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DNA barcoding is useful for taxonomy: a reply to Ebach

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DNA barcoding is all too often derided by taxonomists with little understanding of how far this emerging subdiscipline of systematics has progressed since it was proposed by Hebert *et al.* (2003). A prime example is Ebach's factually incorrect and misleading recent correspondence (Ebach 2011). Ebach and I agree on one point: indeed many readers of *Zootaxa* would have cringed as they read his letter, though perhaps the cause was a tasteless joke. For brevity I will address only three key points he raised about the uses for DNA barcoding.

First, bird strike is no laughing matter as the 155 people who survived US Airways Flight 1549 ditching into the Hudson River in January 2009 will attest. Jokes about "*pâté [de] foie turbine*" do not do justice to the gravity of the subject. Subsequent DNA barcoding analysis of bird remains identified the culprits as Canada Goose (*Branta canadensis* Linnaeus, 1758) (Marra *et al.* 2009). Fortunately aviation authorities recognize the importance of bird species identification following bird strike as it allows them to tailor risk management measures to particular species, and they are funding ongoing research in this area.

Second, the recent literature contains many examples of taxonomists having embraced DNA barcoding to assist with their research. Ebach's claim that none would be interested is patently untrue. Recent examples include taxonomic papers on oomycetes (Bala *et al.* 2010), limpets (Johnson *et al.*, 2008), collembolans (Porco *et al.* 2010), caddisflies (Pauls *et al.* 2010) and moths (Hausmann *et al.* 2010). In addition, taxonomists are using barcoding to associate adult and immature life stages in such disparate taxa as fish (Baldwin *et al.* 2009), frogs (Hiobiarilanto *et al.* 2010) and insects (Stur & Ekrem 2010).

Third, Ebach uses the term "parataxonomy" as a slight on molecular systematists who might not have the same in-depth knowledge of morphology and biology as a taxonomic specialist. I take issue not with this insult but with the implication that we should not trust identifications made by such "non-experts". Consider the multi-billion dollar industry of medical pathology. A technician working in a commercial pathology lab is not a bacterial systematist so why do people trust diagnoses emerging from their laboratories? It is because they are following molecular biological and biochemical protocols for species diagnosis that have been developed by microbiologists, rigorously tested for their specificity and sensitivity and have withstood thorough peer-review. The parallels with DNA barcoders are self-evident. If the molecular systematists (Ebach's "parataxonomists") cranking out barcode sequences do not have the required specialist taxonomic knowledge they collaborate with taxonomists who do. Bear in mind that the DNA barcode is not just a sequence but also comprises, among other things, a voucher specimen with its corresponding collection information and a species determination. As with any taxonomic study the species determination is a hypothesis proposed by a named individual (so that people can gauge for themselves the degree of certainty of the identification) and this can be tested by subsequent researchers through further study of the voucher specimen. The same criteria that apply to a good morphological taxonomic study apply also to barcoding: have sufficient numbers of specimens been sampled, have closely related species been examined to determine the species-specificity of diagnostic character states, and so on. Thus the implication that DNA barcoding is somehow methodologically inferior to morphology-based taxonomy is based largely on ignorance.

A related point often raised by the anti-barcoding lobby, is that barcoding is "not science". It is instructive here to distinguish between the initial process of building and validating a DNA barcode reference library and the subsequent technical process of performing routine identifications. Taxonomic expertise is crucial for the former, and as every researcher who has ever been involved in a DNA barcoding project knows it often comprises multiple iterations of morphology-based and molecular-based investigations to establish where species boundaries lie; this is the scientific part. Subsequently only generic technical skills are needed for running diagnostics tests; this is the technical "not science" part. The elephant in the room here is that once a thorough DNA barcode database has been built and validated,

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taxonomists will no longer have to be consulted for all routine identifications. Provided morphological and barcode-based identifications agree, barcodes provide a diagnostic test that can be implemented cheaper and faster than morphological methods for large sample sizes. Some taxonomists appear threatened by this potential although I suspect most would be happy to be released from routine identification duties to concentrate on the more difficult, and more interesting, taxonomic questions. And there is no shortage of those. "Barcoders" are building an identification system that could be used by parataxonomists (and indeed by anybody) to increase the accuracy of their identifications. While barcoding certainly will not solve all alpha-taxonomic questions, it will rapidly identify those questions that are too complex to be solved with a simple single gene system. It is here that other systematists should concentrate their research efforts for maximal productivity.

Finally, the Barcode of Life Data Systems database (http://www.boldsystems.org/) is undergoing exponential growth and is attracting a rapidly-growing user group who, while not blind to the limitations of DNA barcoding (e.g. Baldwin *et al*. 2011), have voted with their feet. For a balanced and timely review of DNA barcoding, and in particular an explanation of the crucial differences between DNA barcoding and DNA taxonomy, a distinction which many taxonomists still struggle to grasp, see Teletchea (2010). In my experience, sceptical specialist taxonomists may remain unconvinced about the potential of DNA barcoding until they have seen barcode data for their taxa of interest. Perhaps it is our loss that Ebach cannot extract DNA from trilobites!

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