

NOMENCLATURE

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Notes on the new Example 9 in Article 9.8 of the *International Code of Nomenclature for algae, fungi, and plants*

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Examples are the most important guide to the application of the rules in the *International Code of Nomenclature*, so it is important that they are exact and well chosen. In the new *Melbourne Code* (McNeill & al., 2012) there is under Art. 9.8 a new example (Ex. 9) which needs further comment as it is not a good example of how to operate. It concerns how to epitypify a name. Epitypes are a rather recent improvement of the *ICN*, a chosen representative specimen which makes possible an exact interpretation of a type specimen which “is demonstrably ambiguous and cannot be critically identified ...”

The intent of the new example is apparently to show—on the basis of the lichen name *Lichen saxatilis* L. (\equiv *Parmelia saxatilis* (L.) Ach.)—that it also is allowed to epitypify when molecular evidence is needed for exact interpretation of a type, in itself a reasonable move. The example, however, does in my opinion not demonstrate this, and indirectly recommends a practice which I am sceptical of and believe is contrary to sound practice when selecting types reflected in Rec. 9A of the *ICN* (for other kinds of designated types).

Let me start with an inaccuracy in the text of the example which is important in this connection: “No molecular sequence could be obtained from the type ...” It goes on referring to a paper by Molina & al. (2004) where a molecularly characterized epitype has been chosen. When consulting this paper, I found that the authors write that “molecular data are not available for the type”, which is a different thing. I interpret the authors as assuming that it would be pointless to try to get molecular data from such an old specimen, which was the general view at that time. As we now know, it is possible with special techniques and under lucky circumstances to get molecular data also from very old specimens (Hawksworth, 2013).

The apparent problem here, to which there is no answer in the *ICN*, is what *demonstrably* means in these circumstances. My claim is that the authors have not *demonstrated* that the lectotype cannot be molecularly defined, which in my opinion is required as the text is formulated now. A reformulation may be necessary to cover the example.

Furthermore Molina & al.’s (2004) epitype selection is far from recommendable, even if Rec. 9A does not cover epitypes.

Molina & al. (2004) used the only specimen from Sweden in their study to establish an epitype. This specimen was from Umeå in northern Sweden from where the Linnaean lectotype most likely does not originate as it has no *Flora lapponica* numbers, only those of *Flora suecica* and *Species plantarum* (see Jørgensen & al., 1994). A study of the molecular variation of the variable *Parmelia saxatilis* in Sweden (Thell & al., 2011) would have been a better basis to understand the lectotype prior to epitypification. The lectotype of *Lichen saxatilis* was likely collected from the Uppsala area, a region from which it would have been easy to obtain fresh material for molecular analysis. Furthermore the authors did not argue that the lectotype is threatening the current use of the name *Parmelia saxatilis*.

An exemplary way of integrating molecular analysis into epitype selection is found in Kadereit & al. (2013) who epitypified *Salicornia europaea* L. on a specimen from the type locality, one which they also characterized molecularly in a comprehensive molecular study of the group in the region. But even Kadereit & al. did not demonstrate that it is impossible to get molecular data from the lectotype.

There appears therefore to be a need to discuss what *demonstrably* means in the days of molecular evidence, since it will undoubtedly be difficult to get molecules out of old specimens without new techniques. Is it really necessary to test material from old specimens in every case? I believe not, since it would destroy them in the long run. It would be much better to follow the authors cited above: find a modern specimen of the taxon and analyse it molecularly. I suggest that a more suitable formulation of the Art. 9.8 is found, and I hope my note will stimulate a discussion on the topic ahead of the next congress. The question of epitypifying in relation to molecular methods is not solved by the present example, which I find confusing!

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