Comparison chart:
Current ICNP vs. Whitman's proposal vs. distinct registry for the uncultivated

The “discussions related to the use of DNA as type material for bacterial species descriptions” (https://www.the-icsp.org/, accessed on 2020-02-23) are not necessarily ease to follow because the order of the contributions may obscure the logical interrelations of the specific arguments. It thus makes sense to assort the contributions according to arguments. This in turn may best be achieved by grouping the arguments into pros and cons of the distinct nomenclatural codes under discussion: The current INCP (Parker et al., 2019) vs. the ICNP modified as suggested by Whitman (2016).

I have added a third approach, a separate naming system for uncultivated taxa that takes into account the concerns raised by Oren & Garrity (2018), for comparative purposes. This does not mean that this approach is the one I favour. I think it should be discussed more broadly. Indeed, the ballot is not just about the use of genome sequences as nomenclatural types. Rather, the decision is about a specific implementation of this idea by specifically modifying the ICNP. Even researchers sympathetic towards genome sequences as nomenclatural types must consider the consequences of these specific modifications. Alternatives for modifying the ICNP also exist. For instance, impure cultures or dead specimens could be allowed under certain circumstances. Such alternatives should also be taken into account and more broadly discussed.

The contributions taken into account below are those I am aware of as of today (2020-02-23). They are referred to using their author(s) and date. Not all of the e-mails from the debate may have been sent to me.

The juxtaposition below is opinionated but even those who disagree with me may find the separation into distinct arguments to be of use. My own conclusion would favour the ICNP, combined with a distinct system for uncultivated organisms, and the current INCP over the proposal by Whitman (2016).

It has also been argued that the decision should be postponed because most of the affected microbiologists are unaware of it (Christensen-01-13; Dijkshoorn-01-13; Moore-01-15). For an opposing view see Sutcliffe-01-15. I would prefer to put the debate on a broader basis even if this implied a (potentially considerable) delay. Most microbiologists I talked to were unaware of the fact that the decision is scheduled for March 2020.

Benefit	Nomenclatural approach			Comments
	ICNP, 2018 revision	**Whitman 2016/ Whitman et al. 2019 proposal**	**Distinct system for uncultivated organisms**	To avoid nomenclatural chaos, a distinct system for uncultivated organisms would need to use taxon names whose shape immediately clarifies that they belong to that distinct system. The nomenclatural chaos by having two distinct systems in operation for the same

				organisms at the same time (Oren & Garrity, 2018) only occurred because the shape of the names was indistinguishable (as in the case of cyanobacteria in microbiology/botany and anamorphs/teleomorphs in mycology). Most users of taxonomic classifications only take the taxon names into account. One option for generating clearly separate names is, of course, prepending “Candidatus”. In contrast to the current system of Candidatus names, a central registration for names of uncultivated bacteria could be established as well as rules about issues such as types and priorities. One may prefer to not use Latin names in the alternative system (Wink-02-08; Tindall-02-14), which is one among several options for considering the concerns raised by Oren & Garrity (2018).
Provides sufficient incentive for cultivation and deposit	yes	no	yes	If genome sequences were possible as nomenclatural types for names validly published according to the ICNP, the likely outcome would be that even pure cultures would not be used any more as types because depositing them in culture collections is considerably more tedious then depositing a sequence in INSDC, which usually needs to be done anyway (Moore-01-17; Fournier-01-21; Göker-02-08). It has been argued that an incentive for cultivation and deposit remained due to the possibility of publishing emended taxon descriptions (Whitman-01-21; see also Sutcliffe-01-20) but emendations do not have the same weight as proposing names and occur relatively rarely (Zamora et al., 2018; Göker-02-20). See also Willems-01-20. Strains are essential particularly in the clinical context, e.g., for developing vaccines (Christensen-01-16; see also Christensen-01-13; Dijkshoorn-01-13). While there may well be other incentives for isolating strains (Konstantinidis-01-18; Rossello-Mora-01-20), it is still of relevance whether or not the rules of nomenclature support isolation and cultivation.
Provides sufficient incentive for naming uncultivated	no	yes	yes	If a separate naming (and recognition) system for uncultivated microorganisms was used, an incentive for naming them would be provided, or the current incentive (which obviously exists to some extent) increased. At the same time, an incentive for isolation,

bacteria				cultivation and deposit would remain because these measures would still be prerequisites for validly publishing a name under the ICNP. A separate naming system may still create many names that may be regarded as meaningless, particularly if they are only based on the core genome.
Avoids hindering anyone to assign names to (all) prokaryotes	yes	yes	yes	The three “yes” values may be surprising at first sight. However, even the ICNP never hindered anybody to assign a name to some microbe. The ICNP just regulates which names are validly published according to that code. On a similar vein, none of the three systems would guarantee that a taxonomic system is implemented that is particularly suitable according to the views of selected taxonomists. Conversely, no Code has ever hindered microbiologists to name all bacteria or archaea they are aware of. At least to some degree, a naming system for uncultivated microbes has always existed.
Takes sufficiently into account that names are for organisms, not for sequences	yes	no	yes	“Should the proposals be accepted, the meaning of nomenclatural types would change in a fundamental way from physical objects as sources of data to the data themselves. […] Names of taxa are applied to organisms, not to characters of those organisms. Therefore, a physical object should preferably serve as the type of a name, rather than the characteristics of that object” (Zamora et al., 2018). The separate system for uncultivated prokaryotes could be devised so as to provide names for sequences. The epistemological problem caused by using sequences as nomenclatural types for organisms (Nübel-02-07) or vice versa would not occur. (It would still need to solve issues such as the instability caused by updates of INSDC accession numbers, see Tindall-02-14.)
Ensures reproducibility by allowing for a re-examination of organismic type material	yes	no	yes	With a separate system in place, organismic type material would be kept as nomenclatural types for names of organisms under the ICNP. “Such changes [i.e. the permission of sequences as nomenclatural types] are conducive to irreproducible science [and] the potential typification on artefactual data, [...] ultimately causing nomenclatural instability and unnecessary work for future researchers that would stall future explorations of fungal diversity” (Zamora et al., 2018).

				Sequence artefacts may cause the need for many Requests for an Opinion (Tindall-02-14; see also Nübel-02-07). Accession numbers in publicly available databases as recommended by Whitman (2016) are not necessarily stable because the sequence information can be updated. The problem that the Whitman (2016) proposal does not specify quality checks has been highlighted by many (Fournier-01-21, Reubsaet-01-17; Lai-01-16; Brown-02-21).
Avoids over-emphasizing currently accepted methods for genome-based taxonomy	yes	no	yes	We tend to believe nowadays that the current methods are much better than those applied, say, 50 years ago (for a similar comment see Konstantinidis-02-08; Konstantinidis-01-18; Rossello-Mora-01-20). But what will researchers 50 years from now think about the methods we are applying now? The proposal to modify the code strongly relies on the *currently* perceived accuracy of sequencing, assembly and downstream genome-based taxonomy methods (see also Whitman-Sutcliffe-01-13; Konstantinidis-01-14). It does not sufficiently take into account the possibility that these methods may considerably be revised in the future. In contrast, the deposit of type strains in culture collections does not presuppose the reliability of any specific analysis method *and* makes the types accessible to future methods. The Whitman (2016) proposal does not specify quality checks (see also Fournier-01-21, Reubsaet-01-17; Lai-01-16; Brown-02-21) and thus may frequently yield situations in which a Request for an Opinion would be needed (Tindall-02-14). While minimum standards for genome sequencing in taxonomy exist (Whitman-01-17), they are not enforced by the proposal (Moore-01-17). In contrast, the proposal may well pave the way to lowered standards because it contains a number of ambiguous clauses (Göker-02-20; see also Nübel-02-07).
Fosters the taxonomic application of newly developed methods	yes	no	yes	If sequences are used as nomenclatural types, only sequence-related bioinformatic methods can be applied to them. Methods newly developed in the future for sequencing itself or for exploring the phenotype of an organism could not be applied. For this reason, the spectrum of methods is much broader if it can be applied to an organism, let alone a living organism. This was clearly seen by >400

				mycologists in 2018: “By allowing already extracted data, such as a DNA sequence, to serve as type instead of the source of the data, new information cannot be obtained when this is required” (Zamora et al., 2018). See also Fournier-01-21.
Appreciates the role of genome sequencing for taxonomy	yes	yes	yes	While it sometimes depicted otherwise (Whitman-Sutcliffe-01-13 and Rossello-Mora-01-20 could be interpreted in that way), critics of the proposal by Whitman and colleagues do not deny the crucial role of genome sequencing. However, one must keep in mind that microbiology would soon navigate towards to a dead end if sequencing is not accompanied by other methods that allow for making sense of the sequences. As yet huge proportions of bacterial genomes are annotated as hypothetical proteins only or are wrongly annotated. This situation can only be improved by cultivation and subsequent laboratory testing (Overmann et al., 2019).
Enforces more elaborate species-delineation methods	no	no	no	Species-delineation methods using (genome) sequence similarity thresholds are satisfying in all respects. More elaborate approaches in use elsewhere require at least a better representation of the population (Nemec-02-06; Padial et al., 2010; Zamora et al., 2018). “There is an inevitable trade-off between using complex integrative approaches for delimiting species that may provide stable names, and the need to accelerate the pace of taxonomic descriptions” (Padial et al., 2010). The authors make a clear distinction between candidate species, i.e. “clusters of specimens identified through DNA barcoding” (the best equivalent of which in microbiology is species delineation through sequence similarity thresholds) and “species hypotheses [with] stability to their names, which requires a careful and often painstaking and time-consuming labor of species delimitation.” This would also best be implemented by distinct systems for candidate taxa and taxa validly published under the ICNP. Environmental sequences as types may less well be suited for better species concepts than isolates because “a MAG that represents an abundant population is NOT a single-strain description but the average genome of the population/many cells” (Konstantinidis-02-08), hence they would not

				represent the variance of the population (which sequencing distinct isolates could).
Avoids generating huge number of names with low information content and the same status as more informative names	yes	no	yes	“Such changes [i.e. the permission of sequences as nomenclatural types] are conducive to [...] massive creation of names with low information content, ultimately causing nomenclatural instability and unnecessary work for future researchers that would stall future explorations of fungal diversity” (Zamora et al., 2018). See also Nemec-02-06.
Avoids confusion by using names that clearly indicate on which kind of type they are based	yes	no	yes	Because most users of taxonomic classifications only take the taxon names into account, it would not be sufficient to indicate in the designation of the nomenclatural type whether it is a strain, a sequence, or anything else. Moreover, such as designation is only a recommendation in the proposal by Whitman (2016). A separate system for uncultivated bacteria would need to generate names that cannot be confused (see above; Wink-02-08; Tindall-02-14).
Avoids legal issues related to CBD or Nagoya protocol	no	no	no	While it has been argued that using sequences as types could prevent legal restrictions imposed in certain countries (Korpole-02-06, Patil-02-08, Venter-02-08, Venter-02-23) this view has been contested (Moore-02-07, Moore-02-10, Tindall-02-10). In particular, it has been pointed out that similar restrictions will probably soon be enforced regarding sequence information (Overmann-02-09).
Avoids infusing taxonomic opinion into the ICNP	yes	no	yes	General consideration 4 of the ICNP states “Rules of nomenclature do not govern the delimitation of taxa nor determine their relations.” Principle 1.4 of the ICNP states: “Nothing in this Code may be construed to restrict the freedom of taxonomic thought or action”. This means that the ICNP does not govern taxonomy, it governs nomenclature only. For this reason, whether or not a name is validly published must not be dependent on taxonomic opinion. This requirement conflicts with the proposal by Whitman (2016). The proposal would introduce into Rule 18a and Rule 20a that a sequence

		🟥		(or any other “type material”) must unambiguously identify the species or genus to be of use as a nomenclatural type. “In this regard, the key issue is whether or not the species is unambiguously identified, which is an absolute and not quantitative distinction. Either the evidence is sufficient to identify the species or it is not” (Whitman 2016; see also Whitman-Sutcliffe-01-13). However, whether or not unambiguous identification is possible depends on the circumscription or extent of the taxon, which is subject to taxonomic opinion. If the “type material” then conflicted with the new Rules, the taxon name would not be validly published. Thus the proposal would make the status of being valid published dependent on taxonomic opinion.

References

Note: Contributions to the ICSP online discussion are marked by Author-Month-Day.

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Zamora et al. (2018). Considerations and consequences of allowing DNA sequence data as types of fungal taxa. IMA FUNGUS 9(1): 167–175. doi:10.5598/imafungus.2018.09.01.10. *NOTE: This publication critically comments on a largely equivalent suggestion to use sequences as types that was made for fungi. Most of the criticisms equally apply to the Whitman (2016) proposal. The proposal to use sequences as types for fungi was rejected by a considerable majority on the International Mycological Congress.*