



The taxonomy's new clothes: a little more about the DNA-based taxonomy

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The use of DNA sequences, including DNA barcoding, as a taxonomical tool has been happening for some time (Tautz *et al.*, 2003; Hajibabaei *et al.*, 2007; Packer *et al.*, 2009). However, the description of new species based solely on DNA sequences is a new idea (Cook *et al.*, 2010) and a new practice (Brower, 2010). Our aim is not to further polarize the war between advocates of strictly molecular or strictly morphological systematics (following, *e.g.*, Pires & Marinoni 2010). The objectives here are (i) to present some arguments regarding the perils of the proposition of a model (theory) for solely DNA-based descriptions (Cook *et al.* 2010) and the actual publication (practice) of such descriptions (Brower 2010), (ii) to discuss some reasons why we believe that adopting strictly DNA taxonomy for species description, setting aside everything we have learned from classic taxonomy, may not be the best alternative and (iii) to present the point of view about these matters of a PhD candidate and a recently graduated PhD working with taxonomy in a developing country.

Critical theory of DNA-taxonomy

Cook *et al.* (2010:322) advocated there would be no compelling evidence to exclude DNA-only descriptions. In terms of nomenclatural rules, DNA-based descriptions are not in contradiction with the ICZN criteria for name availability (since these descriptions comply with publication adequacies). Nevertheless, the main question regards the significance of these taxa described. In accordance with Ebach & Carvalho (2010), we believe that small uncontextualized differences in sequences of DNA cannot necessarily define distinct taxa. As suggested some time ago by Darwin himself, “*No one supposes that all the individuals of the same species are cast in the same actual mould*” (Darwin 1872:34). A species is a hypothesis of relationship and its proposition relies on the study of a large number of specimens (exception for rare species, species where few individuals are collected or fossils) of the same or from different localities that allow a distinction between intraspecific and interspecific variation. We believe this is one of the most distinctive aspects of morphological based taxonomy in relation to molecular practice that usually covers data from one or few individuals as representative of a given species.

Cook *et al.* (2010) also claim that the classic taxonomic methodology is a virtual black box, that “*taxonomy remains as a ‘closed’ profession*” and that the “*descriptions are traditionally the territory of taxonomists*”. But the molecular approach for species definition does not constitute, in any way, a clearer methodology than the morphological one. The claim that a sequence is not influenced by subjective assessments ignores the difficulty of aligning sequences of different length, distinguishing paralogs from orthologs (exception for DNA barcoding). Selecting appropriate genes for any particular taxonomic study (Lipscomb *et al.* 2003) in addition to the choice of models and analyses for species delimitation can also generate different results (Brower 2006). In molecular taxonomy speech, it seems that the ease of identifying the character states (ATCG)—and consequently the ease of saying ‘this A is different from that T’—obscures the difficulty of establishing homologies among them. Furthermore, it is obvious that species description is the territory of taxonomists, as the structure of proteins regards biochemists or the study of a dinosaur fossil is the territory of paleontologists. Each field of biological sciences has its peculiarities and characteristics and the suitable training for practicing it. Cook *et al.* (2010:323) also claim that DNA sequencing is cheap and easy. But, in our opinion, the matter does not regard the economic viability of DNA-based taxonomy in relation to classic taxonomy, nor the price ratio between DNA sequencing and the purchase of stereomicroscopes. These apparent facilities provided by molecular databases may lead to a harmful robotization of the taxonomical science, where the questions exist just to be quickly solved. The use of DNA sequences for describing new species should be used as an auxiliary tool and treated under a phylogeographic context or through a revision study of taxa, preferably with a large number of individuals.