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Opinion

Do we need Epitypes in Zoology?

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According to the International Code of Nomenclature for algae, fungi, and plants (McNeill et al. 2012) paragraph 9.7, "An epitype is a specimen or illustration 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 of a taxon. When an epitype is designated, the holotype, lectotype, or neotype that the epitype supports must be explicitly cited (see Art. 9.18)". In botany sensu lato, the use of epitypes thus is an immediate measure to supplement, but not replace, old types with new and better information content. Of course, there is some debate about when it is appropriate to designate an epitype, but in principle epitypes are considered useful for example in fungal research (e.g. Hyde & Zhang 2008, Ariyawansa et al. 2014). Surprisingly, there seems to be little public demand for epitypes in zoology. Bouchet & Strong (2010) already emphasized that all global molluscan species names in current use ideally should be compiled into an approved list and be backed by name-bearing types that are informative in the light of modern morphological and molecular research. If types were lost, neotypes should be designated. If types were still existing but not sufficiently informative to unambiguously characterize a species, an epitype could be designated. Since most molluscan species names are based on shells alone, thousands of neotypes and epitypes would have to be established just for molluscs. Bouchet & Strong (2010) concluded that there is not enough (wo)manpower for such an iconic task. Yet, we think it could be beneficial, possible and timely to start with routinely designating neotypes and with establishing epitypes in zoology.

Zoological taxonomy has become integrative and molecular data do play a constantly growing role. In an ideal world, morphology-based species descriptions all are detailed, accurate and comprehensive; name-bearing types and perhaps secondary types are available in public collections for comparison and supplementary genetic study; and original collecting data allow for recollecting more material from the type locality. However, in the real world, things are less perfect and more complicated. Correct species re-identification and species discovery are, among others, commonly hampered by severely deficient original descriptions, unexplored ranges of morphological variation, unknown or destroyed type localities, and non-existing, lost or missing type material. Existing historical type specimens, if not damaged, may provide character-rich exoskeletons in arthropods, and dried tissues, for example in insects and plants, preserve DNA quite nicely for many decades, if stored properly. In contrast, many non-arthropods do not provide exoskeletons at all or, as in molluscs, even perfectly preserved and healthy shells may not necessarily be character-rich. Generally, wet-preserved museum specimens are in high risk of becoming damaged, chemically altered, dry or rotten and DNA tends to degrade rapidly in watery liquids. Old types thus suffered and were finally discarded especially in soft-bodied groups such as sea slugs, in which massive and partly cryptic species diversity has been recently discovered (e.g. Jörger et al. 2012, Padula et al. 2016). There have always been unofficial opinions that even worse than lost types do types that still exist but are damaged or not informative, such as empty shells or formalin-preserved tissue not suitable for molecular barcoding.

What will, for example, some remaining tiny distorted or broken pteropod type shells tell us about the newly discovered species diversity of these organisms threatened by acification of the world oceans? How can we reasonably relate newly collected European land slugs with perhaps hundreds of available historical names connected to some more or less colourless, amorphous, dried or otherwise damaged remainders of type material? If types were definitely lost, we could argue for recollecting material from type localities and designating carefully preserved and studied neotypes for each and every dubious or cryptic species, although neotype designation is not recommended as a standard procedure by the Code of Zoological Nomenclature (ICZN 2000). But what to do, if types, or remainders thereof, still exist? Isn't it sometimes appealing to think of making a clear cut and more or less literally throwing away any existing but obviously meaningless type material?

There are of course many reasons to disagree with formally or physically "getting old and meaningless stuff and its historical burden out of the way" to establish new types that are suitable for genetic analyses, even from a purely pragmatic perspective. First, many

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of the available types, even tiny empty shells, may bear traces of DNA. These are not useful for standard PCR approaches. But the newly developing field of museomics, applying “next generation” sequencing techniques to museum specimens (Prosser et al. 2015), soon may help in many cases, at affordable expenses. Enormous quantities of short sequence fragments are generated, possibly also from formalin-fixed or long-time preserved material, with high throughput platforms such as Illumina. Sequences from many species can be handled simultaneously (tagged and multiplexed) and are assembled using bioinformatics software. The most modern systems already can sequence single DNA molecules. Another reason against establishing a new set of types, when old material still exists, is that further, completely unknown analytical techniques may be developed during the next decades. Maybe shells, tissues, proteins or other biological material will then just be scanned routinely by a whatsoever beam and IDs will be provided instantaneously? What a loss, if we really had ignored, dismissed or destroyed any remaining museum type material by then! However, in the nearer future, many problematic cases will remain without any genetic or other relevant information available from types, and thus connected to uncertainty regarding later re-identification of species. We think we badly need a simple and non-destructive yet effective way of adapting zoological nomenclature and practical taxonomy to the molecular age right now.

Why reinventing the wheel? We may just do in Zoology, what botanists and mycologists already have successfully and reasonably done for decades and designate epitypes, providing essential and relevant information on top of normal primary types whenever needed or beneficial! There is no such official category in current Zoological Nomenclature, though its establishment should be encouraged. In the meantime, researchers and curators already could simply call, use, and publish “epitypes” unofficially, similar to “topotypes” and some other non-official but for certain purposes useful categories, which still are in practical use in museums. We would regard the immediate use of zoological epitypes as a timely preadaptation to improved nomenclatural rules to come. Since epitypes in our understanding are not themselves name-bearing, but a supplement to primary types, we see no direct danger for nomenclatural stability at all. Just the opposite, newly designated epitypes provide best possible data and transparency for long-term securing nomenclatural stability as well as the potential to be revised if better information, for example more conclusive data from the primary type, becomes available.

An epitype in Zoology should provide additional morphological, anatomical, perhaps biochemical and whatever other relevant information – and, of course, should allow for easy sequencing, if possible; there may be some exceptions, e. g. deep sea specimens usually die and partly decompose before they can be fixed and adequately preserved. “DNA-types” as proposed by Jörger & Schrödl (2013) thus could be a special kind of usual type categories (such as “DNA-holotype”) or of epitypes. DNA should be extracted from DNA-epitypes and, if somehow possible, be permanently stored deep-frozen in a public repository such as the DNA bank (link). In the future, information from original types and epitypes may be compared and taxonomy be adjusted, but in the meantime epitypes provide better information, more taxonomic transparency and a more stable nomenclature. In addition, we argue for more deliberate designation of neotypes, i. e. designation of neotypes should be standard practice in the framework of taxonomic revisions, even if there is no immediate necessity, but a clear benefit for long-term stabilizing the taxonomy and nomenclature of a certain group. Again, as for epitypes, neotypes should be selected to provide good-quality DNA that should be stored in special repositories.

In an ideal world, editors of museum journals do not write essays about how to best “ignore” or “circumvent” some existing type material or how to push nomenclatural rules, as some might see it. But taxonomy has become much more powerful by incorporating molecular methods. Accordingly, museums now are required to do more than merely preserving and storing morphological types, and codes of nomenclature tailored to the pre-molecular age need to adopt modern technical possibilities and requirements of the society. In times of global change and biodiversity crisis, zoological taxonomy as a whole needs to be transformed to become more efficient. There may be several ways to reach this goal and it should be allowed to propose and discuss them openly.

In summary, for all species lacking types, we recommend standard designation of neotypes, following reasonable practices of taxonomic revisions and selecting material suitable for sequencing. This will help to get rid of cases of centenary taxonomic uncertainty, without sacrificing our taxonomic heritage or stability. In species with types still existing but damaged, incomplete regarding relevant features or not suitable for sequencing or other taxonomically important analyses, we think that the designation of epitypes would be beneficial. This practice would go along with reliable and published vouchers, additional information and thus better taxonomic decisions. Epitypes may be really charming. As non-name-bearing types, formal danger from epitypes to nomenclatural stability is minimal. On the other hand, an epitype can (and perhaps should) be more than a DNA voucher: providing essential taxonomic information it may become a de facto substitute for true type material in the age of molecular and high-tech taxonomy – but still remains testable and adjustable later.

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