

Introduction to the ongoing discussion of the proposed nomenclatural code for uncultivated prokaryotes with DNA sequences as type

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Formal name of this Code might be:

International Code on the Nomenclature of Prokaryotes Described from Sequence Data (ICNPDS) or informally the SeqCode.

Purpose of this nomenclatural code for uncultivated prokaryotes

The major goal of this document is to create a code for naming prokaryotic taxa based upon their genome sequences as nomenclatural types that might be used for uncultivated and fastidious prokaryotes (Murray et al., 2020). However, SeqCode will accomplish other things as well. 1) The naming rules will be consistent with those of the International Code of Nomenclature of Prokaryotes (ICNP) (Parker et al., 2019), and it is hoped that the nomenclatures formed under both codes will eventually be merged. 2) The ICNP is difficult to read and parts are contradictory. This Code will resolve these ambiguities without contradicting the nomenclature developed under the ICNP. 3) By being more plainly written, less apt to alternative interpretations and easier to understand, it will reduce controversy and confusion. 4) The ICNP requires deposition of type strains in two culture collections and registration of new names by publication in the IJSEM. Since that option is unlikely to be available for taxa described from sequence data in the near future, this Code will suggest alternatives for registration and assigning priority to names.

In accomplishing these goals, the SeqCode is evolutionary and not revolutionary. In fact, it adds no new ideas to the canon of biological naming. For instance, the most controversial aspect of this code is that it does not require physical evidence for the taxon in the form of viable cultures. However, neither did the 1990 ICNB (LaPage et al., 1992), which allowed detailed descriptions and illustrations to serve as nomenclatural types until January 2001 (Parker et al. 2019). Similarly, the International Code of Virus Classification and Nomenclature (<https://talk.ictvonline.org/information/w/ictv-information/383/ictv-code>) does not require deposition of physical samples. The goals of this Code are practical and not philosophical. It seeks to make naming easy and yet clearly regulated. Ease is an important virtue for nomenclatural codes because it encourages wide use. The diversity of prokaryotes is enormous and far exceeds the capacity of any specialized discipline to fully understand. This Code will be inclusive and encourage participation by diverse disciplines.

The SeqCode is not intended to discourage isolation and collection of strains, and investigators are encouraged to name new species using the ICNP when strains are available for deposition in culture collections. Currently, it is not possible to infer the complete potential of Archaea and Bacteria from their genome sequences, and strains remain an important tool for fully understanding the pathogenicity, biotechnological applications, physiology and other properties of species. For these reasons, strains will retain their value even if they are not the nomenclatural types. Lastly, naming the uncultivated facilitates all subsequent investigations and encourages isolation and characterization of strains. Thus, the SeqCode will encourage cultivation of species of prokaryotes known now only from their sequences.

Introduction

Naming is an essential component of scientific investigations, including those in biology. Without the ability to assign precise and unambiguous names, it is impossible to communicate effectively. For

instance, prior to the implementation of the ICNP and formation of the Approved Lists (Skerman et al. 1989), *Mycobacterium tuberculosis*, the causative agent of tuberculosis, had at least nine scientific names (Buchanan et al., 1966). Precise naming is also critical for creation of large databases and the large-scale analyses made possible by computing. Without a single, permanent name, databases would require frequent curation, which would become increasingly difficult as the information content grows. Thus, the absence of a naming system would also preclude the application of modern bioinformatics tools.

In biology, codes of nomenclature have been designed to establish identifiers that have a one-to-one correspondence with natural entities (Winston, 2018). Their goals are often described in sections entitled “General considerations” or “Principles”. Chief among their goals is to ensure that each entity has only a single, unique formal name. This becomes problematic because naming proceeds concurrently with the discovery of biodiversity, and discovery occurs independently by investigators all over the world. Investigators often have different taxonomic opinions and philosophies, and naming must accommodate these differences. Codes seek to knit these divergent efforts into a single, shareable robust nomenclature.

Codes must deal with four fundamentals of naming. The first is the hypothesis that there exists a biological entity deserving of a name. The biological entity is a taxon. The ICNP is purposely ambiguous regarding the nature of these entities and defines them as “any group of organisms treated as a named group in a formal taxonomy” [General Consideration 7(3), Parker et al., 2019]. However, the ICNP does exclude certain things, such as consortia and fossils. This Code uses the same definition.

The second component is evidence for the taxon, which is the nomenclatural type (or just ‘type’). Types have three essential functions. First, they prove the existence of the taxon. Second, they provide a standard for comparison of a new specimen to allow determination of whether it belongs to the same or a different taxon. As a consequence of the latter, the third and one of the most important functions of types is their ~~play a crucial~~ role in the application of names, as exclusion of a type from a taxon warrants creation of a new name. In the ICNP, there are two fundamentally different kinds of types. Firstly, the types for species and subspecies are the experimental evidence for the taxon and have historically been strains or detailed descriptions. In the SeqCode, this kind of type is DNA sequence. Secondly, the types for genera and higher taxa are their subordinate taxa. As a consequence, every taxon is associated with some experimental evidence of existence, either directly as for species and subspecies, or indirectly as for taxa above the rank of species.

Thirdly is the name itself, arguably the least important component. Although Linnaean tradition favours binomial names formed from Latin and Greek, in principle the name could be formed from any source and even arbitrarily (as per Rule 10a of ICNP). Latinization of names was understandable when naming was primarily a European activity and Latin was a common component of their scientists’ education (Winston, 2019). It is less justified in the modern global context, and modification of the International Code of Virus Classification and Nomenclature to permit names that are not Latin binomials is being actively discussed.

Ideally, names should be understandable and easy to form. In practice, naming in the ICNP has required extensive curation by experts and lacks scalability. Thus, while it is not difficult to create a few names during the course of a research project, generating large numbers of names is time-consuming, tedious and prone to error. Nevertheless, the SeqCode uses the same rules of naming as the ICNP so that the names of the two codes can be easily merged at some future time. Fortunately, there are a number of ways to increase the scalability of naming even with the current system. Pallen et al. (2020) recently created the ‘Great Automatic Nomenclator’ or Gan, which can combinatorially generate large numbers of names from a small number of Latin roots. This approach can be generalized in the near future and eliminate the problem of scalability while providing even more options for creating linguistically correct names. An alternative is to create a system of simplified latinization of names such that the names remain consistent

with the ICNP and also avoid more than minimal curation by experts. For instance, naming strategies could be restricted to arbitrary words or words in other languages with standard rules for combining roots. Some biological codes of nomenclature have also relaxed the rules for naming so that strict adherence to Latin is not required. These approaches could also be adopted by the ICNP to make naming scalable.

Fourthly, a code should describe a process or system that allows names to be added as new data or new perspectives are acquired. This process resembles an algorithm, which is a simple set of rules that enables solving of complex problems. By systematically combining the discoveries from a large group of investigators, a consensus nomenclature can be achieved even in the absence of a unified taxonomy. The algorithm must allow for creation of new names as taxa are discovered or when the classification of existing taxa changes. The process of union, transfer and division of taxa must be straightforward so that it is easily understood and readily adopted; and, if conflicts arise, there must be means to objectively resolve them.

Codes attempt to be philosophically neutral on the great issues in systematics. Principle 1(4) of the ICNP states: “Nothing in this Code may be construed to restrict the freedom of taxonomic thought or action” (Parker et al., 2019). However, in practice, absolute neutrality is not really possible (Rossello-Mora and Whitman, 2018). For instance, both the ICNP and the SeqCode are designed to create names for a hierarchical taxonomy and both assume that a hierarchy is both desirable and reflective of nature. Likewise, they also assume that entities called ‘species’ exist in prokaryotic biology. Implicit in these assumptions is that every species belongs to a genus, and every genus belongs to one of each of the higher ranks used in this hierarchy, i.e. family, order, class and phylum. Even if these founding assumptions are incorrect, it is still possible to create a useful nomenclature.

Nomenclatural codes also strive to be independent of taxonomic philosophy. As an example, prior to the mid-1980s, prokaryotic taxonomy was largely determinative and did not necessarily seek to identify natural relationships among taxa described at the higher taxonomic ranks. Consequently, the ICNP placed great importance on the identification of diagnostic properties of the lower taxa. With the development of robust methods to determine genetic relationships, prokaryotic taxonomy transitioned to a phylogenetic approach, resulting in major changes in the nomenclature of individual taxa (Fox et al., 1980; Garrity et al., 2001; Wayne et al., 1987). The ICNP provided the framework that guided this process, and many of the names created under the determinative taxonomy survived the transition to a phylogenetic taxonomy.

However, elements of the ICNP remain poorly suited to a phylogenetic taxonomy. When most of the current edition was written in 1990, the extent of prokaryotic diversity was greatly underestimated. Class was the highest recognized taxonomic rank, and many genera were not assigned to higher taxonomic ranks. For instance, the Approved Lists from 1980 contains only seven names of classes and 58 names in total above the rank of family (Skerman et al. 1989). Moreover, there was no standardization in the formation of class names. At that time, the ICNP heavily emphasized naming species and genera, and rules for naming the higher taxonomic ranks were rarely discussed and remained ambiguous. In contrast, today there are more than five hundred validly published names of ranks above the family (Parte et al. 2020). More than a hundred classes have been named, and the rank of phylum has become widely used even though it has only recently been accepted for incorporation into the ICNP. As a consequence of the ambiguities in the ICNP regarding higher taxa, some of these names were not created in a standard manner, resulting in ambiguities in the nomenclature. The SeqCode will provide a recommendation to help standardize the nomenclature of the higher taxonomic ranks.

In addition to providing guidelines for naming, codes also provide standards for the evidence that can be considered as type. In the current ICNP, the deposition of viable type strains into two service collections in different countries is required evidence. In addition, minimum standards are recommended for specific

taxonomic groups to guide descriptions of novel species, although relatively few have been published. While recognized standards are necessary to prevent the creation of useless names and other abuses, they necessarily restrict the freedom of taxonomic thought. For instance, a restrictive methodological standard (i.e. axenic culture) remains at the heart of the current ICNP, whilst the prohibition of genome sequences as type prevents the expansion of nomenclature to the large numbers of uncultured prokaryotes as well as those that cannot be readily maintained by service collections because of their fastidious growth requirements or due to international laws preventing the export of biological material from some countries (Sutcliffe et al., 2020). Therefore, codes should seek a middle road, where sufficient safeguards exist to limit abuse of the nomenclatural system while still allowing for prokaryotic diversity to be freely explored.

In the SeqCode, a mechanism is proposed to create minimum standards to ensure data quality. The minimum standards are themselves outside the code to allow for flexibility as experimental methods change. Thus, this Code envisions creation of a governing body to review and approve minimum standards. For instance, a number of minimum standards for genome and metagenome-assembled genome (MAG) sequences have already been proposed (Bowers et al., 2017; Chun et al., 2018; Field et al., 2011; Konstantinidis et al., 2017). Upon review, these could either be accepted or an entirely new set of standards could be proposed. In addition, less restrictive minimum standards could be proposed by taxonomic subcommittees with expertise in specific taxa such as fastidious prokaryotes. For instance, it may not be possible at the present time to generate genome sequences for certain obligate symbionts. If experts familiar with these organisms have experimentally validated alternative sequence-based procedures such as multilocus sequence analyses (MLSA), they will be acceptable under this code.

The ICNP distinguishes three categories of names: legitimate, validly published and correct. Legitimate names are formed according to the rules of the code, including being validly published. In the ICNP, validly published means registered either in the Approved Lists or subsequent publication in the IJSEM or its Validation Lists. All legitimate names must be validly published. While in principle all validly published names should be legitimate, this is not always the case. Sometimes names become illegitimate due to discovery of synonyms or changes in the rules of the code. Lastly, correct names must be legitimate but are also those to be used in a particular taxonomy. These distinctions are used in the SeqCode, which will have its own system of registration, the form of which has not yet been decided. One possibility is to use an online registration completed by the authors of new names. Names then become validly published upon acceptance of the description and approval by the list curator.

Like the ICNP, the principle of priority is a key element of the code proposed here. This principle states that the earliest validly published name for a taxon is the correct name for the taxon. This principle ensures the stability of names and that, in a given taxonomic position, each taxon has only one correct name under the code. At the rank of species and subspecies, names are associated with a type, so the earliest name that includes a particular type has priority over any subsequent name and cannot be changed. For instance, if a species is moved to another genus, its species epithet remains the same even though the genus name changes. If it is united with another species, the earliest validly published name remains the correct name. If a species is divided, the taxon that retains the type must retain the original name.

At the rank of genus, the type is a species, and any genus that includes that species must have the earliest validly published genus name of that species. In this fashion, the priority of the genus depends on the priority of its type species. Likewise, if a taxonomy unites two genera, the type species must be the one with the earliest validly published name and, thus, priority. If a genus is divided, the name must be retained by the taxon that retains the type species.

Currently, the ICNP only requires use of names with priority for species and genera. It explicitly allows choice in the type of the higher taxonomic ranks of order and class. For the ranks of family and order, the

code does not provide clear direction, although the earliest names are often chosen as types. This ambiguity is a source of instability and confusion. In a hierarchical taxonomy, the creation of a new genus implies the potential for a new family, order, class and phylum even if they are not named. Thus, the priority of the names of higher taxa should depend upon the priority of the genus name and ultimately that of the type species name. This rule would ensure the stability of the names of higher taxa. For instance, if higher taxa were united, the name would be chosen from the one whose genus name had priority. If a higher taxon were divided, the branch that included the type would retain the name. The newly recognized branch would acquire a name based upon the taxa immediately below it in rank. An entirely new higher taxon could only occur upon discovery of a novel genus.

In contrast, priority of the higher taxa in the ICNP arguably depends on the date of validation of the name and not the priority of the name of the type genus. Since naming higher taxa was not a common practice prior to Garrity et al. (2001), this rule created the potential for instabilities. Therefore, the SeqCode recommends that the types for higher taxa should be chosen on the basis of the priority of their genus names. Because this is a recommendation and not a rule, it does not have to be followed when it causes conflicts with the ICNP. Moreover, to allow the eventual merging of the two codes, correct names validly published under the ICNP prior to January 1, 2022, will remain legitimate under the SeqCode.

The SeqCode proposes two other major changes from the ICNP. The taxonomic ranks with standing in nomenclature are reduced, and the ranks of subgenus, subtribe, tribe, subfamily, suborder and subclass are not included. These ranks are rarely used in the modern literature, and their conceptual and experimental bases are ambiguous (see also Oren, 2019). Many of the Rules of the ICNP deal with naming prior to adoption of the Approved Lists and Validation Lists. Now that all the current names are incorporated into these Lists, these Rules are no longer necessary. Removing them from the SeqCode further simplifies it.

The SeqCode also proposes the creation of two administrative bodies to facilitate its implementation. The International Committee on the Systematics of Prokaryotes Described from Sequence Data (ICSPDSD) will be responsible for the content of the code and administering the infrastructure required for maintenance of registration system for names similar to the Validation Lists of the ICNP. Its functions are similar to those of the ICSP. The ICSPDSD will also appoint a Nomenclature Reconciliation Commission with the authority to resolve disputes regarding the interpretations of the rules and to grant exceptions in unusual circumstances. Its functions are similar to those of the Judicial Commission of the ICSP.

It is the intention in creating this code to produce an easily adoptable solution to the nomenclature of taxa currently excluded from formal naming by the specific insistence in the ICNP that types must be viable cultures. We hope this will provide a service to the wider community working on prokaryotic diversity and, also that in due course, allow the formal nomenclature of all taxa to be brought under a unified framework.

Useful definitions:

Nomenclature: the body or system of names in a particular field.

Name: the label applied to an object. A word or set of words by which a taxon is known, addressed, or referred to. A term used for identification.

Epithet: an adjective or descriptive phrase unique to the person or thing mentioned. The species name is an epithet of the genus name.

Species name: composed of the genus name and species epithet.

Taxon: any group of organisms treated as a named group at a specific category in a formal taxonomy

Circumscription: of a taxon is an indication of its limits or the set of biological entities it contains.

Nomenclatural type (or just type): for a species, it is the evidence for the taxon, such as genome sequence, with which the name is permanently associated. In the ICNP, the type is a viable strain deposited in two publicly accessible culture collections in different countries. For higher taxa, the type is a lower taxon. The nomenclatural type is not necessarily the most typical or representative element of the taxon. **Principle of Priority** states that the correct name of a taxon is the oldest legitimate, validly published name applied to it. It is the fundamental guiding precept that preserves the stability of biological nomenclature. It was first formulated in 1842 by a committee appointed by the British Association to consider the rules of zoological nomenclature. The committee's report was written by Hugh Edwin Strickland.

Legitimate (names and epithets) in accordance with the rules of the code.

Illegitimate (names and epithets) contrary to the rules of the code.

Effectively published (names and epithets) that have appeared in printed and/or electronic matter made generally available to the scientific community.

Validly published (names and epithets) that are effectively published and registered according to the rules of the code.

Correct (names and epithets) which must be adopted for a taxon under the rules in the proposed taxonomy. Note that validly published names may be legitimate but not correct, depending upon the taxonomy. For instance, a taxonomy may merge two species. While both names are validly published and legitimate, only the name of the earlier synonym is correct in this taxonomy.

Homotypic synonym: more than one name associated with the same type [previously referred to as objective synonyms].

Heterotypic synonym: different names associated with different types that in the opinion of the microbiologist concerned belong to the same taxon [previously referred to as subjective synonyms].

Earlier synonym: first validly published synonym [previously referred to as senior synonym].

Later synonym: subsequently validly published synonym [previously referred to as junior synonyms].

Basonym: the earliest validly published name of a taxon which has been changed, often because of reclassification.

Homonymy: when two names are the same but have different types, often due to uniting two genera each of which contain species with the same species epithet or when a genus name is chosen that already is in use among the eukaryotes.

comb. nov. (*combinatio nova*): abbreviation to denote transfer of a species to a new genus. Because the species name includes both the genus name and species epithet, the new name is a combination of the new genus name and the old species epithet.

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Draft of the International Code of Nomenclature of Prokaryotes Described from Sequence Data

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CHAPTER 1. GENERAL CONSIDERATIONS

General Consideration 1

The progress of prokaryotic microbiology requires a precise system of nomenclature accepted by the majority of microbiologists.

General Consideration 2

To achieve order in nomenclature, it is essential that scientific names be regulated by internationally accepted Rules.

General Consideration 3

The Rules that govern the scientific nomenclature used in the biological sciences are embodied in International Codes of Nomenclature.

General Consideration 4

Rules of nomenclature do not govern the delimitation of taxa nor determine their relations. The Rules are primarily for assessing the correctness of the names applied to defined taxa; they also prescribe the procedures for creating and proposing new names.

General Consideration 5

This International Code of Nomenclature of Prokaryotes Described from Sequence Data (ICNPDS) applies to all prokaryotes whose type is either DNA sequence or a taxon whose type is DNA sequence. It is suggested that this code is colloquially referred to as the SeqCode to better distinguish it from the International Code of Nomenclature of Prokaryotes (ICNP), which applies to all prokaryotes whose type is either a strain or a taxon whose type is a strain. The nomenclature of eukaryotic microbial groups is provided for by other Codes: fungi and algae by the International Code of Nomenclature for algae, fungi and plants; protozoa by the International Code of Zoological Nomenclature. The nomenclature of viruses is provided for by the International Code of Virus Classification and Nomenclature.

General Consideration 6

The International Committee on the Systematics of Prokaryotes Described from Sequence Data (ICSPDS) has been established to provide a mechanism for emendations of Rules, exceptions to Rules, and interpretation of the Rules in doubtful cases for the SeqCode.

General Consideration 7

The SeqCode is divided into Principles, Rules and Recommendations.

The Principles (Chapter 2) form the basis of the Code, and the Rules and Recommendations are derived from them. The Rules (Chapter 3) are designed to implement the Principles. Interpretations of the Rules

which lead to contradictions of the Principles are incorrect. The Recommendations (Chapter 3) supplement some of the Rules and do not have the force of Rules. They are intended as guides to desirable practice. Names contrary to a Recommendation cannot be rejected for this reason. The Appendices are included to assist in the application of this Code and do not form the legislative part of this Code.

General Consideration 8

Nomenclature deals with the following:

Terms used to denote the taxonomic ranks and their relative order, e.g., “species”, “genus”, “family”, “order”, “class” and “phylum”.

Names applying to individual taxa. A taxonomic group is referred to throughout the SeqCode as a taxon, plural taxa.

General Consideration 9

The SeqCode is an instrument of scientific communication.

CHAPTER 2. PRINCIPLES

Principle 1

The SeqCode has one fundamental aim, which is to provide a standardized, robust, and stable system of nomenclature for prokaryotes described from sequence data that is compatible with the freedom of scientists to classify prokaryotes according to taxonomic judgments.

Nothing in the SeqCode may be construed to restrict the freedom of taxonomic thought or action.

Principle 2

The nomenclature of prokaryotes is not independent of botanical and zoological nomenclature. When naming new taxa at the rank of genus or higher, names which are already regulated by the International Code of Zoological Nomenclature and the International Code of Nomenclature for algae, fungi and plants must be avoided.

The SeqCode is also not independent of the prokaryotic nomenclature and names regulated by the International Code of Nomenclature of Prokaryotes (ICNP) and formed before January 1, 2022. Before that date, legitimate names formed under the ICNP have priority. After that date, names formed under the ICNP compete with names formed under the SeqCode for priority and are only recognized if they have priority, i.e. are legitimate and validly published prior to names formed under the SeqCode.

Principle 3

The scientific names of all taxa are Latin or latinized words treated as Latin regardless of their origin.

Principle 4

The primary purpose of giving a name to a taxon is to supply a means of referring to it rather than to indicate the characters or the history of the taxon.

Principle 5

The application of the names of taxa is determined by means of nomenclatural types, referred to in the

SeqCode as types.

Principle 6

The correct name of a taxon is based upon valid publication, legitimacy and priority of publication.

Principle 7

A name of a taxon has no status under the Rules and no claim to recognition unless it is validly published and legitimate.

Principle 8

Each taxon 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 the SeqCode. The circumscription of a taxon is an indication of its limits or the set of biological entities it contains. The position or rank is an indication of its parent taxon within a taxonomy.

Principle 9

Aim at stability of names. The name of a taxon should not be changed or replaced without sufficient reason based either on further taxonomic studies or on the necessity of rectifying a nomenclature that is contrary to the Rules of SeqCode.

Principle 10

Names created must be clear enough to avoid errors, confusion, or misunderstandings. Useless names should not be created.

CHAPTER 3. RULES OF NOMENCLATURE WITH RECOMMENDATIONS

Section 1. General

Rule 1a

The SeqCode shall be known as the International Code on the Nomenclature of Prokaryotes Described from Sequence Data (ICNPDS). It will take effect on January 1, 2022. It is suggested that this code is colloquially referred to as the SeqCode to better distinguish it from the ICNP.

Rule 1b

Alterations to the SeqCode can only be made by the ICSPDS in accordance with its statutes.

Rule 2

The Rules of the SeqCode are retroactive except where exceptions are specified.

Rule 3

Names contrary to a Rule cannot be maintained.

Rule 4

In the absence of a relevant Rule or where the consequences or interpretation of a Rule are uncertain, a summary in which all pertinent facts are outlined should be submitted to the Nomenclature

Reconciliation Commission of the ICSPDSD for a ruling.

Section 2. Ranks of Taxa

Rule 5a

The taxonomic categories covered by these Rules are given below in descending taxonomic rank. The Latin equivalents are given in parentheses.

Phylum (Phylum)

Class (Classis)

Order (Ordo)

Family (Familia)

Genus (Genus)

Species (Species)

Subspecies (Subspecies)

Rule 5b

Definitions of the taxonomic categories will inevitably vary with individual opinion, but the relative order of these categories may not be altered in any classification.

Rule 5c

The use of the taxonomic rank of subspecies is optional. All species must be assigned to each of the higher taxonomic ranks.

Rule 5d

Taxa below the rank of subspecies (infrasubspecific subdivisions) are not covered by the Rules of the SeqCode. Any intermediate or informal category, whether below or above the categories cited above, are not covered by the SeqCode.

Section 3. Naming of Taxa

General

Rule 6

The scientific names of all taxa must be treated as Latin. The name of a species is a binary combination of a generic name and specific epithet; names of taxa above the rank of species are single words.

Recommendation 6

To form new prokaryotic names and epithets, authors are advised as follows:

1. Avoid names or epithets that are very long or difficult to pronounce when latinized.
2. A name or epithet must be spelled with only the 26 letters of the standard Latin alphabet.
3. Choose names and epithets that differ by at least three characters from those of closely related genera or species.
4. Words from languages other than Latin or Greek should be avoided when equivalents exist in

Latin or Greek or can be constructed by combining word elements from these two languages. Exceptions: names derived from typical local items such as foods, drinks or geographical localities for which no Latin or Greek names exist.

5. Do not adopt unpublished names or epithets found in authors' notes, attributing them to the authors of such notes, unless these authors have approved publication.
6. The abbreviation M.L. stands for "Medieval Latin" not "Modern Latin". For the latter, N.L. ("Neo Latin") is to be used.
7. When arbitrary names are formed, this has to be indicated and such names have to be easy to spell and pronounce. Arbitrary names should be limited to the scientific sphere of human activity.
8. Authors should not name organisms after themselves or after living co-authors. If genus names or specific epithets are formed from personal names, they should contain only the untruncated family (and rarely the first) name of one person.
9. Give a feminine form to all personal generic names regardless of the gender identity of the person they commemorate.
10. Refrain from naming genera after persons unconnected with natural science.
11. Avoid generic names that are in use in botany, zoology, or virology, in particular well-known names.
12. Names should not be deliberately contentious or abusive of any person, race, religion, political belief, or ideology.

Names of Genera

Rule 7

The name of a genus is a noun, or an adjective used as a noun, in the singular number and written with an initial capital letter. The name may be taken from any source and may even be composed in an arbitrary manner. It is treated as a Latin substantive or noun.

Names of Species

Rule 8

The name of a species is a binary combination consisting of the name of the genus followed by a single word known as a specific epithet. The generic part of the name must begin with an initial capital letter, and the specific epithet must begin with a lowercase letter. Any typographical signs, numbers or additional characters are forbidden to be inserted between generic and specific part of the name or into the name itself.

Rule 9

Formation or usage of identical specific epithets based on different types within the same genus is forbidden.

Example: Nouioui et al. 2018 transferred the species *Lysinimicrobium aestuarii* Hamada et al. 2015 to the genus *Demequina* and gave it a new name *Demequina maris* since *Demequina aestuarii* had been validly published (Yi et al., 2007) and based on different type. This rule avoids the creation of homonyms.

Example: *Bacillus pallidus* Scholz et al. 1988 is based on the nomenclatural type, strain H12; the specific epithet *pallidus* cannot be used for *Bacillus pallidus* Zhou et al. 2008, another bacterium whose name is

based on a different type.

Rule 10

A specific epithet may be taken from any source and may even be composed arbitrarily.

Example: *thetaiotaomicron* in *Bacteroides thetaiotaomicron* derived from a combination of the Greek letters *theta*, *iota* and *omicron*.

A specific epithet must be treated in one of the three following ways.

1. As an adjective that must agree in gender with the generic name. Example: *aureus* in *Staphylococcus aureus*.
2. As a substantive (noun) in apposition in the nominative case. Example: *Desulfovibrio gigas* or other names cited in Trüper and De'Clari (1997).
3. As a substantive (noun) in the genitive case. Example: *coli* in *Escherichia coli*.

Recommendation 10

Authors should attend to the following Recommendations and those of Recommendation 6 when forming specific epithets.

1. Choose a specific epithet that, in general, gives some indication of a property or of the source of the species.
2. Avoid epithets that express a character common to all, or nearly all, the species of a genus.
3. Avoid epithets in the same genus which are very much alike, derived from the same word stems and especially those that differ only in their last letters.
4. Avoid the use of the genitive and the adjectival forms of the same specific epithet to refer to two different species of the same genus.
5. If an ordinal adjective used for enumeration is chosen, then they may include numbers up to ten. Example: *primus*, *secundus*.

Names of Subspecies

Rule 11a

The name of a subspecies is a ternary combination consisting of the three names: a name of a genus followed by a specific epithet, the abbreviation "subsp." (subspecies), and finally the subspecific epithet that begins with a lower-case letter.

Example: *Bacillus subtilis* subsp. *spizizenii* Nakamura et al. 1999.

Rule 11b

A subspecific epithet is formed in the same way as a specific epithet. When adjectival in form, it agrees in gender with the generic name.

Rule 11c

No two subspecies within the same species or within the same genus may bear the same subspecific epithet.

Rule 11d

A subspecies that includes the type of the species must bear the same epithet as the species.

Example: *Bacillus subtilis* subsp. *subtilis* (Ehrenberg 1835) Nakamura et al. 1999

Names of Taxa above the Rank of Genus (Phylum, Class, Order, Family)

Rule 12

The name of a taxon above the rank of genus is a latinized word. Names of a families and orders are in the feminine gender, the plural number, and written with an initial capital letter. Names of classes and phyla are in the neuter gender, the plural number and written with an initial capital letter.

Rule 13

The name of a family, order, class, or phylum is formed by the addition of the appropriate suffix to the stem of the name of the type taxon (see Section 4). These suffixes are presented in Table 1.

Table 1. Suffixes for Taxonomic Ranks^a

Rank	Suffix	Example for the genus <i>Hadarchaeum</i>
Phylum	-ota	<i>Hadarchaeota</i>
Class	-ia	<i>Hadarchaeia</i>
Order	-ales	<i>Hadarchaeales</i>
Family	-aceae	<i>Hadarchaeaceae</i>

^aFrom Chuvochina et al., 2019

Section 4. Nomenclatural Types and Their Designation

General

Rule 14

For each named taxon of the various taxonomic categories listed below, there shall be designated a nomenclatural type. The nomenclatural type, referred to in the SeqCode as “type”, for a species or subspecies is the evidence for a taxon, such as DNA sequence, with which the name is permanently associated, whether as a correct name or as a later heterotypic synonym. For taxa above the rank of species, the type is one of the subordinate taxa, with which the name is permanently associated, whether as a correct name or as a later heterotypic synonym. Formation of names of the taxa above the level of genus are based on the names of the types, allowing tracing which biological entity is included in the taxon. The nomenclatural type is not necessarily the most typical or representative element of the taxon.

Types of the various taxonomic categories are presented in Table 2.

Table 2. Nomenclatural types of taxonomic ranks

Taxonomic category	Nomenclatural type
subspecies	Designated DNA sequence
species	Designated DNA sequence
Genus	Designated species
Family	Designated genus

Order	Designated genus
Class	Designated order
Phylum	Designated phylum

Rule 15

The type of a taxon must be designated by the author at the time the name of the taxon is published.

Rule 16

The type determines the name of a taxon if the taxon is subsequently divided or united with another taxon.

Example: When Ash et al. (1994) proposed that the genus *Bacillus* be divided into the genera *Bacillus* and *Paenibacillus*, the genus which contained the type species *Bacillus subtilis* had to be named *Bacillus*.

Type of a Species or Subspecies

Rule 17a

The type of a species or subspecies is a designated DNA sequence that is compliant with the minimum standards for genome, metagenome-assembled genome or single-amplified genome sequences. The sequence must be deposited in a public database and be readily available for taxonomic studies. Upon recommendations by the ICSP or ICSPDSD subcommittees on the taxonomy of specific groups, the ICSPDSD may approve other minimal standards as suitable types for specific groups.

Rule 17b

The type of a species or subspecies must unambiguously identify the taxon. Names of species based upon types that fail to unambiguously identify the taxon either because of experimental errors, incompleteness or other reasons are not legitimate.

Rule 18 Reference DNA sequences

A reference DNA sequence is not a type but a sequence used in comparative studies. A reference sequence has no standing in nomenclature.

Types of higher taxa

Rule 19

Only taxa with legitimate and valid names may serve as types for taxa higher than the rank of species.

Rule 20a

The nomenclatural type of a genus is the type species that was designated when the genus name was originally validly published.

Rule 20b Retention of type species on publication of a new generic name

The valid publication of a new generic name as a deliberate substitute for an earlier name found for some reason to be illegitimate does not change the type species of the genus.

Example: The deliberate creation of *Xanthomonas* as a substitute for the name *Phytomonas* (not available, as it was already in use as the name of a protozoan genus) does not change the type species,

which was *Phytomonas campestris* and which became *Xanthomonas campestris*.

Recommendation 20

When more than one subordinate taxa are available to serve as type, chose the earliest legitimately named taxon.

Rule 21

deleted

Section 5. Priority, Effective and Valid Publication of Names

Rule 22a

Each taxon above species, up to and including phylum, with a given circumscription, position, and rank can bear only one correct name, that is, the earliest that is in accordance with the Rules of the SeqCode. In a given position, a species can bear only one correct epithet, that is, the earliest that is in accordance with the Rules of the SeqCode.

Note 1. In the case of a species, Rule 22a must be applied independently to the generic name and the specific epithet. Under most circumstances, the specific epithet remains the same on transfer of a species from one genus to another. However, if the specific epithet is currently in use in the name of another species or subspecies in the genus to which the species is to be transferred, a new name must be proposed for the transferred species (see examples in Rule 9 above).

Note 2. In a given position, a subspecies can bear only one correct subspecific epithet, that is the earliest that is in accordance with the Rules of the SeqCode. In the case of a subspecies, Rule 22a must be applied independently to the specific and subspecific epithets. The subspecific epithet remains the same on transfer of a subspecies from one species to another, unless the subspecific epithet has been previously used in the name of another species or subspecies in the genus to which the subspecies is to be transferred.

Rule 22b

The date of a name or epithet is that of its valid publication. For purposes of priority, however, only legitimate names and epithets are taken into consideration.

Rule 22c

The priority of names whose types are DNA sequences will compete for priority with names in any other code after January 1, 2022.

Rule 22d

If two names published after 1 January 2022 compete for priority, priority is determined by the date of the valid publication, either under the rules of the SeqCode or the ICNP. If both names are published on the same date, priority will be decided by the Nomenclature Reconciliation Commission of the ICSPDSD.

Rule 22e

Legitimate names validly published under the ICNP prior to 1 January 2022 remain legitimate in the SeqCode even if there are differences in type or naming style.

Effective publication

Rule 23a

Effective publication under the SeqCode means making the name generally available to the scientific community via printed and/or electronic material for the purpose of providing a permanent record.

Rule 23b

When a name of a new taxon is published in a work written in a language unfamiliar to the majority of workers in prokaryotic biology, the author(s) should include in the publication a description in English.

Rule 23c

The following are not accepted as forms of effective publication.

1. Communication of new names at a meeting, in minutes of a meeting, or in abstracts of papers presented at meetings.
2. Placing of names on specimens in collections or in listings or catalogues of collections.
3. Distribution of microfilm, microcards, or matter reproduced by similar methods.
4. Reports in ephemeral publications, newsletters, or non-scientific periodicals.
5. Inclusion of a name in a published patent application or issued patent.
6. A name associated with metadata in a sequence database.
7. Making available electronic material in advance of publication (e. g. papers in press, preprinting or otherwise making unpublished manuscripts available in electronic format).

Rule 24a Date of publication

The date of publication of a scientific work is the date of publication of the printed and/or electronic matter. The date given to the work containing the name or epithet must be regarded as correct in the absence of proof to the contrary.

Rule 24b

The date of acceptance of an article for publication if given in a publication does not indicate the effective date of publication and has no significance in the determination of the priority of publication of names.

Valid and Invalid Publication and Registration of names

Rule 25

A name of a new taxon, or a new combination for an existing taxon, is not validly published unless the following criteria are met.

1. The name is validly published under the Rules of the ICNP or the SeqCode.
2. Valid publication under the SeqCode requires registration of the name [in manner to be determined].
3. The publication of the name is accompanied by a description of the taxon or by a reference to a previous effectively published description of the taxon.
4. The new name or new combination should be clearly stated and indicated as such. Appropriate abbreviations are: "*phyl. nov.*" for *phylum novum*, "*class. nov.*" for *classis novum*, "*ord. nov.*" for *ordo novus*, "*gen. nov.*" for *genus novum*, "*sp. nov.*" for *species nova*, "*comb. nov.*" for *combinatio nova*. Although words or abbreviations in Latin are usually printed in italics, such abbreviations as the above are frequently printed in Roman or boldface type when they follow a Latin scientific name in order to differentiate them from the name and draw attention to the abbreviation.
5. The derivation (etymology) of a new name (and if necessary of a new combination) must be given.

6. The type of the taxon must be clearly designated. In the case of species or subspecies, the type DNA sequence must be deposited according to Rule 17a and the accession number cited.

Note 1. When a new species or a new combination results in the proposal of a new genus, both the genus name and the new species name or new combination must be validly published. Valid publication of the new species or new combination alone does not constitute valid publication of the new genus.

Rule 26 Valid Publication of a Specific or Subspecific Epithet

A specific (or subspecific) epithet is not rendered illegitimate by publication in a genus (or species) name which is illegitimate.

Section 6. Citation of Authors and Names

Proposal and Subsequent Citation of the Name of a New Taxon

Rule 27

The citation of the name of a taxon that has been previously proposed should include a citation of the effective publication. Include both the name of the author(s) who first published the name and the year of publication. If there are more than two authors of the name, the citation includes only the first author followed by “et al.” and the year. For names formed under the ICNP, reference to the Approved List (Skerman et al., 1980) as ‘AL’ or the Validation Lists as ‘VL’ with its number, for example as VL100, should be given. For names formed under the SeqCode, the Validation Identification Number [in whatever form that ends up as] should be given.

Note 1. Correct citation of a name enables the date of publication to be verified, the original description to be found, and the use of the name by different authors for different organisms to be distinguished.

Proposal and Subsequent Citation of a New Combination

Rule 28

When an author transfers a species to another genus, or a subspecies to another species, then the author who makes the transfer should indicate the formation of the new combination by the addition to the citation of the abbreviation “*comb. nov.*” (*combinatio nova*). This form of citation should be used when the author retains the original specific epithet in the new combination. However, if an author is obliged to substitute a new specific epithet as a result of homonymy, the abbreviation “*nom. nov.*” (*nomen novum*) should be used. The original name is referred to as the basonym.

Recommendation 28

The citation of a new combination should include in parentheses following the citation to the name, the previous name, citation to the effective publication of the previous name and its Validation Identification Number.

Examples:

Marinobacterium iners Tindall 2020 *comb. nov.* (*Pseudomonas iners* Iizuka and Komagata 1964^{AL})

Demequina maris Nouioui et al. 2018 *nom. nov.* (*Lysinimicrobium aestuarii* Hamada et al. 2015^{VP})

Citation of the Name of a Taxon whose Circumscription Has Been Emended

Rule 29

If an alteration of a taxon modifies its circumscription, the author responsible may be indicated by the addition to the author citation of the abbreviation “*emend.*” (*emendavit*) followed by the name of the author responsible for the change. Only alterations that cause significant changes in the circumscription warrant emendation.

Example: *Rhodopseudomonas* Czurda and Maresch 1937 *emend.* van Niel 1944 (see Opinion 49; Judicial Commission).

Section 7. Changes in Names of Taxa as a Result of Transference, Union, or Change in Rank

Rule 30

If the type of a taxon (“A”) is transferred to a new taxon (“B”) where it cannot serve as type because its priority is lower than the existing type of taxon B, a new type for taxon A should be assigned as the remaining member with highest priority, i.e. the earliest one validly published.

Example: to be added

Rule 31

A change in the name of a taxon is not warranted by an alteration of the diagnostic characters or of the circumscription.

Rule 32

When two or more taxa of the same rank are united, then the name of the taxon under which they are united (and therefore the type of the taxon) is chosen by the rule of priority of publication.

Example: White (1930) united *Eberthella* Bergey et al. (1923) with *Salmonella* Lignie's 1900 and retained the earlier name, *Salmonella*. However, if this choice would lead to confusion in prokaryotic biology, the author should refer this matter to the Nomenclature Reconciliation Commission.

Rule 33 Division of a Genus into Genera

If a genus is divided into two or more genera, the generic name must be retained for the genus that retains the type species.

Example: Ash et al. (1994) proposed that the genus *Bacillus* be divided into the genera *Bacillus* and *Paenibacillus*, and so the genus which contained the type species *Bacillus subtilis* had to be named *Bacillus*.

Division of a Species into Species or Subspecies, and of a Subspecies into Subspecies

Rule 34a

When a species is divided into two or more species, the specific epithet of the original species must be

retained for the taxon which includes the type.

Rule 34b

When a species is divided into two or more subspecies, the specific epithet of the original species must be retained for the subspecies which includes the type.

Example: Publication of *Bacillus subtilis* subsp. *spizizenii* Nakamura et al. 1999 automatically created a new subspecies *Bacillus subtilis* subsp. *subtilis*.

Example: Upon the division of the species *Bacillus subtilis* into subspecies, the subspecies containing the type strain must be named *Bacillus subtilis* subsp. *subtilis*.

Note. Although the specific and subspecific epithets in the name of a type subspecies are the same, they do not contravene Rule 12b because they are based on the same type.

Transfer of a Species to Another Genus

Rule 35a

When a species is transferred to another genus without any change of rank, the specific epithet must be retained unless it is already in use in the new genus. In that case, a new name for the specific epithet must be chosen to avoid creating a later homonym.

Example: Bernardet et al. (1996) proposed *Flavobacterium hydatis* nomb. nov. for *Cytophaga aquatilis* Strohl and Tait 1978^{AL} on transfer to *Flavobacterium* because in that genus the name *Flavobacterium aquatile* already existed.

Rule 35b

When the name of a genus is changed, the specific epithets of the species included under the original generic name must be retained for the same species if they are transferred to the new genus.

Union of Taxa of Equal Rank

Rule 36

In the case of subspecies, species, and genera, if two or more of these taxa of the same rank are united, the first validly published legitimate name or epithet is retained. If the names or epithets are of the same date, the author who first unites the taxa has the right to choose one of them, and their choice must be followed.

Rule 37 Union of Species of Two or More Genera as a Single Genus

If two or more species of different genera are brought together to form a single genus, and if these species include the type species of one or more genera, the name of the genus is that associated with the type species having the earliest validly published, legitimate generic name. If no type species is placed in the genus, a new generic name must be proposed, and a type species must be specified.

Example: to be added

Rule 38 Union of Species as Subspecies

When several species are united as subspecies under one species, the subspecies which includes the type strain of the species under whose name they are united must be designated by the same epithet as the species.

Example: to be added

Rule 39a Union of Taxa above Genus under a Higher Taxon

When two or more taxa of the same rank from family to phylum are united under a taxon of higher rank, the higher-ranking taxon should derive its name from the name of the earliest legitimate genus that is a type genus of one of the lower-ranking taxa.

However, if the use of this generic name would lead to confusion, then the author may choose as type a genus which, in their opinion, leads to the least confusion.

Example: to be added

Rule 39b

If no type genera were placed in the taxon, a new name based on the selected type must be proposed.

Change in Rank

Rule 40

When the rank of a taxon of genus or above is changed, the stem of the name must be retained and only the suffix altered.

Rule 41a

When a subspecies is elevated in rank to a species, the subspecific epithet must be used as the specific epithet unless the resulting combination is illegitimate.

Example: *Campylobacter pylori* subsp. *mustelae* Fox et al. 1988 becomes *Campylobacter mustelae* Fox et al. 1989.

Rule 41b

When a species is lowered in rank to a subspecies, the specific epithet must be used as the subspecific epithet unless the resulting combination is illegitimate.

Example: *Bifidobacterium globosum* Biavati et al. 1982^{VP} becomes *Bifidobacterium pseudolongum* subsp. *globosum* Yaeshima et al. 1992, VL43.

Section 8. Illegitimate Names and Epithets: Replacement, Rejection, and Conservation of Names and Epithets

Illegitimate Names

Rule 42a

A name contrary to a Rule is illegitimate and may not be used. However, a name of a taxon which is illegitimate when the taxon is in one taxonomic position is not necessarily illegitimate when the taxon is in another taxonomic position.

Example: If the genus *Diplococcus* Weichselbaum 1886 is combined with the genus *Streptococcus* Rosenbach 1884, *Diplococcus* is illegitimate as the name of the combined genus because it is not the earlier name. If the genus *Diplococcus* Weichselbaum 1886 is accepted as separate and distinct, then the name *Diplococcus* is legitimate.

Rule 42b

Names of prokaryotes validly published under the SeqCode are not to be rejected as homonyms of names of prokaryotes published before 1980 and omitted from the Approved Lists.

Note: Some reasons for which a name may be illegitimate are the following.

1. If the taxon to which the name was applied, as circumscribed by the author, included the nomenclatural type of a name which the author ought to have adopted under one or more of the Rules. Example: If an author circumscribes a genus to include *Bacillus subtilis*, the type species of the genus *Bacillus*, then the circumscribed genus must be named *Bacillus*.
2. If the author did not adopt for a binary or ternary combination the earliest legitimate generic name, specific epithet, or subspecific epithet available for the taxon with its particular circumscription, position, and rank. Example: to be added
3. If it is a later homonym of a name of a taxon of prokaryotes, fungi, algae, protozoa, or viruses. Example: *Phytomonas* Donovan 1909, a genus of flagellates, antedates *Phytomonas* Bergey et al. 1923, a genus of prokaryote (Judicial Commission Opinion 14, 1954).
4. A species or subspecies epithet is illegitimate if it duplicates a specific or subspecific epithet previously validly published for the same genus but whose name is based upon another type. Example: *Bacillus pallidus* Scholz et al. 1988 is based on the nomenclatural type, strain H12; the specific epithet *pallidus* cannot be used for *Bacillus pallidus* Zhou et al. 2008, which is a different bacterium whose name is based upon another type.

Replacement of Names

Rule 43

An illegitimate name or epithet is replaced by the oldest legitimate name or epithet in a binary or ternary combination which in the new position will be in accordance with the Rules. If no legitimate name or epithet exists, one must be chosen. Since a specific epithet is not rendered illegitimate by publication in a species name in which the generic name is illegitimate, authors may use such an epithet if they wish provided that there is no obstacle to its employment in the new position or sense; the resultant combination is treated as a new name (*nom nov.*) and is ascribed to the author. The epithet is, however, is ascribed to the original author. Example: *Pfeifferella pseudomallei* Ford 1928 is an illegitimate combination since *Pfeifferella* is a homonym of a protozoan generic name (Judicial Commission Opinion 14, 1954). The epithet *pseudomallei* can be used for this organism in another genus, *Pseudomonas pseudomallei* Haynes 1957.

Rule 44

A legitimate name or epithet may not be replaced.

Section 9. Orthography

Rule 45

All names comprise only the 26 letters of the Roman (Latin) alphabet. Diacritic signs are not to be used.

Rule 46

Because of the possibility of causing confusion, genus names may not end in the suffixes reserved for higher ranks: -aceae, -ales, -ia, and -ota.

Note: The rule only applies to names formed under the SeqCode after January 1, 2022.

Rule 47a

Any name or epithet should be written in conformity with the spelling of the word from which it is derived and in strict accordance with the rules of latinization. Exceptions are provided for typographic and orthographic errors and orthographic variants.

Rule 47b

In the SeqCode, orthographic variant means a name (or epithet) which differs from another name only in transliteration into Latin of the same word from a language other than Latin or in its grammatical correctness. Changes in suffixes for consistency with the names of higher taxa are orthographic variants.

Examples: *Haemophilus*, *Hemophilus*; Acidobacteria (the class), Acidobacteriia

Typographic and Orthographic Errors

Rule 48

The original spelling of a name or epithet must be retained, except for typographic or orthographic errors.

Example: The original spelling was *Bacillus megaterium*, not *megatherium* (Judicial Commission Opinion 1, 1951).

An unintentional typographical or orthographic error later corrected by the author is to be accepted in its corrected form without affecting the status and date of valid publication. It can also be corrected by a subsequent author who may or may not mention that the spelling is corrected. However, the abbreviation “corrig.” (*corrigendum*) may be appended to the name if an author wishes to draw attention to the correction. Succeeding authors may be unaware that the original usage was incorrect and use the spelling of the original author(s). Other succeeding authors may follow the correction of a previous author or may independently correct the spelling themselves, but in no case is the use of corrig. regarded as obligatory. None of these corrections affects the status and date of valid publication.

Example: *Pasteurella mairi* (sic) Sneath and Stevens 1990. The typographic error later corrected by

Sneath [40] to *Pasteurella mairii*, which may be cited as *Pasteurella mairii* corrig.

Note. The liberty of correcting a name or epithet must be used with reserve, especially if the change affects the first syllable and above all the first letter of the name or epithet.

Orthographic Variants by Transliteration

Rule 49a

Words differing only in transliteration into Latin from other languages which do not use the Latin alphabet are to be treated as orthographic variants unless they are used as the names of taxa based upon different types, when they are to be treated as homonyms.

Example: *Haemophilus* and *Hemophilus*.

Rule 49b

When there are orthographic variants based on the same type, and there is no clear indication that one is correct, then an author has the right of choice.

Personal Names

Rule 50

The genitive and adjectival forms of a personal name are treated as different epithets and not as orthographic variants unless they are so similar as to cause confusion. Example: The epithets *pasteurii* (genitive noun) and *pasteurianum* (adjective) are treated as different epithets.

Gender of Names

Rule 51

The gender of generic names is governed by the following.

1. A Latin or Greek word adopted as a generic name retains the classical gender of its language of origin. Authors are recommended to give the gender of any proposed generic name. Example: *Sarcina* (Latin feminine noun, a package).

In cases where the classical gender varies, the author has the right of choice between the alternatives. Example: *-incola* the gender may be masculine or feminine.

2. Generic names which are modern compounds from two or more Latin or Greek words take the gender of the last component of the compound word. Example: *Lactobacillus* (masculine) milk rodlet from Latin: *lac*, *lactis* (neuter), milk; and *bacillus* (masculine), little staff. If the ending is altered, the gender is that of the new ending in the language of origin.
3. Arbitrarily formed generic names or vernacular names used as generic names take the gender assigned to them by their authors. When the original author failed to indicate the gender, a subsequent author has the right of choice. Example: *Desemzia* Stackebrandt *et al.* 1999, who assigned the feminine gender.

CHAPTER FOUR. RECOMMENDATIONS FOR AUTHORS AND PUBLISHERS

When the type for a species or subspecies is a culture, the superscript “T” will be used immediately following the name or strain identifier. If the type is a sequence, the superscript “Ts” will be used. If the type is a description, preserved specimen or illustration, the superscript “Td” will be used. When the type is a taxon at the rank of genus or higher, the superscript is determined by the nature of the type of the species.

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