

Editorial. DNA barcoding and authorship in taxonomy

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Abstract. New times bring different methods and different approaches on how we study insect biodiversity. Many members of the Flemish Entomological Society actively participate in different DNA barcoding-related projects. Also, many of them exchanged their entomological nets with sophisticated digital cameras and became very enthusiastic recorders of distribution data, biological and morphological traits among insects.

The Editor-in-chief of Phegea asked several questions about morphology and molecules, DNA barcoding and authorship to the Director of the OD Taxonomy and Phylogeny of the RBINS, Head of the Joint Experimental Molecular Unit, Prof. Thierry Backeljau. Our correspondence is presented for the attention of the members of the VVE.

Samenvatting. Nieuwe tijden brengen verschillende methoden en verschillende benaderingen met zich mee in de wijze waarop we de biodiversiteit van insecten bestuderen. Veel leden van de Vlaamse Vereniging voor Entomologie nemen actief deel aan verschillende projecten die verband houden met DNA-barcoding. Velen van hen verruilden ook hun entomologische netten voor geavanceerde digitale camera's en werden zeer enthousiaste rapporteurs van verspreidingsgegevens, biologische en morfologische kenmerken van insectensoorten.

De hoofdredacteur van Phegea stelde verschillende vragen over morfologie en moleculen, DNA-barcoding en auteurschap aan de directeur van de OD Taxonomie en Phylogenie van het KBIN, hoofd van de Joint Experimental Molecular Unit, prof. Thierry Backeljau. Onze correspondentie wordt aangeboden ter vriendelijke attentie van de leden van de VVE.

Résumé. Les temps nouveaux proposent différentes méthodes et différentes approches sur la façon dont nous étudions la biodiversité des insectes. De nombreux membres de la Société flamande d'Entomologie participent activement à différents projets liés aux codes-barres ADN. En outre, beaucoup d'entre eux ont échangé leurs filets entomologiques contre des appareils photo numériques sophistiqués et sont devenus des enregistreurs très enthousiastes de données de distribution, de traits biologiques et morphologiques des espèces d'insectes.

Le rédacteur en chef de Phegea a posé plusieurs questions sur la morphologie et les molécules, le code-barres ADN et les auteurs au directeur du DO Taxonomie et Phylogénie de l'IRSNB, chef du JEMU, le professeur Thierry Backeljau. Notre correspondance est présentée à l'aimable attention des membres du VVE.

Key words: Authorship — DNA barcoding — Morphology — New approaches.

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DNA- barcoding

JDP. You are the authority of the DNA barcoding. Please advise me and my editorial colleagues:

When the DNA barcode difference is 2.1% is it one or two species involved?

When the difference is 3.1% is it one or two species involved?

When the difference is 5.1% is it one or two species involved? etc. etc. etc.



TB. There is no such thing as a "universal" sequence divergence threshold that indicates a species-level differentiation. So, the argument of x % sequence divergence is in itself not valid to claim that two DNA

sequences belong to different species. In fact, this sort of argument was already disproven in the times that allozyme electrophoresis was used to differentiate species by "genetic distances". Anyway, % sequence divergence between species may vary strongly among taxa and the DNA gene fragments used. So it is not the % sequence divergence that should be used for taxonomic purposes, but rather the presence of a "significant" DNA barcode gap (i.e. bimodal distribution of % sequence divergences when intra- and allegedly interspecific sequence comparisons are analysed) and/or the phylogenetic structuring of the sequences involved.

Moreover, if sequence divergence is used as an indicator of species level differences, then the authors should show that the similar patterns of sequence divergences occur in several gene fragments, including both mtDNA and nuclear DNA.

IMPORTANT CONCLUSION: DNA barcoding is not a taxonomic black magic box !

Maybe as a hint: intraspecific % sequence divergences of 5% are not uncommon... in other taxa. We found such divergences in several millipede species. In stylommatophoran snails intraspecific % sequence divergences can be up to 30% (see Prévot *et al.* 2013 in the link further below)!

JDP. An article was published in *Zootaxa* in which the authors present the difference of 3.87% between the populations in India and France as belonging to one pest species. Now as the editor of another manuscript I deal

with very hot disputes between two research teams of China and India about a very similar case. So how big the DNA barcode difference should be that we can say with strong certainty based on the DNA barcode evidence that one or two species are involved?

TB. See my comment above: if the only argument is 3.87% sequence divergence (for which gene fragments?), then the argument does not seem valid to me... What is the % sequence divergence WITHIN the populations of India and France? Anyway, 3.87% sequence divergence is not particularly high, but as I neither know the taxa that are involved here, nor the gene fragments used, I cannot say much, except that mere % sequence divergence is not in itself a reliable taxonomic indicator.

My guess is that the dispute between the Indian and Chinese researchers reflects the political rivalry between India and China, rather than a sound taxonomic debate (Comment of the editor: the rivalry in taxonomy is a known phenomenon of all times, within all ages of taxonomists and in almost all countries).

JDP. It seems a trivial question, but it is very important for the authors because their professional status and position belong upon the published articles and described new pest species. How do the DNA barcoding people decide whether one or two species are involved?

TB. DNA barcoding is a powerful tool, but it is definitely not a magic stick that solves all taxonomic problems! Basically, DNA barcoding still depends largely on the interpretation of the researchers involved. That is why a sound taxonomy should be based on an integration of various data, including DNA. Yet, at the level of DNA, the most common way to decide about taxonomic issues, is to implement various types of species delimitation methods (= statistical and phylogenetic techniques to detect patterns of consistent "genetic gaps" between operational taxonomic units). Yet, even with such species delimitation methods things may remain difficult to interpret in taxonomic terms. Via this link I provide a paper in which various species delimitation methods are used:

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0060736>

Authorship

JDP. On online forums, we, editors, had a discussion about whether we should implement the rule that only actual contributors are the authors. However, knowing that the majority of our authors are from the countries where authorship of articles is perceived as a thank you service to friends, bosses, beloved ones, we decided to leave that upon the corresponding author. We had cases that authors could be even administratively punished if they do not include their bosses as co-authors.

You are the best authority on this ethical question. What are the habits in Belgium? Sorry for this question but this issue is quite often discussed among our authors. They point to a long authorship list of high positioned entomologists and ask us, editors, a similar question.



TB. I think that journal editors should not decide about who deserves to be co-author of the submissions they receive. There are many reasons why people are included as co-author of a paper, so in my opinion I see no logical reason why journal editors should interfere with this. What would be the point or added value to do so? Of course the journal can ask that authors add a short text block indicating the contribution of each author (several journals already do so), but in fact that only takes space and I'm not sure whether it is very helpful. Long authors' lists are indeed an increasing tendency, for which journals use various solutions, including moving the "bulk" of authors to some sort of appendix. Yet, do not forget that often such long authors' lists simply reflect large project contributions... and as a researcher you are supposed to collaborate... i.e. publish jointly... and yes in large complex projects, such collaborations may involve many authors.

Conversely, as a journal you could easily decide that it is a journal policy to allow no more than XX authors on a paper, just as some taxonomic journals have a policy of no longer accepting single species descriptions. Yet, I do not see why a journal would impose "a priori" limits to the number of authors of a paper. What would be the purpose? My feeling is that journal editors can only interfere with the authorships of the submissions they receive in case (some) authors are demonstrably linked to fraud or other "illegal" and "unfair" practices. Yet, in general I do not think that editors should bother about who is included as co-author of the manuscripts they receive. I neither see why the authors themselves would ask to editors to decide about this! I never had such case.

JDP. Thank you very much for your kind attention and reply to this issue also.

With my very best wishes and kindest regards.