

Mycologists' newest unsuccessful effort towards permitting DNA sequences as the nomenclatural types

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In the just ended 12th International Mycological Conference (IMC12) in Maastricht, Netherlands, three proposals related to naming fungal taxa with DNA sequences were all not approved by the vote in 15th August, 2024. These proposals include *F-005* – Allow the naming of fungi from DNA sequences as types; *F-006* – Allow genomic sequences to serve as types of names of organisms treated as fungi; and *F-007* – Add a recommendation on the designation of fungal organisms only known from DNA sequence data. In brief, *F-005* and *F-006* are straightforward to allow DNA sequences and more strictly genomic sequences, respectively, as the nomenclatural types to name fungi, while *F-007* hopes to compromise a way to permit invalidly naming fungi with DNA sequences as the nomenclatural types, in case that *F-005* and *F-006* were rejected. Although the reasons for not approving these proposals are different, this negative vote result from all offline voluntary participants is not surprising, since the guiding vote has indicated similar opinions from the Nomenclature Committee for Fungi and the International Commission on the Taxonomy of Fungi.¹ Moreover, the related proposals were also not approved by the 20th International Botanical Congress in Madrid, Spain convened a couple of weeks prior to the IMC12.

Back to the beginning of taxonomy using binomial nomenclature as a

system in 1753, represented by Linnaeus's publication *Species Plantarum*, it has always asked for physical materials as the nomenclatural types to name fungal taxa. This rule never raised a question, until recently advanced DNA sequencing technology has revealed more and more unnamed and uncultured fungi from environmental samples. Due to lack of available physical materials, such fungi known only from DNA sequences, viz. fungal dark taxa (FDT), cannot be formally named following the International Code of Nomenclature for algae, fungi, and plants (ICNafp). This phenomenon, to some extent, blocks one of the most important aims of fungal taxonomy that is to facilitate convenient scientific communications. Therefore, to name FDT, some mycologists intended to amend the ICNafp to permit DNA sequences as the nomenclatural types.

After comprehensive and wide discussions year by year as well as previous rejections of related proposals, for the first time by the 19th International Botanical Congress in Shenzhen, China in 2017, it seems that almost all fungal taxonomists realize the necessity of naming FDT; nevertheless, it still concerns mycologists on how to amend the ICNafp to achieve this necessity.² The core issue is to set the standard of the DNA sequences as nomenclatural types. Due to the extremely high species number and diverse

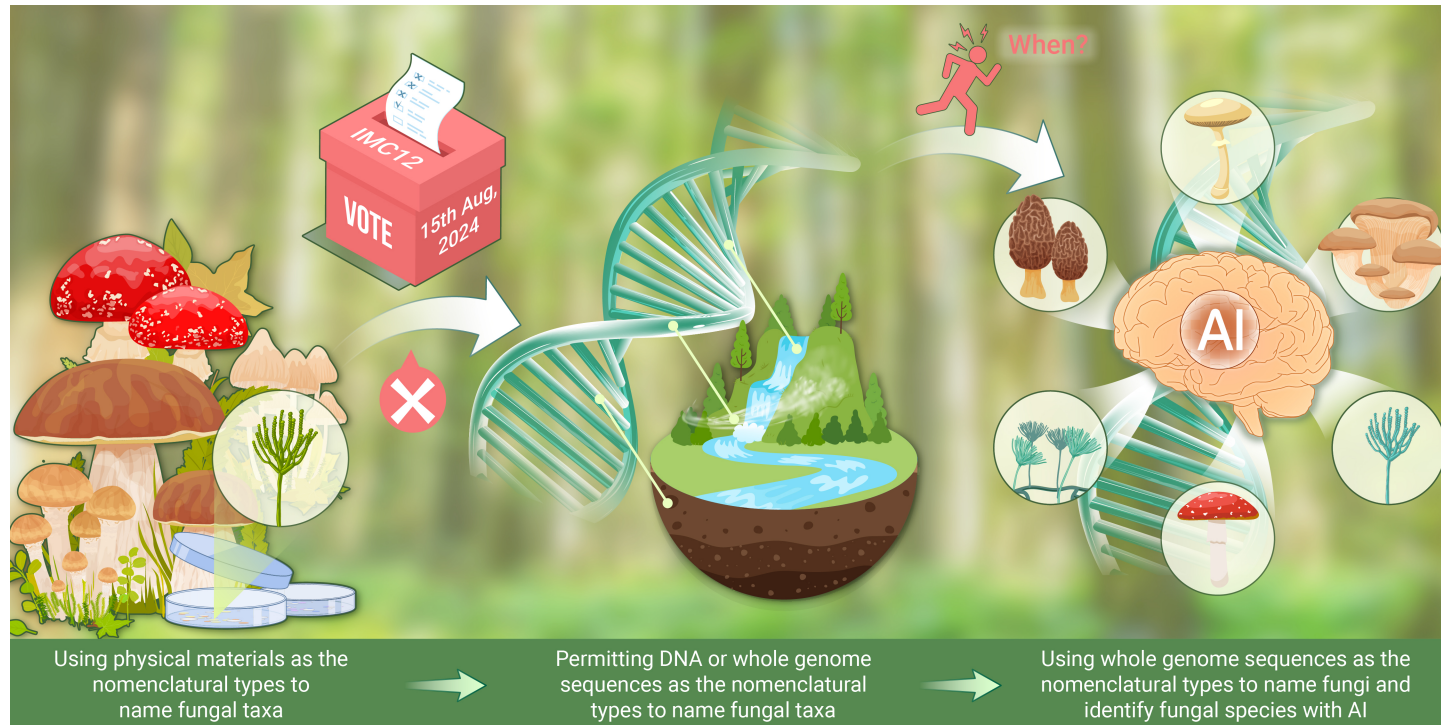


Figure 1. Perspective for prospering the discipline of fungal taxonomy with the technology advancement.

groups of fungi, it is impossible to find a single, or even several, barcoding genes to delimit all fungal species. So, what barcoding genes should be used as nomenclatural types to name FDT is a tough choice. In terms of using whole genome sequences as nomenclatural types, the resolution is high enough to delimit fungal species, but the economic and technological

requirement of sequencing and assembling whole genomes from environmental samples is much higher than using barcoding sequences. This requirement restricts the wide application of whole genome sequences in some labs at the moment, although in our opinion it will be solved very soon with the further advancement of sequencing technology. More intractably,

there are innumerable type specimens deposited in herbaria and fungaria tens or even hundreds of years ago, and it is difficult, if possible, to generate high-quality barcoding sequences and whole genome sequences from these species even with the help of epitypification. Then, there is not a reliable way to judge whether the barcoding sequences and/or whole genome sequences result really from new fungal taxa rather than from previously named but unsequenced species without comparable morphological and other characteristics. For the above-mentioned concerns, no feasible solution is available now, which is postulated as the main reason for rejecting the three proposals.

It is noteworthy that the similar situation of FDT also exists for additional microbial groups. For example, after that the International Committee on Systematics of Prokaryotes has rejected the amendment of the International Code of Nomenclature of Prokaryotes for naming microorganisms with DNA sequences as the nomenclatural types, an independent code, viz. SeqCode was initiated, which permits the whole-genome sequences as the nomenclatural types for prokaryotes regardless of cultivability.³ Although the SeqCode is supported by many microbiologists and goes well now, it also faces several concerns similar to the proposals naming FDT to be solved.⁴ Therefore, it is too early to evaluate the contribution of the SeqCode to the microbial taxonomy. Moreover, in a negative light, the initiation of the SeqCode indeed splits the community of microbiology and taxonomy to some extent. Given above, we suggest that fungal taxonomists, instead of initiating an independent code, should try to solve the concerns about naming FDT with DNA sequences as the nomenclatural types. Until then, the related proposals will come naturally to be approved.

We believe in and would love to see whole genome sequences as the nomenclatural types for FDT or even all fungi happening in the future. However, this is not the only crucial issue for making fungal taxonomy moving forward. In the new era of artificial intelligence (AI), all fungal taxonomists are encouraged to cooperate with AI experts to achieve identifying and delimiting fungal species automatically based on DNA sequences.

This achievement will help to recognize innumerable unnamed fungi in a reasonable time, and thus facilitate to utilize and conserve these fungal resources (Figure 1).⁵

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DECLARATION OF INTERESTS

The authors declare no competing interests.