

POINT OF VIEW

Epitypes are forever: Best practices for an increasingly misused nomenclatural action

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■ INTRODUCTION

The application of names based on nomenclatural types has long been a fundamental principle of botanical nomenclature. This practice, that the name of a taxon is permanently attached to a single element, has fostered stability, reliability, and repeatability that are essential to research on, and communication about, algae, fungi, and plants. In the minds of many, the type of a name takes on an almost mythical status. It is often thought of as an ideal representative of the taxon, one that is well-preserved, that has complete provenance data, that displays all of the critical phenotypic characters, and that is composed of ample material for future study. Yet, the above is rarely the case. Many names were described centuries ago from incomplete or fragmentary material, or material that has become damaged over time. Often a taxon is described from limited material when it is first recognized as distinct, and it is the formal recognition that results in targeted efforts to fully characterize its variation. Not infrequently this results in the discovery that the taxon has a wide range of variation, in which the type may lie at one extreme. This reality, that the type specimen may not necessarily be representative of the taxon whose name it defines, is explicitly recognized by Art. 7.2 of the *Code* (Turland & al., 2018).

Regardless of the underlying causes, in practice, names are often applied based on types in which some critical characters are lacking or poorly preserved. There are even instances in which a name cannot be applied with certainty based on its type. For instance, a type could be identified as belonging to a given species, but when divided into infraspecific taxa the type may not necessarily be identifiable with certainty as belonging to any particular intraspecific taxon. Or a name could be found to be based solely on a centuries-old illustration that does not display the critical characters required to distinguish between several closely related taxa as presently delimited. In such cases, the *Code* allows for the existing type to be supported by an epitype (Art. 9.9). Specifically, an epitype is to be designated when the type it supports is “demonstrably ambiguous and cannot be critically identified for purposes of the precise application of the name to a taxon”.

Based on the above, one may infer that the application of names based on non-ideal types is routine and epitypification

is an unusual, perhaps even extreme measure. However, during the last decade, epitypification has become commonplace, often used in situations that do not meet the criteria outlined in Art. 9.9 of the *Code*. Some authors have advocated epitypification as a means to circumvent detailed and careful study of type specimens (Ariyawansa & al., 2014). In some instances, epitypification has resulted in unfortunate and unforeseen name changes (Mosyakin & McNeill, 2018).

In my opinion, the widespread use of epitypification stems from a fundamental misconception that epitypes supplement the existing type and merely aid in interpretation. This was my belief when I designated an epitype for *Lecanora thelococcoides* Nyl. (Lendemer, 2004). As a nomenclature editor for TAXON, I have found that belief to be similarly widespread. Many also believe that if an epitype is found not to be conspecific with the type it supports, then the epitype can be superseded. Or if the original type is shown to be unambiguous, then the epitype can be overturned. These beliefs are incorrect. Once an epitype is designated it can only be displaced through conservation, or if the type it supports is shown not to be the type of the name (Art. 9.20 & Note 8).

At present, epitypes are often designated in instances that do not meet the standard of demonstrable ambiguity outlined in the *Code*. They are also designated based on the incorrect belief that they can be easily superseded or overturned. Given these factors and the implications that epitypification can have on the application names, I propose the best practices outlined below. These guidelines were inspired by discussion of this issue in the mycological community (e.g., Hyde & Zhang, 2008; Ariyawansa & al., 2014; Jørgensen, 2014), but are intended to apply to any one working on organisms covered by the *ICN*.

■ PROPOSED BEST PRACTICES

- (1) Epitypification should be viewed as an extreme measure, carried out only in the unusual situation that the type of a currently applied name cannot be identified with certainty, preventing the unambiguous application of the name.
- (2) Absence or poor preservation of selected diagnostic characters, ambiguous provenance data, and/or absence of

molecular data should not be considered *a priori* to mean the type is demonstrably ambiguous and that the name cannot be applied with certainty.

- (3) An explicit statement should accompany the designation of an epitype that the current nomenclatural type the epitype supports is “demonstrably ambiguous”.
- (4) An explanation of why the name cannot be applied based on the existing type should be provided (e.g., what diagnostic character is not present in the type, or that geographic provenance is unknown in a circumstance in which the name must be applied to one of a number of allopatric cryptic species).
- (5) When choosing an epitype, preference should be given to recently collected material from the type locality. If material from the type locality is not available, then preference should be given to material from as geographically close to the type locality as is practicable.
- (6) Authors should avoid choosing an epitype that differs substantially in ecology or geographic provenance from the type it supports, even if the two agree phenotypically (e.g., regardless of phenotypic characters, a name for a lichen based on saxicolous material from Sweden should not be epitypified using corticolous material from Brazil).
- (7) An explicit statement should accompany the designation of an epitype that the epitype represents the same taxon as that to which the name is currently applied, and the statement should be supported by citation of specific characters or other critical information.

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