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Article in *Zootaxa* · February 2017

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Should we describe genera without molecular phylogenies?

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For nearly a decade I have published species descriptions and revisions of land snails in peer-reviewed journals. As a systematist, it is often requisite to reclassify species into other, sometimes unnamed genera. Although in most cases editors and reviewers have not commented on the taxonomic changes I have made and the new taxa I described, I sometimes received negative critiques when I described new genera unaided by molecular phylogenetic support. I feel these critiques have become increasingly more frequent, and am convinced that many fellow taxonomists share this experience. Addressing this problem is particularly difficult due to three reasons. First, it is impossible to support these observations with statistical data (i.e. the frequency of similar reviews increasing or not); second, the increasing number of published phylogenetic works reveals more and more cases of polyphyletic genera, which might suggest that morphology-based generic grouping is unreliable, and thus, should be avoided; and third, no publications exist suggesting not to describe genera using (still) reliable morphological foundations. Subsequently, the unsatisfactory review process of taxonomic works is often exacerbated by the biases of reviewers and their inobservance of valuable historic convention in light of the current wave of molecular phylogenies. Moreover, the future value of morphological descriptions for biodiversity assessments (i.e. IUCN) is not even addressed.

Here, I argue against prohibiting descriptions of genera without phylogenetic support, and make suggestions how editors and reviewers should handle "phylogeny-free" genus descriptions. To illustrate my experience, I quote some text from previous reviews and editorial comments that I have received:

Editor of a taxonomic journal, (07.02.2012).

"(...) In particular, I need you to provide much more information regarding your decision to erect new genera; as of now you provide no rationale, and you must fully defend this approach. I frankly would feel much more comfortable if you had corroborating DNA sequence analyses to demonstrate that these are not simply subgenera or even simple groups within already existing genera -- and you have not even minimally done this. There is a strong burden of proof to undertake such splitting, and I expect these decisions to be clearly reasoned and proved with empirical data. If you cannot do this, then I strongly suggest that you place your new taxa into already existing generic entities."

Anonymous reviewer (02.11.2016).

"(...) As for the description of a new subgenus, I am strongly opposed to this taxonomic proposal. Taxonomy serves three possible purposes: (1) the ego of the author, (2) the human desire to classify things, (3) the scientific purpose to conceptualize ideas about the evolutionary relationships amongst organisms. The only purpose this new subgenus serves is 1. (...) As for purpose 3, attempting to conceptualize the evolutionary relationships of species, this decision is even worse. Inevitably, you are making a statement about the evolution of this group and you imply that one species is the sister group of all other species combined based on one character. You have a one in six chance that you are right because your treatment is not backed up by any phylogenetic analysis."

Anonymous reviewer (23.11.2016)

"(...) The taxonomic description of the new species is also good. However, in the absence of molecular sequence data, I consider that there are insufficient grounds for erecting a new genus. (...) As taxonomists living in the 21st century we have a responsibility to investigate the phylogenetic basis of historically-erected genera and sub-genera by the combined study of morphological and molecular data. This is often not possible because of limited funding, and so the best course when describing species new to science is to work with existing generic and sub-generic names and to avoid contributing to taxonomic instability by creating new generic level taxa purely on the basis of a few shell characters."

In the first case, my proposal to erect new pulmonate land snail genera was based on shell and genital anatomical characters, whereas in the latter two cases, I attempted to describe new (sub)genera based on differences of the breathing tubes, a traditional approach used in the respective land snail groups (Kobelt, 1902). In other words, 30–200 years ago the scientific community would not have questioned the establishment of these new genera based on morphology. Naturally, without knowing the background of the above examples, it is not possible to form an opinion whether I was right or wrong when I tried to erect new genera, although this is not my point here. Instead, I aim to show that the preference of existing generic names over erecting new genera is strong.

Are the reviewers right?

Strictly speaking, the reviewers, who disapprove and forbid morphology-based genera may be right. "How do I know that they are really monophyletic?" We cannot know whether a taxon is monophyletic without a proper phylogeny. To investigate this question we have to go back to the definition of the genus. If we define a genus as "a group of species that are more closely related to one another than they are to any species assigned to another genus" (Wood & Collard 1999: 201), then only an appropriate phylogeny would provide satisfactory evidence, although a hypothesis of monophyly based on morphology should be also acceptable. If we define a genus as a group of species defined by apomorphic character states, morphology is sufficient. Regardless of generic definitions or criteria, which are usually not given in genus descriptions, monophyly of genera is, or at least should be assumed (Ebach *et al.* 2006) (although species are not necessarily monophyletic; Schluter & Nagel 1995, Nosil *et al.* 2002). The level of provided supporting evidence should be up to the journal's policy and the taxonomists' personal preference.

In the vast majority of species descriptions, no species criteria are specified. Unlike genera, describing species without molecular support appears acceptable. Species criteria (e.g. presence of reproductive barriers) are mostly assumed rather than tested in species descriptions. On the contrary, assuming monophyly is deemed to be insufficient by some members of the taxonomic community. The reason for this double standard is puzzling. Especially since one might encounter larger difficulties handling synonyms of species than those of genera.

Reviewers suggesting not to describe phylogeny-free genera supposedly aim to minimize the subjectivity of taxonomy caused by the never-ending battle of lumpers and splitters. This goal is admirable. However, taxonomy is a science, and all new taxa that are proposed are hypotheses that can be refuted and falsified (Evenhuis 2008).

Not always a matter of money

Although molecular phylogeny becomes an everyday tool for some proportion of professional taxonomists, it is not available for many researchers due to the lack of funds. Moreover, in Europe, 60 % of new taxa are described by non-professionals (Fontaine *et al.* 2012), who have nearly no chance to support their taxonomic decisions with molecular phylogeny. However, the lack of funds and limited access to molecular laboratories explain only a fragment of cases when molecular phylogeny could not be performed. In many cases it is not possible to perform phylogenetic analysis due to a number of other reasons. For example, the absence of specimens in museum collections potentially containing DNA (e.g. empty mollusc shells and wrongly preserved historical specimens; see Jaksch *et al.* 2016); type localities of species described centuries ago are not precise enough to allow revisiting the original sites; the original sites are destroyed and the targeted species might be extinct in the wild; not to mention fossil taxa, which also need to be placed in the system obviously without molecular support. Furthermore, molecular studies that propose new taxa should also return to morphological characters in light of the molecular phylogenetic trees.

More repercussions than merits

Genera, irrespective of the fact that they are "old" or "new", are testable hypotheses of monophyletic groups that predict the distribution of characters (Platnick 1979; Wheeler 2004). In the absence of molecular support, I cannot see a good scientific reason to prefer existing genera over new genera. The action of placing a species into a genus irrespective of being named or not, is a hypothesis of the species' evolutionary history. Describing new, morphologically well-defined genera is not "unnecessary splitting", but small steps towards understanding evolutionary relationships of organisms. Forcing classification of new species into already named genera could have more repercussions than merits. It would, for example, result in unnecessarily "dumping" of species into well-defined genera, the reduction of diagnostic apomorphic characters in morphologically defined groups. Such practice will turn a well-defined genus into a wastebasket taxon, which may, for instance, create artificial biogeographic "connections" between areas.

Taxonomy and systematics faces several challenges in the 21st Century, and the naming of new genera without phylogeny is certainly not the biggest of these. For instance, incorrect identification of specimens used for molecular studies (Nilsson *et al.* 2006; Groenenberg *et al.* 2011), taxonomic inflation (Isaac *et al.* 2004; Harris & Froufe 2005), and

the increasing gap between phylogeny and classification (Franz 2005) are much more serious problems. On one hand, phylogeny provides us with a powerful tool to hypothesise evolutionary relationships. On the other hand, since the world's biodiversity is largely unknown (some 86% of non-marine eukaryotic species are unknown; Mora *et al.* 2011) and the number of taxonomists is decreasing (Bebber *et al.* 2014; Wheeler 2014), it is not yet the time to regulate morphology-based grouping of species. Instead of criticising their well-trained, professional expertise (gleaned through years of intense study), we should invest more trust in the taxonomic evaluations of the decreasing number of taxonomists as well as allow more freedom for morphology-based grouping. Especially, given that if someone wants to describe something, he/she can find a way to do so in local, small non peer-reviewed journals or self-published books.

One-sided critiques emphasising only the taxonomic value of molecular assessment could well result in the weakening trust of taxonomists (mostly the ones not dependent on impact factors) in peer-reviewed journals, which is already a major problem in today's taxonomy. Morphology is still what makes the organism a tangible entity beyond its DNA.

Necessary changes in the review process

What we need, is better editorial practice. To overcome this recent trend, I suggest considering the following points:

(1) Authors have to justify their conclusions clearly with their data. Also, if the reason is other than no access to molecular laboratory and funds, they should state the reason why molecular phylogeny is not performed.

(2) Editors need to understand the hypothesis-driven nature of taxonomy, systematics and phylogeny, and need to be able to ignore reviewers who do not engage the subject.

(3) Reviewers should refrain from rejecting the description of new genera on the basis of the lack of molecular data. Instead, they should be critical of poorly defined genera, no clear gaps in the morphological continuum, overlapping character states across genus-group taxa, and genera awaiting descriptions based on non-conventional morphological characters.

(4) Taxonomic journals could state whether they allow, discourage or prohibit descriptions of taxa above species level without molecular phylogenetic support. On one hand, this would allow the authors to prepare to the nature of reviews, and choose journals where the lack of sequence data will not result in changing the proposed taxonomic decisions. On the other hand, this would create a rather harmful division in how journals deal with taxonomic submissions.

Acknowledgements

Although I argue against their opinion, I would like to thank the editors and volunteering reviewers of my manuscripts. I am grateful to Adrienne Jochum for her suggestions and corrections of the English, and to an anonymous reviewer for comments on the first draft of the manuscript.

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