

Should universal guidelines be applied to taxonomic research?

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In an attempt to facilitate the integration of various methods of species delimitation, Dayrat (2005) recommends a set of nomenclatorial guidelines. He proposes to restrict the application of new specific epithets where a recent taxonomic revision has not dealt with the totality of names and variation in the group, where specimens are not well-represented in collections, where DNA extraction from type specimens is not possible, and where putative novel species are supported only by a single type of data (e.g. morphological). Dayrat further recommends that putative novel species for which only one type of data exists be described with the abbreviation ‘sp.’, so as to avoid the permanent establishment of a specific epithet, as required by the current codes of nomenclature. Contradicting himself, Dayrat implies that putative novel species supported only by DNA sequences should be named as valid species. If adopted, Dayrat’s guidelines would impede taxonomic progress, diminish the utility of taxonomy to its users (e.g. conservation biologists and biogeographers), and prevent the integration of methods of species delimitation. © 2007 The Linnean Society of London, *Biological Journal of the Linnean Society*, 2007, 90, 761–764.

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Recently, several articles have appeared in the scientific literature discussing the nature of a ‘taxonomic crisis’ and potential strategies by which the taxonomic community might hasten the pace at which biodiversity is discovered and classified (Blaxter & Floyd, 2003; Mallet & Willmott, 2003; Sites & Marshall, 2003). Much of the debate has centred on the relative merits of morphology and DNA sequences in species delimitation and phylogeny estimation (Hebert *et al.*, 2003; Lipscomb, Platnick & Wheeler, 2003; Scotland, Olmstead & Bennett, 2003; Wiens, 2004), but some have focused on the development of high-tech tools for taxonomists (Wheeler, Raven & Wilson, 2004). In a recent issue of this journal, Dayrat (2005) argues for taxonomy to become ‘integrative’ through the use of multiple data types (e.g. morphological, genetic, behavioural, and developmental) in studies of species boundaries. Dayrat suggests that the ‘overabundance

of synonyms’ (Dayrat, 2005: 409) and ‘erroneous species boundaries’ (Dayrat, 2005: 408) are serious and overlooked impediments to taxonomic progress. He even asserts that the abundance of synonyms is so great that it ‘. . . makes the selection of names for well-delineated entities very difficult’ (Dayrat, 2005: 409). He therefore proposes changes to the way taxonomists use nomenclature when treating specimens that putatively represent novel species. Although Dayrat’s goal appears to be admirable, the guidelines he proposes for making taxonomy integrative will create difficulties far greater than those he identifies as impediments to progress.

Dayrat proposes seven guidelines, several of which use absolute terms and identify particular situations where novel specific epithets should not be published. He recognizes that incorrect species delimitation results in erroneous interpretation for a broad spectrum of researchers and managers and thus he proposes to limit the application of new names in an attempt to minimize the problems faced by taxonomists and users of taxonomy. Dayrat’s proposal would

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create a bias that, in many situations, would underestimate biodiversity and hinder the efforts of future researchers. Clearly, ecologists, biogeographers, and conservation biologists encounter problems whether biodiversity is under- or over-estimated (Wiens & Servedio, 2000; Sites & Marshall, 2003). The two problems are analogous to Type I and Type II errors in statistical analyses (Frost & Hillis, 1990). Systematists should avoid both problems.

Dayrat's guidelines may be summarized by the following quotes:

1. 'No new species names should be created in a given group unless a recent taxonomic revision has dealt with the totality of the names available for the group.' (Dayrat, 2005: 410)
2. 'No new species names should be created if the infra- and interspecific character variation has not been thoroughly addressed.' (Dayrat, 2005: 411)
3. 'No new species names should be created based on fewer than a certain number of specimens ... and never with a single specimen.' (Dayrat, 2005: 411)
4. 'A set of specimens differing in some regard from existing species can be described with the abbreviation "sp." (for 'species') and not with a real species name regulated by the codes of nomenclature.' (Dayrat, 2005: 411)
5. 'Ideally, names should only be created for species that are supported by broad biological evidence.' (Dayrat, 2005: 412)
6. 'No new species names should be created if type specimens deposited in a museum collection are preserved in a way that prevents any further molecular study.' (Dayrat, 2005: 412)
7. 'All neotypes designated from now on should be preserved in a way that allows DNA extractions and sequencing.' (Dayrat, 2005: 412)

Some of these guidelines contain suggestions that systematists already follow in many cases (e.g. Min *et al.*, 2005; Rickart *et al.*, 2005; Sanders, Malhotra & Thorpe, 2006). However, the absolute nature of Dayrat's statements renders them extremely difficult to follow in some cases, especially in groups that are poorly represented in scientific collections. In many instances, adoption of these guidelines would seriously impede the description and understanding of the world's biota.

Guidelines 1 and 2 are concerned with the recency of revision of the group in question as well as a systematist's understanding of inter- and intraspecific character variation. First, a systematist contemplating naming a putative novel species should consider the rigour and scope of a previous revision – not its date of publication. Systematists should indeed understand levels of character variation as thoroughly as is possible. However, among poorly collected groups, it may not be possible to obtain a thorough understanding of

this variation. Nevertheless, when this variation is moderately well understood, species names should be published to approximate diversity as accurately as is possible, given current collections and/or prospects for future collections. Many taxa, which are poorly represented in scientific collections, may remain forever poorly represented, especially given current rates of habitat loss, increasing bureaucratic and moral objections to collecting, and a general decline in the rate at which organisms are being collected (Winker, 1996). A recent revision of Sri Lankan frogs of the genus *Philautus* Gistel provides an illustrative example. Manamendra-Arachchi & Pethiyagoda (2005) review this group and describe 27 novel species using morphological characters. Seventeen of the 52 species they recognize are considered extinct and several of these are poorly represented in collections; clearly, opportunities for improved sampling within the genus are limited (Manamendra-Arachchi & Pethiyagoda, 2005). These authors were correct to describe this group as well as possible given current collections and prospects for future collections.

Guideline 3, like many of Dayrat's suggestions, goes too far, and is supported only by anecdotes. Ideally, any systematist would have a large series of every new species, but this often is not possible. We will never discover all of the species, and there will always be taxa that are poorly represented in scientific collections. Should we never name a new species based on a single specimen? Caution should of course be used when samples are limited but, if multiple characters from a single specimen or limited series fall outside the variation known from the apparent sister taxon, publishing a novel epithet may be appropriate. For example, a rodent (*Crunomys fallax* Thomas) was described based on a single specimen in 1898. The genus and species have since been reviewed by Musser (1982a) without any change in status for *C. fallax*. Over a century after the original description, no new specimens have been discovered. Any number of reasons could explain the lack of new material, but the species is clearly supported by the best available data (Musser, 1982a).

I suspect that systematists contemplating describing a putative new species based on a single specimen have, in general, been quite cautious. If Dayrat wishes to demonstrate the need for a minimum number of specimens to be set before a species could be named, I suggest he test this in a statistical framework. It would be possible to compare the rates at which species names have been declared synonyms for sets of species, which were originally described based on a range of sample sizes. If species that have been named based on a single specimen are significantly more often synonymized than those named based on a series of five or 10 specimens, then perhaps Dayrat would

have a point. However, Dayrat's claims, as they currently stand, are not convincing.

If systematists, en masse, decided to follow Guideline 4, the literature would eventually be so full of 'sp.' that confusion would reign supreme. Multiple 'sp.'s would abound in poorly known genera. Communication would be exceedingly difficult. Paradoxically, validly published names later determined to be synonyms are unique, which facilitates tracing their history through the literature. Following the history of a particular 'sp.' through the literature would be substantially more challenging, whether one is a practicing systematist, or a user of taxonomy.

Guideline 5 encourages the use and support of multiple data types before naming putative novel species. Any well-trained scientist will use all available sources of data for assessing a given hypothesis. But when a putative novel species is supported by a single type of evidence, and other kinds of data are neither available, nor likely to be so, publishing a new name is appropriate and necessary. Dayrat provides a perfect example when he highlights the recent discovery of cryptic taxa using DNA sequences (Dayrat, 2005: 409). He apparently forgets that these species are hypotheses, supported only by DNA sequences, and generally not by the 'broad biological evidence' (Dayrat, 2005: 412) he purportedly desires. The extinct species evaluated by Manamendra-Arachchi & Pethiyagoda (2005) again provide an example, as does *C. fallax* Thomas. DNA sequences may never be available for many of these species. In spite of this, it is completely reasonable and desirable to recognize species for which only a single type of data is available, and these data will often be morphological. As with the other guidelines, the individual circumstances of the group, including availability and prospects for additional collections, should be considered.

Dayrat would like to see taxonomy be integrative but, in guidelines 6 and 7, he reveals a preference for molecular methods. Although Dayrat touts the importance of maintaining an interest in morphology, he claims that tissue samples are necessary, and thus implies that DNA provides superior evidence, in these two guidelines. If Dayrat believes morphology is equally important, why does he not demand any standards for the ways morphological material is preserved with type specimens, or that it be preserved at all? Morphology remains the only method for determining relationships with most fossil taxa, which can be crucial to understanding relationships among extant species (Smith, 1998). Although morphology has declined in popularity (Scotland *et al.*, 2003), morphological analyses still produce viable hypotheses of phylogenetic relationships and species boundaries (Messenger & McGuire, 1998; Hillis & Wiens, 2000; Wiens, 2004). Systematics has seen a number of excit-

ing new methods come and go; none has revealed absolute truths. DNA sequences, although enormously helpful, will not resolve all questions. Systematic studies of Philippine mice of the genus *Apomys* Mearns provide an excellent example. Sequences of mtDNA of two largely sympatric species (*Apomys insignis* Mearns and *Apomys hylacoetes* Mearns) are almost identical (Steppan, Zawadzki & Heaney, 2003), but morphology reveals subtle differences (Musser, 1982b) and karyology striking differences (Rickart & Heaney, 2002). If taxonomy is to be truly integrative, we must allow flexibility in the use of a variety of different types of data, rather than require the availability of a single, favoured method. Ideally, specimens should be preserved in ways that maximize their utility; preserving DNA is an important component of this objective. Unfortunately, Dayrat's guidelines ignore the circumstances under which type specimens have often been collected. If formalin-preserved specimens of an undescribed species are all that exist, and that species is now extinct, should it never be named because it did not occur to a collector in the pre-DNA era to preserve a tissue sample in ethanol? Perhaps relatively few species would fall into this category but the same problem applies to taxa that are restricted to areas where collecting is difficult or impossible due to bureaucratic obstacles. Specimens and series of specimens with unique suites of characters should be named, regardless of the availability of tissue samples.

Establishing nomenclatorial rules or codes of conduct that place restrictions on the methods of taxonomy will not rid us of erroneous species delimitation or abundant synonymy. These difficulties are largely the result of (1) differentiation (morphological, genetic, developmental, etc.) being a process, rather than an event; (2) the diversity of species concepts applied by systematists; and (3) our inference of species limits using characters, which are imperfectly correlated with speciation (Frost & Hillis, 1990; de Queiroz, 1998; Mallet & Willmott, 2003; Sites & Marshall, 2003). As long as some systematists view speciation as a process, there will always be disagreements about where to draw the line. It is neither conceivable nor desirable that all systematists adopt a single species concept within the immediate future (Mayden, 1999). Nevertheless, taxonomy should indeed be integrative, and integration should involve consideration of multiple species concepts and character types (when available). Restrictive guidelines that ignore individual circumstances will inhibit progress and discourage collaboration among practicing systematists and users of taxonomy. Science proceeds via the free exploration of ideas, and not by the restriction of methods available to researchers. In contrast to Dayrat, I am convinced that systematic methods are already becoming

integrated, and will increasingly become so when taxonomy is a significant component of an undergraduate biology education and a priority for institutions that oversee, fund, conduct, and publish scientific research.

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