

PISSING AWAY THE EONS¹

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There are lots of things that really bother me about the current biodiversity crisis. But one item near the top of the list is the seemingly imminent loss of so many millions of years of evolutionary history across so many thousands or millions of lineages during the short span of my lifetime. It just would not seem quite such a waste if we were only a few million years out from the last mass extinction event, or if we were not bumping off so many lineages that had survived previous mass extinction events, or if the creationists were right and nothing was more than a few thousand years old anyways.

But how exactly evolutionary history (i.e., phylogeny) might be important to the conservation of biodiversity is not always clear. This intersection of fields is the topic of a new book edited by Andy Purvis, John Gittleman, and Thomas Brooks. All three editors have each published important papers that combine phylogenetics and conservation biology. Their goal here is to “explore the ways in which the wealth of new phylogenetic information can benefit conservation biology” (p. 2). Overall, I think that the book successfully does this, although my satisfaction levels fluctuated considerably from chapter to chapter.

The book consists of 18 chapters divided among four sections: (1) units and currencies, (2) inferring evolutionary processes, (3) effects of human processes, and (4) prognosis. I briefly summarize these below.

SECTION 1—UNITS AND CURRENCIES

The first section deals primarily with species and with the use of phylogenetic diversity as a currency for conservation biology.

¹*Phylogeny and Conservation*. Andy Purvis, John L. Gittleman, and Thomas Brooks, Editors. 2005. Cambridge University Press, Cambridge, U.K. xiii + 431 pp. \$60 SB. ISBN 0-521-53200-0.

This section starts with a useful chapter (Sinclair et al.) that briefly reviews how phylogenies are built and how they might be used in conservation.

I found the next chapter (Agapow) to be frustrating. It complains about disagreements over species concepts and about the large numbers of new species that are being discovered as a consequence of applying the “phylogenetic species concept.” This chapter seems to ignore recent signs of progress in resolving debates over species concepts (e.g., Mayden 1997; de Queiroz 1998), disregards important differences among species concepts used by modern systematists (not everyone who uses phylogenies follows the phylogenetic species concept), presents recent progress in species-level systematics as if it were somehow problematic, and, in the end, offers few constructive suggestions.

The chapter by Avise argues that intraspecific phylogeographic studies are useful for conservation biology, but that interspecific phylogenies may be of more limited value.

Rodrigues et al. use simulations to address a critical question: does prioritizing areas based on the phylogenetic diversity they contain end up preserving more phylogenetic diversity than simply prioritizing areas having the most species? They find only a limited set of conditions in which these two criteria (phylogenetic diversity, species diversity) seem likely to prioritize different areas.

Mooers et al. discuss the idea of quantifying how much “evolutionary heritage” a country “stewards” within its borders (e.g., based on the ages of endemic lineages). Admittedly, it is unclear whether quantifying biodiversity in this way will make a compelling argument for conservation to these governments. Nevertheless, this chapter represents the sort of thinking that the book could have used much more of, in terms of treating

phylogenetic diversity as a commodity to justify conservation outside of academia. More on this below.

SECTION 2—INFERRING EVOLUTIONARY PROCESSES

The second section is ostensibly about using phylogenies to infer evolutionary processes that are relevant to conservation. But it is quite heterogeneous, and I am not convinced that any chapters really did this.

Jones et al. use phylogenies to look at how age of species and species range sizes might be related. They infer that species range sizes seem to decrease over time, and that there are significant phylogenetic effects on geographic range sizes among species.

Smith et al. argue for the need to preserve “evolutionary process” by preserving ecotone habitats. They present many interesting results, but do not yet make a compelling case with this chapter. In my mind, they would need to make a very convincing case indeed to justify preservation of “process” at the expense of preserving extant diversity. They find significant genetic differentiation (in both mitochondrial and nuclear markers) within a species of bird (little greenbul, *Andropadus virens*) that exists in two disjunct areas of rainforest in West Africa and in some adjacent ecotone habitats. They find that more morphometric characters show significant differentiation between the populations in forest and ecotone habitat than between species in the two disjunct forest areas (although there is nevertheless significant differentiation between the two rainforest populations in some characters). They argue that these between-habitat morphometric differences are more important than the genetic differentiation between areas, but for reasons that were not entirely clear to me. They discuss differentiation in songs characteristics between habitats, but do not compare songs between the two disjunct areas (so one cannot tell whether there is more call variation between habitats or between regions), and do not relate call variation directly to reproductive isolation. They devote about a page to the topic of using phylogenies to infer the role of ecotones in speciation.

This section also contains two chapters on the flora of two regions in Africa (Lovett et al. and Midgely et al.), but neither contains phylogenies nor much discussion of the integration of phylogeny and conservation.

Finally, the chapter by Moritz and colleagues discusses the phylogeny and biogeography of reptile, amphibian, and snail species within the rainforests of northeastern Australia. All phylogenies are based on mitochondrial DNA only, without any caveats (i.e., problems with mtDNA data emphasized by Moritz in other papers are not mentioned). This chapter summarizes many years of very interesting research by this group with many potential conservation implications, but it was not always clear to me when reading the chapter what specific evolutionary processes were being addressed.

SECTION 3—EFFECTS OF HUMAN PROCESSES

This section focuses mostly on macroecological analyses that relate various factors to extinction risk using phylogenetic comparative methods. Another study employs similar methods to examine invasiveness. Using data from birds, Brooks et al. show that threat level to species, habitat vulnerability, evolutionary distinctiveness, and endemism of species within habitats are all related to each other. Purvis et al. show that extinction risk and factors that may be related to it (e.g., species range size) show significant phylogenetic signal among primates. They then use supertrees from carnivores and primates to test the possible correlates of extinction risk in these groups. Bennett et al. also examine ecological traits that are related to extinction risk in birds. They find that extinction risk is phylogenetically nonrandom and most closely related to large body size, low fecundity, and long generation times. They also find that species threatened by direct human persecution and introduced predators tend to have large body size and long generation times, whereas species threatened by habitat modification tend to be small and ecologically specialized.

Cardoso et al. describe patterns of primate species richness across different subregions within Amazonia. Like those on African plants, this chapter presents much interesting information, but it was unclear to me how it was related to the general topic of phylogeny and conservation, as phylogeny was not really used.

Finally, Lockwood reviews and tests whether nonnative species tend to have nonrandom taxonomic affiliations (e.g., whether certain families have more established nonnative species in a region than others, after correcting for differences in the global species richness of each group). She finds that some families do indeed tend to be overrepresented among the invaders, suggesting that these groups have some biological traits that promote one or more stages of the invasion process.

SECTION 4—PROGNOSIS

The chapter by Sean Nee argues that most of the major branches of the Tree of Life consist of microscopic lineages, and that there would be little impact on these major branches if all macroscopic life were to go extinct. This is an interesting and amusing read, but perhaps not all that helpful with regard to present-day conservation issues.

Barracough and Davies discuss the possibility of shifting the emphasis of conservation biology toward preserving future speciation rather than present-day biodiversity. These authors argue that such a shift would be ill-advised, particularly given our limited ability to forecast future conditions over even short time scales and the long time scales over which biodiversity evolves.

THE BOTTOM LINE

Overall, I think that this book is worthy of serious attention from evolutionary, systematic, and conservation biologists. I can think of few applications of evolutionary biology and systematics that are as important as conservation biology. The editors appear to have assembled a diverse roster of prominent researchers working in this general area(s). The book is aesthetically pleasing and I detected relatively few editorial mistakes or typos.

The book does have some weaknesses. Based on my reading of the book, the most unambiguously important usage of phylogenies in conservation is in species delimitation. Numerous studies have found that species of conservation concern actually consist of two or more cryptic species, each in greater peril of extinction than was suspected before. But, by my count, the general topic of how one uses phylogenies to delimit species gets one page (p. 43) in a book of more than 400 pages. Many of the chapters focus instead on using phylogenies to facilitate phylogenetically correct comparative analyses, which is hardly new or unique to conservation biology (even though the analyses themselves seem important and worthwhile).

Apart from these two uses, I was disappointed that the book does not make a stronger case for the more practical importance of phylogeny for conservation. For example, how might humans benefit from preserving phylogenetic diversity? Does greater phylogenetic diversity offer the potential for a greater variety of nat-

ural products? What about preserving phylogenetic diversity in the evolutionary neighborhood of important agricultural and domesticated species? I suspect that many of the benefits that we associate with biodiversity in general (e.g., Wilson 1992, 2002), such as greater genetic and phenotypic diversity, may be more closely tied to phylogenetic diversity than to species diversity alone. Overall, I think that a useful opportunity to explore these sorts of pragmatic issues was missed.

This book is a step in the right direction, but I hope it will not be the last. There is certainly much more to be done at the intersection of these fields, and this book should be a useful starting point.

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