

Report of the Special-purpose Committee on DNA Sequences as Types, established at the XIX International Botanical Congress in Shenzhen, China

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Abstract A Special-purpose Committee on DNA Sequences as Types was established at the XIX International Botanical Congress (IBC) in Shenzhen, China in 2017, with a mandate to report to the XX IBC with recommendations on a preferred course of action with respect to DNA sequences as potential types under the *International Code of Nomenclature for algae, fungi, and plants*. This report provides a synthesis of the deliberations from the Special-purpose Committee on this issue. We discuss two potential options for dealing with the problem that many species, especially of microfungi and microalgae, can be discovered and delimited using eDNA sequencing but cannot currently be formally named due to the requirement in the *Code* that either a specimen or illustration be nominated as holotype. One option is to expand the definition of “type” to include DNA sequences, while a second option would allow some taxa to be named without types, the application of their names instead being determined using a DNA sequence. This report should be read in concert with two formal proposals for potential amendments to effect these options, published in this issue of *Taxon*.

Keywords DNA sequences; eDNA; type concept; typification

Background

As discussed in Thiele & al. (2023a), DNA sequences are becoming increasingly important in many core activities of modern taxonomy, including identifying specimens, delimiting species and other taxa, inferring evolutionary relationships between taxa, estimating the phylogenetic structuring of life and establishing robust taxonomic classifications (Blaxter & al., 2022). DNA’s universality and discriminatory power in taxonomy have led to a range of proposals (e.g. Hawksworth & al., 2016; Hawksworth, 2018; Renner, 2021; Hedlund & al., 2022) for DNA sequences to be used for another of taxonomy’s core activities—typifying the names of taxa.

The *International Code of Nomenclature for algae, fungi, and plants* (herein, the *Code*; Turland & al., 2018) requires that the application of names be determined by types and that the types of names of species and infraspecific taxa must be physical specimens preserved in a herbarium or equivalent institution or, in some cases, illustrations (see Art. 7.1 and 8.1). If a physical type specimen or illustration cannot be prepared, a taxon cannot be named.

However, modern methods of DNA sequencing allow the *in silico* assembly of DNA sequences from environmental samples such as soil and water, and studies using these methods have demonstrated the detection, discrimination and characterization (by sequencing) of many thousands (potentially, millions) of novel species and other taxa. Many of these taxa cannot be cultured or purified into a sample using current technologies available even in the best-equipped laboratories. The rules of the *Code* that require a preserved specimen therefore preclude the formal naming of these taxa.

The inability to name such taxa is not just of scholarly interest: it has practical consequences that threaten to impede research, conservation and policy (Thomson & al., 2021). Resolving many environmental challenges needs integration and interoperability of data on biodiversity, and names of taxa provide an essential key to those data and a means to link data together at scales from single organisms to

whole ecosystems (Penev & al., 2022). Naming the Earth’s taxa is important, yet a large number of taxa are unnameable under the *Code*.

Several publications (e.g. Beer & al., 2016; Lücking & Moncada, 2017) have attempted to find ways to deal with this issue through creative use of existing provisions of the *Code*. Given their lack of success, two formal proposals to amend the *Code* by allowing DNA sequences to serve as types were presented to the Nomenclature Section of the XIX International Botanical Congress (IBC) in Shenzhen, China in 2017 (Prop. 308 and 309 in Hawksworth & al., 2016; see also Art. 8 Prop. O and Rec. 8C (new) Prop. A in Turland & Wiersema, 2017). While these were originally intended to deal with fungi only, a friendly amendment from the floor at the Nomenclature Section extended them to all organismal groups covered by the *Code* (Lindon & al., 2020). The proposals were rejected at the Nomenclature Section, and the issue was referred to the present Special-purpose Committee, with a mandate to report on the matter to the XX IBC (Wilson, 2019; Lindon & al., 2020).

The 17 voting members of the Special-purpose Committee, as constituted (Wilson, 2019), were Kevin Thiele (Australia, Convener), Samuli Lehtonen (Finland, Secretary), Maria do Carmo Amaral (Brazil), Wendy Applequist (U.S.A.), Arvind Dhabe (India), Ali Dönmez (Turkey), Kanchi Gandhi (U.S.A.), Quentin Groom (Belgium), Christine Maggs (U.K.), Valéry Malécot (France), Karol Marhold (Slovakia), Angela McDonnell (U.S.A.), Øjvind Moestrup (Denmark), Susanne Renner (Germany), Gary Saunders (Canada), Yijian Yao (China) and Hwan Su Yoon (South Korea). Karen Wilson (Australia, Secretary of the General Committee) and Nicholas Turland (Germany, Rapporteur-général) served *ex officio*. Tom May participated in his capacity as Convener of a parallel Special-purpose Committee on the same issue established by the 11th International Mycological Congress (IMC) in San Juan, Puerto Rico in 2018 (see below). Tom maintained a neutral stance on the merits of the proposals and abstained from formal

votes. Not all members as constituted took an active part in the deliberations of the Committee.

A voluntary survey of Committee members' expertise with respect to DNA methods and nomenclature, and their attitudes towards DNA typification, was conducted before deliberations commenced. Most members (66.7%) who responded to the survey ($n = 12$) regularly used DNA methods in their research and publications and rated their level of expertise as high to very high. Most members (75%) also rated their knowledge of and expertise in nomenclature as high or very high. Nine members nominated their main taxonomic expertise as being vascular plants, two as algae and one as fungi. Committee members' initial attitudes to the use of DNA sequences as types was well-balanced: 25% of responding members strongly supported the use of DNA as types, the same proportion strongly opposed, while the remainder (50%) did not have a strong opinion one way or the other. Most members (58.3%) indicated that they were "fairly committed to [their] position, but could be convinced otherwise", while 25% were "strongly committed and unlikely to change [their] mind". The remainder had no definite views.

The proposals that led to the establishment of the Special-purpose Committee in Shenzhen were also considered at the 11th IMC in San Juan, which governs Chapter F of the *Code* (matters pertaining only to fungi; Hawksworth, 2018; Lücking & al., 2018; May & Redhead, 2018; Thines & al., 2018; Zamora & al., 2018). Here again they were rejected and referred to a parallel Special-purpose Committee established under the IMC, to report to the 12th IMC in Maastricht, The Netherlands in 2024 (May & al., 2018). The present paper does not necessarily represent the views of that mycological Special-purpose Committee.

This paper is the second by the Special-purpose Committee established in Shenzhen. The first paper (Thiele & al., 2023a) provided an initial statement of the problem, an exploration of the issues, a summary of the pros and cons of using DNA sequences as types and a brief outline of potential options. This second paper is a report of the Special-purpose Committee's deliberations and a summary of the development of two potential options for dealing with the naming of taxa that cannot currently be typified using specimens or illustrations. The paper should be read in concert with two formal proposals for amendments to effect these options, published in this issue of *Taxon* (Thiele & al. 2023b,c).

Types, descriptions and diagnoses

Types are central to modern nomenclature; indeed, Principle II of the *Code* establishes their centrality:

"The application of names of taxonomic groups is determined by means of nomenclatural types."

Typification, however, has a long and complex history. In Thiele & al. (2023a), we discussed, in brief, part of this history, focusing on early disagreement as to whether type specimens or descriptions and diagnoses would best serve nomenclature by ensuring the convenient and unambiguous application of names. Type specimens were eventually favoured for this purpose and have been central to the *Code* since the earliest years of the 20th century. Note, however, that until as recently as the Sydney *Code* (Voss & al., 1983: Art. 9.3), descriptions could be used as types if preservation of a type specimen was impossible:

"9.3. If it is impossible to preserve a specimen as the type of a name of a species or infraspecific taxon of non-fossil plants, or if such a name is without a type specimen, the type may be a *description* or figure [our emphasis]."

Article 9.3 was amended in the Berlin *Code* (Greuter & al., 1988) by removal of the words *or description*, on the basis (1) that there was no good argument to retain it in its previous form (McNeill, 1986), (2) that allowing descriptions to serve as types was inconsistent with the provision for neotypification (Greuter & McNeill, 1987) and (3) because it was considered "a denial of the type method" (Brummitt, 1974: 865).

Descriptive statements (in the form of a full description or diagnosis or both) are also central to taxonomy and nomenclature, and either a description or a diagnosis is required for valid publication of new names (Art. 38.1 and 38.2). The *Code* does not specify what form a descriptive statement must take or its content (diagnoses are defined in Art. 38.2), though it is generally understood to comprise a set of key features, usually drawn from morphology but sometimes including chemistry, ecology, etc. Statements describing "properties such as purely aesthetic features, economic, medicinal or culinary use, cultural significance, cultivation techniques, geographical origin, or geological age" are excluded from fulfilling the requirements of Art. 38.1 (see Art. 38.3). When there is doubt as to whether a description or diagnosis qualifies for valid publication, a request for a decision may be submitted to the General Committee (Art. 38.4).

In Thiele & al. (2023a), we discussed the essential attributes of types and descriptive statements and argued that DNA sequences are more akin to descriptions than they are to types. We note here that when the question, whether types or descriptive statements are more effective for the unambiguous application of names, was last seriously discussed, and when the *Code* was amended in 1987 to remove descriptions from consideration for typification in favour of specimens or illustrations, the problem we are seeking to address here (taxa that can be discovered and characterized but not preserved in any pure form) did not exist.

Deliberations of the Special-purpose Committee have led to a conclusion that there are two main options for dealing with this problem. Option 1 would be to amend the definition of "type" in the *Code* to include DNA sequences. Option 2, by contrast, would retain the traditional definition of type but allow some organisms to be named without types, the application of their names instead being fixed using DNA sequences. Both these options have consequences, discussed below.

Option 1. Amending the definition of "type"

Option 1 proposes to amend the definition of "type" to include, in certain prescribed circumstances, DNA sequences. On face value, this may appear to be relatively simple and minimally disruptive. The primary change would be to amend Art. 8.1 to allow a type to be a specimen, illustration or DNA sequence. Other Articles that reference types (e.g. Art. 9.1 and 9.9) would also need to be amended accordingly. Principle II would remain unchanged: the application of names of taxonomic groups would continue in all cases to be determined by means of nomenclatural types. Furthermore, as DNA sequences can be considered somewhat analogous to illustrations (Turland & Wiersema, 2017) or descriptions (Thiele & al., 2023a), the former of which are allowed as types and the latter of were allowed until 1987, allowing sequences to act as types could be seen as consistent with historical application of the *Code*.

However, while this option appears to have the advantage that the Principles of the *Code* would remain undisturbed, some members of the Special-purpose Committee felt that its apparent simplicity is deceptive. Principle II—that the application of names is determined by means of types, not descriptive statements—has governed

nomenclature for almost 40 years (since the *Berlin Code*), and including DNA sequences, which are more akin to descriptions than to specimens, would substantially change the meaning and intent of the type method.

Allowing descriptions to serve as types prior to 1987 was, in our opinion quite rightly, deemed to deny the type method (Brummitt, 1974: 865); likewise, illustrations can be regarded as compromising the type method as well. Originally, illustrations and descriptions were allowed as types to circumvent exactly the problem the Special-purpose Committee was established to solve: situations where type specimens cannot reasonably be preserved or are uninformative. However, this was considered as an exception for special cases only, and the number of names typified by illustrations remains negligible compared to the number of names typified by specimens. By contrast, the number of DNA-typified names could, in the not-so-distant future, exceed the number of specimen-typified names, thereby leaving specimen types as exceptions. This would substantially undermine Principle II as presently applied. Hence, some Committee members felt that Option 1 would be destructive to the integrity of the type method, because it would redefine the concept of a type well beyond its historical meaning.

In addition to typification, the *Code* requires names of new taxa to be accompanied by a description or diagnosis or a reference to one (Art. 38.1). This poses a problem for names based on a sequence only, because it is often not possible to obtain information about the taxon beyond the sequence, apart from some possible ecological and distributional information. Because the sequence is akin to a description, the Committee considered it appropriate to allow DNA sequences to also act as descriptions (or diagnoses) in cases where no other descriptive information is possible, therefore requiring amendments to Art. 29.1, 38.1 and 39.2 concerning effective and valid publication.

The Committee also determined that a protologue consisting of a citation of a sequence identifier alone, acting simultaneously as a type and description, would be inadequate to allow others to assess the justification or merits of a new taxon. The proposed amendment to Art. 39.2 would require the inclusion of selected informative (i.e. diagnostic) parts of the sequence in the protologue. The same effect could be achieved by making diagnoses obligatory, but this would disrupt the practice in use for names typified by specimens or illustrations.

Option 2. Allowing type-less names

Option 2 proposes to amend the *Code* to allow, in certain prescribed circumstances, taxa to be named without types. At first, this may seem to be a more substantial break from (recent) tradition than retaining the primacy of the type approach and redefining “types” to include DNA sequences (Option 1). It has the advantage, however, that many of the (many) provisions of the *Code* that relate to typification would remain essentially unchanged: types would still be either specimens or illustrations, the effect of the amendments being that some names could be validly type-less.

The starting point of amendments under Option 2 would be a modification of Principle II. As discussed above, this records a resolution of the 19th century debate as to whether specimens or descriptive statements (descriptions or diagnoses) are better for unambiguously fixing the application of names. The Committee considered two alternatives for incorporating type-less names into the Principles, one to amend Principle II only and one to also add an additional Principle on type-less names. When the Committee voted on these alternatives it was evenly split; accordingly, the simpler alternative was adopted and a proposal included to amend Principle II as follows:

“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.”

To give effect to the amended Principle and to allow, in prescribed circumstances (see below), taxa to be named without types, the Committee opted to propose the addition of a new Section to Chapter II, the title of which would be generalized from “Status, Typification, and Priority of Names” to “Status, Application, and Priority of Names”. A new, dedicated Section provides the advantage that all key provisions pertaining to type-less names would be conveniently gathered together, leaving those provisions that pertain to typification largely undisturbed.

The proposals introduce a new term to the *Code*, that of “*reference DNA sequence*” (abbreviated to “*reference sequence*”). This is a permanently stored sequence in an approved, openly accessible public repository that can be used to fix the application of type-less names, in the same way that types are used to fix the application of conventionally typified names.

While allowing type-less names in narrowly prescribed circumstances (and using a description in the form of a DNA sequence to fix their application) may seem a radical departure from recent *Codes*, the option was available until as recently as 1987. Further, while the *Code* requires the designation of a holotype for any new name, many older names in current use lack a type (usually because none was designated in their protologues, or through loss), and nomenclature has not been seriously compromised by these. Indeed, the type-less names proposed here would be comparable with the diagnosis-based nomenclatural system of Linnaeus, except that many DNA sequences provide vastly more information than Linnaeus’s morphological diagnoses. Solving the problem of “dark” taxa—ones that can be discovered but not named under present rules—is a comparable modern challenge to that faced by Linnaeus. Some members of the Special-purpose Committee believe that allowing type-less names for these taxa provides an effective, workable solution to the problem, one that adheres to the fundamental *raison d’être* of the *Code*—the control of nomenclature and the ability to unambiguously fix the application of the names of taxa.

Limiting the scope of the proposed amendments

Of the previous proposals to amend the *Code* to allow DNA sequences as types, two (Hawksworth & al., 2016; Hawksworth, 2018) were limited to organisms treated as fungi and were unrestricted in application within that group (i.e. any fungus could be described using the provisions), while one (Renner, 2021) was open to all taxonomic groups and was unrestricted in its taxonomic application (thereby allowing even macroscopic organisms for which physical types are possible, such as vascular plants, to be typified solely on the basis of a DNA sequence).

The Committee discussed whether the proposed amendments should be restricted in some way, or unrestricted, and voted unanimously in favour of restricting the scope of the amendments (11 in favour, 1 abstention).

We then considered three potential ways to effect such a restriction: (1) restricting the provisions to certain taxonomic groups (such as fungi and algae); (2) restricting the provisions to certain circumstances (such as when, for technical reasons, it is impossible or not feasible in practice to preserve a specimen); or (3) restricting the provisions to certain taxonomic groups under certain circumstances (i.e. a combination of (1) and (2), such as restriction to

microfungi and microalgae when it is impossible or not feasible in practice to preserve a specimen).

After discussion, consensus was readily reached in favour of option (3)—to restrict the provisions to circumstances where preservation of a physical type (or preparation of a useful image) is not technically feasible *and* to always exclude vascular plants and bryophytes (which are always macroscopic and hence can always be typified) from the proposed new provisions. To clarify the circumstances, we propose a Note to be added, explaining that preservation of a specimen (Option 1) or typification (Option 2) is regarded as technically not feasible if and only if physical specimens, illustrations or cultures cannot reasonably be obtained using technologies available to an author at the time of publication. Preservation of a specimen or culture is not considered unfeasible if a 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. A justification for the infeasibility of obtaining a specimen is also required (see below).

The Committee also considered whether the provisions could apply to fossil organisms. The *Code* defines fossil-taxa as follows:

“1.2. A taxon (diatom taxa excepted) the name of which is based on a fossil type is a fossil-taxon. A fossil-taxon comprises the remains of one or more parts of the parent organism, or one or more of their life-history stages, in one or more preservational states, as indicated in the original or any subsequent description or diagnosis of the taxon (see also Art. 11.1 and 13.3).”

“13.3. For nomenclatural purposes, a name is treated as pertaining to a non-fossil taxon unless its type is fossil in origin (Art. 1.2). Fossil material is distinguished from non-fossil material by stratigraphic relations at the site of original occurrence. In cases of doubtful stratigraphic relations, and for all diatoms, provisions for non-fossil taxa apply.”

Note that taxa of diatoms, even ones known only from fossils, are treated as non-fossil for nomenclatural purposes, in line with long tradition in that taxonomic group (Greuter & Hawksworth, 1999).

The chemical stability of DNA means that “fossil” DNA (i.e. DNA of extinct organisms) is increasingly being sequenced from fossil and subfossil specimens. Given the restrictions discussed above, names based on such specimens would continue to be conventionally typified. However, the excellent preservation of DNA at low temperatures and anoxic environments also allows DNA to be sequenced from some fossil environmental samples such as permafrosts (e.g. Murchie & al., 2022). Therefore, taxa that are now extinct could, at least theoretically, be discovered and characterized using DNA sequences, and the provisions would allow such taxa to be named using relevant sequences.

Ensuring the quality of sequence-based nomenclature

A major concern of the Committee was a set of related issues around sequence quality and veracity. One issue was the lack of accepted and stable standards for the “taxonomic quality” of a sequence, including source (e.g. nuclear, plastid or mitochondrial), quality, length, informativeness, etc., and the difficulty of maintaining such standards in the face of rapid technological development (Thines & al., 2018; Thiele & al., 2023a). A second issue was that sequence-based nomenclature may be more susceptible than specimen-based nomenclature to taxonomic malpractice and even deliberate scientific fraud (such as by “correcting” or editing a sequence before uploading it to a repository; Thiele & al., 2023a). A

third issue relevant to environmental DNA sequencing is the possibility of hybrid and chimeric sequence assemblies.

A second, somewhat related, important issue concerned the management of names in genera that comprise a mix of sequenced and unsequenced taxa. If a sequence is detected in an environmental sample and assigned to such a genus, it may be difficult (though not impossible) to exclude the possibility that the sequence is from one of the unsequenced taxa: naming it on the basis of the sequence may therefore create a junior synonym. Unfettered sequence-based naming in such genera has the potential to create many such synonyms, necessitating subsequent work by more careful taxonomists to resolve the resultant mess.

The Committee concluded that all these important issues relate to the quality of taxonomic science, not nomenclature, and hence are best dealt with outside the rules of the *Code*, which deliberately deals only with matters of nomenclature (by providing the means to manage the establishment and application of names), not taxonomy. Nevertheless, the Committee was of the view that some mechanism for ensuring quality and veracity was needed. By unanimous vote, members decided that type-less names or names typified on a DNA sequence should only be validly publishable in a restricted set of qualifying journals, with the journals responsible, through normal peer-review and editorial processes, for ensuring that sequences are adequate and verified.

To effect this, the Committee proposes a set of Articles to empower the General Committee to maintain a list of specified journals in which, and only in which, DNA-based names can be effectively published.

Priority

The Committee considered the possibility that specimens, if obtained, should supersede DNA sequences as types (Option 1) or that typified names should be given priority over type-less names (Option 2, similar to the *Candidatus* names of prokaryotes; Parker & al., 2019). Relevant situations would be, for example, two names that were independently published, one with a DNA sequence and one with a specimen type, or a name published based on a sequence but with a specimen subsequently obtained. Ensuring the “superiority” of the conventional type method was regarded as desirable by some Committee members. However, in both these circumstances, the determination that the specimen and sequence comprise the same taxon necessarily indicates that the sequences are acting effectively to fix the application of their respective names, thereby obviating any need to replace them. Establishing a “two-tiered” system would in effect create a parallel nomenclatural system for sequence-based names under the *Code*. While this is one possible path forward (Zamora & al., 2018; Lücking & al., 2021), the Committee felt that priority should operate normally whether the names are sequence-based or specimen-based.

Attitudes of the Committee at the end of deliberations

The voluntary survey that was conducted when the Committee began its work was repeated after deliberations concluded, to assess shifts in overall attitudes towards the use of DNA sequences for fixing the application of names. Of the respondents ($n = 10$), 80% strongly believed or were inclined to believe that DNA sequences should be able to be used to fix the application of names, while 10% strongly believed or were inclined to believe that they should not, with 80% strongly or fairly committed to their view and 20% more neutral. A clear majority of members (70%) definitely intended

or indicated they were highly likely to vote in favour of one or other of the two sets of proposals, while 30% remained uncommitted. No responding member indicated that they were definitely or highly likely to vote against both proposals. Note that we chose not to ask which of the two sets of proposed amendments members favoured, because several members preferred to wait for community and sector discussions before opting for a preference.

There was a general shift in attitude by the conclusion of the Committee's work in favour of the use of DNA sequences for fixing the application of names, mainly resulting from those members who began the deliberations in a neutral frame of mind becoming more in favour and more committed.

Concluding remarks

The use of DNA sequences to typify names has divided the botanical and mycological communities in recent years, with enthusiastic supporters and resolute detractors of a sequence-based nomenclature. To date, all proposals for sequence-based names have been rejected.

At the beginning of its deliberations, the Committee established several important general principles (outlined in Thiele & al., 2023a), the most important of which was that opinions about the merits or otherwise of sequence-based *taxonomy* had no place in our discussions—the Committee's mandate was to explore the value or otherwise of sequences for fixing the application of *names* only. We believe this helped to set aside some differences between protagonists for either position.

Carefully restricting the Committee's proposals, to only circumstances where type specimens are impossible to obtain, also helped allay some concerns of those who were initially opposed to sequence-based names. The focus of the Committee became whether it was possible to solve a real and present problem, acknowledged by all Committee members—that many species can be detected and characterized by sequencing DNA from environmental samples but cannot be named under the *Code*.

Our first paper clarified the Committee's view that DNA sequences are more akin to descriptions than type specimens. Indeed, it may be that at least part of the opposition by some people to DNA typification stems from the (perhaps unconscious) belief that DNA typification would inherently violate core tenets of the *Code* as presently understood. Although the Committee is divided on how best to resolve this issue, we all agree that the adoption of a DNA-based nomenclature would represent a fundamental change to the *Code*, and our proposals are likely to be among the most important issues to consider at the XX International Botanical Congress.

With these considerations, the Committee was divided on how DNA-based nomenclature could best be reconciled with the *Code*, without compromising its integrity. Some felt that expanding the type concept to include DNA sequences was least disruptive, while others felt that preserving the conventional type method but relaxing the requirement for typification (by allowing some names to be type-less) offered a better way forward.

In either case, the Committee unanimously agrees that the *Code* cannot be a static document but rather needs to adapt over time. The problem facing those who can detect and characterize new taxa using DNA sequencing but not name them is a problem at the heart of taxonomy and nomenclature in the 21st century and was unimaginable until recently. Naming of sequence-based taxa outside the *Code* could lead to serious disruptions and throw taxonomy into confusion.

We believe that the Committee's proposals to amend the *Code* are moderate and workable, and we urge the botanical community to critically consider our deliberations and ensure the widest possible discussion so that an acceptable solution can be found to the problem for which the Committee was established.

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(329–338) Proposals to permit DNA sequences to serve as types of names in prescribed circumstances

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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* (Hawksworth & al. in *Taxon* 65: 899–900. 2016; Hawksworth & 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 (Hawksworth & 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 first of these options; an alternative set of proposals (Thiele & al. in *Taxon* 72: 1146–1148. 2023) deals with the second. 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 extending such a well-established and foundational principle as the type concept. Nevertheless, the Committee believes that the proposed amendments below (or the alternative proposals in Thiele & al. in *Taxon* 72: 1146–1148. 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.

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.