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# Good habits come first in Science too: a reply to Straka and Starkzomski

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I thank Straka and Starkzomski for their thoughts [1]. They have, however, critically misread my proposal. They state that I suggested that taxonomically-challenged studies should be “thrown out” or “dismissed”, words and concepts that I did not use [2]. Rather, I explicitly stated that authors of submitted papers should be asked to simply state how the species involved in a given study were identified, and that this action would thus “induce a critical shift in the quality of the papers,” “instantaneously highlight the papers with potential taxonomic errors,” and “elevate the excellence of the science being published.” None of these statements imply or suggest rejection of any evolutionary or ecological studies. Neither do they imply any willingness to discourage the formulation of relevant questions in ecosystems where the taxonomy is poorly known.

More puzzling is the statement by Straka and Starkzomski that “studies with incomplete taxonomy can still have valid and important findings...”, a point that I did not raise, but that I will comment on. I did not ask for justification of incomplete taxonomic data but instead I suggested that we learn where the names (whatever their origin) came from, what literature was used, or who identified the taxa. I agree that studies with justified deficient or unconventional taxonomy can be meaningful for a variety of reasons, e.g., [3,4]. That said, many workers tend to believe that using diversity indices will somehow validate bypassing the fundamental stage where one has to actually identify the taxa in a study. This is wrong, as is the willingness to combine old historic and new data sets regardless of taxonomic validation; mostly because the taxonomic criteria and standards for validation vary among taxa and over time, and because taxonomic errors in understudied taxa are likely to remain overlooked. Within the ecological and evolutionary context, diversity indices are built by taking into account a number of taxonomic units that need to be reliably identified. It is indeed up to scientists and their circumstances whether they do or do not identify the taxa in their studies, or if they do it by themselves or with the help of experts; but in all cases they should be able to specify what they did. Relying on “large sample sizes and taxonomic breadth”, as Straka and Starkzomski suggest, to circumvent obfuscated and vague taxonomy does not validate or strengthen one’s results. Were this so, our work in evolution and ecology

would be as simple as to collect large samples across multiple phyla. A similar misconception is that ecologists dealing with enormous (and sometimes overwhelming) numbers of taxa are exempted from reliable taxonomic work. In fact, it is nearly impossible to find rigorous evolutionary or ecological works where, to quote Straka and Starkzomski, “confirmed taxonomy designations are... unnecessary”.

I agree with these authors that there are inevitably systems where the identification of species is challenging: we all deal with these on a regular basis. But abdication of revealing these challenges does not reinforce one’s results. Taxonomic misidentifications can lead to wrong conclusions and serious error cascades [5], even if framed in valid ecological and evolutionary theories. By providing the best methodological transparency possible, scientific journals will help to solve these problems more efficiently. “Guiding authors to reliably use taxonomic names” [2] is about creating good, verifiable, and replicable habits toward more transparent, integrated, and reliable knowledge (see supplementary material).

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## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.tree.2012.08.016>.

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