

(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.

(329) Amend Art. 8.1 as follows (new text in bold):

“8.1. The type (holotype, lectotype, or neotype) of a name of a species or infraspecific taxon is either a single specimen conserved in one herbarium or other collection or institution, or a published or unpublished illustration (but see Art. 8.5; see also Art. 40.4, 40.5, and Art. 40 Ex. 6); **a holotype may also be an effectively published DNA sequence (see Art. X.1).**”

This amendment expands the definition of types to include DNA sequences. Note that sequences may only be holotypes. Lectotypes and neotypes, by definition, cannot be sequences, because lectotypification and neotypification are only relevant for historical names that have been or will be typified by specimens (or illustrations), and Art. 40.5 as amended below restricts the use of DNA sequences as types to circumstances where conventional typification using specimens or illustrations is not technically feasible.

(330) Amend Art. 9.1 as follows (new text in bold, deleted text in strikethrough):

“9.1. A holotype of a name of a species or infraspecific taxon is the one specimen, ~~or~~ illustration (but see Art. 40.4), **or DNA sequence (see Art. X.1)** either (a) indicated by the author(s) as the nomenclatural type or (b) used by the author(s) when no type was indicated. As long as the holotype is extant, it fixes the application of the name concerned (but see Art. 9.15).”

(331) Amend Art. 9.9 as follows (new text in bold, deleted text in strikethrough):

“9.9. An epitype is a specimen, ~~or~~ illustration, **or (solely for names with a DNA sequence as a holotype) a DNA sequence.** An epitype is selected to serve as an interpretative type when the holotype, lectotype, or previously designated neotype, or all original material associated with a validly published name, is demonstrably ambiguous and cannot be critically identified for purposes of the precise application of the name to a taxon. Designation of an epitype is not effected unless the holotype, lectotype, or neotype that the epitype supports is explicitly cited (see Art. 9.20).”

Note that, if this proposal is adopted, only holotypes or epitypes may be DNA sequences, and epitypification using a DNA sequence would only be available for names originally typified using a DNA sequence (i.e. names that cannot be adequately typified using a specimen or illustration). In all other cases, an epitype would be a specimen (or illustration). The intent is to allow a further sequence to be used to epitypify a name typified with a DNA sequence that is subsequently found to be inadequate for unambiguously fixing the application of a name. DNA sequences cannot be used for lectotypification and DNA sequences cannot be isotypes, syntypes or paratypes, because, by definition, these kinds of types will always be specimens (and DNA typification is restricted to cases where specimens cannot be obtained). Similarly, neotypification is only relevant when an existing type specimen or illustration has been lost, so the replacement can and should be a specimen or illustration.

(332) Amend Art. 9.21 as follows (new text in bold):

“9.21. Designation of an epitype is not effected unless the herbarium, collection, or institution in which the epitype is conserved is specified or, if the epitype is a published illustration, a full and direct bibliographic reference (Art. 41.5) to it is provided **or, if the epitype is a DNA sequence, both (a) the identifier issued for the epitype sequence by an approved online repository (see App. X**

and Art. X.1) is cited, and (b) selected informative portions of the epitype sequence are specified.”

(333) Amend Art. 29.1 as follows (new text in bold):

“29.1. Publication **(with the exception of DNA sequences used for typification; see Art. X.1)** is effected, under this *Code*, by distribution of printed matter (through sale, exchange, or gift) to the general public or at least to scientific institutions with generally accessible libraries. Publication is also effected by distribution on or after 1 January 2012 of electronic material in Portable Document Format (PDF; see also Art. 29.3 and Rec. 29A.1) in an online publication with an International Standard Serial Number (ISSN) or an International Standard Book Number (ISBN).”

(334) Amend Art. 38.1 and 39.2 as follows (new text in bold) and add a new Note after Art. 38.1:

“38.1. In order to be validly published, a name of a new taxon (see Art. 6.9) must (a) be accompanied by a description or diagnosis of the taxon (see also Art. 38.7 and 38.8) or, if none is provided in the protologue, by a reference (see Art. 38.13) to a previously and effectively published description or diagnosis (except as provided in Art. 13.4, **39.2(b)**, and H.9; see also Art. 14.9 and 14.14); and (b) comply with the relevant provisions of Art. 32–45 and F.4–F.5.”

“*Note Ibis.* For the purposes of Art. 38.1, if the type of a name of a new taxon is a DNA sequence, the sequence itself is treated as a description or diagnosis.”

“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 holotype sequence by an approved online repository (see Art. X.1(b)(1) and App. X) and (2) specification of selected informative portions of the holotype sequence (Art. X.1(b)(2)).**”

These amendments allow a DNA sequence to act as a description in cases where no other descriptive information is possible.

(335) Amend Art. 40.5 (new text in bold) and add a new Note as follows:

“40.5. For the purpose of Art. 40.1, the type of a name of a new species or infraspecific taxon of microscopic algae or microfungi (fossils excepted: see Art. 8.5) may be an effectively published illustration **or, on or after 1 January 2026, a DNA sequence**, if there are technical difficulties of specimen preservation or if it is impossible to preserve a specimen that would show the features attributed to the taxon by the author of the name.”

“*Note x.* For the purposes of Art. 40.5, preservation of a specimen is regarded as technically unfeasible if and only if physical specimens or cultures cannot reasonably be obtained using technologies available at the time of publication. Preservation of a specimen is not considered unfeasible if a type specimen could not be obtained merely for reasons of inconvenience, lack of access, or if a specimen was lost or otherwise not collected when it could have been.”

The intent of this amendment and Note is to restrict the scope of DNA typification to only cases where conventional typification using specimens is not technically feasible, in order to be minimally disruptive to established conventional practice for macroscopic organisms that can be conventionally typified. Note that, in some or

many cases, the addition of DNA sequences to protologues for macroscopic organisms may be highly desirable, but these will act as descriptive or diagnostic information rather than as types.

(336) Add the following new Articles in Chapter V Section 2 after Art. 40.5, as follows:

“X.1. In order to be validly published with a DNA sequence as type (see Art. 40.5), a name must (a) be published in an approved journal (see App. Y, Art. X.2(b)) and (b) be accompanied in the protologue by (1) citation of the identifier issued for the type sequence by an approved online repository (see App. X and Art. X.2(a)), (2) specification of selected informative portions of the type 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.2. 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. 9.21(a) and X.1(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 and X.2 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. For example, this provision removes the need to prescribe in the *Code* the properties of DNA sequences (such as source, length, etc.) needed to meet quality requirements for typification, leaving such matters, in effect, to the editors and peer reviewers of these designated journals (chosen and managed by the General Committee as specified in Art. X.2). The Special-purpose Committee felt that quality assurance is a scientific issue and is 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 (X.1(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 (X.1(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.

(337) 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 its holotype is a DNA sequence and it meets the requirements of Art. X.1.**”

(338) 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 DNA sequences as types (Art. X.1 and X.2).** 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.1(b)(2), (3) and (4).

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