

REPLY / RÉPILIQUE

Reply to the comment by L. Prendini on “Identifying spiders through DNA barcodes”¹

Paul D.N. Hebert and Rowan D.H. Barrett

Abstract: Our paper on spiders provides an early demonstration of the power of DNA barcoding; we believe that its conclusions will prove scalable to all eukaryotes. We further anticipate that the “Barcode of Life” movement will soon lead to automated systems for species identification and discovery. However, we emphasize that these systems will operate within a Linnaean framework and that collaborations between molecular and morphological taxonomists are critical.

Résumé : Notre travail sur les araignées fournit une des premières démonstrations du potentiel des codes-barres d’ADN et nous croyons que ses conclusions pourront s’appliquer à diverses échelles à tous les eucaryotes. Nous prédisons aussi que le mouvement du « Code-barre de la vie » entraînera la mise au point de systèmes automatisés pour l’identification et la découverte des espèces. Nous insistons, néanmoins, que ces systèmes s’élaboreront dans un contexte linnéen et que la collaboration entre les taxonomistes moléculaires et les morphologistes en sera un élément essentiel.

[Traduit par la Rédaction]

Ironically, the submission date of Lorenzo Prendini’s (2005) commentary on our paper coincides with the First International Conference on the Barcode of Life hosted by the Natural History Museum (London). The enthusiasm among the 220+ delegates and the grand projects that were launched at this meeting (Marshall 2005) contrast sharply with Prendini’s restrained endorsement of DNA barcodes. We do not agree that barcodes are just one more implement in a bristling quiver of approaches that taxonomists can use to document and catalogue biodiversity. We say this because they represent an important shift from the usual recognition of species by breaks in analog gradients of, for example, size, shape, and colour. By exploiting the digital nature of DNA sequences, barcoding will enable the development of automated identification systems for known species, regardless of life stage or gender. By democratizing and speeding access to identifications, barcoding will help to resolve the “taxonomic impediment” (Janzen 2004).

We also emphasize the critical need for the acceleration of species discovery because un-named species gain no protection from biodiversity accords at international (e.g., Conven-

tion on Biological Diversity) or national (e.g., Endangered Species Act in the USA) levels. We further note that because deep genetic divergences are the rule, even between closely allied species (Hebert et al. 2003a, 2003b, 2004a; Hogg and Hebert 2004), DNA barcoding is a powerful approach for the discovery of new species. Despite this capability, we emphasize that the discovery of previously undescribed species is augmented when information on morphological and ecological characters are fused with DNA barcodes (Hebert et al. 2004b). Hence, we urge strong collaborations between barcoders and taxonomists, and we can point to a growing number of such partnerships that are significantly advancing both the barcode registry and our understanding of species diversity.

Prendini (2005) devotes much of his communication to a discussion of the varied reasons why DNA barcodes will fail to deliver, but the main contention lies with the scalability of our results. This critique is hardly novel, because every technological or scientific advance must weather this challenge. The 1903 Wright Flyer was surely awkward, but powered flight soon proved scalable to a planetary level. In a similar fashion, a few studies, such as our work on spiders, have now revealed the possibility that DNA barcodes will enable the identification of life to soar. Results presented in London indicate that DNA barcoding holds promise for species recognition in all eukaryotic lineages. As a consequence, analytical facilities are ramping up capacity to support increasingly ambitious projects and the major genomics repositories (DDBJ (DNA Data Bank of Japan), EMBL (European Molecular Biology Laboratory), NCBI (National Center for Biotechnology Information)) are developing protocols to organize the looming flood of barcode sequences. Work on animals is most advanced and projects on birds and fishes

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P.D.N. Hebert.² Department of Integrative Biology and Biodiversity Institute of Ontario, University of Guelph, Guelph, ON N1G 2W1, Canada.

R.D.H. Barrett. Department of Biology, McGill University, Montreal, QC H3A 1B1, Canada.

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²Corresponding author (e-mail: phebert@uoguelph.ca).

will soon deliver global barcode coverage (Marshall 2005). Large-scale projects on varied invertebrate groups, as well as on flowering plants, are also underway. In short, the barcode community is responding to the scaling challenge with projects that tackle major compartments of biodiversity in a comprehensive way.

A DNA-based future can herald several possible fates for the Linnaean system — from outright dismissal to revitalization. Those who support the move to a PhyloCode (Cantino and de Queiroz 2000) argue for the replacement of Linnaean taxonomy with a system founded on phylogenetic principles. Other proposals, such as those favouring a DNA-based taxonomy, also anticipate abandoning our current system of classification (Tautz et al. 2003). DNA barcoding, however, promises a gentler treatment of the Linnaean system. A large-scale DNA barcode program may swamp the immediate ability of the taxonomic community to describe all of the newly discovered species, but this “problem” can be countered through an interim taxonomic designation for “species-in-waiting” (Hebert et al. 2004a). The assembly of barcode libraries will also transform the way that identifications are made, provoking a move from morphological keys to automation. However, this work will be executed within a system whose coordinates are firmly Linnaean. More importantly, DNA barcodes will be a great enabler of the primary goal of the Linnaean enterprise — the registration of life’s diversity. It’s for this reason that we urge collaboration rather than contest between those who explore diversity through DNA or through morphology. Once these partnerships are in place, taxonomy really will take flight.

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