

## Meeting Report: “Path Forward for Naming the Uncultivated” Workshops

**Overview and impact.** ISME funding was an important contribution to a series of virtual workshops discussing plans for development of a code of nomenclature that would accommodate uncultivated and fastidious microorganisms with genome sequences, including metagenome-assembled genomes (MAGs) and single cell-amplified genomes (SAGs). The workshops were held during the first two weeks of February 2021, each at two different times to accommodate global participation. Both workshops included homework for participants to prepare and frame the interactive portion and included dedicated sessions to gather feedback. The workshop website, including 11 prerecorded talks, 9 slide presentations, >40 manuscripts, meeting recordings, and breakout group reports and summaries are an invaluable resource for microbiologists. This website and all content are currently being transferred to the ISME website for long-term availability.

The workshops were highly anticipated and attended by a broad group of microbiologists from all over the world, including young scientists. The workshops garnered 848 registrants and at least 575 attendees from at least 42 countries on six continents for one or more workshop (**Figure 1**). A post-workshop survey captured more detailed information for 94 participants. Those participants identified with a broad range of subdisciplines within microbiology (**Figure 2**), including 42 identifying as microbial ecologists and 30 identifying as systematists. These two communities do not often interact, and the strong participation of both groups was a strength of the workshops. 26% of respondents identified as graduate students (**Figure 3**). We note that training for microbial systematics is almost non-existent, despite the large number of scientists using taxonomic names. Thus, career development was a significant outcome of the workshops. 95% of respondents said the content and outcomes of the workshops will be useful to them and/or their field (**Figure 4**), and 90% said they are likely to use SeqCode in the future (**Figure 5**). *Given the strong participation and near-unanimous support for SeqCode, the SeqCode committee has moved to finalize and publish the SeqCode and develop databases and committees to implement it.*

**Summary of Workshop 1.** The first workshop focused on the limitations of the *International Code of Nomenclature for Prokaryotes* and introduced the *International Code of Nomenclature of Prokaryotes Described from Sequence Data*, for which we propose the practical synonym SeqCode. Pre-recorded talks were given by Ramon Rossello-Mora, Kostas Konstantinidis, Aharon Oren, Ed Moore, Alison Murray, and Barny Whitman, with each talk connected to key literature, including a current draft of the SeqCode. Those presentations and readings were background for a related panel discussion to discuss the pros and cons of a SeqCode, key aspects of the current draft SeqCode, and some contentious parts of SeqCode. Panelists included Barny Whitman, Kostas Konstantinidis, Ramon Rossello-Mora, Ed Moore, Marike Palmer, Nikos Krypides, Svetlana Dedysh, Iain Sutcliffe, Maria Chuvochina, Donovan Parks, Phil Hugenholtz, Stephen On, and Andy Holmes. This discussion led to breakout groups to discuss eight unresolved issues in the current draft:

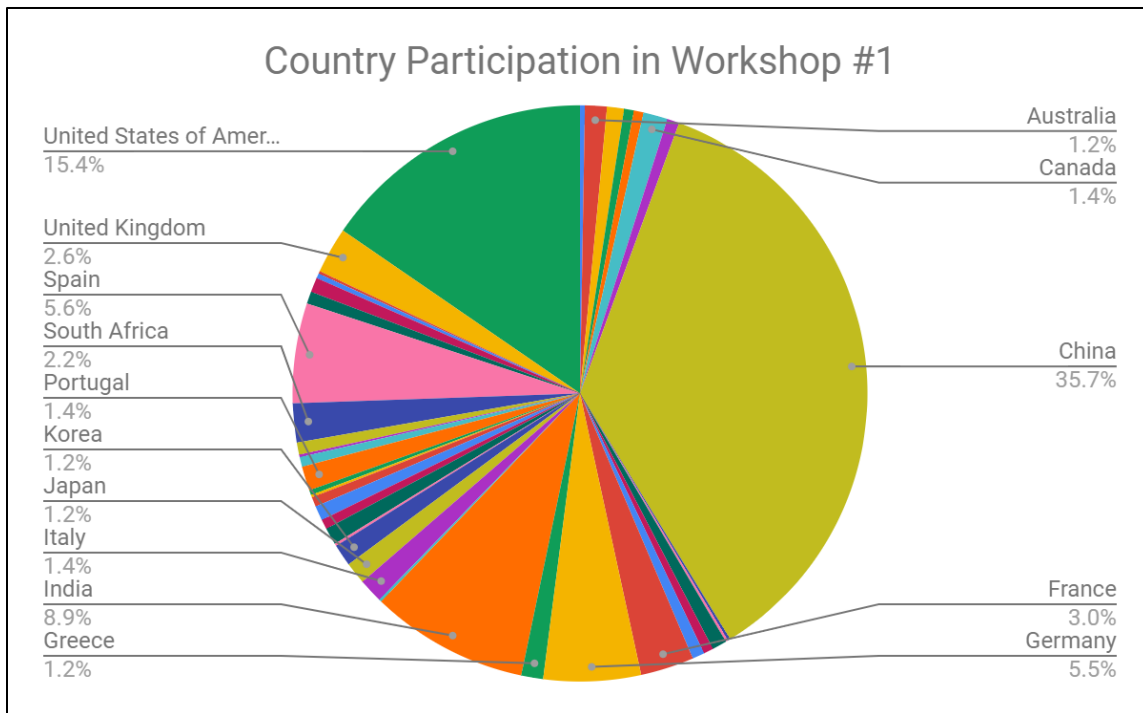
1. Should the SeqCode be restricted to uncultured organisms?
2. Should the SeqCode allow replacement of sequences as types with strains as types [should they become cultivated]?
3. Should the SeqCode specify that priority of higher taxa depend on the priority of the genus and species?

4. Should the SeqCode include a proposal for an Approved List to incorporate the current Candidatus taxa if they include a DNA sequence as type and are otherwise compliant with the SeqCode?
5. Should the SeqCode include a digital protologue as part of the naming process?
6. How should the SeqCode be managed and revised?
7. Should the SeqCode require 'perfect Latin'?
8. Should the SeqCode include the rank of subspecies?

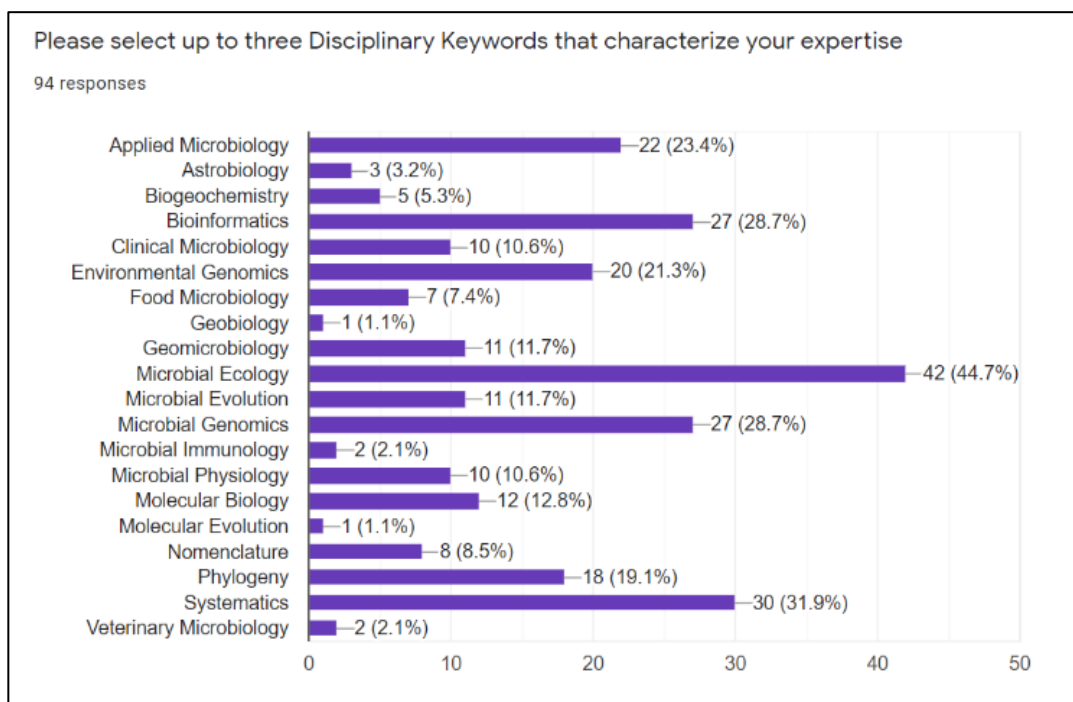
Each breakout group of  $\leq 10$  participants discussed one of these questions for ~ 1 hour and recorded their opinions in a Google Doc and PowerPoint, which was shared with all participants. Those responses are currently being used to inform revisions to the current draft of SeqCode.

**Summary of Workshop 2.** The second workshop began by summarizing the breakout group reports from Workshop 1. Then, we sought advice from systematists working with eukaryotes and viruses who are similarly implementing changes to take advantage of modern data streams, particularly next-generation sequence data, and engaged key databases for advice about implementation of SeqCode and best practices for integration of SeqCode names into their data structures. For the first part, *Translating Between Nomenclature Systems*, pre-recorded talks were given by Susanne Renner (plant systematist), Vincent Robert (curator of Mycobank), Chris Lane (protist systematist), and Arvind Varsani (virus systematist). During the online meeting, these four also formed a panel to discuss questions from the organizing committee and participants. For the second part, *Integration of International Organizations, Standards, and Databases*, nine database and standards experts provided slides on the implications of SeqCode implementation and this same group formed a panel discussion. The participants included Iain Sutcliffe (ICSP), Juncai Ma and Linhuan Wu (WDCM Data Resources), Jorg Overmann (DSMZ), Nicole Dubilier and Phil Hugenholtz (ISME), Conrad Schoch (NCBI Taxonomy), Donovan Parks (Genome Taxonomy Database), Emiley Eloë-Fadrosh and Scott Tighe (Genomics Standards Consortium), Kostas Konstantinidis (Microbial Genomes Atlas), and Jongsik Chun (EzBioCloud Database). The workshop ended with an open discussion and forward-looking high-level synthesis.

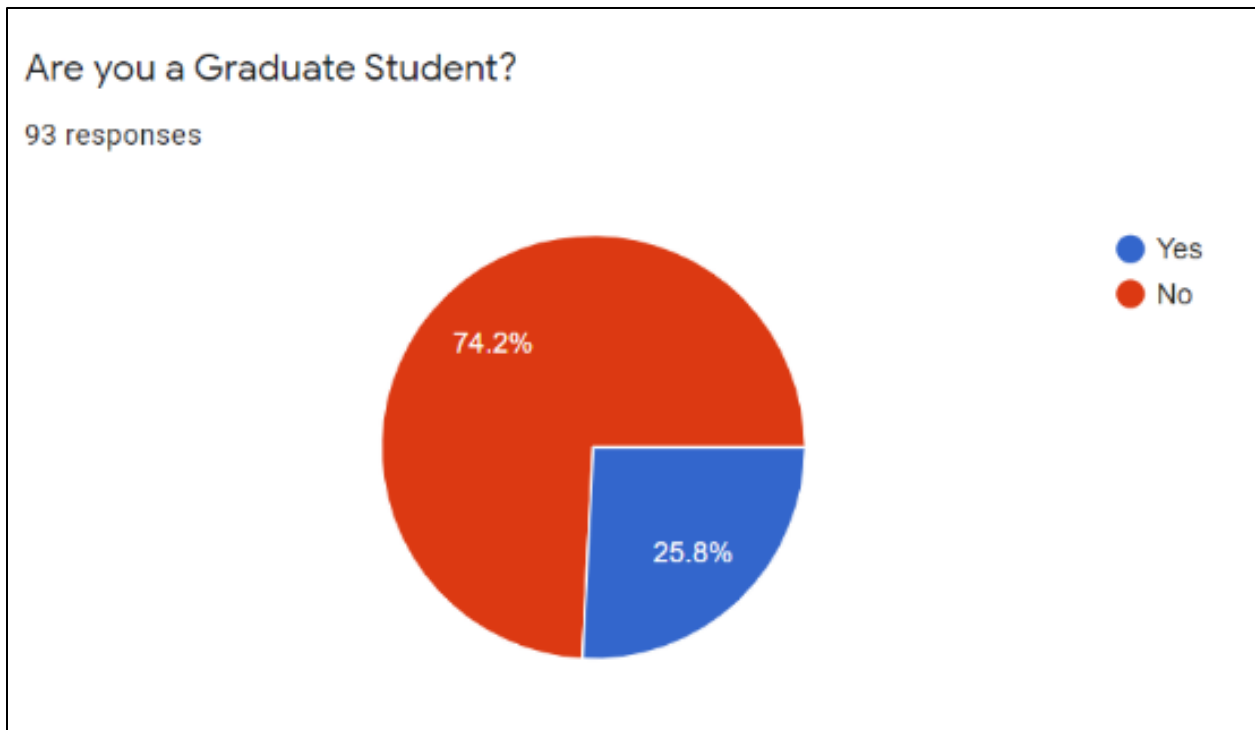
**Acknowledgement of ISME support.** ISME support was recognized by including the logo on the meeting website and verbally acknowledging ISME support at the beginning of each workshop. ISME will also be acknowledged in the SeqCode publication and other outcomes.



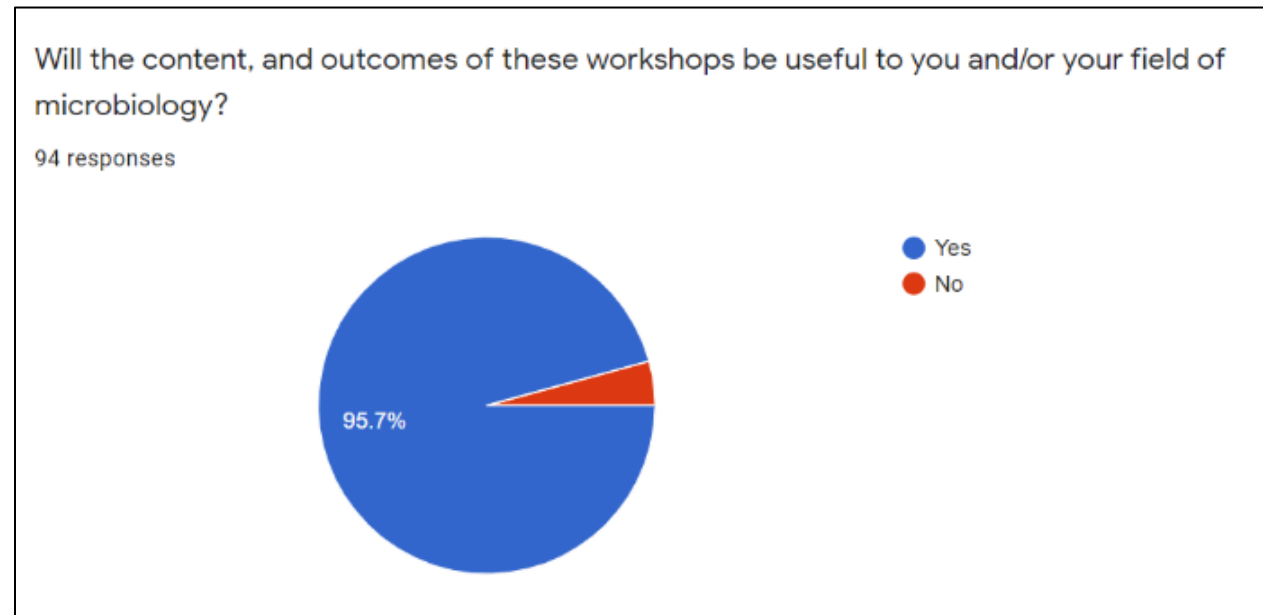
**Figure 1. Strong international footprint.** At least 40 countries from six continents participated in online workshops. Highest representation was from China (261), USA (113), India (65), Spain (41), Germany (40), France (22), UK (19), South Africa (16), and Portugal (10). Countries not listed: Argentina, Belgium, Brazil, Chile, Colombia, Cyprus, Czech Republic, Denmark, Finland, Israel, Malaysia, Mexico, Netherlands, New Zealand, Pakistan, Peru, Poland, Russia, Saudi Arabia, Sweden, Switzerland, Taiwan, United Arab Emirates.



**Figure 2. Broad engagement within microbiology subdisciplines.** Microbiology subdisciplines of SeqCode workshop participants, indicating broad participation and strong participation in both microbial ecology and systematics.



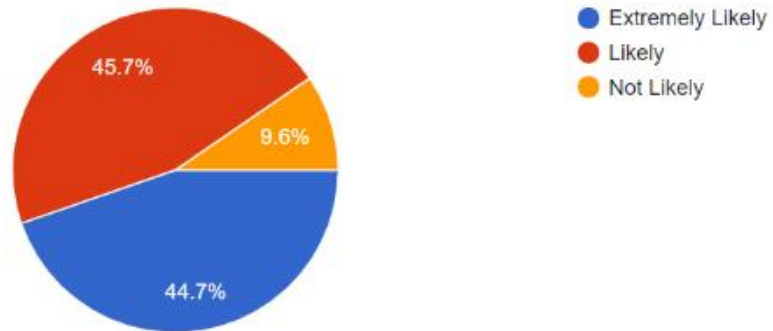
**Figure 3. Strong graduate student participation.** Over 25% SeqCode workshop participants responding to the post-workshop survey were graduate students. This was a very rare opportunity for training in microbial systematics.



**Figure 4. Value of the SeqCode workshops.** Almost all respondents indicated that the workshops and their outcomes will be valuable for them and/or their field of microbiology.

How likely are you to use the SeqCode to name organisms that are represented only by sequence data (i.e. not available in culture)?

94 responses



**Figure 5. Strong community support for SeqCode.** Nearly all participants indicated they will likely use SeqCode in the future. Strong community support is clear justification for implementation of SeqCode.