

REPLY

Complementary Uses of Molecules and Morphology: A Reply to Lee

To the Editor:

In a recent note, Lee (1997) responded to our comments (Hedges and Maxson, 1996) about the differential use of molecules and morphology in phylogenetic analysis. It is unlikely that a consensus will be reached in the immediate future, and we welcome his alternative viewpoint. However, it is important that differences in our views are not based on errors and therefore we wish to clarify some inaccuracies in his paper.

To our suggestion of using molecular trees to interpret morphological and behavioral evolution, Lee argues that the reverse also is true: one must use a behavioral or morphological tree to interpret molecular evolution. While that is an option, it is unlikely to be used. For example, if the evolution of a developmental gene is of interest, then an independent phylogeny could be constructed from other sequence data. Moreover, as morphological and behavioral data have a large subjective component, sequence data from genes other than the one of interest have the added advantage of being objective, and hence more robust.

Contrary to Lee (1997) we did not "claim that morphological data are subject to high levels of convergence," only that they are more "susceptible to adaptive convergence" than molecular data. There is an important distinction. Lee points to two molecular studies where different genes yielded different phylogenies as being "clear evidence of sequence convergence." This is not true, because he is referring to trees that are statistically unresolved. That is different from a significantly discordant result, which is rare among molecular studies (and even then unlikely to be due to convergence). Lee also confuses substitution biases, which are well known in molecular data, with adaptive sequence convergence, which is not (Doolittle, 1994).

Molecular phylogenetics is going through a transition phase, from studies involving a few hundred basepairs and low statistical confidence to those with kilobases of data and highly resolved phylogenies. Debates concerning different approaches in data analysis should be timely, but also prospective. Lee's suggestion that molecules and morphology should "work as equal partners" is unrealistic. The advantage of combining a small set of characters from behavior or morphology with thousands of sites across many genes is unclear, even if it were justified from a statistical standpoint. We prefer a *complementary* approach where organismal evolution is emphasized and explored through molecular phylogenies and comparative methods.

REFERENCES

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