

Phenetic and DNA taxonomy; a comment on Waugh

Sir,

This correspondence attempts to clarify two important issues relevant to the DNA barcoding initiative raised in Waugh's⁽¹⁾ otherwise, cogent and useful review. The first issue concerns the way that Waugh presents the analytic approach to DNA-barcoding data, and the second involves a broader issue with respect to the role of DNA barcoding in modern biology. Both issues are of great importance as to how we view DNA barcoding, and solutions to both will broadly change the way that the taxonomic sciences are accomplished if the view of taxonomy that is expressed by Waugh⁽¹⁾ is the way that the initiative proceeds. It is not the purpose of this correspondence to say whether these approaches are right or wrong, or which one to choose, but rather, to try to put all the cards on the table so that we can make better decisions about how this important scientific endeavor moves forward.

Phenetic taxonomy—again

An alarming bias was reported in this review on how DNA-barcoding data can be analyzed in animal taxonomy. The presentation in the review is patently phenetic. Distances are touted throughout the review as the preferred means of analysis for DNA barcoding. This preference is evident in both the figures used to explain how DNA sequences can be used to establish taxonomic boundaries, and in the papers referenced. This bias toward distances in the review appears to be an effect of the first cohort of DNA-barcoding papers to be published. In fact, of the 15 papers cited by the author to demonstrate the feasibility of DNA barcoding all of these use sequence distances and 14 out of 15 of these come from the same laboratory, or from collaborators with that laboratory. Because the researchers from this laboratory have only used phenetic approaches in their analyses, it appears to the casual reader, that distance-based analysis is the preferred approach of DNA barcoding. Reference is also made in the review to distance approaches in other groups of organisms such as bacteria, protists and plants, and these too attempt to utilize distances as the currency of species identification.

The bottom line is that distances are at odds with the way that modern (and not so modern) taxonomy is accomplished.^(2,3) The grand majority of modern taxonomy is accomplished with characters, or diagnostics to be more exact. This is why, when taxonomic keys are used to determine the membership of a specimen in a species either in the field or in the laboratory, fixed characters are used. While some recent papers in animal taxonomy might use DNA distance information to shore up their diagnosis of new taxa, when a species is described, distances are not normally used in the description.

Nor would they be accepted as the sole source of information for a new species description.⁽²⁾ While the sole paper cited by Waugh⁽¹⁾ as using DNA barcodes in a species description,⁽⁴⁾ lists the DNA sequence information as part of the formal description, it does not present distances or diagnostic characters as part of the description. A glaring exception to this statement on distances is how bacterial taxonomy is accomplished. With bacteria, a 70% chromosomal DNA–DNA hybridization level and a 3.0% 16S rDNA divergence of a new species with its closest relative is used as a boundary for species description. Whether or not this approach is useful to a taxonomy of bacteria is debatable.^(5,6)

A character-based approach can be easily applied to DNA barcoding.^(3,7–9) There are five reasons to consider DNA diagnostics as a tool for DNA barcoding. (1) Diagnostic DNA sequence characters can be extracted from COI sequences (and any other fragment of DNA for that matter) quite easily and efficiently without recourse to a model of evolution. (2) In the case of DNA sequence diagnostics, there is no need to discuss arbitrary cutoffs for what is significant, or what is not, (as there is with phenetic approaches) because diagnostics are either there or they aren't. (3) A DNA diagnostic is part of the organism, and is extractable from the organism without recourse to comparison to anything else. (4) Diagnostics avoid DNA sequence changes in organisms that have occurred as a result of anagenetic change (autapomorphic change versus synapomorphic change) which can often times confound distance comparisons. (5) Diagnostics are more technically adaptable (see DeSalle et al.⁽³⁾ for a discussion) to development of the handheld barcoding device Waugh⁽¹⁾ mentions in the review.

Taxonomy is species discovery, DNA barcoding is species identification and DNA taxonomy is something completely different

The second major problem that needs further appraisal and clarification in the context of Waugh's⁽¹⁾ review, is the issue of how DNA barcodes can be used in modern biological endeavors such as community ecology, biodiversity studies, evolutionary biology, conservation biology and behavioral ecology. Several examples are listed by the author, but there is a general blurring of two major and very different objectives that have been attributed to DNA barcoding. Waugh⁽¹⁾ is correct when he suggests that identification of specimens to their species epithet is a major role for DNA barcoding. However, it is not clear what the role for DNA barcoding in species discovery or taxonomy is in this review. This problem of blurring the distinction of species identification and discovery is one that has haunted the DNA-barcoding initiative from its inception and has been specifically discussed by DeSalle⁽¹⁰⁾ and Rubinoff.⁽¹¹⁾

This problem has been blurred even more by the use of another term often times associated with DNA barcoding

called DNA taxonomy.⁽¹²⁾ DNA taxonomy as it was originally described, and papers supporting it cited by Waugh, would use DNA sequences alone to accomplish taxonomic revision in groups of organisms.^(13,14,15) It is the sole use of DNA in taxonomy that most taxonomists cringe at. And it is DNA taxonomy that poses the biggest life change to taxonomy so far, not DNA barcoding. If DNA taxonomy is accepted as a means of doing taxonomy, then there will be a major shift in the way that we think about naming and systematizing species. To further clarify the distinctions amongst taxonomy and DNA barcoding, it can be pointed out that the integrated taxonomy approach is more precise and DNA barcoding is more heuristic and exploratory. DNA taxonomy, in contrast, wants to be both precise and exploratory. While Waugh recognizes much of this distinction, there is still the hint of merger of DNA barcoding and DNA taxonomy in the review and this correspondence hopes to give more clarity to the distinction between these two different approaches.

Further on down the road

Some decisions need to be made with respect to how DNA barcoding will affect biology in the future. As Waugh⁽¹⁾ points out, the biodiversity crisis is so acute that some relief is needed in order to solve problems arising from the crisis, and that DNA barcoding can be an important tool in this endeavor. However, some care and attention is needed in order to make sure that DNA barcoding is effective, and integrated into the approaches of the initiative. If DNA barcoding adopts a solely phenetic-based analytical approach, it is evident that classical taxonomy will not respond well to the endeavor. As with any conflict it will need to be resolved for progress to be made. There are three major outcomes to conflict resolution in this context. (1) Taxonomists will learn to use distances in their descriptions of species and will embrace the approach. (2) DNA barcoders will learn to use diagnostics, and distances will be a secondary kind of information in taxonomic descriptions or not used at all. (3) A hybrid of the two approaches needs to be developed. More pointedly, the blurring of species identification (DNA barcoding), species discovery (integrated taxonomy) and DNA taxonomy needs to be rectified. Due to

the general incompatibility of these three concepts, any fuzzy vision of these three approaches if left unattended will cause more trouble than clarity, further on down the road.

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