Review of: *Species Diagnostics Protocols: PCR and Other Nucleic Acid Methods*, edited by J. P. Clapp

Steven A. Nadler  
*University of California - Davis, sanadler@ucdavis.edu*

Follow this and additional works at: [http://digitalcommons.unl.edu/parasitologyfacpubs](http://digitalcommons.unl.edu/parasitologyfacpubs)  
Part of the Parasitology Commons

[http://digitalcommons.unl.edu/parasitologyfacpubs/705](http://digitalcommons.unl.edu/parasitologyfacpubs/705)
**BOOK REVIEW...**


This edited book is part of the Methods in Molecular Biology series (Vol. 50) and consists of 27 chapters contributed by 40 authors. The premise of the book is that nucleic acid-based methods will become commonplace "where there is a requirement to identify rapidly organisms that are small, immature, or present in large numbers." Molecular taxonomic approaches have greatest utility for recognition of cryptic species, evaluation of life cycle stages that are normally not diagnostic, and assessments of extremely small individuals that would require substantial preparation for identification (Black and Munstermann, 1996). Molecular taxonomy is certainly not new to parasitology, although in the future such approaches are likely to be applied more routinely in other subdisciplines, including the study of parasite communities.

Examples of taxonomic work in this volume tend to follow a similar pattern. A series of specimens is first identified using traditional methods, and these individuals serve as a benchmark to characterize molecular patterns for the potential pool of taxa to which unidentified specimens must be assigned. This, of course, presupposes that the alpha taxonomy of the group of interest is fairly well understood, and that an appropriate pool of "usual suspects" can be selected in advance for evaluation of the unidentified specimens.

Four chapters of the book concern organisms causing parasitic diseases of humans including leishmaniasis (G. J. J. M. Van Eys and S. E. O. Meredith), African trypanosomiasis (G. Hide), malaria (G. Snounou), and onchocerciasis (T. R. Unnasch and S. E. O. Meredith). Other chapters include identification procedures for organisms that may also interest parasitologists, including mosquito vectors of malaria, e.g., Anopheles species complexes, and viruses such as dengue and HIV. Of course, techniques discussed in chapters focusing on other organisms could easily be applied to various parasites.

A wide variety of approaches employing nucleic acids are included in this volume, and most of the protocols take advantage of the polymerase chain reaction (PCR) to amplify sufficient quantities of DNA for comparison. One chapter (N. Springer et al.) that parasitologists should take special note of concerns the use of fluorescent oligonucleotide probes for the identification of protozoan endosymbionts. Selective hybridization of specifically designed oligonucleotide probes is a method that holds great promise for identification of microscopic organisms. In general, the experimental protocols are sufficiently detailed and organized to be used right at the laboratory bench. Most chapters contain a separate Notes section cross-referenced to steps of the experimental protocol. This organization keeps the protocols uncluttered, yet provides background information and important tips for troubleshooting unsuccessful experiments. The individual chapters vary substantially with respect to the amount of molecular biology experience needed to undertake a particular procedure. This book is not a "do it yourself manual" for biologists lacking molecular training. Nevertheless, the detail of most chapters with respect to lists of required equipment, reagents, and step-by-step methods is admirable.

The strength of this volume is its thoroughness in presentation of procedures; its weakness is that virtually no discussion of analytical or theoretical issues is provided, although this is typical of books detailing methods. One exception is the chapter by W. C. Black, who discusses the use of cluster analysis to determine if arbitrary PCR (random amplified polymorphic DNA and arbitrarily primed PCR markers) patterns are species specific and useful for diagnosing unknown specimens. This chapter will be instructive for investigators interested in using AP patterns (which typically display intraspecific polymorphisms) for species diagnosis. Researchers requiring additional information on methods of data analysis or the relationship between speciation and molecular genetics, should probably consult other recently published books (e.g., Schierwater et al., 1994).

**LITERATURE CITED**


Steven A. Nadler, Department of Nematology, University of California, Davis, California 95616-8668.