Parasite Diversity and Diversification
Evolutionary Ecology Meets Phylogenetics

The development of molecular tools has dramatically increased our knowledge of parasite diversity and the vectors that transmit them. From viruses and protists to arthropods and helminths, each branch of the Tree of Life offers an insight into significant, yet cryptic, biodiversity. Alongside this, the studies of host–parasite interactions and parasitism have influenced many scientific disciplines, such as biogeography and evolutionary ecology, by using comparative methods based on phylogenetic information to unravel shared evolutionary histories.

*Parasite Diversity and Diversification* brings together two active fields of research, phylogenetics and evolutionary ecology, to reveal and explain the patterns of parasite diversity and the diversification of their hosts.

This book will encourage students and researchers in the fields of ecology and evolution of parasitism, as well as animal and human health, to integrate phylogenetics into the investigation of parasitism in evolutionary ecology, health ecology, medicine and conservation.

*Serge Morand* is CNRS researcher at the Institute of Evolutionary Sciences at the University of Montpellier II, France. His research focuses on the evolutionary ecology of host–parasite interactions and population ecology of parasites and pathogens. He is conducting several projects on the impacts of global changes on the links between biodiversity and health in Southeast Asia, using rodent-borne diseases as a model. He is the co-author of several articles and books on these fields.

*Boris R. Krasnov* is Professor and Head of the Mitrani Department of Desert Ecology in the Jacob Blaustein Institutes for Desert Research at the Ben-Gurion University of the Negev, Israel. He is interested in the various aspects of ecology and evolution of host–parasite relationships. Parasitic fleas on small mammals represent his main study model of parasite–host associations, although he studies some other parasite taxa as well. He is an author of three monographs, editor and co-editor of three collections and author of more than 200 scientific publications.

*D. Timothy J. Littlewood* is a Merit Researcher and currently Head of the Life Sciences Department at the Natural History Museum, London. His main research interests include: the systematics of platyhelminths (flatworms), and other phyla, particularly with a view to revealing evolutionary patterns associated with parasitism; the development and application of molecular tools for species diagnosis, life-cycle completion and biodiversity assessment; and mitogenomics and phylogenomics pursued by means of next-generation sequencing.
Parasite Diversity and Diversification

Evolutionary Ecology Meets Phylogenetics

Edited by

SERGE MORAND
CNRS, University of Montpellier, France

BORIS R. KRASNOV
Ben-Gurion University of the Negev, Israel

D. TIMOTHY J. LITTLEWOOD
Natural History Museum, London
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Contributors

Julie M. Allen
Illinois Natural History Survey, University of Illinois at Urbana-Champaign Champaign, Illinois, USA

Marina S. Ascunce
Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA

Ahidjo Ayouba
UM1 233, Institut de Recherche pour le Développement (IRD) and University of Montpellier 1, Montpellier, France

David Bass
Department of Life Sciences, The Natural History Museum, London, UK

Frida Ben-Ami
Department of Zoology, George S. Wise Faculty of Life Sciences, Tel-Aviv University, Tel-Aviv, Israel

Frédéric Bordes
Institut des Sciences de l’Evolution, CNRS-IRD-UM2, University of Montpellier 2, Montpellier, France

Bret M. Boyd
Florida Museum of Natural History and Genetics and Genomics Graduate Program, University of Florida, Gainesville, Florida, USA

Rodney A. Bray
Parasites and Vectors Division, Life Sciences Department, Natural History Museum, London, UK

Aurélie Chambouvet
Department of Life Sciences, The Natural History Museum, London, UK; Biosciences, University of Exeter, Geoffrey Pope Building, Exeter, UK
List of contributors

Philippe Christe
Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland

Julien Claude
Institut des Sciences de l’Evolution, CNRS-IRD-UM2, University of Montpellier 2, Montpellier, France

Yves Desdevises
Observatoire Océanologique de Banyuls-sur-Mer, Université Pierre et Marie Curie, UMR CNRS Biologie Intégrative des Organismes Marins, Banyuls-sur-Mer, France

Carl W. Dick
Department of Biology, Western Kentucky University, Bowling Green, Kentucky, USA

Katharina Dittmar
Department of Biological Sciences, Graduate Program of Ecology, Evolution and Behavior, University at Buffalo, The State University of New York, Buffalo, New York, USA

Ashley Dowling
Department of Entomology, University of Fayetteville, Fayetteville, Arizona, USA

Bryan G. Falk
Division of Invertebrate Zoology and Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, New York, USA

Martín García-Varela
Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, México D.F., México

Rebecca Rose Gray
Department of Zoology, University of Oxford, Oxford, UK

Michael W. Hastriter
Monte L. Bean Museum, Brigham Young University, Provo, Utah, USA

Hadas Hawlena
Jacob Blaustein Institute for Desert Research and Department of Life Sciences, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel

Tine Huyse
Biology Department, Royal Museum for Central Africa, Tervuren, Belgium, and Laboratory of Biodiversity and Evolutionary Genomics, Department of Biology, KU Leuven, Leuven, Belgium
List of contributors

James C. Iles
Department of Zoology, University of Oxford, Oxford, UK

Tania Jenkins
Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland

Boris R. Krasnov
Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede-Boqer Campus, Midreshet Ben-Gurion, Israel

Armand M. Kuris
Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara, USA

Tommy L. F. Leung
Zoology, School of Environmental and Rural Sciences, Faculty of Arts and Sciences, University of New England, Armidale, New South Wales, Australia

D. Timothy J. Littlewood
Parasites and Vectors Division, Life Sciences Department, Natural History Museum, London, UK

Peter V. Markov
Department of Zoology, University of Oxford, Oxford, UK

Camilo Mora
Department of Geography, University of Hawaii at Manoa, Honolulu, Hawaii, USA

Serge Morand
Institut des Sciences de l’Evolution, CNRS-IRD-UM2, University of Montpellier 2, Montpellier, France

Solon F. Morse
Department of Biological Sciences, Graduate Program of Ecology, Evolution and Behavior, University at Buffalo, The State University of New York, Buffalo, New York, USA

Steve Nadler
Department of Nematology, University of California, Davis, California, USA

Sigrid Neuhauser
Department of Life Sciences, The Natural History Museum, London, UK; Institute of Microbiology, Leopold-Franzens University Innsbruck, Innsbruck, Austria
List of contributors

Roderic Page
Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK

Bruce D. Patterson
Center for Integrative Research, Field Museum of Natural History, Chicago, Illinois, USA

Martine Peeters
UM1 233, Institut de Recherche pour le Développement (IRD) and University of Montpellier 1, Montpellier, France

Gerardo Pérez-Ponce de León
Departamento de Zoología, Instituto de Biología, Universidad Nacional Autónoma de México, México D.F., México

Susan L. Perkins
Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, USA

Timothée Poisot
Department of Biology, University of Quebec at Rimouski, Rimouski, Quebec, Canada

Robert Poulin
Department of Zoology, University of Otago, P.O. Box 56, Dunedin 9054, New Zealand

Oliver G. Pybus
Department of Zoology, University of Oxford, Oxford, UK

David L. Reed
Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA

Thomas A. Richards
Biosciences, University of Exeter, Geoffrey Pope Building, Exeter, UK

Klaus Rohde
Zoology, School of Environmental and Rural Sciences, Faculty of Arts and Sciences, University of New England, Armidale, New South Wales, Australia

Lajos Rózsa
MTA-ELTE-MTM Ecology Research Group, Budapest, Hungary
List of contributors

Andrea Šimková
Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic

Arne Skorping
Department of Biology, University of Bergen, Bergen, Norway

Melissa A. Toups
Department of Biology, Indiana University, Bloomington, Indiana, USA

Piotr Tryjanowski
Institute of Zoology, Poznań University of Life Sciences, Poznań, Poland

Maarten P. M. Vanhove
Laboratory of Biodiversity and Evolutionary Genomics, Department of Biology, KU Leuven, Leuven, Belgium; Biology Department, Royal Museum for Central Africa, Tervuren, Belgium; Department of Botany and Zoology, Faculty of Science, Masaryk University, Brno, Czech Republic; and Institute of Marine Biological Resources and Inland Waters, Hellenic Centre for Marine Research, Anavyssos, Greece

Zoltán Vas
Department of Zoology, Hungarian Natural History Museum and Department of Biomathematics and Informatics, Faculty of Veterinary Science Szent István University, Budapest, Hungary

Andrea Waeschenbach
Parasites and Vectors Division, Life Sciences Department, Natural History Museum, London, UK

Lucy A. Weinert
Department of Veterinary Medicine, University of Cambridge, Cambridge, UK

Michael F. Whiting
The College of Life Sciences, Brigham Young University, Provo, Utah, USA

Quin Zhu
Department of Biological Sciences, Graduate Program of Ecology, Evolution and Behavior, University at Buffalo, The State University of New York, Buffalo, New York, USA
Foreword

So nat’ralists observe, a flea
Hath smaller fleas that on him prey;
And these have smaller fleas to bite ’em.
And so proceeds Ad infinitum.

Jonathan Swift, 1733

In 1988, while doing a PhD on biogeography in New Zealand, I wandered into my university’s geology library and idly browsed the latest issue of Nature. At that time any self-respecting graduate student in systematics knew that the ‘good stuff’ wasn’t to be found in Nature, but rather in the pages of Systematic Zoology (now Systematic Biology) or Cladistics. But this issue was different for it contained Mark Hafner’s and Steve Nadler’s elegant study of pocket gophers and their lice. By today’s standards this was a small data set: eight mammals and their ten parasitic insects. Hafner and Nadler used unweighted pair group method with arithmetic mean (UPGMA) to cluster genetic distances computed from allozymes from these taxa, a tree-building method disdained by right-thinking graduate students who read every issue of Cladistics. But the match between the two trees was striking, not only in the topology but also the relative genetic distances. A few years earlier, David Penny and colleagues had sought to show that evolution was a proper, testable hypothesis (Karl Popper’s influence was everywhere in systematics in the 1980s) by demonstrating that the probability of multiple phylogenies for different proteins for the same taxa being at all similar was vanishingly small. Hafner and Nadler had gone one better and found closely matching trees for different taxa.

Since Hafner and Nadler’s study, phylogenetics has been transformed by the ease of obtaining DNA sequence data. Initially it seemed simple: sequence a marker and build a tree. But as more loci were sequenced it became clear that multiple loci could mean multiple gene trees (it is worth remembering that Hafner’s and Nadler’s allozyme study had more loci than many early DNA studies). Phylogenetics was capable of generating tangled trees, much like those emerging from comparative studies of host–parasite coevolution. At the same time, sequencing made possible phylogenetic studies of organisms whose morphology carried little, if any, discernible trace of their history. Many of these organisms were themselves associated with other organisms. What seemed like relatively simple associations between, say, a mammal and a louse became
on further inspection complex, multi-layered assemblages involving hosts, parasites and parasite endosymbionts.

The chapters in this book make a compelling case for why the study of host and parasite taxa and their interactions is so engaging. Beyond the intriguing biology, and the visual appeal of matching evolutionary trees, there are tractable questions that can be tackled using a range of methods, from genomics to experimental ecology. Modern coevolutionary studies have brought Swift’s verse to life. 

Roderic Page