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Editorial

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Why we shouldn't let sleeping dogmas lie: a partial reply to Craig*

RANDALL D. MOOI[1] & ANTHONY C. GILL[2]

[1] *The Manitoba Museum, 190 Rupert Ave., Winnipeg, Manitoba R3B 0N2, Canada*
E-mail: rmooi@manitobamuseum.ca (corresponding author).
[2] *Macleay Museum and School of Biological Sciences, University of Sydney, NSW 2006, Australia*
E-mail: anthony.c.gill@sydney.edu.au

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Now, when I have spoken on these matters in the past, it has sounded to some as if I had taken upon myself the task of denigrating paleontology and individual paleontologists. That is not so. I am concerned with what I find is a real problem.—Nelson, 1969 in Williams and Ebach, 2004: 711

We were reticent to respond to Craig (2011), for worry that this might lead to an ongoing, futile exchange on who does and who does not understand homology and the workings of systematics. No reply, too, would be a reply of a sort. However, Craig's missive provides an opportunity to explore additional aspects of the issues/crises at hand. Before we do so, we would point out that in Mooi & Gill (2010a) we did not say that molecules cannot provide homology (as Craig implied), but instead argued that current popular methods are phenetic and do not discover this homology. Numerical methods do not differentiate homology from homoplasy in morphology consistently, either, and thus are a disservice to the molecular and morphological evidence; the phenograms produced do not necessarily appropriately or accurately reflect the relationships the data can provide.

Craig (2011) begins with an acknowledgment that it is a good idea to challenge dogmatic thinking – just so long as it is not his dogma ("long-settled debates"). This is reminiscent of a comment by an anonymous *Molecular Phylogenetics and Evolution* reviewer of a rejected manuscript discussing similar issues where the main criticism was that we (with others) had the audacity to write a paper where "Its purpose is to question the foundation of molecular phylogenetics, a well-established field." Craig and that reviewer would prefer we let sleeping dogmas lie. It is ironic that in other exchanges (Mooi & Gill 2010b, contra Smith 2010; Gill & Mooi 2011 contra Wiley *et al.* 2011) we are labeled as dogmatic, whereas Craig chastised us for attacking dogmatism.

The single paragraph history of the term homology in Craig (2011) finished with what amounted to a case closed (perhaps one of the "long-settled debates" p. 38). The issues of homologue and homology have been examined for over 150 years in comparative biology and systematics and, using other terminology, some would argue for several hundred years before that (Williams & Ebach, 2008). Contrary to Craig's claims, we are well aware of the efforts to apply notions of molecular homology within the numerical cladistic paradigm, and it is that embrace of numerical cladistics that we had commented on. We note that there has been considerable discussion regarding homology since Craig's favoured source on the matter, Patterson (1988). In Patterson (1988: 621) there are some statements that deserve reflection: "In molecular phylogenetics, there is no exact equation between homology and synapomorphy...". And Craig (2011: 39) misread Patterson in suggesting "Homology in sequence data may be detected in *ways* that are not possible with morphological data (Patterson 1988)" (our italics). Patterson (1988: 610, our italics) actually stated: "Molecular sequence homology is 'detectable' in *a way* that morphological homology is not, primarily because molecular sequences are one-dimensional." We read his comments on the one-dimensionality of gene sequences ("…an Adenine is an Adenine…and so forth" of Craig 2011: 39) as a disadvantage of these data, not an advantage. At least some molecular workers agree: "There is an oft-repeated claim that sequences are easier to deal with than phenotypic characters because DNA sequences consist of only 4 types of nucleotides. However, it is straightforward to see that this fact makes homology assessment harder, not easier" (Morrison 2009:

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