Evolutionary Pathways in Nature

A Phylogenetic Approach

Reconstructing phylogenetic trees from DNA sequences has become a popular exercise in many branches of biology, and here the award-winning geneticist John Avise explains why. Molecular phylogenies provide a genealogical backdrop for interpreting the evolutionary histories of many other types of biological traits (anatomical, behavioral, ecological, physiological, biochemical, and even geographical). Guiding readers on a natural history tour along dozens of evolutionary pathways, the author describes how creatures ranging from microbes to elephants came to possess their current phenotypes. If you want to know how the toucan got its bill and the kangaroo its hop, then this is the book for you. This book also provides a definitive answer to the proverbial question: 'which came first, the chicken or the egg?' This scientifically educational yet entertaining treatment of ecology, genetics and evolution is intended for college students, professional biologists, and anyone interested in natural history and biodiversity.

John C. Avise is a distinguished professor of Ecology and Evolutionary Biology at the University of California, Irvine.

Evolutionary Pathways in Nature

A Phylogenetic Approach

JOHN C. AVISE
Department of Ecology and Evolutionary Biology
University of California

Illustrations by Trudy Nicholson

CAMBRIDGE
UNIVERSITY PRESS

CAMBRIDGE UNIVERSITY PRESS
Cambridge, New York, Melbourne, Madrid, Cape Town, Singapore, São Paulo

Cambridge University Press
The Edinburgh Building, Cambridge CB2 2RU, UK

Published in the United States of America by Cambridge University Press, New York

www.cambridge.org
Information on this title: www.cambridge.org/9780521857536

First published 2006

Printed in the United Kingdom at the University Press, Cambridge

A catalog record for this publication is available from the British Library

ISBN-13 978-0-521-85753-6 hardback
ISBN-10 0-521-85753-8 hardback

ISBN-13 978-0-521-67417-1 paperback
ISBN-10 0-521-67417-4 paperback

CONTENTS

PREFACE

Many biologists now incorporate molecular phylogenetic analyses into their explorations of nature. Using sophisticated laboratory techniques, they uncover "DNA markers" or "genetic tags" that uniquely identify each creature. Furthermore, details in the submicroscopic structures of these natural labels offer tantalizing clues to how living organisms were genealogically linked through bygone ancestors. Thus, lengthy DNA sequences housed in the cells of all organisms carry not only the necessary molecular genetic instructions for life, but also extensive records of phylogeny, i.e. of evolutionary ancestry and descent.

During the replication and transmission of DNA from one generation to the next, mutations continually arise. Many of these spread through populations (via natural selection, or sometimes by chance genetic drift), thereby cumulatively altering particular molecular passages in each species' hereditary script. In recent years, scientists have learned how to read and interpret the genealogical content of these evolutionary diaries – these "genomic autobiographies" – of nature. Results are summarized as phylogenetic diagrams that depict how particular forms of extant life are connected to one another via various historical branches in the Tree of Life.

Phylogenetic analysis has become a wildly popular exercise in many areas of biology, but phylogenies estimated from DNA sequences are seldom the ultimate objects of scientific interest. The primary value of each molecular phylogeny lies instead in its utility as historical backdrop for deciphering the evolutionary histories of other kinds of biological traits such as morphologies, physiologies, behaviors, lifestyles, or geographical distributions. By mapping such organismal features onto species' phylogenies estimated from molecular data, biologists can address fascinating questions of the following sort. Did the bipedal hop arise once or multiple times in kangaroo evolution? From what type of ancestor did toucan birds evolve their banana-like bills? How often during evolution have reptiles lost their limbs? Are the antifreeze proteins in Arctic and Antarctic fishes functionally similar by virtue of shared ancestry or convergent evolution? By what evolutionary routes have some fishes evolved powerful electrical discharges? Did Jamaican land crabs derive their peculiar forms of offspring care from a common ancestor? Did walkingstick insects evolve from flyingsticks or vice versa, and how often? How have certain bacteria acquired their magnetic compasses? On how many occasions have distinct algal and fungal lineages joined forces in lichen symbioses? Where on the planet have phylogenetic appraisals uncovered cryptic species and conservation-relevant hotspots of global biodiversity? Can the ancient breakup of the supercontinent Gondwanaland account for the modern distributions of particular lineages of birds and mammals in the Southern Hemisphere? Where and when did the viruses responsible for the AIDS epidemic enter the human species? And, which came first: the chicken or the egg?

By highlighting studies that have provided scientific answers to these and many additional questions, I intend to illustrate the power (and also some limitations) of comparative phylogenetic perspectives in biological research. Several available textbooks describe, in depth, how molecular data are gathered in the laboratory and analyzed at the computer. My approach here will not be to recount the many operational details of molecular phylogenetics (although introductory background is provided). Rather, my intent is to serve as a naturalist guide on a biological expedition into the remarkable world of nature, as viewed through the evolutionary prism of molecular phylogeny. In each of 67 essays arranged into six topical chapters, I describe how a DNA-estimated phylogeny provided historical framework for interpreting a puzzling ecological feature or evolutionary process in organisms with unusual anatomies or lifestyles, or in creatures with special significance to one or another biological field such as ethology, natural history, biogeography, conservation, biochemistry, physiology, epidemiology, or medicine.

Through this case-history approach, I hope to provide a fun yet educational introduction – for amateur naturalists and students to professional biologists – to how comparative phylogenetic analyses have helped to solve some of nature's most intriguing mysteries. Another goal is to encourage a deeper appreciation of the many intellectual and aesthetic treasures of the biological world. As more and more people become educated about nature's ways, perhaps societies will learn to cherish life's variety and strive harder to preserve what remains. Tragically, through human actions, populations and species today are being driven to extinction at rates seldom experienced in the planet's long history. To terminate any lineage now is to lose forever a genetic wisdom that was honed along an epic evolutionary journey lasting nearly four billion years. Paradoxically, life is both fragile and tenacious. Extinction continually threatens, and once realized can never be undone. However, having withstood and adapted to countless environmental challenges over the geological eons, each extant lineage is also a hardy and proven survivor, surely deserving of our deepest respect and admiration.

ACKNOWLEDGMENTS

Doug Futuyma, Blair Hedges, David Hillis, Kirk Jensen, Judith Mank, Axel Meyer, David Reznick, DeEtte Walker, John Ware, and several anonymous reviewers provided helpful comments on various portions of the text. I am especially grateful to Trudy Nicholson for producing the beautiful plant and animal drawings that grace this book.