Opinion

DNA taxonomy '2.0'

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Tautz et al. (2002) claimed that DNA taxonomy offers a reliable tool for species identification and description. The former is broadly accepted and applied in the Barcoding endeavour, having generated millions of barcodes worldwide. The latter, basing species descriptions on molecular characters, has since led a shadowy existence, with few cautious attempts published. Apparently, it has remained a paradigm for metazoan taxonomy that "DNA sequences alone are not sufficient to characterize a species (…)" (Tautz et al. 2002). This attitude may have helped protecting the well-established morphology-based taxonomic system from erosion, but it has also ignored the diagnostic value of molecular data and impeded recognition of morphologically cryptic species.

Jörger & Schrödl (2013) demonstrated that molecularly delimited cryptic sea slug species can be formally described and named based entirely on diagnostic nucleotides without violating the International Code of Zoological Nomenclature or long-standing taxonomic practice. The advances towards establishing a practical standard for DNA taxonomy include robust and testable diagnoses, deposited vouchers, and a new category of name-bearing type material ('DNA-types' of extracted DNA). This showcasing of DNA taxonomy bridges the gap between molecular species delineation (i. e. discovery as 'candidate species', 'molecular taxonomic units' etc.) and their formal recognition as named species, and therefore as testable hypotheses as well.

Nevertheless, in our opinion the paradigm remains essentially justified: species descriptions, even those based predominately on molecular characters, should always include phenotype information at a feasible level in order to stay connected to the taxonomic history and to provide necessary information for other disciplines and future research. Inspired by Tautz et al. (2003), this is a plea for drawing on the unique diagnostic potential of molecular characters for modern species descriptions, but without losing the power of morphology (or other informative character sets). After 10 years, DNA taxonomy '2.0' has matured into a valuable component of an integrative taxonomic framework, enabling a more realistic view on global biodiversity.

References

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