



Quis custodiet ipsos custodes? A call for community participation in the governance of the SeqCode[☆]

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ABSTRACT

Codes of nomenclature that provide well-regulated and stable frameworks for the naming of taxa are a fundamental underpinning of biological research. These Codes themselves require systems that govern their administration, interpretation and emendment. Here we review the provisions that have been made for the governance of the recently introduced Code of Nomenclature of Prokaryotes Described from Sequence Data (SeqCode), which provides a nomenclatural framework for the valid publication of names of *Archaea* and *Bacteria* using isolate genome, metagenome-assembled genome or single-amplified genome sequences as type material. The administrative structures supporting the SeqCode are designed to be open and inclusive. Direction is provided by the SeqCode Community, which we encourage those with an interest in prokaryotic systematics to join.

Introduction

The Code of Nomenclature of Prokaryotes Described from Sequence Data (the SeqCode) was introduced in 2022 to provide a nomenclatural framework for the naming of prokaryotes based on sequence data as types (Hedlund et al., 2022). As reviewed elsewhere (Konstantinidis et al., 2017; Murray et al., 2020; Palmer et al., 2022; Whitman et al., 2022; Whitman et al., 2024), the SeqCode is considered necessary because of the exclusion of uncultured and many fastidious *Archaea* and *Bacteria* from the system of valid naming under the International Code of Nomenclature of Prokaryotes (ICNP). This exclusion resulted from requirements introduced on 01 January 2001 for the deposition of type strains of species in at least two international culture collections (ICNP Rule 30, Oren et al., 2023). Notably, Rule 30 also excludes naming under the ICNP of strains from countries that have restrictions on the distribution of biological resources (da Silva et al., 2023). Consequently, the SeqCode was drafted by an *ad hoc* Steering Committee following workshops held to engage with the wider community (Murray et al., 2020; Hedlund et al., 2022; Whitman et al., 2022).

Codes of nomenclature provide principles and rules for naming biological taxa, typically under the Linnean system, and so also require systems of governance. The International Society for Microbial Ecology

(ISME) agreed to act as the parent organisation for the SeqCode (<https://www.isme-microbes.org/seqcode-initiative>), and it was evident during its development that statutes to formalise the SeqCode governance were needed. Several models for organisation of committees that govern codes of nomenclature were examined by the *ad hoc* Steering Committee (Table 1). Such committees generally restrict their memberships to experts in the field, although some also include mechanisms for wider participation by the community. For instance, the International Committee on Systematics of Prokaryotes (ICSP), which maintains the ICNP, is largely comprised of delegates nominated from the national microbiology societies that are members of the International Union of Microbiological Societies (IUMS), with one delegate from each member society, and is supplemented with a typically small number of co-opted members. At the time of writing, it has 34 members, more than half of whom are from Europe, an acknowledged lack of diversity and representation (Sutcliffe et al., 2022). Only voting members of the ICSP can approve amendments of the ICNP.

Similarly, the International Commission on Zoological Nomenclature (ICZN) is entrusted with the authority to amend and interpret the International Code of Zoological Nomenclature. At the time of writing, this commission is comprised of 26 commissioners. Election of commissioners now takes place via an international ballot using an online voting

[☆] “Who will guard the guards themselves?”.

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Table 1
Codes and administrative structures governing biological nomenclature.

Nomenclatural Code	Governing Body	Constituency	Constitution/ Statutes
International Code of Nomenclature for algae, fungi, and plants	International Association for Plant Taxonomy; International Mycological Association	Nomenclature Section of the International Botanical Congress; International Mycological Congress	https://www.iapt-taxon.org/nomenclature/div_iii_1.html
International Code of Nomenclature of Prokaryotes	International Committee on Systematics of Prokaryotes	Bacteriology and Applied Microbiology Division of the International Union of Microbiological Societies	Whitman et al. (2019)
The International Code of Virus Classification and Nomenclature	International Committee on Taxonomy of Viruses	Virology Division of the IUMS	https://ictv.global/about/statutes
International Code of Zoological Nomenclature	International Commission on Zoological Nomenclature	Section of Zoological Nomenclature, International Union of Biological Sciences	Articles 77 and 84, https://www.iczn.org/the-code/the-code-online/
SeqCode	Committee on the Systematics of Prokaryotes Described from Sequence Data	The SeqCode Community	https://www.isme-microbes.org/governance

platform (Harvey et al., 2022). Members of the international zoological community are invited to register to vote via relevant mailings and websites; in the most recent ballot, votes were received from 425 registrants from 50 countries (Harvey et al., 2022). Changes to the Constitution of the ICZN, all amendments to the International Code of Zoological Nomenclature, and new members of the ICZN must be ratified by the International Union of Biological Societies. A similar but complex model is now employed by botanists and mycologists. Under Division III of the International Code of Nomenclature for algae, fungi, and plants (the ‘Botanical Code’, Turland et al., 2018), the Botanical Code may only be amended by the Nomenclature Section of an International Botanical Congress, which typically occurs every six years (Landrum et al., 2017; Turland et al., 2018). Prior to each congress, a guiding vote or ‘mail ballot’ of the members of the International Association for Plant Taxonomy, members of the nine Permanent Nomenclature Committees and authors of proposals to amend the Code is conducted for proposals published since the last congress. Ultimately, changes to the Botanical Code also require a vote of the Nomenclature Section of the International Botanical Congress following, in part, the recommendations of the guiding vote. The votes at the Nomenclature Section are conducted in person and include both personal and institutional votes, with one personal vote per member of the Section and a maximum of seven institutional votes per institution (typically herbaria) (Landrum et al., 2017; Turland et al., 2018). The Nomenclature Section of the 2017 ‘Shenzhen’ Congress comprised 155 members, and when institutional votes were also considered, the constituency comprised 582 possible votes representing 44 countries (Lindon et al., 2020). The need to reform this system to include virtual participation has been recognised (Landrum et al., 2021), whilst separate provisions are made for the governance of those parts of the Botanical Code for organisms treated as fungi via the Fungal Nomenclature Session of an International Mycological Congress (Turland et al., 2018).

Following the publication of the SeqCode, draft statutes for the future governance of the SeqCode were made public for comment and discussion in September 2022 by emailing to various lists of taxonomists

and via the Slack platform (<https://seqco.de/connect>). No comments were received and so, in October 2022, version 1.0 of the Statutes (Supplementary File 1) was adopted and posted within the SeqCode Registry (<https://disc-genomics.uibk.ac.at/seqcode/>; Whitman et al., 2022; Whitman et al., 2024; Ernster & Rodriguez, 2024) and on the ISME website (<https://www.isme-microbes.org/governance>). As a result, starting from 1 January 2023, the governance of the SeqCode is administered by the Committee on the Systematics of Prokaryotes Described from Sequence Data (hereafter, the SeqCode Committee). This is comprised of two elements, namely the ‘SeqCode Community’ and the five administrative components (Fig. 1). The function of the SeqCode Community is to support the open and inclusive development, promotion and operation of the SeqCode via transparent democratic structures, including election of the Officers of the various administrative components. Membership of the SeqCode Community is open to all members of the ISME as well as other microbiologists who have a demonstrable connection to microbiology either through their employment or publications. We strongly encourage all people with an interest in prokaryotic systematics to join the SeqCode Community. Applications can be made either directly to the Secretary of the Executive Board (see below) or via an online sign-up form (<https://seqco.de/join>; <https://www.isme-microbes.org/seqcode-information>). The open membership structure of the SeqCode Community is intended to bring major decision making on nomenclatural matters directly to the microbiological community, giving better representation to diverse interests and user groups. In this regard, it is notable that both the ICZN and the governance of the Botanical Code have in recent years similarly moved towards more open and inclusive democratic structures (Landrum et al., 2021; Harvey et al., 2022).

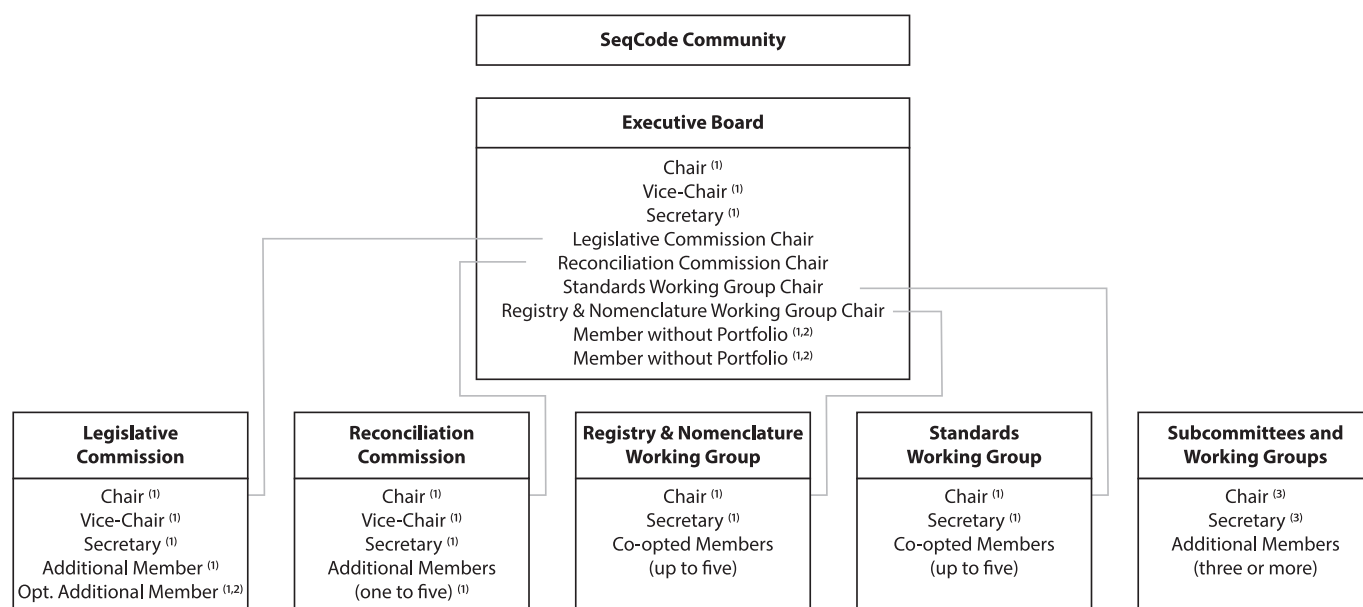
The administrative components of the SeqCode Committee are (a) the Executive Board, (b) SeqCode Legislative Commission, (c) SeqCode Reconciliation Commission, (d) Registry & Nomenclature Working Group, and (e) Standards Working Group. Each has elected officers (as a minimum, Chair and Secretary; Fig. 1). The Executive Board provides administrative oversight of the SeqCode Committee as a whole. The Chairs of the four other administrative components participate as *ex officio* members of the Executive Board. Following an email call in late October 2022 for candidates, also encouraging recipients to register for the SeqCode Community, elections of the first officers were conducted by an email ballot in December 2022 of the registered members of the SeqCode Community. 73 members participated (63 %), and those elected began their terms of office on 1st January 2023. Minutes of the meetings of these administrative components are made public via a dedicated Zenodo Community space (<https://zenodo.org/communities/seqcode>).

The functions of the other four administrative components are summarised as follows:

- Like the ICNP, which has been through multiple revisions since 1948 (Oren et al., 2023), the SeqCode is expected to be a living document that will be refined over time. The **Legislative Commission** is the only body authorized to amend the SeqCode, as defined in Rule 2 of the SeqCode (Whitman et al., 2022). The process by which amendments to the SeqCode can be proposed is outlined in Article 11 of the statutes (Supplementary File 1) and is coordinated by the Legislative Commission. Indeed, a proposal to amend the SeqCode was recently published (Whitman et al., 2023) and is currently being balloted on.
- The SeqCode **Reconciliation Commission** is the judicial branch of the SeqCode Committee and is the only body authorized to render formal decisions on the application and interpretation of the SeqCode, as defined in Rule 3 of the SeqCode (Whitman et al., 2022). Article 12 of the SeqCode statutes (Supplementary File 1) describes the process by which requests for a decision by the Reconciliation Commission can be made. Functionally, the Reconciliation Commission is comparable to the Judicial Commission of the ICSP (Whitman et al., 2019). The Reconciliation Commission also

SeqCode Committee

The Committee on the Systematics of Prokaryotes Described from Sequence Data



⁽¹⁾ Elected by the ballot of the General Membership

⁽²⁾ Optional post

⁽³⁾ Elected by the members of the Subcommittee or Working Group

Fig. 1. The structure of the SeqCode committee and its administrative components. In addition to the offices shown, the SeqCode Statutes allow for ISME to delegate a non-voting observer to the Executive Board.

considers whether exemptions to the recommended quality standards for type sequence data can be applied in particular circumstances (Rule 18a, see below). An example of one such decision is an exemption regarding the proposed type material associated with the name *Omnitrophus fodinae* (10.5281/zenodo.10366526).

- The **Registry & Nomenclature Working Group** serves to maintain the SeqCode Registry, which records names validly published under the SeqCode (Whitman et al., 2022; Whitman et al., 2024). Members of the Working Group also provide the necessary expertise in Latin needed for curation of the Registry and provide advice to registrants on the formation of grammatically correct names.
- The **Standards Working Group** monitors technical developments in the generation and quality control of the sequence data used as types for SeqCode names (Hedlund et al., 2022). SeqCode Rule 18a requires adherence to minimal standards for sequence data used as type, and the Standards Working Group is able to make recommendations to the SeqCode Community on which standards should be adopted (such recommendations requiring ratification by vote of the SeqCode Community).

In addition to these administrative components, the statutes of the SeqCode Committee allow for the formation of Subcommittees on the taxonomy of specific groups and of *ad hoc* 'Task & Finish' Working Groups. At this time, no groups of this type have been formed.

After its first two years of operation the SeqCode is well established, with significant interest from the microbiological community as judged from citations and Altmetrics of the SeqCode paper (<https://www.nature.com/articles/s41564-022-01214-9/metrics>), >300 registered users of the SeqCode registry and >219 validly published SeqCode names to date. An important aspect of the SeqCode is the open nature of the SeqCode Community and that the SeqCode itself is a community-

driven resource. Consequently, we hope that persons interested in prokaryotic systematics will register to join the SeqCode Community and actively participate in its further development.

Finally, it is also important to highlight that the SeqCode complements rather than competes with the ICNP, and recognition of priority of ICNP names is built into the SeqCode for this reason. Indeed, we hope that, in due course, the two Codes may eventually be merged into a unified Code of Nomenclature for all prokaryotes regardless of cultivation status (Whitman et al., 2024). We appeal to members of the Executive Board of the (ICSP), which maintains the ICNP, to engage in mutually respectful discussion in this regard with the Executive Board of the SeqCode Committee and the SeqCode Community.

CRediT authorship contribution statement

Iain C. Sutcliffe: Writing – review & editing, Writing – original draft. **Luis M. Rodriguez-R:** Writing – review & editing. **Stephanus N. Venter:** Writing – review & editing. **William B. Whitman:** Writing – review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.syapm.2024.126498>.

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