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Comment on “Taxonomy and the DNA Barcoding Enterprise” by Ebach (2011)

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Since Linnæus (1735) proposed a now globally adopted classification scheme, taxonomists have benefited greatly from the ‘Linnæan Binomial Enterprise’. Ebach’s (2011) concerns, particularly that taxonomy “is slowly dying off”, were around well before DNA barcoding began. Here we discuss the integrative potential of DNA barcoding with morphology, which contrary to Ebach’s comments, has proved a useful addition to the taxonomists tool-kit; such molecular applications to taxonomy are not new and have been widely used by taxonomists for over 30 years (e.g., Kitchener *et al*. 1984).

We argue that taxonomy, like the vast majority of disciplines, must continue to develop in response to changing technologies. Taxonomy is not the static science as Ebach portrays. Scanning Electron Microscopy (S.E.M.) is a good example of a valuable tool that has assisted taxonomists since it became commercially available around 1965; and now the use of environmental S.E.M., confocal microscopy and mini-CT scanners are proving useful as taxonomic tools (e.g., http://digimorph.org/). DNA barcoding enters this category. It has the added advantage that its application crosses many facets of science and we agree with Ebach that the benefits of DNA barcoding in biosecurity, food sciences and forensics are certainly a clear highlight (see also Mitchell 2011).

Ebach rightly points out that the “*…payoff for the taxonomist is funding and elevated importance in their home institution*” (p.67), but several of his subsequent statements are confusing. For example, Ebach fears that “*The proposed solution…is to re-vamp taxonomy as a service industry to provide ready identification and classifications for non-taxonomists.*” (p.67) and thus “*…liberate other fields, such as ecology, to practice species identification without any taxonomic training*” (p.67). Are these not already practices that have been undertaken by taxonomists since the Linnæan classification scheme was widely adopted? Most biological disciplines currently rely on taxonomy to formalise the model organisms they study. In fact, taxonomy, through binomial naming, is the basal hypothesis that one deals with entities with homologous properties among individuals. So why is this an issue? Type material lodged in museums is, we assume, for others to identify and compare specimens with in the future. Other scientific fields have benefited from taxonomic expertise since museums and other institutions became the repositories of our publicly available natural antiquity.

Before DNA barcoding, taxonomists were no less involved than today in routine identification for other fields of study, rather taxonomists pursue their own goals (from description of new species to phylogenies). Often the identifications of specimens not done by specialists were error prone and/or did not reach the species level. It is not entirely clear why Ebach assumes that “*most readers of Zootaxa would be cringing…*” (p.67) if non-taxonomists practice species identifications using taxonomic tools, namely published descriptions and keys provided by taxonomists for identification purposes (one of the goals of taxonomy); such practices have been around as long as taxonomy itself and are constantly being updated as new species are described or revised, and they continue to adapt to new technologies (e.g., Cranston 2005; Maddison *et al*. 2007). This view appears to revolve around the phrase “parataxonomists”, which is clearly an issue for Ebach, and refers in this case to a biodiversity study of ants identified to genus in Madagascar (Smith *et al*. 2005). Simply put, this brings a name to assistants to taxonomists in field collection, sorting and identification of taxa using available taxonomic tools (i.e., keys elaborated by taxonomists), a practice that is common-place (see Krell 2004 for a discussion of ‘parataxonomy vs. taxonomy’).

It appears that Ebach has two real issues. The first relates to how taxonomists could use DNA barcoding as a taxonomic character; he suggests that “*…nowhere do we find its uses for taxonomy*” (p.67). The second issue relates to

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the perceived decline of taxonomists as a result of DNA barcoding; “*Rather than hire taxonomists, museums can now hire parataxonomists and barcoders at a fraction of the cost of training taxonomists*” (p.67) and thus “*Ironically, industry no longer has to spend a penny to procure barcoding data and taxonomic expertise, while at the same time taxonomy and taxonomic expertise is slowly dying off*” (p.67). A critical oversight in Ebach’s arguments is that the decrease in taxonomists began long before DNA barcoding, and initiatives have been implemented to tackle this issue. For example, in 1995 the U.S. National Science Foundation (NSF) initiated the Partnerships for Enhancing Expertise in Taxonomy (PEET) (Rodman 2007), and the Australian Biological Resources Study (ABRS) also provides considerable funds for taxonomic studies.

Below we discuss DNA barcoding as it applies to current uses in taxonomy and we explore where taxonomy could benefit more in the future. We see two alternatives for taxonomists: to ignore barcoding or to be involved, and briefly discuss these below.

(1) Ignore DNA barcoding (and all molecular approaches) and leave these to purely molecular researchers. What would be the outcome? It would limit opportunities for funding in biodiversity projects, which increasingly rely on molecular approaches. Disconnecting taxonomic activities from DNA barcoding would bring further collateral damage. Would DNA barcoding die? No, it would likely grow and generate an alternative classification routinely used as a proxy for species, a practice which is already widely accepted for microorganisms, keeping loose connections with morphological taxonomists (e.g., Fox *et al.* 1977; Hedi *et al.* 2009). The paucity of morphological characters in these groups led to the reliance on molecular taxonomy; this is not the case for most taxa currently studied and described in taxonomic journals. If taxonomists ignore DNA barcoding it will develop as an independent taxonomic tool, and DNA barcoding will gain increasing popularity within the scientific community, at the expense of alpha-taxonomy.

(2) Be involved, taking advantage of DNA barcoding for taxonomy. It is difficult to deny the value of DNA barcoding for taxonomy, and Ebach does not discuss the issue. For linking molecules to the huge corpus of knowledge about organism morphology and biology, taxonomic input is essential, and this integration is a primary objective of DNA barcoding (see Hajibabaei *et al.* 2007), but it is up to taxonomists to get involved. DNA barcoding brings an independent set of characters obtained in a relatively easy way, and directly comparable between species and populations. In complement to morphological assessment, it greatly helps to disentangle species complexes and separate sibling species (e.g., Porco *et al.* 2010a; Dinca *et al.* 2011), to highlight cryptic diversity and potential new species overlooked by morphological analysis (e.g., Hausmann *et al*. 2009; James *et al.* 2010; Saunders & McDonald 2010), to unambiguously link juveniles to adults of the same taxon when they are morphologically different (e.g., Valerio *et al.* 2009; Potapov *et al.* 2010; Richard *et al.* 2010), and to allow species-level identifications in groups that require the use of characters that are only present in one sex. Moreover, protocols for recovering DNA from specimens of small arthropods non-destructively while preserving them as voucher specimens (Paquin & Vink 2008; Porco *et al.* 2010b) provide the opportunity to further examine ‘anomalies’, such as cryptic diversity.

Overlooked diversity is probably the most fruitful field for DNA barcoding applications, and the one which is most directly linked to current taxonomic concerns. Numerous barcoding examples have revealed hidden diversity, flagging it for further morphological scrutiny, but also tagging it for studies in other disciplines (e.g., Hendrich *et al.* 2009; Saunders & McDonald 2010; James *et al.* 2010). A simple search (keywords "new species", "description" or "revision") of the International Barcode of Life literature database (http://ibol.org/resources/scientific-publications/) provides 22 examples where DNA barcoding has benefited taxonomists since 2009 alone, and there are likely to be many more (using Google™ scholar, the same keywords with "barcoding", returned 102 articles in *Zootaxa* alone). Ebach is correct in his assertion that “*Many taxonomists ... find themselves largely responsible for addressing specimens which have unidentifiable barcodes (often assumed to mean ‘new species’) or revising problematic taxonomic groups in order to streamline classifications*” (p.67); this is, after all, the core business of taxonomy. In this context DNA barcoding also enables taxonomists and the wider scientific community to link the corpus of knowledge about a particular taxon to a name, and eventually to revive species discarded as synonyms. For example, DNA barcodes were used to resolve the species complex *Oenochroma vinaria* Guenee, 1858 (Lepidoptera: Geometridae) with a DNA barcode from the type specimen (Hausmann *et al.* 2009), and barcoding of the type specimen of the earthworm *Lumbricus terrestris* Linnæus (1758), along with one of its major synonyms (James *et al.* 2010), is also emblematic in this respect. This approach maintains the taxonomic legacy vivid in today’s science, linking past knowledge to present findings, and demonstrates that, contrary to Ebach’s statement that “*Taxonomists…have little use for barcodes*” (p.67), taxonomists and the rest of scientific community can mutually benefit from integrating such a tool. In fact, more and more taxonomists now routinely provide a DNA barcode as part of the species description (e.g., Porco *et al.* 2010b; Palacios-Vargas *et al.* 2011).

Currently, DNA barcoding is one of many useful tools on the bench of the taxonomist, not the competitor. In making easier the exploration of taxonomic diversity where morphological tools are at their limits, it streamlines a timeconsuming process and affords the taxonomist time to pursue more interesting and relevant questions. It may not be the ‘shining bullet’ but it certainly offers a valuable ancillary tool for taxonomists.

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