SeqCode, a nomenclatural code for prokaryotes described from sequence data

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Abstract

Most prokaryotes are not available as pure cultures and therefore ineligible for naming under the International Code of Nomenclature of Prokaryotes. Here we summarize the development of the SeqCode, a code of nomenclature under which genome sequences can serve as nomenclatural types. The SeqCode operates through self-registration (https://seqco.de/), provides a reproducible and objective framework for all prokaryotes, regardless of cultivability, and facilitates communication across microbiological disciplines.

Manuscript body

It is widely recognized that the requirement of the International Code of Nomenclature of Prokaryotes (ICNP) for deposition of axenic and viable cultures as nomenclatural types has hindered the development of a nomenclature for uncultured and fastidious cultured prokaryotes (Archaea and Bacteria) and thus effective communication of microbial diversity (Konstantinidis et al., 2017; Murray et al., 2020). For example, as-yet-uncultivated taxa account for ~85% of the phylogenetic diversity of prokaryotes (Nayfach et al., 2021), and named prokaryotes account for only <0.2% of total species (Sutcliffe et al., 2021). By excluding the uncultured majority, a substantial portion of the tree of life is relegated to poorly ordered, ambiguous, and often synonymous names or alphanumeric codes, the latter of which have limited mnemonic value (Miller 1956).

To address this problem, Murray et al. (2020) proposed two paths, which were endorsed by 121 authors and signatories from 22 countries and six continents (Murray et al., 2020). 'Plan A' was based on proposals by Whitman (2015) that DNA sequences could serve as nomenclatural types and be incorporated into the existing ICNP infrastructure. However, the International Committee on Systematics of Prokaryotes (ICSP) rejected Whitman's proposal (Sutcliffe et al., 2020), thus triggering "Plan B", which called for a new code of nomenclature (Murray et al., 2020). To further engage the community in the implementation of "Plan B", we organized a series of online workshops (https://www.isme-microbes.org/reports-sponsored-events) that garnered 848 registrants from a broad range of microbiology disciplines and 42 countries. Ninety percent of participants reported that they would use a new code that accepts DNA sequences as types (https://www.isme-microbes.org/sites/default/files/reports/Path_forward_Naming_Uncultivated.pdf). Given strong participation and near-unanimous support, we acted on a variety of community recommendations (Table S1) to complete the SeqCode (formally The International Code of Nomenclature of Prokaryotes Described from Sequence Data; see Additional Information) and made progress on systems to implement it.

The SeqCode uses genome sequence data as common currency for typification of both cultivated and uncultivated microorganisms and follows the tenets of the ICNP by observing similar rules of priority. In essence, these rules state that the earliest validly published name for a taxon in a

particular position is the correct name, observing historical precedent and stabilizing nomenclature. The SeqCode also recognizes the priority of ICNP names provided they do not violate the priority of SeqCode names, thus minimizing divergence between the systems. Taxonomic names will be captured in the SeqCode Registry, a simple self-registration portal through which names and nomenclatural types (e.g., genome sequences for species) are registered, validated, and linked to metadata. In the best-case scenario, data will be entered and reviewed prior to publication, allowing automated checks and curators to guide users through the naming process. Following peer review and publication of the manuscript describing the taxa, the manuscript Digital Object Identifier (DOI) is entered into the Registry, completing the valid publication of the name/s (Figure 1, Path 1). However, the SeqCode also enables registration of previously published names, such as *Candidatus* names that conform to its rules. In that case, the *Candidatus* designation could be dropped, and the names given priority under the SeqCode (Figure 1, Path 2; see Additional Information). While the SeqCode itself is necessarily comprehensive, we have also developed resources to guide the community, including a glossary and examples (see Supplementary Information). Table 1 summarizes recommended minimal standards for sequences and reporting requirements. We endorse high quality standards for use of the SeqCode but expect standards to evolve to keep pace with community feedback and methodological improvements.

Potential users may ask: (i) What is the difference between *Candidatus* status and valid publication under the SeqCode? In reply, *Candidatus* is a provisional status lacking priority and standing and is relegated to a non-legislative appendix of the ICNP. *Candidatus* status was developed for organisms for which "more than a mere nucleic acid sequence is available". Since its inception, visualization of the taxon in a natural sample has been recommended (Murray and Stackebrandt 1995; Parker et al., 2019), but this is rarely implemented. It has been argued that *Candidatus* names should be granted priority under the ICNP (Whitman et al., 2019); however, this proposal was also rejected (Sutcliffe et al., 2020). As a result, many *Candidatus* names may prove to be ephemeral. (ii) What are the consequences for taxonomic names that are published in primary literature but not validly published under the SeqCode? Although the community is free to publish taxonomic names that do not comply with codes of nomenclature, we argue that codes of nomenclature and taxonomic frameworks serve the greater community by promoting objectivity, best practices, communication, and data interoperability. However, the unique restrictions of the ICNP regarding viable and accessible type strains have alienated many microbiologists and engendered a sense of normalcy in publishing names outside of the regulation of the ICNP. The SeqCode addresses this problem by providing an efficient and user-friendly resource that serves the common interests of the wider research community. The SeqCode embraces Findability, Accessibility, Interoperability, and Reusability (FAIR) principles, and the Registry was developed with interoperable data structures to promote sharing SeqCode names across global biodiversity inventories within microbiology and the broader biology research communities (e.g., NCBI (Schoch et al., 2020), GTDB (Parks et al., 2018), MiGA (Rodriguez-R et al., 2016), LPSN (Parte et al., 2020), Catalogue of Life (Roskov et al., 2019), Global Biodiversity Information Facility (GBIF 2020)).

In closing, we emphasize a few important points. First, the SeqCode is not intended to discourage cultivation. Cultivation of mixed or pure cultures enables testing properties predicted from genomes under controlled conditions. Furthermore, investigators are strongly encouraged to deposit strains to culture collections to improve strain stability and availability, enable assessment of reproducibility of phenotypic traits, provide resources for biochemistry and biotechnology, and promote international cooperation. Second, like all other codes of nomenclature, the SeqCode does not provide rules or recommendations on the delineation of taxa. Existing and improving approaches and data structures are available for that purpose (e.g., Parks et al., 2020; Rodriguez-R et al., 2018), and proposals for novel taxa must be settled through peer review. Finally, this is the first version of the SeqCode and we hope that it will evolve as the community engages in further developing the system. Because of our desire to serve the broad microbiology research community, we will engage the community to gather feedback and develop bylaws for SeqCode administration. This code is driven by bottom-up desires to improve communication across the microbial sciences. Thus, we view this 'SeqCode v1.0' as a necessary first step toward a unified system of nomenclature to communicate the full diversity of prokaryotes, and we will cooperate with the community toward building this vision.

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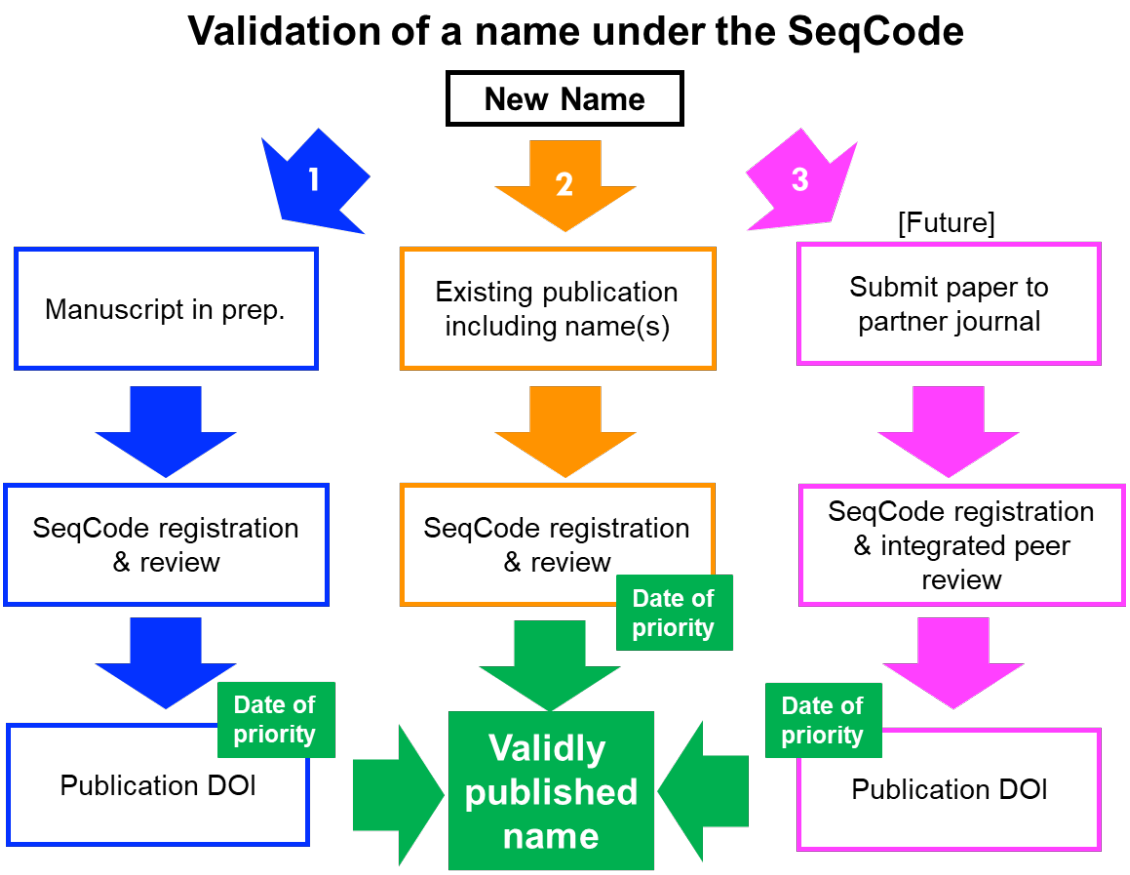

Figure 1. Validation process of a name under the SeqCode. Currently, two mechanisms exist, with a third possible in the future. The recommended mechanism (left arrow, Path 1) involves draft registration of the name and metadata into the SeqCode Registry prior to publication. Automated data quality and name synonymy checks in conjunction with curator review will lead to provisional acceptance of proposals that comply with SeqCode rules. Completion of the registration process requires the DOI of the effective publication. Once the proposal is accepted and the DOI entered, the registration is complete, marking the time and date of priority. The second (middle arrow, Path 2) is for names that are already published, such as *Candidatus* names. It requires draft registration of the name and metadata into the SeqCode Registry. SeqCode curators review compliance with the SeqCode rules before accepting the proposal. Acceptance of the proposal completes registration and marks the time and date of priority. At that point, the *Candidatus* designation can be removed. The third mechanism could be developed in partnership with one or more journals in the future (right arrow, Path 3) and would involve simultaneous peer review and SeqCode Registry curator review as an integrated path to the validation of proposed names. Issue of the DOI of the accepted paper marks the time and date of priority.

Table 1. Data quality and reporting requirements and recommendations for an isolate genome, MAG, or SAG to serve as the nomenclatural type for a species named under the SeqCode. Requirements will be checked as part of the validation process on the SeqCode Registry. Recommendations are suggested best practices to guide authors and peer reviewers to ensure high quality data supporting species to be named. See Supplementary Information for examples.

Information	Requirements	Recommendations
Included in publication proposing new species names under SeqCode[a]		
Name	Required for all names	1. Etymologies for all proposed names are recommended. 2. Names with mnemonic cues are recommended.
Interpretation of biological properties	None	Indicate inferred or demonstrated physiological traits and ecological information, such as habitat in the manuscript body and/or protologue.
Designated genome	None	1. Indicate access to genomic assembly (e.g., INSDC accession). 2. Indicate access to raw data (e.g., SRA accession). 3. Demonstrate compliance with GSC standards for isolate genomes (Field et al., 2008) and high-quality SAGs and MAGs (Bowers et al., 2017). 4. Include as much metadata as possible in the publication (see Field et al., 2008).
Evidence of the species, taxonomic rank, and position	None	1. Demonstrate the uniqueness of the species with respect to existing named species and justify the taxonomic rank and position (e.g., Jain et al., 2018, Karthikeyan et al., 2019; Parks et al., 2020; Rodriguez-R et al., 2018). 2. For MAGs and SAGs, compare multiple high-quality genomes representing the species in more than one sample (e.g., Supplemental Information).[b]
Data quality[c] and availability necessary for completion of SeqCode Registry		
Type genome assembly quality	1. >90% complete and <5% contaminated; 16S and 23S rRNA genes >75% complete (modified from Bowers et al., 2017). 2. Isolate genome read coverage ≥50x (Field et al., 2008).	1. >80% of tRNAs present (modified from Bowers et al., 2017). 2. High genome integrity (contig # <100; N50 >25 kb; max. contig >10 kb). 3. MAG/SAG read coverage ≥10x.
INSDC data availability	1. Assembly available in INSDC database. 2. Raw data available in INSDC databases (e.g., Sequence Read Archive)[d].	1. Data submission using MIxS Checklists in INSDC databases (https://gensc.org/mixs/). 2. Include as much metadata as possible in INSDC.

SeqCode Registry	Type genome assembly and raw data INSDC accession numbers, taxon name, etymology, rank.	Provide as much contextual data as possible to facilitate downstream genome comparisons with respect to provenance.

a. There are purposefully few requirements for the effective publication to accommodate existing and future publications that don't adhere to all recommendations. Critical data will be captured on the SeqCode Registry (Figure 1).

b. Comparison of 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.

c. Data quality can be assessed by automated pipelines or other approaches. Exceptions for lower data quality should be justified by authors in the effective publication.

d. Not required for names effectively published before January 1, 2023, to allow for existing published names (e.g., existing *Candidatus* names) and names currently undergoing peer review to be validated under the SeqCode.

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