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Comment

Availability of new Bayesian-delimited gecko names and the importance of character-based species descriptions

Leaché & Fujita [1] present an empirical example of Bayesian species delimitation (BSD; [2]) to recognize three new species of African geckos from within the range of the widespread taxon *Hemidactylus fasciatus*, Gray 1842. As with any new method, BSD will undoubtedly generate questions and discussions about its practicality and assumptions. However, the use of this method of delimiting species does not obviate the need to adhere to the practice of describing or defining species on the basis of intrinsic characters.

In order for any species name in zoology to be available, it must satisfy the applicable provisions of Articles 11–20 of the *International Code of Zoological Nomenclature* (1999) (hereafter 'the *Code*'). Relevant to this issue, 'To be available, every new name published after 1930 . . . must be accompanied by a description or definition that states in words characters that are purported to differentiate the taxon (Article 13.1.1, p. 17)' where a character is 'any attribute of organisms used for recognizing, differentiating, or classifying taxa' (Glossary, p. 101). Leaché & Fujita [1] do not provide descriptions or definitions for their new taxa, only putative diagnoses (recommended but not required under the *Code* (Recommendation 13A)), and these are based not upon characters but upon degree of support under their species delimitation model (e.g. 'This species includes all populations that cluster with those from the Togo Hills included in this study with strong support in the Bayesian species delimitation model'). Although geographical location could be argued to be an organismal attribute, (i) Article 12.3 and, by implication, Article 13.1 [3] clarify that the mention of a locality does not in itself constitute a description, and (ii) Leaché & Fujita [1] have not actually used locality as a character, but as an indicator of the cluster to which populations belong. The new names they propose thus lack definitions or descriptions of *organismal* attributes (characters) as required by the *Code* and their diagnoses consist solely of extrinsic relational statements about *populations*. The new names proposed for members of the *H. fasciatus* group (*Hemidactylus coalescens*, *Hemidactylus eniangii*, *Hemidactylus kyaboboensis*) fail to conform to Article 13 and are *nomina nuda*, and thus unavailable under the *Code*.

The diagnoses of their new species are similar to the definitions of clade names under phylogenetic taxonomy, but their species descriptions are also unavailable under the *PhyloCode* [4], which defers to 'provisions of the appropriate rank-based code (e.g. . . . ICZN)' for species availability.

The unavailability of Leaché and Fujita's gecko names rests on more than a technicality. We emphasize this point to highlight *the very purpose* of the taxonomic protocols inherent in the *Code's* adherence to character-based species definitions. The application of Leaché & Fujita's approach would no doubt facilitate the description of many new species, and in light of the ongoing biodiversity crisis facing the planet [5] and the need to describe new species before they are lost to extinction [6], this might be viewed positively. However, the deleterious impact of premature taxonomic inflation to conservation efforts is well documented [7–9]. Thus, our concern is that the conservation benefit from a flood of superficial new species descriptions might be outweighed by the cost of taxonomic instability and confusion. For example, unambiguous allocation of a specimen to one of Leaché & Fujita's new species of *Hemidactylus* could only be accomplished by its incorporation into their species delimitation model. This would necessitate the collection of DNA sequence data and replication of their analytical protocol for each unknown sample. Alternatively, specimens could be compared directly to the cited type material but, in the absence of informative diagnostic characters, this would effectively entail a re-analysis of the entire *Hemidactylus fasciatus* group.

The *Code's* requirement for a character-based description or definition forces taxonomists to make comparisons with similar or related forms and to identify features intrinsic to the organism. Character differences not only reflect lineage independence, but also they make the associated species names the very currency of communication in systematic biology. Although we suspect few biologists believe either that all descriptions under the *Code* employ a uniform degree of rigor, or that the biological reality of a species is dependent upon the enumeration of a set of diagnostic characters, the focus on characters, no matter how artificial, allows for comparability. This decreases taxonomic ambiguity and instability, and results in a system of names that can be used both by taxonomists and by the much larger community of consumers of taxonomic information. Characters must be included by all authors publishing new species descriptions, whether or not they use new or traditional means of species delimitation.

We submit that there are at least three alternative approaches that are superior to creating unavailable names. First, genetic characters can be used to satisfy

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Article 13.1.1 of the *Code* [10], just as morphological characters do (e.g. [11]). Second, evolutionarily distinct lineages (i.e. 'candidate species' *sensu* [12]) may be left unnamed until additional data allow for proper descriptions (e.g. [13,14]). Finally, morphology can be studied in conjunction with application of the Bayesian model.

Leaché & Fujita [1] stated 'In terms of *H. fasciatus*, we are not aware of any morphological or ecological characteristics that differentiate these lineages,' but it is unclear whether a morphological survey or analysis was undertaken. Although some organisms exhibit limited interspecific external variation owing to extreme morphological conservativeness and/or homoplasy [15], descriptions of many 'cryptic' gecko species have successfully used tree-based data (gene tree monophyly and distance data) in conjunction with explicit character-based descriptions and diagnoses (e.g. [16,17]). Corroborating their new method with a set of differentiating characters would have been an excellent way to bolster Leaché & Fujita's [1] test of BSD. Any single method of inference can be misleading, but the agreement between independent classes of data can result in increased confidence in hypotheses such as species delimitations [18].

We do not deny that the populations of West African *Hemidactylus* named by Leaché & Fujita [1] represent valid taxa under any of several lineage-based species concepts [19]. The Bayesian approach to species delimitation may well provide objective criteria for discerning species boundaries using genetic data and we favour further exploration of this approach, especially if used in combination with surveys of characters that can be used to recognize species. If, however, as in the paper by Leaché & Fujita, Bayesian species *descriptions* have as their sole underpinnings the degree of support for a pattern of clustering under a particular model, we regard them as both practically unworkable and philosophically inadvisable.

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