

A page outlining “How to use this book” would also be helpful to inform and inspire the potential user and to convey the author’s vision for how it could be used. I would also like to see a brief note about the importance of conserving indigenous vegetation and the need for readers to be mindful that all plants covered in the book are significantly depleted and many are extremely rare. We should never assume that such things are sufficiently understood. The emphasis on structural detail may encourage readers to look at plants more closely and while this is a positive thing, they should be

encouraged to examine specimens carefully in situ with a hand lens rather than picking them. Legislative protection and permit issues are also relevant in this context and warrant a mention.

However, these are minor points, especially when considered alongside the numerous positive features of this book. *Flora of the Otway Plain and Ranges I* is an outstanding piece of work and I recommend it highly to anyone with an interest in bushland plants and their conservation. There is a place where head and heart unite and it’s a good place to go. This book takes me there.

Tangled trees

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***Tangled Trees: Phylogeny, Cospeciation, and Coevolution.* By Roderic D. M. Page (editor). University of Chicago Press, Chicago, IL. Published 2003. x+350 pp. ISBN 0-226-64466-9 \$US32.50 (paperback); ISBN 0-226-64467-7 \$US85 (hardback).**

All systematists know that the study of historical processes benefits greatly from a phylogenetic perspective, and they also know that the notions of co-evolution and co-speciation have been of general interest to biologists for many a long year. It therefore can come as no surprise that the last 20 years has seen many developments integrating the study of phylogenetic congruence into studies of co-evolution and co-speciation in host–parasite, mutualistic and symbiotic systems. This book is intended to bring together many of these developments, from both the theoretical and practical sides. It concentrates on host–parasite systems as exemplars, but the principles and practice have wider relevance.

In spite of the subtitle, this book isn’t really about co-evolution in the broad sense. If it was, then it would need to include a wider range of discussions about co-adaptation between parasites and hosts. For example, there is nothing here about epidemiology modelling, which is a large part of the practical study of host–parasite co-evolution, nor is there anything about parasites and their transmission vectors (as opposed to hosts). If you are looking for that type of thing, then the book by Poulin et al. (2000) would be a better bet. Instead, the book reviewed here is very much about co-phylogeny, and as such it is probably of more direct relevance to systematists than would be a more general book on co-evolution. Moreover, by focusing on the topics that it does, this book provides unique material about co-phylogeny and co-speciation, presenting

both an introduction to the topic and a detailed exploration of its ramifications.

If you are interested in this topic, then this is pretty much the only book available, so that it needs to cover a lot. The Introduction and first four chapters provide a good coverage of many aspects of the methodology and theory, while the remaining eight chapters provide a feast of empirical examples. However, principles and practice are neatly tied together by most of the authors.

There is still some way to go before we have a robust methodology for co-phylogeny mapping, as the theory is more complex and the practice is messier than we would like. This book summarizes what has been achieved so far and raises many of the methodological issues that still need to be addressed. These latter issues include the effects of phylogenetic uncertainty, concurrent timing of proposed co-speciation events, and distinguishing real co-speciation from other co-evolutionary events (e.g. resource tracking), as well as statistical tests of co-phylogenetic congruence in the face of increasing levels of host switching. There is plenty here to keep the theoreticians occupied for quite some time to come.

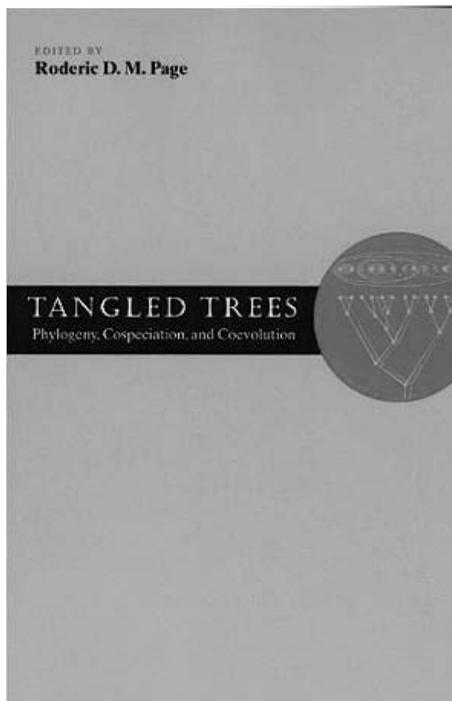
As far as methodology is concerned, it is valid to ask how up-to-date this book is. The genesis of the book was in 1997, the associated symposium was held in 1999, the Preface is dated 2001, and the book is copyrighted for 2003. Has the study of co-phylogeny changed much since then? The answer is both “yes” and “no”. The two main games in town are still Brooks Parsimony Analysis (BPA) on one hand and Reconciliation Analysis (RA) on the other, as presented in this book. These two general approaches have received several comparative reviews in the literature (the most recent being that of Stevens,

2004), and they still make regular appearances in empirical studies (although BPA may be more popular in biogeography studies rather than in host–parasite studies). For the interested, BPA has been subjected to a long series of commentaries over the past five years in both *Cladistics* and the *Journal of Biogeography*. More recently, the PACT method of Wojcicki and Brooks (2004) has been introduced, to replace the previous BPA methods, although no computer program yet exists. Perhaps the biggest limitation of RA is that the main computer program, TreeMap v.2, is still listed as a beta release after more than 3 years, with no manual, although the paper by Jackson & Charleston (2004), will give you some useful hints on usage and interpretation. The recent release of the competing Tarzan program (Merkle & Middendorf, 2005) might liven things up in this area, especially as it is claimed to be faster and to deal with larger data sets. Of the few alternative methods, the approach implemented in the TreeFitter program is discussed in the book chapter by Ronquist, and data-based methods are discussed by Huelsenbeck et al. and Johnson & Clayton, but the ParaFit method (Legendre et al. 2002) gets no mention at all.

As far as empirical practice is concerned, it is the biological basis of co-evolution that is of most interest. The book authors address this basis from many different perspectives, reflecting the diversity of potential causes and influences that creates much of the co-phylogeny messiness. Most of the factors discussed are ecological ones, including geography and demography, with a strong genetics and comparative flavour. Thus, macroevolutionary patterns are interpreted as the product of microevolutionary events. However, few of the authors provide broad syntheses, preferring instead to illustrate their points with a specific example. The example parasites include pinworms (Nematoda), retroviruses, and (inevitably) lots of lice.

In terms of empirical studies, another collection of papers appeared in 2004 in *Systematic Biology* 53(1):92–173, based on a symposium held in 2002. This collection of seven papers (plus introduction) focuses on co-evolution in

a slightly broader sense than the co-phylogeny one discussed here. It is a worthwhile addition to the growing literature on the historical aspects of inter-species interactions, as well as a neat complement to the collection in this book.



The book editor notes that two groups of organisms are not explicitly represented by empirical examples in his collection: plants and bacteria. The absence of plants, at least, probably gives the book a biased assessment of co-phylogeny, in the sense that researchers seem to find it much harder (although not impossible) to detect examples of co-speciation involving plants (e.g. the recent studies of Brändle et al. 2005; Machado et al. 2005; see also the discussion by Percy et al. 2004). That is, co-phylogeny studies between animal parasites and animal hosts may actually be preferentially sampling “successful” examples of co-speciation, and thus giving us a rather one-sided view of co-evolutionary processes. If this turns out to be a general phenomenon

(and it is certainly a testable hypothesis), then a review of botanical studies would have been a useful addition to this volume.

In the absence of bacteria, perhaps the most intriguing choice of host–parasite relationship in the book is that of malaria (Sporozoa; Protozoa) and their lizard hosts. This is interesting because the study of co-phylogeny between Sporozoan endoparasites and their hosts is almost non-existent (see also Ricklefs et al. 2004), and yet such studies could actually be even more useful within this group than they are elsewhere. For example, one problem with studying the evolution of these unicellular organisms is trying to date any of the hypothesized events. There is no fossil record, for instance, that can be used to provide “known” dates for historical events, from which other phylogenetic events could then be dated. Therefore, dating usually involves untestable assumptions about fixed rates of molecular evolution (e.g. Morrison 2005). One solution to this problem might be to search for examples of unequivocal occurrences of co-speciation, because if the host speciation has a known date then this would also provide a reference date within the parasite phylogeny. The

practical limitations of such an approach should be obvious (e.g. the co-speciation time may be pre-emptive, synchronous or delayed), and there are theoretical problems as well, such as potential coalescent effects (e.g. the very large population sizes of protozoans means that discrepancies between gene trees and species trees are to be expected, due to deep coalescence). Nevertheless, this approach is no different in principle to using geological events to date biological events, and it shows the potential of co-phylogeny studies to contribute to evolutionary studies of “difficult” groups.

Not unexpectedly, given finite space, there are many topics that are not covered by the chapters of this book and many problems that are not addressed by the authors. Perhaps the most obvious of these is the lack of consideration given to life-history stages. Many parasites, for example, pass through several distinct stages in their lives, with different life-history stages obligately parasitizing different types of host. Many Sporozoa have their sexually reproductive phase in one host (the definitive host, e.g. a carnivore) and an asexual stage in another host (the intermediate host, e.g. a herbivore), while parasitic Platyhelminthes commonly have up to three hosts during their life (e.g. a mollusc, a fish and a bird). The question, then, is: which of these hosts is the parasite co-speciating with? Presumably it is only one of them, as it seems unlikely that it could be several of them simultaneously. Unfortunately, all of the case studies in this book consider only parasites with a direct (i.e. one-host) life cycle, and so we do not get an answer to this question. Even for those parasites (e.g. malaria) that have an obligate transmission vector, the vector has also been ignored in co-phylogeny (but not co-evolutionary) studies.

This issue of multiple hosts is not a trivial one for studies of co-evolution in the more general sense. As one specific example, my only contribution to the genre has been to test the (possibly hare-brained) idea that parasites of human-associated hosts might preferentially show recent demographic expansions as a result of the rapid expansion of human populations in the last 10,000 years (Morrison & Höglund 2005). However, the empirical test of this hypothesis ended up being restricted to Nematode parasites with a direct life cycle, because multi-host parasites usually have only one human-associated host (thus confounding the hypothesis test), and the asexual stages have almost no within-population genetic variation (which is necessary for the calculations). This produced a very biased test of the co-evolutionary hypothesis. Moreover, the decision to use only mitochondrial DNA sequences effectively excluded all data from plant-parasitic nematodes (which had all been studied using RAPDs and

microsatellites), thus producing exactly the sort of additional taxonomic bias that I referred to above. These sorts of methodological problems need to be addressed and their potential for producing misleading generalizations evaluated, but the book authors leave most of them for future consideration.

Another issue worth raising is the fact that taxon sampling in parasitology is opportunistic more often than not, to a much greater extent than occurs in studies of non-parasitic organisms. Infected hosts cannot always be identified a priori, and then only at autopsy can the parasite be located (particularly endoparasites), so that co-evolutionary studies can be wildly inaccurate (especially if they involve estimates of prevalence or intensity). Furthermore, for some parasite groups only those species with domesticated animals or plants as their host have been studied. This means that many phylogenetic trees of parasites are very incomplete, unless they refer to a relatively small group of species that has been specifically targeted for a particular study. It is difficult to evaluate whether it is even worth doing a co-phylogeny study under these circumstances, as this limited sampling only compounds the sorts of methodological limitations highlighted in this book. So, there is very little empirical evidence that can be used to evaluate just how biased are the well-known instances of host–parasite co-speciation. The book authors remain optimistic, but only time will tell.

For any systematist embarking on a host-parasite study for the first time, or for a biologist wanting a readable entrée into the topic, this book is a good place to start, as it still provides the only comprehensive introduction to the theory and practice of co-phylogeny analysis. For the seasoned practitioner of co-evolution who has still not fully appreciated the potential benefits of a phylogenetic perspective, this book provides a critical synthesis of much of the current thinking as well as coverage of the possible future directions. It should enthuse anyone with an interest in the historical aspects of inter-species interactions.

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Conference reports

Eighth International Mycological Congress, Cairns, 2006

The eighth International Mycological Congress was recently held in Cairns on 20–25 August; the first time that the Congress has come to the Southern Hemisphere. There were about 700 delegates from more than 50 countries, with the largest contingents from Australia, the United States and Japan. Symposia were held in five concurrent sessions during each day. There were also more than 600 posters across ten themes, which paralleled the diversity of topics in the symposia: Phylogeny, Systematics and Evolution; Mycorrhizae; From Genomics to Proteomics; Food Mycology and Mycotoxins; Plant and Fungal Pathogens; Animal Pathogens; Cell Biology and Physiology; Population Genetics; Biodiversity and Conservation; and Industrial Mycology. The Congress was preceded by various workshops, on topics such as Insect Pathogens, Rust Fungi and Hypogeous Fungi.

The first of five Plenary Addresses was a fascinating overview of the ‘Fungal tree of life’ by Franz Oberwinkler, who included an update of the fast-changing classification of fungi. Oberwinkler stressed the importance of links between fungi and their plant hosts in understanding the evolution of both plants and fungi. The final plenary by Mike Wingfield on ‘Emerging fungal diseases threaten world forests’ included mention of Guava Rust on Myrtaceae and Heteropyxidaceae (both Myrtales) in South America, which is a fungus that we will be hearing a lot more about in Australia (although we hope we never see it here – see Pam Catchside’s article in the last issue of the newsletter). David Hawksworth gave an entertaining special lecture on ‘Mycology and Mycologists’, which included a glimpse into the good old days at the then Commonwealth Mycological Institute, where men in suits sat smoking pipes while looking down microscopes.

The Cairns Convention Centre provided an excellent venue, with sufficient room for all the different activities, and a convivial meeting place in the main hall, where displays and a café were provided. There was also plenty in the Cairns

region, especially as far as the natural surrounds of rainforest and reef, to entertain delegates, overseas and Australian alike. The number of delegates was about half that at the previous Congress, which was held in Oslo. I did hear the odd grumble about how far some people had come to attend, but given the reverse is usually the case I reckon its not too much to ask to have the Congress in the Southern Hemisphere every couple of decades. Trond Schumacher, President of the International Mycological Association, which is the sponsoring organisation of the Congress, pointed out that part of the reason for moving Congresses around is to stimulate mycology in the host country. The Congress was certainly one of the largest ever gatherings of Australian mycologists, and there was also a good representation of mycologists from Asia and South Africa, although unfortunately not so many from other parts of Africa or South America.

Most papers included at least a little, and often a lot, of molecular data. Even some of the reports based on PhD studies utilised four or five DNA regions across numerous species. A symposium on DNA barcoding included some interesting presentations where the utility of barcoding (using a standard sequence such as COX1 or ITS) was tested in genera where the taxonomy is already well-known, such as in certain groups of *Penicillium* and *Trichoderma*. The approach worked well enough, although there were some species that could not be differentiated on these sequences. Symposia on Gondwanan Fungi and Phylogeography both included papers which utilised molecular data across the global diversity of particular genera, families or orders. Intriguing suggestions are emerging from these approaches that the basal members of some groups are from Gondwanan regions: *Armillaria* in Africa, the Hysterangiales in Australia and *Laccaria* in various regions of the Southern Hemisphere. Such results certainly mean that taxon sampling, up to now a little light on south of the equator, must be more complete as far as