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Editorial

How Systematic and Applied Microbiology will deal with two nomenclature codes (ICNP and SeqCode) for prokaryotes, and which classification standards are recommended for new taxa descriptions

Summary

Recently, a new code of nomenclature for prokaryotes having genomes as nomenclatural types has been published and has subsequently, therefore, come into effect. The editors of Systematic and Applied Microbiology (SAM) want to outline how the journal will deal with the resulting two independent codes (ICNP and SeqCode) for the period during which they will coexist. SAM is keen on supporting both initiatives as long as the taxonomic descriptions of the taxa for which the new names are proposed are of high quality and, therefore, add value to the classification of both cultivated and uncultivated prokaryotes. Here, we describe what the minimal requirements and recommendations are for manuscripts of new taxa descriptions to be published in SAM.

Recent debates among taxonomists and molecular ecologists have brought microbiology to an unprecedented crossroads where two independent nomenclatural codes have come into effect. The International Code of Nomenclature for Prokaryotes (ICNP; (Parker et al., 2019)), currently undergoing extensive amendments (Oren et al., 2021), has been the basis for naming prokaryotes for the last 60 years and, since 2001, considers only pure cultures deposited in two different strain collections as type material. On the other hand, and after our suggestion to take action (Konstantinidis et al., 2017), some microbiologists, including several molecular ecologists and taxonomists, created the new Code of Nomenclature of Prokaryotes Described from Sequence Data (SeqCode; (Hedlund et al., 2022; Whitman et al., 2022)), which considers genome sequences deposited in one of the INSDC repositories as type material. This represented a straightforward solution for advancing scientific communication concerning the taxonomy of uncultivated taxa with a stable nomenclature. ICNP and SeqCode extensively overlap but the latter includes several improvements that make nomenclature more accessible, easier to apply and easier to communicate (Whitman et al., 2022). Besides the improvements and the implementation of genome sequences as type material, SeqCode includes an online self-registration system (https://seqco.de/) that represents the main mechanism for generating an official record and establishing the priority of names. The validation of the names is undertaken via the registry platform, where either the DOI of the original publication is included, or the authors can register their names before obtaining the DOI, which would allow them to receive feedback and correct a nomenclature in their manuscript while it is under review. In contrast, the validation of names under ICNP rules, with the protologues published outside the International Journal of Systematic and Evolutionary Microbiology (IJSEM), are checked by the list editors of the IJSEM upon receiving the original publication and the deposition certificates of the type strains. Once checked, the names are added to the Validation Lists that are published regularly by IJSEM.

The editors of Systematic and Applied Microbiology (SAM) authoring this present editorial recognize the value of having an alternative code that will allow uncultivated taxa to be stably named, although they also understand the challenges that the scientific community will face in this regard. Given the fact that SeqCode recognizes the priority of names validly published under the rules of the ICNP, which will minimize the divergence between the systems (Hedlund et al., 2022), SAM is willing to publish new taxa named using either nomenclatural code, but following their own requirements and rules. Consequently, authors should decide and state under which code they are proposing new names. In addition, in the case where cultivated and uncultivated taxa are to be named in the same manuscript, the names can be independently formed based on ICNP and SeqCode rules, respectively. In all cases, SAM editors will ask authors to recognize the priority of the names proposed under SeqCode, which will be considered legitimate. Names published later for the same taxon under the ICNP will be considered as synonyms.

At all times, SAM encourages the description of new taxa based on cultures, naming them following the nomenclatural rules of the ICNP, and the deposition of type material in two culture collections, as stated in Table 1. SAM will only consider publications for cases where the deposit of the strains is challenging (e.g. symbionts, fastidious growers, compromised deposits) or for other well-justified reasons, naming genomes from the type strain cultures under SeqCode. Making the reference material available through public collections is a priority for the editors of SAM, as it has significant scientific value (Stackebrandt et al., 2014). On the other hand, SAM strongly encourages the description and naming of MAGs and SAGs under SeqCode if they conform to the requirements listed in Table 2. Our editorial policy aims to treat classifications equally for nomenclatures formulated under both codes, always endorsing the highest quality taxonomic descriptions, with the hope that a single nomenclature, resulting from the convergence of the two systems, will be achieved in the near future.

Please note that beyond the nomenclatural rules of the two codes, we also discuss below the standards required to classify taxa, even

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though the two represent distinct components of taxonomy. SAM is committed to the publication of excellence in taxonomy, and this discipline has three major components (Cowan, 1971): (i) Classification, which is the procedure for describing new taxa by exploring their diagnostic properties and placing them within the homonymous classification system that is expected to be operational, universal and predictive; (ii) Nomenclature, which is the only official discipline in taxonomy ruled by the ICNP and SeqCode codes, and pursues naming taxa with accurate rules and recommendations for a stable naming framework; and (iii) Identification, which is the "raison d'être" of taxonomy and supports accurately placing newly observed organisms as members of known taxa. Consequently, the editors will continue to uphold high standards of quality for genomes and taxonomic descriptions when editing submitted manuscripts.

Most of the relevant requirements for taxonomic papers can be obtained in the Guide for Authors [here]; in addition, and as

Table 1
Requirements and recommendations for describing cultivated taxa to be named under the ICNP rules. Note that SAM distinguishes between single and multiple strain descriptions, which are treated differently.

Description of cultivated taxa and naming under the ICNP rules
Name and designated type strain
Required
The taxon name and the designated type strain collection numbers need to be given in the main manuscript in the form of a protologue table, and a template is given here. Taxon names need to be written in italics, and the designated types and culture collection numbers should be suffixed with a superscript^T. For example: *Salinibacter altiplanensis* (AN15^T = IBRC-M 11031^T = CECT 9105^T). The deposit certificates need to be submitted together with the manuscript.
Protologue
Required
If taxa are named under the ICNP rules, protologues must be given in the form of a table in the manuscript. Descriptions in the supplementary material are not allowed because only permanent records are considered for validation of names. For instructions on how to name under the SeqCode rules see Table 2. The required fields for the protologue are available in the online template.
The required basic information is:
- Name (formed with mnemonic cues).
- Etymology.
- Designated type strain and two culture collection numbers.
- Genome with an INSDC accession number of the designated type strain that meets minimum quality requirements (Bowers et al., 2017). The requirements given in Table 2 apply to the quality of the genomes.
- The 16S rRNA gene accession number of the designated type strain. The gene must be almost complete (>1,400 bp) if resulting from PCR amplification or complete if resulting from genome sequencing.
- In the case of a new genus, designate the type species.
- In the case of higher taxa, designate the type genus.
- Diagnostic genomic and phenotypic properties, inferred and demonstrated physiological traits. Ideally, a phenotypic discriminative profile using relevant physiological studies is desired.
Optional
The following are optional but highly recommended for more informative taxa descriptions:
- Include as much metadata as possible (see (Field et al., 2008)).
- As commercial biochemical tests and simple phenotyping using standard laboratory tests often do not reveal relevant properties, a more exhaustive, genome-based description of (potential) phenotypic properties is recommended instead (e.g. metabolic prediction based on functional gene annotation bioinformatics).
- It will benefit the study to include ecological information, such as habitat, environmental physicochemical properties, inferred interactions with other organisms, such as symbiosis, syntrophy, and other properties that may be relevant for the description.
- Chemotaxonomic properties, such as fatty acids, polar lipids, respiratory quinones or polyamines, unless required by the respective taxonomic subcommittees, may be regarded as optional, given that these can also be determined retrospectively (Sutcliffe et al., 2021).
- Some fields of relevant metadata are already given in the available online template in order to guide the acquisition of such data, and these can be added as new lines in the protologue template.
Type material data quality
Required
For taxonomic descriptions with nomenclature according to the ICNP rules, the type material is a living pure culture. This must be deposited in two culture collections from different countries, and the cultures must be fully available to third parties without any restriction, following the recommendation of the ICNP.
Multiple strains ≥2
SAM recommends that authors acquire multiple non-clonal strains of the same taxon, ideally from different origins.
Required
With the description of multiple strains, it is required that:
- There is proof of non-clonality of the strains. For this purpose, different genome-based methods can be applied. However, for a fast-check at the initial editorial desk-based evaluation, genome fingerprinting techniques, such as PCR-RAPD profiles (Sikorski et al., 1999), should be applied, and an image should be provided in the supplementary material showing distinct fingerprints. Note that if some strains show identical fingerprints, indicating clonality, these will be considered as a single strain. If all strains of the same taxon show the same fingerprint, the description will be considered as an SSSD.
- All (non-clonal) strains described in the manuscript (or a subset if >10 isolates) should be genome-sequenced in order to perform pairwise comparisons that will allow taxon circumscriptions.
- The monophyletic origin is a premise for recognizing a taxon. Therefore, all strains in the study must be placed within a phylogenetic framework. SAM requires that at least a 16S rRNA phylogenetic tree is provided, and the guidelines for this are given in the text.
- Genome coherence has to be evaluated using one of the OGRIs (Chun and Rainey, 2014).
- All strains must be phenotypically evaluated in order to reflect the intraspecific diversity.
Optional
The following are optional:
- In cases of large collections (>10 strains), and if well-justified, sequencing and phenotyping of only part of the collection will be allowed.
- Phylogenetic inference based on additional trees beyond the 16S rRNA gene, as indicated in the text, using different gene sets (or their translated products), such as ribosomal proteins, or core genes, is encouraged in order to further support and/or demonstrate the robustness of the classification.
- Chemotaxonomic markers should be determined for the whole collection, as appropriate.
- To increase the interest of the study, it is highly recommended to check the abundance of the new taxon in the sample of origin by means of culture-independent methods, such as fluorescence microscopy using specific probes (FISH), 16S rRNA gene amplicon sequencing, and/or by metagenomic read recruitments.
- To increase the importance of the study, SAM highly recommends screening for the presence and relative abundance of the new taxon in the publicly available 16S rRNA gene amplicon and metagenomic datasets. Read recruitments against the genome using the publicly available metagenomes can reveal relative abundance, biogeographic distribution and ecological patterns that increase the usefulness of the taxonomic description. For an example, see the study of the geographical distribution of *Hydrotalea lipotrueae* (Gago et al., 2021).

Table 1 (*continued*)

Description of cultivated taxa and naming under the ICNP rules
Single strain species descriptions (SSSDs)
If only one isolate has been obtained, SAM will consider such manuscripts for review only under exceptional cases
Required
To compensate for the absence of multiple strains, SAM requires increasing the interest of the study by: - Providing a high-quality genome, ideally fully closed, and comparing the gene composition with the closest relatives. - Providing an exhaustive phenotypic description, ideally finding relevant traits in the genome and proving the expression of the capabilities. - Providing ecological information for the isolate by reporting its relative abundance in the sample of origin by means of culture-independent methods, such as FISH, 16S rRNA gene amplicon sequencing or metagenome read recruitments. - Providing the biogeographical distribution by means of screening for the presence and relative abundance of the new taxon in the publicly available 16S rRNA gene amplicon and metagenomic datasets. Read recruitments against the genome using the publicly available metagenomes can reveal relative abundance, biogeographic distribution and ecological patterns that increase the usefulness of the taxonomic description. For an example, see the study of the geographical distribution of *Hydrotalea lipotrueae* (Gago et al., 2021).
Optional
Any additional information that increases the value of the contribution that goes beyond SSSDs will be welcomed, such as: - Evaluating the pan- and core-genomes of, for example, the genus where the strain has been classified. - Revealing taxonomically non-relevant traits, such as prophages, mobile elements and genomic islands that can increase the broader interest of the strain.

Table 2

Requirements and recommendations for describing uncultivated taxa to be named under the SeqCode rules. The SeqCode is less restrictive than ICNP in linking a taxonomic description to a publication that is considered to be a permanent record. SeqCode requires that only new names are given in the publication proposing the name, and the full or succinct protologues, including the designated type material, can be given in the supplementary material. The SeqCode registry is available at (https://seqco.de/) and is the basis for name validation and priority establishment. SAM will follow these rules but endorse certain more restrictive requirements in order to ensure further (higher) data quality for the future. This table includes all details concerning data quality and reporting requirements, as well as recommendations for an isolate's genome, metagenome assembled genome (MAG), or single amplified genome (SAG) used to serve as the nomenclatural type for a species named under SeqCode, obtained largely from (Hedlund et al., 2022).

Description of taxa and naming under the SeqCode rules
Name and designated type genome
Required
The taxon name and the designated type genome, with an INSDC accession number, need to be given in the main body of the manuscript or in a table if protologues are included in the supplementary material. Exceptionally, isolate-based descriptions with a nomenclature formulated under the SeqCode rules will be recognized by SAM if the strains, due to any specific reason, cannot be deposited in two different culture collections. Taxon names need to be written in italics and the genome designated names and accession numbers suffixed with a superscript^{TS}. For example, see *Wolframiiraptor gerlachensis* (Wger_A8^{TS} = GCA_021323375.2^{TS}).
Protologue
Required
The description of the taxon must be given either in the manuscript or in the supplementary material (if there are >10 protologues) depending on the volume of descriptions given in the contribution. The required fields in the protologue are given in the template, which is downloadable here. The basic information required is: - Name (formed with mnemonic cues). - Etymology. - Interpretation of the biological properties, inferred or demonstrated physiological traits, as well as ecological information, such as habitat, environmental physicochemical properties, inferred interactions with other organisms, such as symbiosis, syntrophy, and other properties that may be relevant for the description. - Designated genome assembly (e.g. INSDC accession) and access to raw data (e.g. SRA accession). - Given registry number after submission to the SeqCode Registry system. - Include as much metadata as possible (see (Field et al., 2008)). Some fields of relevant metadata are already provided in the online template.
Optional
Optional information can include: - In cases where the authors wish to provide additional metadata fields, these can be added as new lines in the protologue template.
Registry
Required
Data quality will be assessed by using available automated pipelines or other approaches. Exceptions for lower data quality should be justified by the authors in the main body of the manuscript. - The assembly should be available in one of the INSDC databases. - Raw data (reads) should be available in the INSDC databases (e.g. Sequence Read Archive). This is not required for names effectively published before January 1, 2023, in order to allow for existing published names (e.g. existing *Candidatus* names) and names currently undergoing peer review to be validated under SeqCode.
Optional
There are several optional fields in the registry form which, if left empty/non-filled, will not lead to the invalidation of the entry. For details check (https://seqco.de/).
Type material data quality
Required
Genomes, MAGs and SAGs should have minimal standards of quality to be recognized as type material. Lower standards may lead to erroneous classifications and/or confusion that will promote undesired instability in the system. The major requirements for adequate (high) quality are: - Assembly quality for MAGs and SAGs: >90% complete and <5% contaminated (modified from (Bowers et al., 2017)). - For isolates as for MAGs/SAGs, read coverage ≥10x (Field et al., 2008). - Provide evidence of the discreteness of the species, taxonomic rank and position, including the uniqueness of the species with respect to existing validly named species, as well as justifying the taxonomic rank and position based on genomic and 16S rRNA gene data. - Check for congruence between the genome-derived and 16S rRNA taxonomic assignments (e.g. (Karthikeyan et al., 2019)). - For MAGs and SAGs, compare multiple high-quality genomes representing the species from more than one sample (multiple high-quality genomic assemblies from multiple samples can support the non-chimeric nature of MAGs and provide confidence of the assembly for both MAGs and SAGs) or justify why multiple samples and/or MAGs are not available. - 16S rRNA gene >75% complete, and passes chimera checks. - >80% of tRNAs present in order to further ensure high completeness of the genome (modified from (Bowers et al., 2017)).
Optional
Genomes, MAGs and SAGs of high quality are desirable for representing a stable nomenclatural type. Therefore, we also suggest reporting: - High genome integrity (contig # <100; N50 >25 kb; max. contig >100 kb).

Table 3
Protologue table template (available online) to be used for a new genus and species. This information needs to be published as a table in the manuscript submitted to SAM, since the standard written descriptions are not necessary. This will be considered as the formal description for the name and, therefore, the effective publication of a new taxon.

Guiding Code for Nomenclature [req]	Indicate whether the rules of the **ICNP** or **SeqCode** have been followed.
Nature of the type material [req]	Indicate the **strain** or **genome sequence**
Genus name [req]	Add the generic name (e.g. *Salinibacter*)
Species name [req]	Add the full name (e.g. *Salinibacter altiplanensis*)
Genus status [req]	Select the adequate status **(gen. nov. / nom. rev.)**
Genus etymology [req]	**[N.B. Genus etymology is only for new genus proposals; never for extant genera]** Add the genus etymology (e.g. Sa.li.ni.bac'ter. L. fem. pl. n. *salinae* salterns, salt-works; N.L. masc. n. *bacter* masc. equivalent of the Gr. neut. n. *bakterion* a rod; N.L. masc. n. *Salinibacter* a rod from salt-works).
Type species of the genus [req]	**[N.B. Type species of the genus is only for new genus proposals; never for extant genera]** Indicate the designated type species of the genus by adding the full specific name (e.g. *Salinibacter ruber*).
Specific epithet [req]	Add the specific epithet (e.g. *altiplanensis*).
Species status [req]	Select the adequate status **(sp. nov. / comb. nov. / nom. rev.)**
Species etymology [req]	Add the specific epithet etymology (e.g. al.ti.pla.ne'nsis, N.L. masc. adj. *altiplanensis* of the Argentinian Altiplano).
Designation of the Type Strain [req under ICNP]	Provide the designation of the strain as in the manuscript (e.g. AN15^{T}). Note that a superscript T must follow the strain designation(s).
Strain Collection Numbers [req under ICNP]	Provide at least two collection numbers of two international repositories (e.g. IBRC-M 11031^{T} = CECT 9105^{T}). Note that a superscript T must follow the strain designation(s).
Designated Genome, MAG or SAG [req under SeqCode]	Provide the designation of the genome, MAG or SAG as in the manuscript (e.g. Wger_A8^{TS}). Note that a superscript TS must follow the genome designation(s)
Type Genome, MAG or SAG accession Nr. [INSDC databases] [req under SeqCode]	Add the genome accession number(s) with the repository identifier (e.g. GenBank = GCA_021323375.2^{TS}). Note that a superscript TS must follow the genome designation(s) if following the SeqCode rules. If following the ICNP rules, no suffix is needed.
Access to raw data (e.g. SRA accession) [opt under SeqCode]	Add the accession number to the raw data from where the MAGs were assembled and binned (required for names after January 1, 2023).
Registry number [req under SeqCode]	Add the registry number available at (https://seqco.de/).
Genome status [opt]	Complete/incomplete.
Genome size [opt]	Add the genome size in kbp (e.g. 3,580).
GC mol% [opt]	Add the GC mol% (e.g. 64.41).
16S rRNA gene accession nr. [req]	Provide the gene accession number(s) (e.g. LT160741).
Description of the new taxon and diagnostic traits [req]	Provide the phenotypic, genotypic and, if possible, ecological description of the new taxon emphasizing the traits used to diagnose it. This text can be as long as the normal written protologues in standard publications. In addition, add data here on chemotaxonomy, if determined.
Country of origin [opt]	Add the country of origin (e.g. Argentina).
Region of origin [opt]	Add the region of origin of isolation (e.g. Salar de Antofalla).
Date of isolation (dd/mm/yyyy) [opt]	Add the isolation date.
Source of isolation [opt]	Add the source of isolation (e.g. hypersaline lake).
Sampling date (dd/mm/yyyy) [opt]	Add the sampling date.
Latitude (xx°xx′xx″N/S) [opt]	Add the latitude coordinates.
Longitude (xx°xx′xx″E/W) [opt]	Add the longitude coordinates.
Altitude (meters above sea level) [opt]	Add the altitude in meters.
Number of strains in study [opt]	Add the number of strains in the study.
Source of isolation of non-type strains [opt]	Add the source of isolation of the additional strains.
Information related to the Nagoya Protocol [req]	Add here the permit number(s) and country of origin and/or local authority from where the permits had been obtained.

Note that SAM requires the inclusion of the accession number of the deposit of the genome sequence and 16S rRNA genes in one of the INSDC databases.

- All descriptions made following the nomenclatural rules of the ICNP must be given as a table in the main manuscript, as their validation in the IJSEM will require a permanent record and supplemental material is not considered (yet) to be permanent.
- The full descriptions made following the nomenclatural rules of the SeqCode can optionally be given in the supplemental material, since the permanent record is not a requirement for the SeqCode, although the registry system rules the priority and validation of the names. However, SAM requires that the name and designated type material are given in the main text. Therefore, in case of numerous taxa descriptions, SAM will consider publishing a supplementary table with all the complete protologues of the required information but, in addition, a single table with all new names and their designated type material must be given within the main body of the manuscript. For example, see *Wolframiiraptor gerlachensis* (Wger_A8^{TS} = GCA_021323375.2^{TS}).
- In the protologue table, [req] indicates required and [opt] indicates recommended but optional. [req under ICNP] indicates the requirements that have to be taken into account when naming under the ICNP rules, and [req under SeqCode] indicates the requirements that have to be taken into account when naming under the SeqCode rules. The table template can be downloaded here.
- If you are publishing a new species in an existing genus with a validly published name, the second column must be the description of this new taxon, and the fields ***Genus status, Genus etymology*** **and** ***Type species of the genus*** can be removed. If you have more than one species, you only need to add a third, fourth, fifth … column - one for each description.
- If you are publishing a new genus in addition to a new species, the second column must be the description of the genus, and then the fields ranging from ***Specific epithet*** **to** ***GC mol %*** may be filled in with a dash indicating an empty field. The genus description must be followed by the type species of the genus in a third column, and additional species will follow in the fourth, fifth … columns. Should you have two or more genera, just provide the Genus, Type species, Species, … repeating the column series or, alternatively, you can generate one table for each different genus.
- Please add a superscript T to the designated type strain name and strain collection numbers (e.g. AN5^{T}; IBRC-M 11031^{T} = CECT 9105^{T}) if you name under the ICNP rules.
- Please add a superscript TS to the designated type genome name and strain collection numbers (e.g. Wger_A8^{TS} = GCA_021323375.2^{TS}) if you name under the SeqCode rules.
- Empty rows (i.e. fields where no information is available) must be removed.

guidelines for authors and reviewers, the editors want to emphasize that SAM:

- requires the almost complete 16S rRNA gene sequence (>90% of total length) to be used for reconstructing the genealogical backbone of the organisms under study and recommends that this reconstruction represents the consensus topology for the evaluation of distinct trees generated using different algorithms, (neighbor-joining, maximum parsimony and maximum likelihood), different sets of filters (depending on whether you are looking for ancient or modern lineages and filtering-out poorly aligned or hypervariable regions), and eventually different outgroups, and sets of sequences under study (i.e. trying to balance the number of reference and new sequences among the tree branches) in order to assess the robustness of the branching order. The LTP database (Ludwig et al., 2021), which contains all available type strain sequences, can be an excellent source of reference sequences for phylogenetic reconstructions with taxonomic purposes.
- encourages the use of genome sequences to select subsets of genes in order to reconstruct phylogenies. A reasonable practice will be to reconstruct trees based on core-genes or subsets of universal genes, such as the ribosomal proteins, single-copy universal genes, or the gene selection used by the Genome Taxonomy Database (GTDB; (Parks et al., 2018)).
- considers Multi Locus Sequence Analysis (MLSA) to be a robust tool for reconstructing protein-coding gene phylogenies but always recommends the use of a large number of genes (>12; (Soria-Carrasco et al., 2007) to ensure the stability of the branching orders.
- recommends evaluating the position of the new taxa using both concatenated alignment of protein-coding genes and 16S rRNA gene sequences, and reporting on the congruency (or lack) of the topologies of the resulting trees.
- requires genome sequencing of all strains in a study (or a subset of the strains if the collection is too large), at a high quality, not necessarily closed but with a low number of contigs and at least 10x coverage for each genome, in order to perform whole genome pairwise comparisons. Note that the SAM requirement of a sequenced genome for taxonomic purposes was implemented in 2016 and there have been no exceptions to this requirement in publications since then. Besides the Overall Genome Relatedness Index (OGRI; (Chun and Rainey, 2014) parameters, SAM editors encourage the use of genomic information that goes beyond pure classification and helps in understanding intraspecific genetic diversity and biogeography, as well as inference of ecological and metabolic traits, among others.
- encourages the exploration of new methods to infer or determine the phenotype from genome sequences or other types of data. Since finding discriminative phenotypes may not always be straightforward, the use of commercial batteries of metabolic tests should be considered for isolate-based taxonomic descriptions. Chemotaxonomic characters, unless required by the respective taxonomic subcommittees or demonstrated to be highly discriminative for the taxon studied, may be regarded as optional, but the retrospective evaluation of such characters in a wider taxonomic framework is recommended (Sutcliffe et al., 2021).
- encourages the collection of a large number of strains, MAGs or SAGs, which are not clonal varieties of each other, since only this allows the genetic and phenotypic diversity to be assessed within a species.
- will only take Single Strain Species Descriptions (SSSDs) for publication under exceptional, well-justified cases, as shown in Table 1. These cases include, but are not limited to, fastidious microorganisms or exceptional metabolisms, taxonomic uniqueness or isolates that originate from extraordinary cultivation approaches. To increase the interest of the SSSDs contribution, we recommend linking them to metadata (e.g. in ecology using molecular approaches, such as metagenomics and single cell identification by fluorescence *in situ* hybridization). For example, the biogeographical distribution of a new species can be assessed by read recruitment plots using publicly available metagenomes (e.g. (Gago et al., 2021)).
- will only take MAGs and SAGs descriptions if these conform to the minimal requirements given in Table 2, or in well-justified cases when some of the minimum requirements are not met.
- requires the protologues to be published in the main body of the manuscript, as in Table 3, using the template that can be downloaded [here].
- contrarily to the ICNP that requires a permanent record in order to validly publish the names, SeqCode allows the protologues to be published as supplementary material. However, SAM will only allow protologues to appear as supplementary information if the number of descriptions is large (e.g. > 10). In this latter case, the main body of the manuscript should contain a table with the new names and the designated type materials (i.e. the genome accession numbers), and the protologues will be given in the supplementary material.
- as with the SSSDs, SAM expects that the value and impact of a manuscript will increase by adding information that goes beyond simple genome descriptions. For MAGs and SAGs, their detection in more than a single sample is desirable and assessing their biogeographical distribution should be evaluated. Although not compulsory, the use of alternative molecular methods to detect and quantify the abundance of MAG/SAGs in samples, such as fluorescence *in situ* hybridization, is recommended.

With the recommendations specified here, we hope to encourage authors and reviewers to help SAM publish the highest quality taxonomic proposals and advance the cataloguing of both cultivated and uncultivated prokaryotes. By treating the descriptions formulated equally under either the ICNP or SeqCode, we will be contributing towards the future reconciliation of both codes.

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