Need morphology always be required for new species descriptions?

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Abstract. Despite the widespread and common use of DNA-sequence data to estimate phylogenies, support or contest classifications, and identify species using barcodes, they are not commonly used as the primary or sole source of data for describing species. This is possibly due to actual or perceived pressure from peers to include morphology as the primary source of data for species descriptions. We find no compelling evidence to exclude DNA-only descriptions, or to insist that morphology always be included in a species description. It is not the data type *per se* that is important, but the science behind the taxonomic conclusions. Using alternative kinds of data for descriptions should not cause problems for taxonomy if links are kept with type specimens.

Introduction

For centuries, species have been delimited and described on the basis of morphological features observable by the naked eye or with the assistance of light microscopes. For most of that time, morphological characteristics, behaviours and specimen locality details were the only types of data available to taxonomists. This is no longer the case. The invention and uptake of DNA sequencing technology has resulted in an explosion of additional data: roughly 10% (~160 000 spp.) of all described species are represented by DNA-sequence data in National Center for Biotechnology Information (NCBI) and European Molecular Biology Laboratory (EMBL) databases. DNA-sequence data are now routinely used to characterise variation within and among species (e.g. Monaghan *et al*. 2005; Pons *et al*. 2006), as well as to estimate relationships among species, yet outside microbiology (e.g. O'Rourke *et al*. 2004) DNA-sequence-based taxonomic descriptions are rare.

We are in a time of global biodiversity crisis (e.g. Koh *et al*. 2004) and the 'taxonomic impediment' is reported as a major hurdle to managing biodiversity (Convention on Biological Diversity, http://www.cbd.int/, verified July 2010). The question posed here is now highly relevant: should we be able to forgo morphology and formally describe a species using DNA sequences alone? We find no compelling evidence to exclude DNA-only descriptions and suggest that species description could proceed more efficiently with greater flexibility in the kinds of data accepted for taxonomic descriptions.

The evolving practice of taxonomy

Some primary aims of taxonomists are to delimit, describe and identify species. These are three quite different, but related,

activities and it is important to recognise the distinctions among them (e.g. see Moritz and Cicero 2004). Species delimitation is the process of determining what a species is and, hence, requires an associated species concept. Once a species is delimited, it can be described, and resources such as keys, diagnoses and DNA-barcode libraries (e.g. Hebert *et al*. 2003) can be developed to help users of taxonomy to distinguish it from other species (identification).

Many kinds of data, including allozymes (e.g. Harvey *et al*. 2007), scanning (e.g. de Bivort and Giribet 2004) and transmission electron microscopy (e.g. Mladineo and Bocina 2006), DNA-sequence data (e.g. Kuusela *et al*. 2008), geographic distribution (Brooker and Hopper 1991), as well as traditional morphology, have been used to delimit and identify species. These practices are generally accepted and little disputed, except for some aspects of DNA barcoding (e.g. Omland *et al*. 2006; Rubinoff *et al*. 2006). However, there are differences of opinion on what are considered suitable data for taxonomic descriptions (e.g. Dunn 2003). This might be because descriptions are traditionally the territory of taxonomists. Whereas geneticists and others commonly contribute to species delimitation (e.g. Dobzhansky and Epling 1944), and it is common practice for non-taxonomists to develop and apply molecular tools for identifying already described species (e.g. Cavalieri *et al*. 2008), taxonomy remains a relatively 'closed' profession. The perceived schism (e.g. Dunn 2003) between the use of morphology and DNA for taxonomic descriptions is likely reinforced by the widespread use of the term 'DNA taxonomy' (e.g. Vogler and Monaghan 2007), which singles out the primary use of DNA data as being somehow different from 'taxonomy'. However, taxonomy, as a science, should not be restricted to certain types of data.

If you can't see it's different, why bother describing it as different?

This is a question that has been asked of each of the authors at some time. The answer to the question relates to 'what is a species?'. The species concept to be used is the first question upon which a taxonomist needs to decide – without it, species delimitation is not possible. However, taxonomists are rarely explicit about their methods of species delimitation – the types of entity they seek to characterise (i.e. their species concepts) must be largely inferred by the reader. At the most basic, a species might be 'a morphological kind that is different from other such kinds' (Mayr 1996). For some practising taxonomists, this might be sufficient. For most biologists (taxonomists included) and for many users of taxonomy, it is important to capture other aspects of biodiversity (e.g. gene pools, genetic diversity, phenotypic diversity, evolutionarily distinct lineages), rather than to identify only morphological discontinuities (e.g. Hey 2001).

In our experience, most practising taxonomists use morphological features as clues about the discreteness (or otherwise) of gene pools, niche occupants and units of divergent evolution. Many probably even agree with De Queiroz (2007) that species are theoretical entities, 'separately evolving metapopulation lineages', with several time-dependent properties that can be used for species delimitation. The important point is that the species concept used determines what sorts of data can help to delimit the species. Only under the most basic 'morphological kind' concept are data restricted to morphological characters.

For species delimitation under most of the other generally used species concepts, including the biological species or related concepts, the value of DNA-sequence data is immense (Tautz *et al*. 2003). A single string of nucleotides is no more the 'essence' of a species than a handful of morphological features, but genomes are enormous – DNA-sequence data provide much power to circumscribe species. Hence genetic data, including DNA sequences, are often now incorporated in taxonomic decisions, even if not directly included in species descriptions (e.g. Gullan *et al*. 2003; Andriaholinirina *et al*. 2006). Indeed, several of us (the authors) have used genetic data to verify morphology-based decisions before publishing solely morphological descriptions and diagnoses – one reason being peer pressure to conform to entrenched 'morphology has priority' practices.

Because biologists are commonly interested in species for ecological and evolutionary reasons, cryptic species (multiple species which were originally considered to be a single species on the basis of morphology, or morphologically indistinguishable species) are as relevant as morphologically differentiable species (Trontelj and Fišer 2009). There are many examples of how DNA-sequence data have shed light on biologically distinct species that had not been clearly recognisable on the basis of morphology alone (e.g. reviews of Bickford *et al*. 2007; Pfenninger and Schwenk 2007). Individual examples of cryptic species discovered through DNA-sequence data (with the term 'DNA barcoding' now often misapplied) include the Neotropical skipper butterfly (*Astraptes fulgerator*) – 'ten species in one' (Hebert *et al*. 2003), and two species of African elephant (Roca *et al*. 2001). On the other hand, DNA-sequence data have also

been used to demonstrate that species previously recognised on morphology alone do not represent distinct biological units (e.g. quagga and zebra, Leonard *et al*. 2005).

There is little argument that multiple kinds of data have a role to play in helping to delimit species, and that not all data are always equally useful. The question of whether the data (e.g. a single gene region) are sufficient to delimit a species is another issue (e.g. Omland *et al*. 2006; Edwards and Bensch 2009), and applies to all types of data. Assuming that one is dealing with well delimited species, how then should one describe a species for the first time?

Species descriptions

For plants and animals, species are typically described by their morphology, albeit sometimes with descriptions supplemented by additional data such as geographic location (e.g. Brooker and Hopper 1991), supporting genetic evidence of species distinction (e.g. Gullan *et al*. 2003; Andriaholinirina *et al*. 2006) or DNA sequences from the type specimen (e.g. Cook 2003; Perkins and Austin 2009).

Species need to be unique and identifiable. Each species must have a unique name under its respective code. Each name must be tied to a type specimen. None of these requirements precludes a description based on DNA sequences alone, and arguments against DNA-based species descriptions (e.g. Dunn 2003; Lipscomb *et al*. 2003) usually do not claim that DNA sequences cannot distinguish species. A major argument against using DNA sequences alone to describe a species assumes that identification of DNA species will be more challenging to most people (e.g. Cameron *et al*. 2006).

Many identification exercises are challenging, for example determining which species of armoured scale insect is infesting a consignment of bananas in quarantine. This is an example of identifying species, not of describing species, but we consider it a useful exercise to consider the cost and accessibility of using different kinds of data to identify organisms because it has been argued that DNA sequencing is too expensive for developing countries, whereas it is sometimes proposed that morphology can be done by 'anyone' (e.g. Cameron *et al*. 2006). Under the traditional expert-centred paradigm, the job of identifying the armoured scale insect requires a person with years of training and with access to specialised resources, such as slide-making sundries, a powerful compound microscope, a comprehensive reference collection and a massive taxonomic library to dissolve body contents, stain the cuticle, prepare slide mounts, observe minute details under powerful magnification and consult the specialised diagnostic resources. None of these resources is cheap or easy to acquire, and each requires space and maintenance. In addition, this process is time-consuming and few improvements in efficiency can be achieved at scale. Also, as armoured scale insect taxonomy is based entirely on the morphology of adult females, if the banana consignment contained only immature specimens, identification would be impossible.

In comparison, out-sourced DNA sequencing is cheap and easy. A single technician with a general training in molecular techniques could prepare specimens to send out for sequencing – one hundred specimens a week could be done easily and

relatively cheaply, or many hundreds a week if more expensive kits and plates are used. DNA-sequence data have the additional advantage that they can be used to identify all life history stages and just about all body parts (Sperling and Roe 2009). Returned sequences could be matched against databases for an almost instantaneous identification. However, reference databases are not yet comprehensive enough to allow identification of most species – a situation unlikely to change in the near future.

Another issue with current DNA-sequence databases is that taxa are represented by heterogeneous loci; to make a DNA-based identification, one would need to have some idea as to what higher grouping the organism belonged so that appropriate gene regions and primers could be used. Although an admirable idea, standardised COI barcoding (Hebert *et al.* 2003) will not, and cannot, work for all species (e.g. Rubinoff *et al.* 2006). However, for a growing number of pest species, useful data are becoming available (e.g. Edwards *et al.* 2008) – but again, there typically needs to be some idea of what the species might be.

Herein lies what appears, at first, to be a major problem – if species are described by DNA sequences alone, and diagnostic markers or primers are heterogeneous across taxa, one must draw on some other source of information to determine how exactly to proceed with a DNA-based identification. However, as pointed out above, identification and description are two different processes. Identification tools are not restricted to characters that were used in the original description. If they were, then DNA-based identification would not be possible for most organisms given that most species descriptions do not include DNA sequences. It follows, then, that if a species were to be described on the basis of DNA sequences, there would be no impediment to someone developing identification tools that included morphology. For example, an interactive (Lucid) key could be developed for an entire group that had been described by DNA alone. The crucial factor is that type specimens are available for examination, and this is currently required under the respective codes (see below).

Would there be two independent systems?

It has been argued (to us) that allowing DNA-sequence-based descriptions might create two independent systems of taxonomy, one based on morphology and the other on DNA. Before a taxonomist describes a new species, he/she needs to check that the species has not already been described. Typically that involves comparison of the morphology of the putatively undescribed species with the morphology of specimens stored in collections or described in the scientific literature. If some species had been described solely on the basis of DNA-sequence data, a taxonomist might not be able to perform the necessary comparisons without sequencing individuals from the potentially unnamed taxon. However, he/she would be able to compare the new specimens with the type material of the DNA-described species, as types are required under the codes (see below) no matter what form the description. A more difficult task is often in the other direction, where a taxonomist wishes to compare DNA sequences of a new specimen with that of a morphologically

described species – there is often no DNA resource material available. If all new species descriptions of plants and animals included both morphological and DNA-based data, as proposed by Tautz *et al.* (2003) and Perkins and Austin (2009), a more universal, rather than more restrictive, taxonomy would result. This practice is now common for publication of new fungal species names (see any issue of *Persoonia*). At a minimum, authors of newly described species should facilitate the possibility of future DNA work by vouchering suitable material. This could be as simple as choosing the most suitable specimen (e.g. recent collection, at least some tissue well preserved in a lasting way) as the holotype.

How can a DNA-based description work?

If species are discovered on the basis of data other than morphology, how much effort, time and resources should be put into trying to find and illustrate distinguishing morphological features for individual species descriptions? We argue that this would depend on the researcher and the potential uses of the knowledge of the species. In many cases, it is probably more important to have species recognised and named, than to wait years to find and/or illustrate any distinguishing morphological characters. Blanquer and Uriz (2008) describe several decades of lag-time between species discovery and description because of delays caused by needing to find and illustrate morphological differences. The taxonomic process could be accelerated by judicious use of DNA-sequence-based descriptions, as long as good science still underlies the taxonomic decisions. If distinguishing morphological features are later found or described, they could be added to the tool set for distinguishing (identifying) the species. What follows is an example of how this could work.

In a genus description, an author describes the features that are common to all species in that genus, and may also summarise the variation across species in certain attributes. Each species description inherits those attributes from the more general or abstract class. A species description could also function in a similar way. In the case of a group of cryptic species, a species-group description could describe the morphological attributes shared among those species, and a species-group diagnosis could make it clear how to morphologically recognise the group as a whole. Often, this description would be equivalent to, or an improved version of, the morphological description of the originally recognised species before it was discovered to be a cryptic-species complex. Each species description would inherit those attributes from the species-complex description, but also comprise the features that are actually diagnostic for the species – the DNA sequences, diagnostic sites and/or DNA synapomorphies. A specimen would be vouchered as usual and DNA sequences deposited in GenBank or EMBL, but DNA should also be vouchered and stored so that it can be accessed if required in the future. As long ago as 1991, Reynolds and Taylor (1991) flagged that DNA-only, and combined DNA-and-morphology-based, descriptions would begin and urged herbaria to prepare for curating DNA type material. However, most museums and herbaria are still not prepared for curating genomic material, although frozen tissue collections for

phylogenetic work are becoming more common (e.g. South Australian Museum). In many cases, authors who use DNA-sequence data in taxonomic decisions and descriptions need to curate material in their own institutions (e.g. Cook 2003).

In many circumstances, additional data, such as host use or geographic location, might also help distinguish among cryptic species and these attributes should also be incorporated in the description. However, in the case above, we believe the absence of any other data should not preclude the publishing of a species description with diagnosis by DNA-sequence data alone. The following is a simplified and hypothetical example of what a DNA-sequence-data-only description could look like:

Crypsis cryptes species-complex

Morphological description of species complex here.

Crypsis cryptes (Author)

Information about how it was determined that this collection is representative of the original type of the originally described species.
Material examined. *Location and/or host data. Any other biological data available.*
gene A: ACCGTTAGGT<u>T</u>TACGTAWCGAT<u>C</u>GGGCTA.
This species is distinguished by this gene from all others in the species complex by the two underlined synapomorphies.
gene B: TTGCTCTCGTTAAGAGG<u>G</u>GACACCC<u>ATG</u>GCC.
This species is distinguished by this gene from all others in this species complex by the underlined synapomorphies, which include the triple nucleotide motif ATG.
gene C: TTAGCCAGTYAGCAA<u>TATATATA</u>GCGCGCTAC.
This species is distinguished by this gene from all others in this species complex by presence of four repeats of the (TA) motif (underlined).

Crypsis quasicryptes, sp. nov.

Material examined. *Location and/or host data. Any other biological data available.*
gene A: ACCGTTA<u>A</u>GTCTACGTAWCGATGG<u>C</u>GCTA.
This species is distinguished by this gene from all others in this species complex by the two underlined synapomorphies.
gene B: <u>A</u>TGCTCTCGTTAAGAGGG<u>A</u>GACACCCCTCGCC.
This species is distinguished by this gene from all others in this species complex by the two underlined synapomorphies.
gene C: TTAGCCAGT<u>A</u>AGCAATATATAGCGCGCTAC.
This species is distinguished by this gene from all others in this species complex by the underlined synapomorphy.

Are such descriptions allowed under the current codes?

Neither the ICBN (International Code of Botanical Nomenclature, http://ibot.sav.sk/icbn/main.htm) nor the ICZN (International Code of Zoological Nomenclature, http://iczn.org/) has rules about what constitutes a description. Thus, neither code specifically excludes the use of DNA-sequence data alone to describe a species. However, despite no rules against it, a manuscript that uses DNA-sequence data alone to distinguish species is unlikely at present to be viewed favourably by most reviewers or editors for publication in the specialist botanical or zoological literature. Nonetheless, taxonomic decisions based on data other than morphology are not without historical precedence

(e.g. Dobzhansky and Epling 1944) and a growing number of contemporary (e.g. Halt *et al*. 2009) precedents.

Conclusions

Taxonomy is now beyond the stage where it is limited to only morphology, behaviour and distributions, and we argue that, whenever possible, DNA sequences should be obtained or that some type material be vouchered in a way that will allow future DNA work. We recognise that, in some instances, DNA sequences on their own might not be a viable alternative to traditional morphological descriptions, just as morphology-only descriptions are not always appropriate. However, there are circumstances when DNA sequences might be sufficient and effective as the only description of a species. We would urge reviewers and editors to encourage authors to include relevant DNA sequences in their descriptions, and to maintain an open mind about the use of DNA sequences as the only data in a species description. We reiterate Reynolds and Taylor's (1991) plea that herbaria, and museums, prepare for curating DNA type material. The increased use of DNA sequences in taxonomy is inevitable. If we continue to choose to reject or ignore it, then 'mainstream taxonomy' is running the risk of becoming a backwater.

Acknowledgements

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