

Will *The Phylogenetic Handbook* eliminate all the ‘blood, sweat and tears’ that can accompany phylogenetic and molecular evolutionary analyses for the ‘non-card carrying’ phylogeneticist? Of course not. I am confident, however, that the use of this book as a guide can significantly reduce the trauma frequently associated with such analyses. To get a sense of its utility, I went ahead and ran some data sets of my own through a handful of the analyses that are outlined in the practice sections of the book. I found that stumbling blocks remain when it comes to properly installing or executing software, or to properly formatting data sets so that they run smoothly through various software packages. In addition, the software packages that are highlighted in the practice sections of *The Phylogenetic Handbook* might simply not be the particular software packages that you would like to use. There are, for example, many software options for multiple sequence alignment or for phylogenetic analysis using the maximum likelihood criterion, but only a few are presented in the corresponding practice sections of the handbook. You will have to navigate the installation and the execution of these other software packages on your own. This might seem daunting, but at least the theory section of the handbook can equip you with the knowledge needed to make informed decisions about your methodology (and keep in mind that, although this new edition of *The Phylogenetic Handbook* is highly informative and user-friendly, nothing compares to befriending your local phylogenetics guru).

Of course, there are limits to what can be included in the handbook itself. To get around the drawback that only select software is presented in the practice sections, it would be excellent to see additional content added to the website. It would be especially helpful to include on the website the same type of step-by-step practice exercises that are presented in the handbook for additional, commonly used software packages, such as DIALIGN, RAXML, GARLI, and PAML. Such additions to the website would, however, only further the usefulness of this already very handy handbook. I am convinced that its background, theory and practice sections are invaluable for guiding readers through the proper design and execution of phylogenetic and molecular evolutionary analyses, and recommend *The Phylogenetic Handbook* whole-heartedly to anyone whose work might venture in this direction.

Models for the future

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doi:10.1242/dev.039271

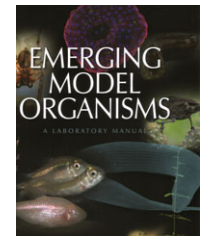
Emerging Model Organisms: A Laboratory Manual, Vol. 1

Edited by Richard R. Behringer, Alexander
D. Johnson and Robert E. Krumlauf

Cold Spring Harbor Laboratory Press (2009) 592 pages
ISBN 978-087969872-0
\$89 (paperback)

Any biologist who has worked with a genuine ‘model organism’, be it plant or animal, mould or microbe, knows the powerful insight into biology that can be provided by such species. In part this insight derives from the intrinsic characters that underlie their initial adoption as models, such as a rapid generation time and ease of husbandry. But their usefulness also depends on the extent to which their intrinsic traits have been built upon; the sheer depth of knowledge of how they work; the development of extensive resources in the form of genes, mutants and transgenic lines; and the establishment of incisive experimental methods. When combined, these allow a fidelity of experimentation that is, at least to me, breathtaking. The arguments as to why we as a scientific community should invest so much in such organisms are overwhelming. With such a focus of resources we can go further, faster; we can then take the details of what we learn and apply them to situations of economic and therapeutic need. We may also seek to establish the underlying principles of how such organisms work, and then apply these in a predictive manner across the tree of life. The success of these approaches should be apparent to all.

Why, then, should we be interested in taking into the laboratory other species, variously known as non-model organisms, new model organisms or, in the case of this book, emerging model organisms? One powerful argument is that every model system has its own unique evolutionary history and hence its own set of adaptations, specialisations and caveats. The workhorses of developmental biology, the fruitfly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*, are a case in point; immensely powerful in many ways, it has recently become clear that both species have lost a surprisingly large number of genes



that were present in the common ancestor of the bilaterians, and that are still found in our own genome (Kortschak et al., 2003; Miller and Ball, 2008; Putnam et al., 2007; Technau et al., 2005). New models will be needed to bring the power of invertebrate genetics to bear on the functions of these genes.

A second argument, and one that I suspect motivates many (including myself), is the drive to understand the evolutionary basis for the diversity of life. Studies restricted to a few species will never illuminate how enigmatic groups such as the cephalopods evolved from their snail-like molluscan ancestors, or how vertebrates evolved the complex cranial senses, jaws and brains associated with their transition to a predatory lifestyle. For these questions, we need to focus on species that diverged at informative points in evolution. For these reasons (and others), many researchers have been turning to a host of different species, some previously studied in other contexts and others essentially new to experimental

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biology. *Emerging Model Organisms* is aimed at helping such adoption by providing centralised collections of information on resources, tools and protocols for a wide diversity of relevant species.

The book is divided into 23 chapters, each describing a different species and each written by a research group with expertise in the area. The species chosen are mostly multicellular, reflecting a focus on developmental biology, and range from the social amoeba *Dictyostelium* (which has such a well-developed research community, resources and tools it could uncharitably be called a ‘well-emerged’ model organism) to the dogfish *Scyliorhinus*, in which little is currently possible experimentally beyond

the descriptive. Many species that could have been included are absent, and hence a second volume is planned: a list of species for inclusion in volume two is given at the front of volume one. This list is now a bit out of date and a more comprehensive list can be found on the relevant website (www.cshprotocols.org/emo). Volume one has a heavy bias towards animals (there are only three plant species included: a moss, a snapdragon and a tomato), and there are only three more plants on the list of eighteen species proposed for volume two. Plant biologists take special note, if something you want to see included is missing or you are angered by the omission of your pet emerging model, the editors openly invite suggestions (you can email them to submitprotocols@cshl.edu).

Each chapter is written to a template, with sections on the general background and history of the organism, its uses, how to find them and keep them, the status of current genomic and genetic resources, and detailed experimental protocols. Different authors invariably bring their own style to their chapter, with some providing much more depth in areas than others. However, the common framework ensures the core relevant information is ever-present. The experimental protocols that accompany each section are a real plus, as they often include those little bits of informal ‘how to...’, as well as the basic experimental steps that can also be found in publications. Any experimentalist knows the value of this lab knowledge when embarking on something new. I also appreciated the sections on resources (genetic and genomic), as many authors are part of ongoing projects and have included information on their status and how to access data; something that is impossible to find from publications and often hard to track down on the Web.

Will this information help a lab trying to set up a system that is new to them? The answer is undoubtedly, yes. I have been through this process several times, and know it is easy to underestimate the difficulties involved with sourcing specimens, establishing breeding conditions and developing resources and experimental techniques. I would strongly recommend anyone starting work on one of the species covered in this book to read the chapter dedicated to it first. In fact, even if your species is not covered, reading a chapter on a closely related taxon might still be surprisingly helpful. I do, however, have one negative thing to say in this context. There are a couple of species in

the book that my lab and I know well, and in one chapter we found a number of errors; little things, like protocol stages mis-numbered, conflicting information in different protocols, taxa misnamed. Easy to spot if you know the species and protocols well, but less so if you are coming to them fresh. I suspect this is a matter of proofreading and that these errors are probably chapter-specific. It won’t prevent me from using the book, but it reinforces that, even with such detailed experimental descriptions provided by world experts, you still need to make sure you understand what you are doing at each step and why. Uncritical pursuit of a protocol is inherently risky.

Overall, should you buy this book? Whilst reading a chapter on an organism on which you were initiating work would be highly recommended, I wouldn’t suggest buying the book just to get the information on one species; instead individual chapters can be bought online more cost effectively from www.cshprotocols.org/emo. As I write, a few of the volume two chapters are also available, and I imagine others will come online as they are completed. I did, though, enjoy browsing the various species in volume one much more than I anticipated. I think this stems from the ‘Background Information and Uses’ sections found in each chapter, which together summarise a diversity of data that

can only otherwise be found from reading numerous, sometimes arcane, papers or from sporadic focused reviews like the *BioEssays* ‘My Favourite Animal’ series. From this perspective, having a copy lying around the lab is a nice idea. The adaptability and plummeting cost of genomics, the widening applicability of gene knockdown methodology and a sustained interest in applying these to a wider diversity of species means opportunities to explore new systems will continue to arise. My copy will be in the lab in the hope that students, postdocs and indeed myself will leaf through it in between experiments, and maybe, one day, exploit what they learn.

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Fleshing out the skeletal system

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doi:10.1242/dev.040576

The Skeletal System

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Cold Spring Harbor Laboratory Press (2009) 365 pages
ISBN 978-087969825-6
£61.75/\$95 (hardcover)

One of the most prominent features of vertebrate evolution is the formation of the skeletal system, which consists of cartilage and/or bone. The skeletal system is essential to all vertebrate species; it provides the body with shape and form, supports it, protects the internal organs, allows body movement, houses blood stem cells, stores minerals and

even acts as an endocrine organ to regulate general metabolism and homeostasis. However, for some time, the biology of the skeletal system escaped most people’s attention because it was viewed as not being quite so ‘alive’ as other tissues and because the high mineral content of the skeleton led people to believe that it consists largely of ‘pieces of rock’. Thanks to the recent application of genetic, molecular and cellular tools to the study of the skeletal system, the past two decades have seen a tremendous explosion of seminal discoveries about this biological system. Now one can never deny

