

(339–348) Proposals to permit DNA sequences to be used for fixing the application of names in prescribed circumstances

Kevin R. Thiele,¹ Quentin Groom,² Susanne S. Renner³ & Samuli Lehtonen⁴

1 *The University of Western Australia, School of Biological Sciences, 35 Stirling Hwy, Crawley, Western Australia 6009, Australia*

2 *Meise Botanic Garden, Nieuwelaan 38, 1860 Meise, Belgium*

3 *Washington University, Department of Biology, One Brookings Drive, St. Louis, Missouri 63130, U.S.A.*

4 *Biodiversity Unit, University of Turku, 20014 Turku, Finland*

Address for correspondence: Kevin R. Thiele, kevin.thiele@uwa.edu.au

DOI <https://doi.org/10.1002/tax.13032>

First published as part of this issue. See online for details.

Many microorganisms can be detected and characterized using traces of their DNA in environmental samples, such as soil, water, air or other organisms. Some or many of these may be new taxa. However, new taxa cannot be named under the *Shenzhen Code* (Turland & al. in *Regnum Veg.* 159. 2018) unless they can be typified using either a specimen (Art. 8.1), a metabolically inactive culture (Art. 8.4) or an illustration (Art. 8.1, 40.4 and 40.5). Because of these provisions of the *Code*, taxa that can be detected and characterized using DNA sequences but that cannot be isolated, cultured or illustrated, are currently unnameable. This is an important challenge, given that naming, documenting and characterizing the Earth's biodiversity is a core activity of taxonomy, and environmental DNA (eDNA) is allowing the discovery and documentation of significant, and previously hidden, parts of that biodiversity.

Several previous proposals to amend the *Code* (Hawskworth & al. in *Taxon* 65: 899–900. 2016; Hawskworth & al. in *IMA Fungus* 9: (i)–(vii). 2018) have attempted to solve this problem. None has been successful. A proposal discussed at the Nomenclature Section of the Shenzhen International Botanical Congress (Hawskworth & al., l.c. 2016), after failing to gain sufficient votes for adoption, was referred to a Special-purpose Committee on DNA Sequences as Types, for consideration. The present proposals result from the deliberations of that Special-purpose Committee.

The Committee established the following important general principles, which inform its proposals:

(1) The remit of the Committee (and hence of the proposals) is to deal with the use of DNA sequences for fixing the application of names; questions about the merits or otherwise of DNA-based *taxonomy* are out of scope.

(2) Any option to name organisms based on DNA sequences should be restricted to taxonomic groups and circumstances where conventional typification (using specimens or illustrations) is not technically feasible, and should not apply to macroscopic organisms such as vascular plants, bryophytes, macro-fungi and macro-algae, or their fossils, where conventional typification is technically feasible. In these cases, DNA sequences may or may not have a role in discriminating and characterizing taxa, but they are excluded from being used to fix the application of names.

(3) The question of the adequacy of a given sequence for the purpose of fixing the application of a name (e.g. whether nuclear, chloroplast or mitochondrial sequences are allowable; how many base pairs or how many regions are adequate) is a scientific question, and is best dealt with using mechanisms outside the formal provisions of the *Code*.

(4) If sequences are used for establishing new names, they must be made freely available in designated online repositories.

The Committee discussed (Thiele & al. in *Taxon* 72: 965–973. 2023) the history of typification and the nature of types, and concluded that DNA sequences are more akin to descriptions than they are to specimens. The Committee considered two options to solve the problem described above (i.e. taxa that can be detected and characterized but that cannot be named): (1) broadening the definition of “type” to include DNA sequences (despite the fundamental differences between sequences and specimens) and (2) establishing a new concept in the *Code* of type-less names (taxa that can be named without a type, on the basis of a sequence).

This set of proposals deals with the second of these options; an alternative set of proposals (Thiele & al. in *Taxon* 72: 1143–1145. 2023) deals with the first. Some members of the Special-purpose Committee expressed a preference for the first option while others preferred the second; for this reason, the Committee has opted to provide both sets of proposals for consideration.

It was with some trepidation that the Committee considered this option for fixing the application of names outside the well-established and foundational principle of the type concept. Nevertheless, the Committee believes that the proposed amendments below (or the alternative proposals in Thiele & al. in *Taxon* 72: 1143–1145. 2023) comprise an important evolution of the *Code*, which must adapt to the new technologies that have resulted in the discovery of many taxa that cannot presently be named.

An advantage of this option is that the important concept of typification, which has underpinned nomenclature for more than a century, is left unchanged. Types remain either specimens or (in some circumstances) illustrations, and all Articles of the *Code* that refer to types keep their traditional meaning. The proposed amendments establish a new mechanism for fixing the application of names using DNA sequences, and restrict the application of that mechanism to narrowly prescribed circumstances where conventional typification is unachievable.

The authors of these proposals are all members of the Special-purpose Committee on DNA Sequences as Types, but not all members of the Committee agreed to author these proposals.

Members of the Committee consider these proposals to be modest and to have the desired effect (allowing the naming of organisms that cannot currently be named under the *Code*) while at the same time being minimally disruptive for taxonomy and nomenclature. Adopting one or the other set of proposals will solve a real, present problem that limits our ability to taxonomically characterize and name the Earth's biodiversity, but will not “open the floodgates” to

unrestricted and uncontrolled DNA-based taxonomy and nomenclature. If both sets of proposals are rejected, the problem will persist, and grow rapidly as the technologies that allow the discovery and characterization of the many taxa that cannot be isolated, cultured or otherwise prepared into specimens become more widespread and effective.

(339) Amend Principle II as follows (new text in bold):

“The application of names of taxonomic groups is determined by means of nomenclatural types **where typification is technically feasible, and by means of a description based on a reference DNA sequence where it is not.**”

The Special-purpose Committee recognizes that amending a Principle of the *Code* is a major step. Principle II is in effect a statement of the resolution (in favour of specimens) of an important historical debate as to whether specimens or descriptions are the most effective way to fix the application of taxonomic names (see Thiele & al. in *Taxon* 72: 965–973. 2023). Given that DNA sequences are more akin to descriptions than they are to specimens, some members of the Committee felt that “simply” including DNA sequences under the definition of “type”, while potentially pragmatic, brings with it the danger of mixing concepts that are fundamentally different in kind. This amendment to Principle II preserves the traditional definition of type while allowing for the naming of taxa that cannot be typified.

(340) Amend the title of Chapter II as follows (new text in bold, deleted text in strikethrough):

“STATUS, ~~TYPIFICATION~~, APPLICATION, AND PRIORITY OF NAMES”

This amendment gives clarity to this chapter’s scope, which, if these amendments are adopted, will carry a new Section with provisions for type-less names, as well as the existing Section 2, which deals with typification.

(341) Amend Art. 6 Note 1 as follows (new text in bold):

“*Note 1.* For nomenclatural purposes, valid publication creates a name, and sometimes also an autonym (Art. 22.1 and 26.1), but does not itself imply any taxonomic circumscription beyond inclusion of the type **or reference DNA sequence** (see Art. X.1) of the name (Art. 7.1).”

This is the first of several instances where the phrase “or DNA reference sequence” should be added after “type”. If this proposal is accepted, the Editorial Committee is asked to deal with subsequent instances, including but not limited to Art. 9, 10, 22, 26, 40, 48 and 52.

(342) Amend Art. 7.1 as follows (new text in bold):

“7.1. The application of names of taxa at the rank of family or below is determined by means of nomenclatural types (types of names of taxa), **except as provided by Art. X.1.** The application of names of taxa at the higher ranks is also determined by means of types when the names are formed from a **typified** generic name (see Art. 10.10) **or by reference sequences when the names are formed from type-less generic names (see Art. X.7).**”

(343) Add a new Section “Type-less names” to Chapter II with the following new Articles and Note:

“X.1. On or after 1 January 2026, when typification is not technically feasible, a name of a taxon other than a vascular plant or

bryophyte may be published without a type, the application of the name instead being fixed using a DNA reference sequence (Art. X.9).”

“*Note 1.* For the purposes of Art. X.1, typification is regarded as technically not feasible if and only if physical specimens, illustrations, or cultures cannot reasonably be obtained using technologies available at the time of publication. Preservation of a specimen or culture is not considered unfeasible if a type specimen or culture could not be obtained merely for reasons of inconvenience, lack of access, or if a specimen or culture was lost or otherwise not collected or prepared when it could have been.”

“X.2. A reference sequence of a type-less name is that sequence to which the name of the taxon is permanently attached, whether as the correct name or as a synonym. The reference sequence is not necessarily the most typical or representative sequence of a taxon.”

“X.3. The reference sequence of a new combination or name at new rank (Art. 6.10) based on a type-less name is the reference sequence of the basionym even though it may have been applied erroneously to a taxon now considered not to include that reference sequence (but see Art. 48.1).”

“X.4. The reference sequence of a replacement name (Art. 6.11) for a type-less name is the reference sequence of its replaced synonym even though it may have been applied erroneously to a taxon now considered not to include that reference sequence (but see Art. 41 Note 3 and 48.1).”

“X.5. The reference sequence of an autonym of a type-less name is the same as that of the name from which it is derived.”

“X.6. The reference sequence of a name of a genus or of any subdivision of a genus erected to accommodate only species with type-less names at time of publication is the reference sequence of a name of one of those species. For purposes of designation or citation of a reference sequence, the species name alone suffices, i.e. it is considered as the full equivalent of its reference sequence (see also Rec. 40A.3).”

“X.7. The reference sequence of a name of a family or of any subdivision of a family is the same as that of the generic name from which it is formed (see Art. 18.1), if the generic name has a designated reference sequence (Art. X.8). For purposes of designation or citation of a reference sequence, the generic name alone suffices.”

“X.8. In order to be validly published a type-less name must (a) be published in an approved journal (see App. Y, Art. X.9(b)) and (b) be accompanied in the protologue by (1) citation of the identifier issued for the reference sequence by an approved online repository (see App. X and Art. X.9(a)), (2) specification of selected informative portions of the reference sequence, (3) a statement as to why it is believed that the taxon is novel and unnamed, and (4) an explanation of why a type specimen could not be isolated, cultured, or otherwise prepared.”

“X.9. The General Committee, after seeking advice from relevant specialist Committees and international societies, has the powers to (a) appoint one or more localized or decentralized, open and accessible electronic repositories to issue the identifiers required by Art. X.8(b)(1) (see App. X), (b) ratify a list of approved journals for valid publication of names with DNA sequences as types (see App. Y), and (c) cancel or alter such appointments or ratifications at its discretion.”

Articles X.1–X.7 are the equivalents, for type-less names, of Art. 7 for typified names. Articles X.8 and X.9 have the effect of restricting the range of journals that can be used to publish new names typified using DNA sequences. While such a provision has been discussed but not effected for names in general, the Committee felt that the new provisions proposed here would benefit from such a restriction, and that quality assurance is a scientific issue best dealt with in this manner.

Requiring justification from the author(s) of a new name as to why a DNA sequence may be appropriately used to typify the new name (Art. X.8(b)(3)) is intended to discourage authors from, for example, erecting a new species based on a novel DNA sequence in a genus that includes species that have not yet been sequenced (and hence could be the source of the sequence). Requiring justification for the impracticability of obtaining a type specimen (Art. X.8(b)(4)) is intended to discourage authors from, for example, erecting a new species that is likely to be macroscopic and/or capable of being isolated or cultured.

(344) Add a new Note after Art. 38.1:

Note Ibis. For the purposes of Art. 38.1, if a name is type-less, the reference sequence itself is treated as a description.”

(345) Amend Art. 39.2 as follows (new text in bold):

“39.2. In order to be validly published, a name of a new taxon published on or after 1 January 2012 must be accompanied *(a)* by a Latin or English description or diagnosis, or by a reference (see Art. 38.13) to a previously and effectively published Latin or English description or diagnosis (for fossils see also Art. 43.1), **or, *(b)* on or after 1 January 2026, by both *(1)* citation of an identifier issued for the reference sequence by an approved online repository (see App. X and Art. X.9(a)) and *(2)* specification of selected informative portions of the reference sequence (see Art. X.8).**”

(346) Amend Art. 40.1 as follows (new text in bold, deleted text in strikethrough):

“40.1. Publication ~~on or after 1 January 1958~~ of the name of a new taxon at the rank of genus or below is valid only when *(a)* **on or after 1 January 1958**, the type of the name is indicated (see Art. 7–10; but see Art. H.9 Note 1 for the names of certain hybrids) **or *(b)* on or after 1 January 2026, a reference sequence is designated for a name that meets the requirements of Art. X.1.**”

(347) Amend Art. 44.2 as follows (new text in bold, deleted text in strikethrough):

“44.2. A name of a new species or infraspecific taxon of non-fossil algae ~~published on or after 1 January 1958~~ is not validly published unless *(a)* **on or after 1 January 1958** it is accompanied by an illustration or figure showing the distinctive morphological features, or by a reference to a previously and effectively published such

illustration or figure, **or *(b)* on or after 1 January 2026 a reference sequence is designated for a name that meets the requirements of Art. X.1.**”

(348) Amend Div. III Prov. 7.9 as follows (new text in bold, deleted text in strikethrough):

“7.9. The General Committee is charged with: *(a)* receiving proposals to conserve, protect, or reject names, proposals to suppress works, and requests for decisions (Art. 14.12, F.2.1, 56.2, F.7.1, 34.1, 38.4, and 53.4) and ~~for referring these proposals or requests to the specialist committee(s) concerned (receipt and referral of proposals and requests are automatic upon their publication).~~ ~~The General Committee is also charged with;~~ *(b)* considering recommendations of the specialist committees and either approving or overturning those recommendations or referring them back to the specialist committees for further consideration; *(c)* **maintaining a list of approved repositories for storing sequences and issuing sequence identifiers; and *(d)* maintaining a list of approved journals for valid publication of names with reference DNA sequences (Art. X.8 and X.9).** The General Committee may also communicate an international standard format in addition to, or as a successor to, Portable Document Format (PDF) for effective publication of electronic material (Art. 29.3) and is empowered to ratify a list of institutional votes drawn up by the Committee on Institutional Votes (see Prov. 3.1).”

Through Prov. 7.9(c) the General Committee maintains a necessary degree of control over aspects of the use of DNA sequences for fixing the application of names that appropriately fall outside the provisions of the *Code* itself. By approving journals and maintaining App. Y, the General Committee will ensure that sufficient scientific rigour is maintained, by the journal editors, over matters such as sequence type, length and the scientific justifications required for Art. X.8(b)(2), (3) and (4).

Acknowledgements

We thank John H. Wiersema, Nicholas J. Turland, Tom W. May and Anna M. Monro for helpful suggestions that improved the manuscript, and all members of the Special-purpose Committee on DNA Sequences as Types, including those who chose not to co-author these proposals.