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OPINION

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DNA barcodes on their own are not enough to describe a species

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INTRODUCTION

Earth's biodiversity is still so poorly known that only about two million (Bánki et al., 2021) of the estimated nine million or more eukaryotic species (Larsen et al., 2017; Mora et al., 2011) have been described. This puts taxonomists in a race against time to discover biodiversity before it is lost as a result of the Anthropocene mass extinction. Each species description is the result of an often long and time-consuming process that has involved collecting specimens, processing them, discovering their correct place in the tree of life and describing the species and its diagnostic characters from other related species. Currently, about 18,000 species are described each year, which means that species are going extinct at least as fast as they are named (Ceballos et al., 2015; De Vos et al., 2015; Zamani et al., 2021). This 'taxonomic impediment' has been recognized as a serious problem (de Carvalho et al., 2007) and has led to several proposed solutions (e.g., Engel et al., 2021; Rodman & Cody, 2003).

In response to the slow and often cumbersome process of describing species, Meierotto et al. (2019) proposed what they later named a 'minimalist' approach. They named 18 new species of Costa Rican braconid wasps based almost solely on their consensus COI barcodes while neglecting to give differential diagnoses to those already described species in the same genera that lacked barcodes. This approach was criticized by Zamani et al. (2021), shortly before Sharkey, Janzen, et al. (2021) named 403 braconid species in the same way while also responding to the criticism. Later, Sharkey, Brown, et al. (2021) published a more detailed response in which they defended their approach. The 'minimalist' approach has also been recently criticized or commented on by Ahrens et al. (2021), Engel et al. (2021), Fernandez-Triana (2021) and Meier et al. (2021).

In this article, we continue this discussion by responding to Sharkey, Brown, et al. (2021). We summarize the main points of concern raised by us (and others) regarding the 'minimalist' approach, expand on some points discussed earlier and explain why we think morphology should remain an integral part of species descriptions. To be clear, we oppose the view of Meierotto et al. (2019) and Sharkey, Janzen, et al. (2021) on DNA barcoding as the only source of information for species *delimitation* and *description* purposes, and not as a valuable tool in an initial survey of biodiversity.

COI BARCODES ARE NOT SUITABLE ON THEIR OWN

The default assumption of Sharkey, Janzen, et al. (2021) is that COI barcode clusters (Barcode Index Numbers [or BINs] computed by BOLD systems) equate to species. This assumption has been heavily criticized, especially by Meier et al. (2021), who pointed out that the algorithm by which BOLD systems groups DNA barcodes is not public; no one else can reproduce the results or assess their reliability. Moreover, the results are not stable. Meier et al. (2021) reanalysed the publicly available data of Sharkey, Janzen, et al. (2021) and found that many of the barcode clusters changed when more data were added. In their opinion, the minimalist approach risked replacing a 'dark taxonomic impediment' (species have not been named) with a 'superficial taxonomic impediment' (species are so poorly and unreliably named, they will need to be redescribed before they can be used).

Sharkey, Brown, et al. (2021) have defended their approach by stating that they do not simply assign names to barcode clusters. Whenever a BIN obviously consists of more than one species, they provide additional morphological or rearing data that differentiate the species. While this is true, it remains the case that most of the species were based solely on the BIN to which they belong. Sharkey et al. also argue that many (morphologically) cryptic species cannot be told apart by anything other than their barcode. There is some truth to this latter argument, and in these cases, a barcodes-only *diagnosis* could be acceptable. However, in our opinion, this should always be justified case by case instead of adopting barcodes-only as the default criterion. An attempt to distinguish cryptic species morphologically should be made, and morphological diagnostic characters should be given, which identify the species complex, if not each individual species in it.

We have little to add to the thorough analysis of Meier et al. (2021), except to emphasize the fact that many of Sharkey, Janzen, et al.'s (2021) species are based solely on *consensus* barcodes. These refer to a character state that does not exist – it is the consensus sequence of an unspecified number of individuals (presumably also the holotype) – and as such does not have real existence, nor can it be used by itself to diagnose unknown specimens. Stating the barcode of the holotype (over or in addition to the consensus barcode) would, in our opinion, have been preferable, even if not sufficient.

DO WE NEED CODE-COMPLIANT NAMES IN CONSERVATION?

One of the main arguments made by Sharkey, Janzen, et al. (2021) for their approach is based on conservation efforts: 'Applied users of biodiversity information (conservation biologists, ecologists) do not need to know how many notopleural setae a fly has; however, they need to identify specimens, know which species are present in a given area and where else a given species might occur'.

While it is true that there is an urgent need to speed up species discovery, the idea that conservation efforts *need* pronounceable, code-compliant names has been challenged (e.g., Meier et al., 2021). The morphospecies concept has been used for centuries to generate biodiversity inventories. If the only thing needed is raw numbers of species, 'genospecies' and BINs work just fine and do not compromise taxonomy. Any conservation purpose that the minimalist approach is supposed to achieve can be reached without undermining integrative taxonomy and without producing code-compliant names.

We would also emphasize that taxonomy done for its own sake, to its own high standards, both fulfils its mission to document and understand the historical context of species diversity and makes species identifiable. There is no need to treat taxonomy as solely existing for the needs of the end-users, as we do not treat astronomy with the sole purpose of launching rockets into space. Even if sacrificing taxonomic rigour did result in faster species discovery and better conservation results, we should at the very least thoroughly consider if the sacrifice—to whatever degree—is worth the price, before doing so.

AN ELITIST APPROACH

Zamani et al. (2021) argued that the minimalist approach risks hindering taxonomy in developing countries, due to DNA barcoding often not being feasible there. Ahrens et al. (2021) and Fernandez-Triana (2021) also raised concerns about the cost and availability of DNA barcoding. Proponents of the minimalist approach (Meierotto et al., 2019; Sharkey, Brown, et al., 2021; Sharkey, Janzen, et al., 2021) argue that DNA-barcoding is becoming cheaper, and technological developments will make it more accessible. We claim that the minimalist approach is elitist in several ways, and that this elitism would slow down the rate of species description by excluding a significant portion of current and future taxonomists.

First of all, barcode-based descriptions without any morphological treatment require the employment of a barcode every time, for every specimen, in every sampled area. If only the COI barcode is available, every specimen collected in a given area needs to be sequenced merely to be identified and sorted – a process that must be done every time a new locality is sampled. To put the situation in perspective, Aguiar and Santos (2010) have collected more than 7000 specimens of Cryptinae (Ichneumonidae) in Brazil. If all these species of Cryptinae of Brazil were diagnosed based solely on DNA barcodes without any morphological context, then even if the price of barcoding were low (USD$1 per specimen), it would take $7000 simply to identify all of the specimens collected in the two forests. Hopkins et al. (2019) collected more than 100,000 parasitoid wasps in the tropical forest of Uganda, most of which are still unprocessed and unpublished. Do we need to barcode them all to estimate the diversity? If that is the case and since barcodes are not available for the existing species, then more than $100,000 should be spent simply to discover for example, that 456 specimens of these belonged to Rhyssinae, that six species of this subfamily are present in Uganda (Hopkins et al., 2019) and that two of those species were new to science.

With these numbers at hand, it is extremely difficult to accept the idea that the barcode by itself is truly money-saving. Only those with funding and/or laboratory facilities would be able to find out if their specimens belong to new species or not. Taxonomy would become a preserve of the elite, mainly established, large-scale research projects based in high-income countries. Not only is this unfair and against the principles of the Access and Benefits Sharing and Nagoya protocols, in the long run, it would slow down the rate of species descriptions, due to the fact that there are fewer people doing the descriptions.

There is a second point that renders the minimalist approach elitist, and it goes beyond political boundaries: the total elimination of non-professional taxonomists. According to Fontaine et al. (2012), 60% of the new species in Europe are described by non-professional taxonomists. These taxonomists do not focus only on charismatic species; their descriptions have represented 52.7% of the dipteran species, 26.7% of the mite species and roughly 50% of Hymenoptera. As Fontaine et al. (2012) mentioned, non-professionals are also needed to put names on species identified with molecular techniques. However, despite their invaluable work, they do not have direct access to molecular techniques due to the expenses involved and/or the lack of expertise in analysing sequence data. Therefore, eliminating the morphological approach for a barcode-only practice would alienate an entire group of invaluable experts from the taxonomic discipline and thus reduce our capacity to describe a majority of new species and produce valuable taxonomic treatments. In this way, the barcode-only approach would become detrimental specifically for the purpose that Sharkey, Brown, et al. (2021) keep mentioning, which is describing species before it is too late.

We also feel that Sharkey, Brown, et al. (2021), in their implementation of the minimalist approach, missed an opportunity to facilitate taxonomy in collaboration with Costa Rican biodiversity scientists. They could have scattered part of their (para)types in several institutions. Instead, none of the many hundreds of specimens were deposited in Costa Rican collections, nor even outside of Canada. This substantially subverted any opportunities at building the capacity of the Costa Rican scientific community in their study, a strategy argued to combat the taxonomic impediment (Britz et al., 2020). While type specimens are perhaps not as important as their barcodes in minimalist taxonomy, their location is still not irrelevant; indeed, Sharkey, Brown, et al. (2021) argue that minimalist descriptions are a ‘first pass’, to be updated with morphological data later on. This is only possible if the specimens are accessible.

PARALLEL TAXONOMIC SYSTEMS

A major concern is that the minimalist approach is incompatible with established (largely morphological) taxonomy. Ahrens et al. (2021) in particular feared this will lead to two competing taxonomic systems, one of which describes species based on DNA barcodes, the other mainly based on morphology, and both ‘consider the [species] names of the other faction doubtful’. Sharkey, Baker, et al. (2021) and Sharkey, Brown, et al. (2021) do not give a solution to this problem but suggest waiting until the gap between the systems is bridged by adding morphological data to the minimalist descriptions and/or by sequencing existing type specimens. In our opinion, this problem on its own is enough to make the minimalist approach untenable.

Maintaining parallel systems leads to a plethora of problems. Most of the species that have evolved are now extinct, and many of these were morphologically distinct from their living relatives (Wiens, 2004). Are we to ignore 99% of the species that have ever lived and completely exclude palaeontology from our study of evolutionary history (Novacek & Wheeler, 1992) until the minimalist descriptions are eventually updated with morphological data? Many, if not most taxonomists cannot sequence their taxa, either because of cost, antiquity or conservation value of old museum specimens, or legislation such as the Nagoya protocol does not allow it. Do they have to wait until sequencing technology and costs have improved, or do they need to be dependent on either a well-funded lab or funding from a high-income country? All of these problems can be avoided by writing an integrative description in the first place.

Having said this, we believe that the use of DNA-based analyses for an initial sorting of new and known species is extremely useful as a first step, but for complete and robust species hypotheses, the barcode sequence need to be accompanied by other evidence, in this case by good-quality diagnostic photographs and minimal diagnosable morphological characters. In the case of Meierotto et al. (2019), this would have been possible, as morphological characters for the new species were given in Meierotto (2018). We presume that these characters were not mentioned in the article itself due to a wish to demonstrate the minimalist method. We feel that providing these should not have involved too much work for Sharkey, Janzen, et al. (2021) either, considering that there are 23 authors on the article. In fact, Sharkey, Baker, et al. (2021) recently took a step in this direction, by including some morphological diagnoses among very similar species.

In the context of parallel taxonomies, we feel we should briefly clarify a misunderstanding, which is specific to Sharkey, Baker, et al. (2021) and Sharkey, Brown, et al., 2021), not the minimalist approach in general. Meierotto et al. (2019), when first proposing the minimalist approach, failed to merge their new DNA barcode-based species with existing species for which barcodes are not available. No sequences were provided for the already known species of *Zelomorpha* Ashmead and *Hemichoma* Enderlein (except for *Z. arizonensis* Ashmead) nor any morphological diagnosis for the new ones (except for host data for most species, but outside the diagnoses). Instead, it was stated that Michael Sharkey had seen the types of the existing species and verified they were different. When Zamani et al. (2021) raised this issue, Sharkey, Brown, et al. (2021) misunderstood, believing that they were being asked for evidence that Sharkey had seen the types. This is not the case. The request was (and still is) for the scientific evidence – the *data* – which led Sharkey to believe the species were distinct and therefore new. Such evidence could have been molecular (e.g., if the authors had sequenced the relevant historical type material), or it could have been morphological or even biogeographical (e.g., if the existing species were obviously not Costa Rican). The concern here is that none of the readers of Meierotto et al. (2019) can assess the reliability of the species hypotheses for themselves since they have not been presented with the data.

DESCRIBING SPECIES IS NOT THE BOTTLENECK

The minimalist approach only makes sense if delimiting and describing species is a major bottleneck. This is not usually the case. Our experience (Zamani et al., 2021; Hopkins et al., 2019; Sääksjärvi et al., 2004) points to the fact that it is the field sampling, processing and databasing of the specimens that consumes most of the time. These may take years in total. Engel et al. (2021) argue that species discovery is limited by a shortage of appropriately trained taxonomists, and more generally of funding and resources for collecting and analysing specimens – and that technical approaches such as DNA barcoding are of little use in solving the problem. Fernandez-Triana (2021) points out that the Costa Rican braconids which both he and Sharkey, Janzen, et al. (2021) study are only available due to the 'herculean' efforts of a team which includes parataxonomists, technicians and scientists from Costa Rica and elsewhere. When taking these hidden efforts into account, the time and money saved by minimalist taxonomy may be relatively insignificant.

CONCLUSIONS

Overall, Sharkey, Baker, et al. (2021) and Sharkey, Brown, et al. (2021) are asking taxonomists to abandon their own scientific and intellectual goals because the requirement of research, scholarship and deep thought is inconvenient. While we do believe that barcode clusters are indeed useful as grouping statements, there is no compelling reason why they should be described as species. Quite the opposite, we present compelling reasons for not doing so. In a time of mass extinction, there is little value in a total withdrawal from careful descriptive work. Moreover, considering the arguments presented here and in Zamani et al. (2021), Ahrens et al. (2021), Engel et al. (2021), Fernandez-Triana (2021) and Meier et al. (2021), we strongly suggest that the production of code-compliant names solely on the basis of DNA barcoding be discouraged. Still, if this trend continues, then we propose that the next step should be taken from within the specific expert-based societies, catalogues or databases, similar to what has been suggested by Wüster et al. (2021) on the numerous cases of taxonomic upheaval and vandalism in herpetology. There are a few rare taxa where this approach might make sense, and it will be up to the taxonomic community to establish, both within and outside the code, which cases warrant treatment in this manner. Wüster et al. (2021) have demonstrated that as a last resort, the community is able to reject bad practices when they crop up, and we expect that the community can be relied upon to suppress names that are deemed insufficient, even if they are strictly code-compliant.

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DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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