJSEM *Candidatus* List.

Note. Possible exceptions to Rule 69(2), Rule 69(3) and Rule 69(4) are defined in Rule 68(2).

Rule 70

The nomenclatural type of a pro-validly published *Candidatus* name at the rank of species or subspecies may be replaced by another nomenclatural type, provided that the replacement type meets the requirements of Rule 69. Such a proposed replacement must be published in the IJSEM.

- (1) The possible reasons for replacing the nomenclatural type of a *Candidatus* species or subspecies are the following:
 - (a) The nomenclatural type is no longer available.

(b) The kind of the proposed replacement type is preferred over the kind of the nomenclatural type as indicated in Rule 69(1).

(c) The proposed replacement type is of the same the kind as the designated nomenclatural type, but the proposed replacement type is of higher quality.

- (2) The proposal of a replacement type in the IJSEM must state the reason for the replacement in sufficient detail. The proposal must also provide evidence that the replacement type belongs to the species or subspecies according to the taxonomic view expressed in the effective publication of the name of the species or subspecies.
- (3) The proposal of a replacement type is void if it does not meet the requirements set out in this Rule. Doubtful cases should be referred to the Judicial Commission (Appendix 8).

Note. A replacement type must not be proposed if it meets the requirements of Rule 30. If it does, it should be used instead to propose the name of the species or subspecies for valid publication, provided that this can be done in accordance with Section 5 and Rule 72 of this Code.

Candidatus names with nomenclatural pro-standing

Rule 71

If a taxon with a given circumscription, position, and rank has no correct name (Rule 23a), the taxon can bear only one pro-correct name, i.e., the pro-validly published and pro-legitimate name with the earliest date of pro-valid publication (Rule 68). Exceptions to pro-priority can be made by conservation or rejection.

- (1) A pro-validly published name or epithet cannot be conserved over a validly published name or epithet, but a pro-validly published name or epithet may be conserved by the Judicial Commission over another pro-validly published name or epithet by analogy with Rule 56b.
- (2) The Judicial Commission may, by analogy with Rule 56a, place a pro-validly published name or epithet on the list of rejected names or epithets. Such rejection equally applies to validly published names or epithets.

Note. A taxon for which there is neither a validly published and legitimate name, nor a pro-validly published and pro-legitimate name, has neither a correct name nor a pro-correct name.

Rule 72

From 1 January 2025, when proposing a taxon name for the purpose of its valid publication under this Code (Rule 27), a pro-validly published and pro-legitimate *Candidatus* name, or epithet thereof, must be reused under certain conditions, depending on the taxonomic view expressed by the authors in the effective publication (Rules 25a–25b) containing the proposal. Under all other conditions, a pro-validly published and pro-legitimate *Candidatus* name, or epithet thereof, must not be reused. This Rule is not retroactive.

- (1) If a name above the rank of species is proposed for the purpose of its valid publication under this Code, and if, in the taxonomic opinion of the authors, the proposed name is a synonym of a pro-validly published and pro-legitimate *Candidatus* name of the same rank, then that *Candidatus* name must be reused, unless to do so would contravene a Rule of this Code.
- (2) If a name at the rank of species or subspecies is proposed for the purpose of its valid publication under this Code, and if, in the taxonomic opinion of the authors, the proposed name is a synonym of a pro-validly published and pro-legitimate *Candidatus* name at the same rank and in the same position, then that *Candidatus* name must be reused, unless to do so would contravene a Rule of this Code.
- (3) If a name at the rank of species or subspecies is proposed for the purpose of its valid publication under this Code, and if, in the taxonomic opinion of the authors, the proposed name is a synonym of a pro-validly published and pro-legitimate *Candidatus* name at the rank of species or subspecies and in a different position, then the final epithet of that *Candidatus* name must be reused, unless to do so would contravene a Rule of this Code.
- (4) The reuse of a pro-validly published and pro-legitimate *Candidatus* name at a given rank when proposing a name for valid publication, without considering the two names to be synonymous, is permitted where this is a necessary condition for proposing the reuse of a pro-validly published and pro-legitimate *Candidatus* name considered to be synonymous at another rank, provided that both names are proposed in the same effective publication.

(a) The reuse of a pro-validly published and pro-legitimate *Candidatus* name at or above genus rank when proposing a name for valid publication, without considering the two names to be synonymous, is permitted if the proposed name serves as the nomenclatural type of a taxon of higher rank. The name of that taxon of higher rank must be proposed in the same effective publication and reuse a pro-validly published and pro-legitimate *Candidatus* name that is considered synonymous at that rank.

(b) Such an action causes the *Candidatus* name that is reused but not considered synonymous with the name proposed for valid publication to become pro-illegitimate. It is therefore advisable to propose directly

a replacement name for this *Candidatus* name. It is recommended that this replacement name indicate the relationship to the original name for which it serves as a replacement [see Appendix 9(A)]. In the case of names at the rank of species or subspecies, such replacement names must retain the final epithet, unless this would contravene a Rule of this Code.

Example. If the hypothetical genus named '*Candidatus* Dedyshiibacter' was the nomenclatural type of '*Candidatus* Dedyshiibacteraceae', and if authors intended to validly publish the name of another genus in the same family, as well as the name of the family, then they could propose the name '*Dedyshiibacter*' for that genus in order to serve as the nomenclatural type of '*Dedyshiibacteraceae*'. If so, the authors should immediately propose a replacement name, such as '*Candidatus* Dedyshiibacteroides', for '*Candidatus* Dedyshiibacter'. If not, a name other than '*Dedyshiibacter*' would need to be proposed for the new genus.

Note. Although Rule 72(4) provides for a possible exception to Rule 72(1), Rule 72(2) or Rule 72(3), it is recommended to choose, among the solutions in accordance with the Rules, the solution which retains the most commonly used names or, if this cannot be determined, the solution that results in the overall lowest number of replacement names.

Rule 73

The original authors of a *Candidatus* name or epithet reused under Rule 72, whether or not as a synonym, are cited by giving the name of the taxon, followed in parentheses by the word '*ex*' and the name of the original authors and the year of pro-valid publication (see Rule 14b and Rule 33c Note 2). Where other authors are subsequently to be cited in parentheses (Rule 34b), this form of citation is retained by analogy with the perpetuation of '*ex*' in Rule 33c Note 2. Rule 73 is retroactive, but failure to comply with it does not alter the nomenclatural status of a name.

Note. The original *Candidatus* name from which a reused epithet is taken is known as the pro-basonym, not the basonym (Rule 34a).

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Conflicts of interest

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