



Neither molecular nor morphological data have all the answers; with an example from *Macrobrachium* (Decapoda: Palaemonidae) from Australia

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Much controversy still seems to surround the role of molecular data in general, and DNA barcoding in particular, within the taxonomic community. This has led to numerous “call and response” pairs of papers, most recently Ebach (2011) and Mitchell (2011), but preceded by many other pairs, such as Packer *et al.* (2009) and Hołyński (2010). There have been numerous calls for a more “integrative” approach to taxonomy (Mitchell 2011; Stevens *et al.* 2011), which itself has generated point and counterpoint papers (Dayrat 2005; Valdecasas *et al.* 2008). This of course is how science progresses (although Max Planck suggested that science advances “one funeral at a time”, en.wikiquote.org/wiki/Max_Planck, accessed 20 March 2011).

If one looks carefully at many of these papers, there is almost always an acknowledgement of the utility of the “other” type of data, such as “We emphasize that DNA barcoding is not a substitute for conventional taxonomic approaches” (Costa *et al.* 2007) or “Sometimes molecular analysis may be the most convenient way to clarify the taxonomical assignments between sexes, developmental stages, castes etc.” (Hołyński 2010). Surely, eventually a point is reached when, to paraphrase U2’s Bono, “There’s been a lot of talk about this, maybe too much talk” (Under a Blood Red Sky, 1983), and perhaps we should all just get on with it.

It seems pretty obvious to us that both types of data are extremely useful, have their own strengths, weaknesses and purviews (with some overlap), and one would be foolish to ignore either of them out of hand. Both DNA barcoding and morphological descriptions are often the tip of the scientific iceberg and a starting point for further scientific analyses. Neither morphological characters nor DNA sequences fully define a living, breathing biological organism, any more than your passport photo fully reflects you.

An example from freshwater prawns

We think that these sorts of discussions are best carried out with reference to real data rather than as philosophical debates, and so we present some new data on Australian freshwater river prawns *Macrobrachium* (Palaemonidae) to show the utility and futility of both molecular and morphological data. In the spirit of full disclosure, we need to admit that we are both evolutionary biologists who primarily use molecular data, but with an interest in taxonomy, if perhaps no great skills in it; but we know people who have. We were sent an unidentified juvenile specimen (Queensland Museum accession number W29088) from the Northern Territory, Australia, by Dave Wilson of Aquagreen. Juvenile *Macrobrachium* can be notoriously difficult to identify accurately to species using traditional morphological methods (Holthuis 1950) because many of the commonly used taxonomic characters are conserved between species in juveniles, and because most morphological identification requires adult males (Short 2004). We asked Dr John Short of BioAccess Australia to examine the morphology of this specimen for us. He determined that it was an undeveloped, sexually immature male that could not be distinguished from *M. equidens* (Dana) at that stage of development, and would also be hard for many people to distinguish from *M. novaehollandiae* (De Man) (J. Short, pers. comm.).

At this stage, we were pretty confident that we could identify it using fairly prosaic “DNA barcode”-type methods (Costa *et al.* 2007). This was because this genus is well known in Australia, both morphologically, thanks to a comprehensive taxonomic revision by Short (2004), as well as molecularly, as all 13 species known to occur in Australia have been sequenced (many in Murphy and Austin 2004). Therefore matching our new sequences from an unknown juvenile specimen to existing sequences from identified specimens should have been straightforward.

We followed a well-worn “pedestrian” (Goldstein and DeSalle 2010) path by sequencing portions of two mitochondrial genes; cytochrome oxidase I (COI, the “DNA barcode”) and 16S ribosomal rDNA (16S, the most