

PERSPECTIVE

Naming and gaming: The illicit taxonomic practice of 'nomenclatural harvesting' and how to avoid it

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Abstract

We coin the term 'nomenclatural harvesting' to identify a distinct form of taxonomic vandalism, in which practitioners generate taxon names for operational taxonomic units (OTUs) identified in phylogenetic trees published by others, even when there is no scientifically useful or practical basis for doing so. This practice can destabilize the nomenclature of scientifically established groups by swamping them with questionable new names, and this may have broader impacts in the application of taxon names to clinical toxinology, studies of biodiversity and conservation, and it may contribute to further erode the trust placed by the public in science. A change to Article 73 of the *International Code of Zoological Nomenclature* and the addition of suitable language in publications presenting taxonomic decisions to authenticate research effort and specimen work would alleviate the problem.

There are few achievements in the publishing activities of biologists that produce greater permanence than naming a taxon. While there are, of course, many other worthy endeavours in biology, taxonomy carries with it a certain glamour, not least because in the system of binominal nomenclature proposed by the Swedish botanist Carl Linnaeus (1707–1778), the authors' names become inextricably linked with the taxon names they coin. This Linnaean system has served biologists well but, ever since its inception (Linnaeus, 1758), it has also been a realm of misdeeds. Linnaeus himself, for example, named the plant genus *Sigesbeckia* for Johann Georg Siegesbeck (1686–1755), one of his vocal critics, and intended it as an insult (Barber, 1980; Chamovitz, 2012): *Sigesbeckia orientalis* Linnaeus, 1753 is a small, smelly, unsightly weed. To add injury to insult, a less obvious misdeed in this case is that Linnaeus's original spelling incorrectly eliminates the letter 'e' in the third position of Siegesbeck's name.

Over the decades and centuries, Linnaeus's binominal system reached ever greater prominence as a standard to categorize and stabilize organismal biology, and it became necessary to trace taxon names, so that duplication and confusion could be addressed or avoided. As a consequence, different areas of biology developed 'codes' of nomenclature, according to which the availability of such nomina could be governed. These

include the *International Code of Nomenclature for Algae, Fungi, and Plants* (McNeill et al., 2012) and the *International Code of Zoological Nomenclature* (hereafter, the *Code*; ICZN, 1999, 2012), to name but two. While this effort has provided an important mechanism to ensure biologists can communicate effectively about specific taxa, some have expressed that these accounting systems do not go far enough in prescribing the conditions whereby nomina become valid and available (Kaiser, 2013; Yanega, 2013) while others have lamented the problem with nomenclatural nihilism (Dubois, 2015; Evenhuis, 2008). Especially nowadays, when a significant amount of information about species and museum specimens is available via online sources and when rapid modes of publication allow anyone to publish (see Rich, 2016 for the direction in which this can go), it is easy to circumvent or thwart the noble intention of the codes – to assist with and streamline scientific processes. Unscrupulous individuals can and do jump freely into taxonomy to satisfy their 'mihi itch' (Evenhuis, 2008) by engaging in a practice called 'taxonomic vandalism' (Jäch, 2007), creating taxon names without proper scientific work to back them up. In the following paragraphs, we describe a distinct variation of this phenomenon we dub 'nomenclatural harvesting' and provide possible solutions for mitigating the problem.

Taxonomic vandalism vs. nomenclatural harvesting

In recent years, we have diagnosed the output of taxonomic vandalism as obviously flawed and divorced from proper scientific process (Denzer et al., 2016; Kaiser et al., 2013). We analysed this practice in the field of herpetology (see below) and recommended that the research community ignore the offending publications and any taxonomic decisions proposed therein. This initiative was implemented successfully, and some nomina of vandalized taxa have by now been overwritten with aspidonyms (names designed to shield science from taxonomic vandalism), without acknowledging the publication that gave rise to the problematic taxon name. While such a community action violates Article 23 of the *Code* (the Principle of Priority), it has emerged as a nearly unanimously accepted remedy against taxonomic vandalism (Wüster et al., 2021) that does not require the tedious scientific process of sinking ‘fake names’ into the synonymy of the taxa from which they were extracted.

A key difference between ‘traditional’ taxonomic vandalism (using minimal morphological variation or geographic isolation to serve as a vague basis for a new taxon) and nomenclatural harvesting is that harvested molecular phylogenies do provide a scientific backbone for the coined nomina, which are based on real taxonomic concepts demonstrated by previous authors that may not be synonymized easily. Whereas it is generally quite straightforward to show the scientific deficiencies of taxonomic vandalism and the haste with which it is often perpetrated (naming as many new taxa as possible in the hope that some of them will stick), nomenclatural harvesting relies on naming monophyletic clades that may constitute valid OTUs or candidate species, and the only procedural omission is a detailed interpretation of such clades. In those cases, a reversal of harvesting is not easily accomplished: a revisor of the taxonomy would have to disprove the original study, not the harvester’s actions.

We generally define as nomenclatural harvesting the activities of someone who scans the scientific literature for the mention of unnamed organismal groups or for figures of phylogenies with identifiable clades, and who then names them without studying the physical organisms involved (i.e. individuals in nature or museum specimens), without regard for the ongoing taxonomic work by others on the group(s) in question and without any sound scientific rationale (Fig. 1). Such action often involves a form of plagiarism, with the naming author relying exclusively on characters described in earlier (and even historic) publications, without adding any new relevant information (for some examples, see Denzer et al., 2016).

With the advent of online publication and the opportunity to rapidly disseminate electronic copies of scientific articles, nomenclatural harvesting is easy. Gone is the time when taxon names could ‘settle’ into nomenclature. Taxon concepts – which, by the definition of the scientific method, are hypotheses, to be re-examined, tested and understood over time – are being produced at a fast rate and, as long as some minimal aspect of the rules of nomenclature laid down in the relevant

code is fulfilled, these concepts can become permanent even when they may be deeply flawed scientifically. It is an ideal situation for someone to cut in – inappropriately – and produce large quantities of taxon names.

Why does nomenclatural harvesting matter?

The science of taxonomy is a key element of biology because it provides the scientific community with the necessary concepts so that communication about specific groups of organisms (e.g. genera, species) can be unequivocal and effective using binominal nomenclature (Cotterill, 1997). The unscientific process of nomenclatural harvesting leads to doubt about these concepts, and while this may appear as a bearable nuisance to researchers working outside taxonomy, it can have profound specific and general consequences in basic and applied biological research. In clinical toxinology, for example, antivenom production and use are often species-specific, and when species are split up or reassigned to different genera without an acceptable evidential trail (Sutherland, 1999) then the uncertainty over names brought on by nomenclatural harvesting may literally become a matter of life and death after envenomations. At a broader scale, nomenclatural harvesting confounds our ability to characterize biodiversity when unwarranted, harvested names dilute the verifiable number of different organisms present in a biome (Wilson, 1985, 2004). This is of particular importance when it comes to the identification and protection of threatened taxa: splitting up or changing the names of species protected by the Convention on International Trade in Endangered Species, better known as CITES, or listed in the *IUCN Red List of Threatened Species* can cause inadvertent loopholes exploitable by for-profit collectors and at least temporarily thwart recognition by enforcement agencies. Lastly, during the COVID-19 pandemic, we have already witnessed a politically motivated erosion of public trust in medical science. The uncertainty surrounding the products of nomenclatural harvesting, should they be left unchallenged, would further diminish the standing of the scientific discipline in the eyes of the public.

Nomenclatural harvesting in herpetology

Herpetology, the zoological discipline involving the study of amphibians and reptiles, has been plagued with nomenclatural harvesting to such an extent that in recent years a single author has managed to register over 2000 nomenclatural acts with *Zoobank*, the online version of the *Official Register of Zoological Nomenclature* kept by the International Commission on Zoological Nomenclature (ICZN). Strictly speaking, all of these registered names could perhaps be considered available and used in publications. However, based on the specifics of how these names were produced, the herpetological community has decided against their use (Wüster et al., 2021), journal editors of herpetological publications are boycotting them (Measey, 2013), and most publications will not even mention or acknowledge the existence of those taxon names except to



FIGURE 1 The nomenclatural harvester shown here “plucks” unnamed OTUs off a phylogenetic tree in order to claim easy fame by naming them without scientific rationale or ethical concerns. The cartoon was drawn at our request by the Colombian artist Camilo Triana (trianacartoon.wixsite.com).

criticize them (Kaiser, 2014; Kaiser et al., 2013). For example, in a recent publication, Wood Jr. et al. (2020) regarded all nomenclatural acts (ten new genera, six new subgenera and ten new species) of a harvesting author as nomenclaturally unavailable. These authors demanded that the ICZN use its plenary power to declare those acts null and void, and that to avoid harvesting above the species level, taxonomists should propose subgenera when publishing phylogenies including newly identified supraspecific clades.

An underlying question for this output level of herpetological taxon names is its scientific legitimacy: how can a single author possibly study and name many hundreds of new taxa

(more than any earlier herpetological authors in their lifetimes) in merely a few years? While this can be done in some animal groups (Jäch, 2006, 2007 – beetles; Buschinger, 2007 – ants) it has, to the best of our knowledge, never been done without specimen work. This appears to be the first attempt to upend the taxonomy of an entire zoological discipline without the completion of basic data gathering and by producing taxonomic decisions outside of the framework of the scientific method. The reason for this level of output is that easy recipe we term nomenclatural harvesting.

Phylogenetic studies often yield several clades within genera that had previously been considered monophyletic. This

result is not necessarily an indication of true diversification, such as of recognizable phenotypic characters, it may merely be an indication of unexpected genetic diversity within a single group, and it may point in the direction of incipient diversification at a level meaningful for taxonomy. Many of these studies are still limited in terms of the investigated genes (although this limitation is being lifted as molecular techniques now allow rapid throughput of large numbers of gene sequences) and weighting these sometimes-preliminary results too heavily for the purposes of producing taxonomic decisions can be premature. As a consequence, authors of these studies will typically abstain from naming each of the clades and perhaps refer to them as operational taxonomic units (OTUs; Sokal & Sneath, 1963) in need of further (morphological) studies, or perhaps candidate species (Hedin et al., 2015; Pyron et al., 2016), whose formal descriptions may be beyond the scope of the phylogenetic focus (and the journal where the paper is being published). OTUs and candidate species are an invitation for nomenclatural harvesting. Sometimes a single such 'taxon-ripe' publication is sufficient to name new taxa, in particular new genera, as the following examples show. Please note that instead of using taxon names produced by nomenclatural harvesting, which we consider unscientific and unavailable for the purposes of zoological nomenclature, we use the taxon level preceded by a superscripted asterisk. Thus, *Genus indicates a genus name derived via nomenclatural harvesting. Furthermore, we do not cite publications containing illicit nomenclatural acts, as this would lend credibility and imply acceptance of the respective publications.

Harvesting from morphological studies

In a study of lacertid lizards Arnold et al. (2007) wrote the following sentence:

Timon consists of two distinct units: the *Timon lepidus* group of the western Mediterranean region (*T. lepidus*, *T. pater*, *T. tangitanus*) and *T. princeps* of southwest Asia.

In their description of *T. princeps* these authors distinguished the Mediterranean *T. lepidus* group from *T. princeps* as follows:

[N]asal process of premaxilla broad in *T. lepidus* group but more slender in *T. princeps*.

They further stated regarding hemipenis morphology that *T. princeps* had

long recurved spines on lobe flanks.

In 2015, an author not associated with the Arnold et al. paper named a new, monotypic genus based on the analysis of Arnold et al. (2007). This author defined the new genus, with *T. princeps* as the type species, as follows:

*Genus is separated from *Timon* by having long recurved spines occurring on the hemipenial lobe flanks, a state not seen in *Timon*. In ... *Genus the nasal process of premaxilla is slender, versus broad in the genus *Timon*.

This author examined no specimens, had no experience with these lizards and had no way to verify the accuracy of the characteristics used by Arnold et al. (2007).

In a similar case, Denzer and Manthey (2009) reported on their examination of the holotype and only known specimen of *Gonocephalus mjobergi*. In their article, these authors gave a full description of the specimen and concluded that the species was not only lacking several characteristics typical for the genus *Gonocephalus* but presented additional characters that would justify the removal of *G. mjobergi* from *Gonocephalus*. They abstained from naming a new genus based on autapomorphies, given that this would be of no phylogenetic relevance and limited taxonomic use, and deferred a decision until more material became available for study. In 2014 a different author erected and named a new genus to accommodate *G. mjobergi* by simply copying and pasting the full description and diagnosis given by Denzer and Manthey (2009). This particular case was documented by Denzer et al. (2016).

Harvesting from molecular studies

In the case of phylogenetic studies using only a molecular data set, a harvesting author would need at least one additional publication, in the absence of any specimen work conducted by the harvesting author, in order to name a new taxon. The *Code* (ICZN, 1999, 2012) does not currently allow the naming of taxa without 'a description or definition that states in words characters that are purported to differentiate the taxon' (Article 13.1.1) or 'a bibliographic reference to such a published statement' (Article 13.1.2). However, even this can be an easy task when one resorts to plagiarism, as the following example shows.

In a broad molecular analysis of snake relationships, Pyron et al. (2011) stated that,

The genera *Buroma*, *Oxyrhabdium* and *Psammodynastes* cannot be placed confidently within the existing subfamilies of Lamprophiidae.

This prompted a harvesting author to write,

Many molecular studies, including that of Pyron et al. (2011), were effectively unable to place *Oxyrhabdium* within any existing families,

and to erect a new family and subfamily to accommodate the only two known species of this genus. The author presented a diagnosis for the family by copying and pasting word-for-word the generic diagnoses given by Boulenger (1893) and Taylor (1922). At the same time, a separate family and subfamily were erected to accommodate the two known species of *Psammodynastes*.

Harvesting at different taxon levels

Naming taxa above the taxon level of species is relatively easy and straightforward. There is no need to study or even know the whereabouts of actual specimens since, typically, these were described in earlier publications. In such situations, the actual type specimen relevant to the nomenclatural act was already designated and deposited in a museum collection. The only action necessary to legitimize a nomenclatural harvest would be to designate a type species in the case of a new genus or a type genus in the case of taxa above the genus level. Of course, diagnostic characters can easily be copied and pasted from earlier publications.

Naming species or subspecies involves a more in-depth literature search because the *Code* requires the designation of type specimens. But even this can be an easy task if the author of an original study published a list of specimens examined in an appendix or referred to particular specimens within a publication as the following example shows.

In a review of the corytophanid lizard genus *Laemanctus*, McCoy (1968) described two specimens (USNM 48097, 48099) that had been collected in the ‘mountains near Santo Domingo (= Petapa)’ in Oaxaca, Mexico. McCoy considered these two specimens aberrant and ‘intergrades between [*Laemanctus*] *longipes* and *deborrei*’. In 2015 these ‘intergrades’ were described as a new species by a harvesting author, and the specimens designated as holotype and paratype were USNM 48097 and 48099, respectively. The actual description followed the same scheme as the ones mentioned earlier, simply copying the characters published by the original authors. McCoy (1968) wrote,

These populations have 42–47 scales at midbody (Fig. 1) and anterior dorsal head scales which are intermediate in size between the very large ones of *longipes* and the smaller scales of *deborrei*.

The description of the new species by the harvesting author was as follows:

42–47 mid-body scale rows and anterior head scales that are intermediate between the very large ones seen in *L. longipes* Wiegmann, 1834 (those being nearly double the size of the posterior casque ones) and the very distinctly small ones (not distinctly larger than those on occipital region) seen in *L. deborrei* (Boulenger, 1877).

No further morphological data were presented since the harvesting author did not examine any of the specimens designated as types. Nor did this author ask collection staff at the USNM or a collaborator to examine the specimens and to provide additional information (as a Research Associate of the USNM, HK confirmed this by speaking to collection staff).

Preventing nomenclatural harvesting at the species level

Given the obvious nature of nomenclatural harvesting, such deviant behaviour should readily be preventable. In the case of

new species names reaped by harvesting, the *Code*'s Article 73 actually provides a Recommendation that could prevent the problem.

Recommendation 73B. Preference for specimens studied by author. An author should designate as holotype a specimen actually studied by him or her, not a specimen known to the author only from descriptions or illustrations in the literature.

We urge the ICZN to promote this recommendation to a binding article in the next edition of the *Code*, by adding it to Art. 73.1.3. and changing the word ‘should’ to ‘must’. The revised article would read:

Article 73.1.3. The holotype of a new nominal species-group taxon can only be fixed in the original publication and by the original author (for consequences following a misuse of the term “holotype” see Article 74.6). An author must designate as holotype a specimen actually studied by him or her, not a specimen known to the author only from descriptions or illustrations in the literature.

This would ensure that species could not be named without examination of the relevant specimen(s). Publications that are nevertheless solely based on harvesting clades from phylogenetic studies or previously unnamed taxa published in taxonomic review articles and do not involve specimen work by authors would therefore not be *Code*-compliant and the nomina they generate would not be available for the purposes of zoological nomenclature. At the end of a publication dealing with new species or other taxonomic decisions at the species level, a lead author would have to specifically authenticate that relevant type specimen(s) were studied. The author of the lizard study mentioned above could have phrased a statement as follows:

I hereby confirm that I personally examined the type specimens relevant to this study as part of preparing this publication.

Adjusted wordings would apply to indicate that multiple authors participated in a study or when specimens were examined by personnel of the institution where the specimens are housed (see below). Should it turn out that the actual specimen(s) had not verifiably been studied, this would automatically lead to revocation of the name(s) in the publication, which would not be available for nomenclatural purposes and which would be considered as having never become available in zoological nomenclature in the first place. Transforming Recommendation 73B to a binding article would amount to one level of taxon filtration to eliminate illicitly produced names (Kaiser, 2013) by essentially using the existing *Code*.

We wish to clarify that, to ensure that a solution like this remains practical, it needs to account for some exceptional circumstances, in particular when considering specimen access. For example, some institutions are unable to loan out material

and, in situations where type specimens are held in different collections, it may be difficult to examine complete sets of type specimens. In such cases, a collaborator (not necessarily an author) acknowledged in the publication, or a responsible person employed by the respective collection, may be asked to provide the necessary morphological and meristic data of the type specimen(s). In the acknowledgments of the publication the author of the lizard study described above could have explained this assistance as follows:

I was unable to personally examine the type specimens due to the current policy at the [collection name] not to loan out specimens to private individuals. Instead [name of collaborator or collection manager] examined the type specimen on my behalf and provided the data necessary to support the species description.

This type of statement can easily be edited to accommodate different numbers of specimens or multiple authors.

Additionally, it should be considered obligatory to inform the respective collection that a specimen (or specimens) from their collection was designated as type material. Again, a short statement should serve this goal:

The [collection name] has been informed that [specimen identifiers and numbers] have been designated as the holotype and paratype of *Species.

The *Code* so far only *recommends* (Recommendation 73C.6) but does not *mandate* (our italics) that author(s) provide the name of the collection where types are held and their accession number(s).

Finally, digital photographic records of specimens, in particular types, are a first step towards virtual museums. In future, this may facilitate the examination of some characters, but not all, without physically studying specimens. A harvester may take advantage of this situation to claim that a specimen has been examined personally. This can be prevented by demanding that a new species or subspecies description must be accompanied by a photographic record of the type material, either taken by the author(s) or licenced to the author(s) by the institution holding the type material.

Preventing nomenclatural harvesting above the species level

When it comes to nomenclatural harvesting above the species level, preventative measures are more difficult to invoke. Among taxonomists working in a common organismal field, collegiality and ethics would dictate that an author of a recently published study, who is actively involved in research in the field, is informed when another author intends to use that author's data before using it to name a new taxon, especially when the naming of new taxa could be a logical next step from the initial publication (ICZN, 1999: Appendix A. Code of Ethics. Principle 2). This would be to extend a common courtesy, and the original author(s) would perhaps be interested in a collaboration that could add new data and new

perspectives, potentially strengthening the case for naming a new taxon. Additionally, this would ensure that the actual specimen(s) would be studied by at least one of the authors. Unfortunately, based on experiences of recent years, the concepts of collegiality and ethical behaviour would likely be lost on a nomenclatural harvester and cannot be presumed.

As a rule, examination of previously described material should also be made mandatory for naming taxa above the species level. This may sound labour-intensive and, in some cases, may constitute a seemingly superfluous task, but in our experience (Kathriner et al., 2014; Kieckbusch et al., 2016; Mecke et al., 2016), a careful look at specimens may uncover inadvertent errors by earlier authors. We would also like to note that most phylogenetic studies, in particular molecular studies, do not normally involve type specimens. Typically, tissue samples for molecular studies come from recently collected specimens that were identified as a particular species based on literature work or by specimen comparisons. The vast majority of these identifications will be correct, but mistakes can (and do) happen. It is therefore of critical importance that molecular studies only include material for which a voucher specimen has been deposited in a publicly accessible collection. Otherwise, should such misidentified specimen(s) emerge in a new monophyletic position that could be considered as a new supraspecific taxon, then any nomenclatural action would be misleading and could be destabilizing. The specimen that was the source of the tissue sample must be compared with the relevant types of the species group under consideration in order to confirm its taxonomic status. Only once the identity of the tissue source is ascertained can a taxonomic decision be supported (see Kathriner et al., 2014 for an example of resulting confusion).

Recently, Wood Jr. et al. (2020), who had been exposed to nomenclatural harvesting on a large scale, proposed that authors of phylogeny-based revisionary studies should provide short diagnoses, designate type species and name monophyletic clades on a supraspecific level as subgenera within the publication. While this will prevent the introduction of new names by a potential harvester, the onus for action remains on the authors instead of being regulated by the *Code*. Premature naming of clades may also be counterproductive since it may not provide the desired stability promoted by the *Code* for any newly named groups. As an alternative, we propose that in situations where a phylogenetic study yields potential supraspecific taxa a time-limited moratorium (of a yet-to-be-defined time frame) could be imposed on formally naming these taxa, unless this is done by the authors of the original study or by taxonomists who have been given permission by the original authors to formulate and publish taxonomic decisions. A corresponding article would have to be added to the next version of the *Code*.

Outlook

We strongly recommend that the ICZN immediately, but certainly in the next edition of the *Code*, introduces new rules to prevent nomenclatural harvesting and taxonomic vandalism. A recent initiative (ICZN Case 3601) to place one illicitly coined

genus name on the *Official Index of Rejected and Invalid Generic Names in Zoology* and a self-published journal on the *Official Index of Rejected and Invalid Works in Zoological Nomenclature* resulted in an unsatisfactory and somewhat equivocal ruling by the ICZN (Opinion 2468). The main reasoning behind the ruling was that

The Commission operates within the strict confines of nomenclature and judgments based on the quality of taxonomy or on ethical principles remain beyond the mandate of the Commission. . .

The commission did not vote in favour of making this genus name available and to validate the journal, nor did it vote in favour of suppressing the name and regarding the journal as unpublished. We feel that, if no further steps are taken by the ICZN, most taxonomists may continue to disregard entries by vandalizing and harvesting authors in *Zoobank* and consequently not adhere to a range of rules prescribed by the *Code*. Article 23 (the Principle of Priority) in particular could be violated in many cases. It is the task of the ICZN to stand in the service of the scientific community to ‘promote stability and universality in the scientific names of animals’ (Preamble of the *Code*), not to protect rogue operators who produce taxon names unscientifically with minimal adherence to the *Code*. If the ICZN insists, with justification, that the community of taxonomists should adhere to the *Code*, it must be prepared to make user-friendly, *Code*-compliant decisions and to implement measures to prevent activities that impinge upon the credibility and integrity of science by condoning the exploitation of loopholes in the current system. Otherwise, as one ICZN Commissioner has stated (Krell, 2021), the following may apply:

Whereas the rejection of taxonomies is common and unproblematic in the scientific discourse, the rejection of available and valid names, not to mention a validly published work, is a rare occurrence and in conflict with the *Code*. However, extraordinary circumstances might justify such extraordinary measures.

The *Code* can be adapted, and this adaptation can be done rapidly, as shown in a recent response (ICZN, 2017) to a scientific debate about the necessity of a preserved holotype (Ceriaco et al., 2016; Krell & Marshall, 2017; Pape et al., 2016). Similarly, the implementation of minor changes to the *Code* can prevent the nomenclatural malpractice we decry above in the future. We are aware that our recommendations for preventing nomenclatural harvesting can only serve as a first proposal, but we hope to encourage an urgent and more detailed discussion about this matter.

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