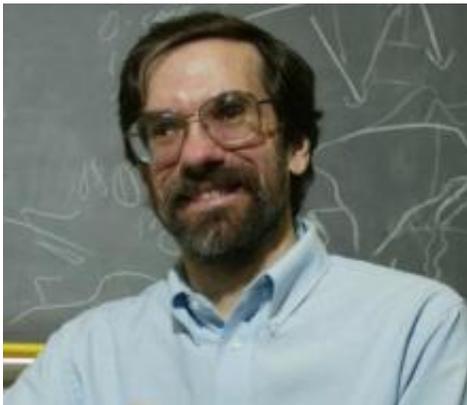


Analysis finds strong match between molecular, fossil data in evolutionary studies

April 28 2009



David Jablonski, the William Kenan, Jr. Professor in Geophysical Sciences at the University of Chicago. Jablonski specializes in numerical analyses of large-scale patterns in evolution. Credit: Jason Smith

During a seminar at another institution several years ago, University of Chicago paleontologist David Jablonski fielded a hostile question: Why bother classifying organisms according to their physical appearance, let alone analyze their evolutionary dynamics, when molecular techniques had already invalidated that approach?

With more than a few heads in the audience nodding their agreement, Jablonski, the William Kenan Jr. Professor in Geophysical Sciences, saw more work to be done. The question launched him on a rigorous study that has culminated in a new approach to reconciling the conflict

between [fossil](#) and molecular data in evolutionary studies.

For more than two decades, debate has waxed and waned between biologists and [paleontologists](#) about the reliability of their different methods. Until now, attention has focused on the dramatically different evolutionary history of certain lineages as determined by fossils or by genetics.

Scientists using molecular techniques assert that genetics more accurately determines [evolutionary relationships](#) than does a comparison of physical characteristics preserved in fossils. But how inaccurate, really, were the fossils? Jablonski and the University of Michigan's John A. Finarelli have published the first quantitative assessment of these assumed discrepancies in the [Proceedings of the National Academy of Sciences](#).

They compared the molecular data to data based on the kinds of features used to distinguish fossil lineages for 228 mammal and 197 mollusk lineages at the genus level (both wolves and dogs belong to the genus *Canis*, for example).

No matter how they looked at it, the lineages defined by their fossil forms "showed an imperfect but very good fit to the molecular data," Jablonski said. The fits were generally far better than random. The few exceptions included freshwater clams, "a complete disaster," he said.

Jablonski and Finarelli (Ph.D.'07, University of Chicago), then decided to push their luck. They looked at the fits again, but this time focused on geographic range and body size. The result: a "spectacularly robust" match between the fossil and molecular data.

Jablonski interprets the results as good news for evolutionary studies. The work backs up a huge range of analyses among living and fossil

animals, from trends in increasing body size in mammal lineages, to the dramatic ups and downs of diversity reported in the fossil record of evolutionary bursts and mass extinctions.

"Our study also points the way toward new partnerships with molecular biology, as we straighten out the mismatches that we did find," he said.

More information: "Congruence of morphologically-defined genera with molecular phylogenies," by David Department of Geophysical Sciences, University of Chicago; and John A. Finarelli, Department of Geological Sciences, University of Michigan, *Proceedings of the National Academy of Sciences*, Online Early Edition, week of April 27-May 1, 2009.

Source: University of Chicago ([news](#) : [web](#))

Citation: Analysis finds strong match between molecular, fossil data in evolutionary studies (2009, April 28) retrieved 21 May 2024 from <https://phys.org/news/2009-04-analysis-strong-molecular-fossil-evolutionary.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.