

EDITORIAL

The taxonomic impediment: a shortage of taxonomists, not the lack of technical approaches

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For almost 30 years, there have been active discussions about the taxonomic impediment and the challenge this represents to address the current human-induced biodiversity crisis. From the start (*Systematics Agenda 2000, 1994*), the term ‘taxonomic impediment’ has been ambiguous, designating both the insufficiency and inadequacy of the resources put to the service of taxonomy (the taxonomic impediment *sensu stricto*) and its main consequence, the wide discrepancy between the reality of specific biodiversity and our knowledge of it (the taxonomic gap; *Dubois, 2010; Raposo et al., 2020*). The total number of species on our planet is unknown, and its various estimates (using different methods) are widely divergent, but consensus exists that we are far from having inventoried half, and most likely one-tenth, of the species still present on earth today (*González-Oreja, 2008*).

Meanwhile, the biodiversity crisis has developed, so that it is now doubtless that a large part of these species will become extinct in the current and coming decades due to anthropogenic actions. This should put taxonomic urgency (*Wheeler et al., 2004; Dubois, 2010*) at the top of the priority list for biological sciences in our ‘century of extinctions’ (*Dubois, 2003*). It is clear that, despite its efforts, conservation biology will not significantly reduce the rate of extinction, even for vertebrates on which most attention is concentrated (*Hoffmann et al., 2010*). The main duty of scientists regarding this situation should be to reduce, as much as possible, the taxonomic gap and to store specimens and tissues that will testify to the vanishing biodiversity of our planet. Once safely stored, research on this material will be possible, even if the species have fallen to extinction in the interim.

Taxonomy is an undervalued biological discipline. This is mainly due to several misconceptions about taxonomy that are widespread in the scientific community. Among these are: (1) the idea that, because taxonomy uses ‘type specimens’, the discipline is typological and non-evolutionary; (2) that taxonomists only study morphology; or (3) that their work is ancillary, merely providing identification of specimens used in other biological studies, such as molecular phylogeny, ecology or conservation biology.

So-called ‘type specimens’ are in fact just vouchers that serve as ‘name-bearers’, allowing objective allocation of names to taxa and are not meant as being ‘typical’ of the taxon (*Simpson, 1940*). Taxonomy, as with every other science, is based on explicit concepts and on the formulation and testing of hypotheses. It requires an integrative approach where scientists benefit by working collaboratively to synthesize the results of data derived from morphology, behaviour, bioacoustics, ecology, geography, molecules, chemistry, history and other diverse fields of inquiry. In this sense it is perhaps the most integrative of all biological disciplines (*de Carvalho et al., 2008*). The identification of specimens is a (useful) practical outcome of taxonomy, but not the core of the discipline, which consists of taxonomic revisions in which the circumscriptions and relationships of taxa are (re)-evaluated (*Löbl, 2018*). Taxonomy is indeed a descriptive science that tests explicit hypotheses, in the same fashion as stellar science and planetary probes represent nothing more than high-tech descriptive sciences (*Grimaldi & Engel, 2007*). Of course, most great finds in science, from gravity to evolution, stem from description of observations.

The source of the ‘taxonomic impediment’ is unclear, but is perceived by some as meaning that the pace of taxonomic work is too slow and laborious, and restricted to the painstaking study of morpho-anatomy, thus insufficient to meet the challenge of documenting biodiversity before it is driven to extinction by anthropogenic alteration and destruction of our ecosystems. Accordingly, various attempts to ‘innovate and speed up’ the taxonomic process have emerged. Some simplistic proposals, mostly based on technological approaches, have been presented as ‘revolutionary’, e.g. replacing descriptions and hypotheses of species with a DNA barcode (wrongly dubbed a ‘diagnosis’; *Sharkey et al., 2021*), or replacing name-bearing specimens held in public curated collections with photographs of species live in the field (*Ceríaco et al., 2016*).

The difficulty in appropriately understanding and addressing the taxonomic crisis results from its multifactorial causes. Among them, the following three are particularly important (*de Carvalho et al., 2005*;

The Buffon Symposium, 2008; Boero, 2010; Wheeler, 2014; Prathapan *et al.*, 2018; Britz *et al.*, 2020; Dubois *et al.*, 2021): (1) the lack of recognition of taxonomy as a robust science by peers and policy-makers; (2) the considerable lack of well-trained professionals, having both solid theoretical and practical backgrounds; (3) the many legal, administrative and ideological barriers that exist regarding the collection and storing of specimens, without which no proper scientific taxonomy can exist.

Many of the problems of taxonomy stem from the dismissive attitude of the scientific community toward this scientific discipline, its unwillingness to appropriately support taxonomic work, a concomitant elimination of academic positions and a growing suspicion towards fieldwork and specimen collection. The search for ‘miracle solutions’ to taxonomy is mostly based on technology rather than manpower. Technological innovations may bring useful tools aiding taxonomic work, but will never replace it. If the population of taxonomists was growing, and if they were given the financial and practical means to carry out well-organized field surveys and collection campaigns worldwide (Dubois *et al.*, 2021), then the taxonomic impediment could rapidly erode away.

The poor image for taxonomy among biological sciences, its concomitant devaluation of taxonomic publications (taxonomic treatments, monographs and new species publications are rarely cited outside taxonomy, even if they are used by other disciplines), and shortage of professional positions and research grants, have played a devastating role in the development and recruitment for the discipline.

There is a global lack of academic education in taxonomy and of properly trained taxonomists, i.e. scientists who distinguish and classify taxa according to explicit concepts and data-based hypotheses, and name them respecting nomenclatural rules and checking type specimens. The theoretical weaknesses of some of the simplistic approaches mentioned above testify to the ignorance of their supporters of the basic tenets of scientific taxonomy (Amorim *et al.*, 2016; Santos *et al.*, 2016). Regardless of technical problems related to the naming of the ‘new taxa’ erected by ‘revolutionary’ protocols (Bauer *et al.*, 2011), such proposals are scientifically questionable.

The case of DNA barcoding is emblematic in this respect. This technique may be useful to identify specimens, i.e. to allocate them to species already recognized by proper taxonomic work or to associate otherwise challenging polymorphic or cryptic taxa. As such, it may be useful in ecology, conservation biology, environmental monitoring and other domains, but it is inappropriate as the sole basis for taxonomic work, which consists in delimitating species and ascertaining their relationships. The use of arbitrary

‘threshold values’ as measured by this methodology to ‘distinguish species’ is nothing but a recent avatar of phenetic taxonomic methods that were dismissed long before the onset of DNA sequencing.

Such approaches actually worsen the challenge by addressing a red herring lurking in the notion of the taxonomic impediment. Moreover, they are based on the assumption that the goal of taxonomy is the mere placing of a name in a taxonomic hierarchy rather than acknowledging that the number, although interesting, lacks practical value in addressing the biodiversity challenges of today (de Carvalho *et al.*, 2014). The goal is not to build mere lists of taxa, just as listing diseases or chemical elements are not the goals of medicine or chemistry, but such lists are integral to all of these disciplines. However, names divorced from suitable breadths of adequate information confuse rather than advance our agendas. Instead, we need means to efficiently, accurately and quickly (but not compromising the former actions) establish the existence of discrete evolutionary units called species, which will allow for their later identification in the lab and field, as well as an understanding of how those species interact with their environment. A cavalierly produced list of species with names dissociated from proper scientific species concepts is no more valuable than knowing the number of different pills in a jar, but failing to know which are stimulants, depressants, painkillers or hallucinogens.

Aside from the aforementioned considerable shortage in brains and hands, a major factor in the taxonomic crisis results from the difficulties encountered by taxonomists to study and collect specimens in the field, store them safely in well-curated collections and make them available to colleagues for study. For a significant increase of our knowledge of biodiversity, collecting new specimens in the field will remain the rate-limiting step (May, 2004). New species are not found in the computers and sequencers of the big cities of the ‘North’, but in the natural and anthropized habitats of the entire planet and, especially, in the more biodiverse ‘South’ (Dubois *et al.*, 2021). Molecular phylogenetics, taxonomic databases and ‘big data’ derived from existing taxonomic information are, indeed, useful tools, but they do not increase our current knowledge of the species that have not yet been collected or studied. In our century of extinctions, immediate effort must be dedicated to collaborative fieldwork and collections, while there is still time.

Organic evolution is not teleological. It results from a variable combination of ‘chance and necessity’ (Monod, 1970), i.e. of genetic variation and natural selection, and as such is not deterministic and predictable. The only way to know it in-depth is to study the organisms themselves, not merely ‘models’ derived from a superficial knowledge of small subsamples.

Efforts to establish new taxa based on the structure of a fragment of one particular gene, or to replace biological vouchers with photographs, actually exacerbate the taxonomic impediment. As in all sciences, there is a need for best practices. In order to attend to the current crises, we need more than ever an adherence to the best standards for producing taxonomic science and communicating it using the proper technical language of scientific nomenclature. This includes a synthesis of extensive data sources to support taxon circumscriptions and hypotheses, and suitable vouchers for their later verification and scientific replication. Specimens are needed so that future generations have a record of life at present, sometimes the sole data we shall ever have for species if it is soon to be lost. Future generations may use these specimens to verify our hypotheses in the face of changing concepts of species and gather data that today are undreamt of – in the same way we today may extract DNA or employ CT-scan data of Linnean or Darwinian specimens to gain insights that those historical collectors could never have imagined themselves.

Instead of relying solely on barcodes and/or photographs, we need intentional and mindful syntheses of molecular, morphological and other data to aid the progress of our knowledge of the vanishing biodiversity. Recent ‘revolutionary protocols’, if adopted by the community, would make the toil of every taxonomist far greater (Meier *et al.*, *In press*). Taxonomists would be faced with a tremendous hurdle toward actually identifying thousands of specimens that may pass before them and may be crucial for ecological, conservation, agricultural or climate-change studies. Every specimen would require partial or complete destruction, depending on the size of the sampled organisms, in order to match the DNA diagnoses, transforming an afternoon’s worth of study into days or weeks. Rather than moving on to tackle the next taxonomic challenge, our diminished force of taxonomists would be bogged down in attempts to place specimens into seemingly known species, with the potential for greater errors if any should attempt to rely solely on photographs, which in many cases fail to properly allow for distinguishing between closely similar or cryptic taxa.

Best practices in taxonomy are critical for addressing the current biodiversity crisis. Innovation is good, but it should improve on an existing situation rather than exacerbate difficulties or worse, revert to 18th- or 19th-century one-character (barcode or single gene) taxonomic approaches. Taxonomy needs to be rebranded to the scientific community as a modern, active and important discipline, and taxonomists need to come together to demand sufficient funding, training and employment for taxonomic researchers.

COMPETING INTERESTS

The authors declare no competing interests.

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