

EVOLUTION,  
SCIENCE,  
AND  
SOCIETY

EVOLUTIONARY BIOLOGY AND THE  
NATIONAL RESEARCH AGENDA



A companion document serves as an executive summary. To receive copies of either report, or for more information, please consult our web site via <http://www.amnat.org> or contact one of the Chairs listed below.

Prepared by delegates representing the following scientific societies. These societies have all endorsed the final document.

American Society of Naturalists  
Animal Behavior Society  
Ecological Society of America  
Genetics Society of America  
Paleontological Society  
Society for Molecular Biology and Evolution  
Society for the Study of Evolution  
Society of Systematic Biologists

Additional endorsement by:

American Institute of Biological Sciences

With financial sponsorship from:

A.P. Sloan Foundation  
National Science Foundation

Editorial Chair:

Douglas J. Futuyma, State University  
of New York–Stony Brook

Organizational Chair:

Thomas R. Meagher, Rutgers, The State University  
of New Jersey

Steering Committee:

Michael J. Donoghue, Harvard University  
James Hanken, University of Colorado  
Charles H. Langley, University of California–Davis  
Linda Maxson, University of Iowa

Working Group:

Albert F. Bennett, University of California–Irvine  
H. Jane Brockmann, University of Florida  
Marcus W. Feldman, Stanford University  
Walter M. Fitch, University of California–Irvine  
Laurie R. Godfrey, University of Massachusetts  
David Jablonski, University of Chicago  
Carol B. Lynch, University of Colorado  
Leslie Real, Emory University  
Margaret A. Riley, Yale University  
J. John Sepkoski, Jr., University of Chicago  
Vassiliki Betty Smocovitis, University of Florida

Designed and produced by the Office of University  
Publications, Rutgers, The State University of  
New Jersey

## CONTENTS

### EXECUTIVE SUMMARY 1

### PREAMBLE 2

### I. INTRODUCTION 3

### II. WHAT IS EVOLUTION? 3

### III. WHAT ARE THE GOALS OF EVOLUTIONARY BIOLOGY? 5

- A. Subdisciplines of Evolutionary Biology 5
- B. Perspectives from Evolutionary Biology 7

### IV. HOW IS EVOLUTION STUDIED? 8

### V. HOW DOES EVOLUTIONARY BIOLOGY CONTRIBUTE TO SOCIETY? 11

- A. Human Health and Medicine 11
- B. Agriculture and Natural Resources 14
- C. Finding Useful Natural Products 17
- D. Environment and Conservation 17
- E. Applications beyond Biology 19
- F. Understanding Humanity 19

### VI. HOW DOES EVOLUTIONARY BIOLOGY CONTRIBUTE TO BASIC SCIENCE? 20

- A. Accomplishments in the Study of Evolution 20
- B. Contributions to Other Biological Disciplines 24

### VII. WHAT DOES THE FUTURE HOLD FOR EVOLUTIONARY BIOLOGY? 27

- A. Applied Science 27
- B. Basic Science 31

### VIII. MECHANISMS FOR MEETING THE CHALLENGES OF THE FUTURE 35

- A. Advancing Understanding through Research 35
- B. Advancing Understanding through Education 37
- C. Advancing Understanding through Communication 38

### IX. CONCLUSION 39

### BIBLIOGRAPHY 41

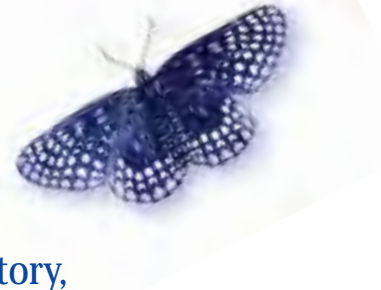
### APPENDICES 43

- I. Evolution: Fact, Theory, Controversy 43
- II. How This Document Was Produced 44
- III. Glossary of Frequently Used Terms 44
- IV. Matching Evolutionary Research to Agency Missions 45





evolutionary biology is the study of the history of life and the processes that lead to its diversity.



Based on principles of adaptation, chance, and history,

evolutionary biology seeks to explain all the characteristics of organisms, and, therefore, occupies a central position in the biological sciences.

#### **RELEVANCE OF EVOLUTIONARY BIOLOGY TO THE NATIONAL RESEARCH AGENDA**

The twenty-first century will be the “Century of Biology.” Driven by a convergence of accelerating public concerns, the biological sciences will be increasingly called on to address issues vital to our future well-being: threats to environmental quality, food production needs due to population pressures, new dangers to human health prompted by the emergence of antibiotic resistance and novel diseases, and the explosion of new technologies in biotechnology and computation. Evolutionary biology in particular is poised to make very significant contributions. It will contribute directly to pressing societal challenges as well as inform and accelerate other biological disciplines.

Evolutionary Biology has unequivocally established that all organisms evolved from a common ancestor over the last 3.5 billion years; it has documented many specific events in evolutionary history; and it has developed a well-validated theory of the genetic, developmental, and ecological mechanisms of evolutionary change. The methods, concepts, and perspectives of evolutionary biology have made and will continue to make important contributions to other biological disciplines, such as molecular and developmental biology, physiology, and ecology, as well as to other basic sciences such as psychology, anthropology, and computer science.

In order for evolutionary biology to realize its full potential, biologists must integrate the methods and results of evolutionary research with those of other disciplines both within and outside of biology. We must apply evolutionary research to societal problems, and we must include the implications of that research in the education of a scientifically informed citizenry.

To further such goals, delegates from eight major professional scientific societies in the United States, whose subject matter includes evolution, have prepared this document. It includes contributions by other specialists in various areas. Feedback on earlier drafts was elicited from the community of evolutionary biologists in the United States, and the draft was made public on the World Wide Web. The delegates arrived at a series of recommendations that address the areas that follow.

#### **ADVANCING UNDERSTANDING THROUGH RESEARCH**

To capitalize on evolutionary biology as an organizing and integrating principle, we urge that:

- evolutionary perspectives be incorporated as a foundation for interdisciplinary research to address complex scientific problems
- evolutionary biologists work toward building meaningful links between basic research and practical application
- evolutionary biology play a more explicit role in the overall mission of federal agencies that could benefit from contributions made by this field

#### **ADVANCING UNDERSTANDING THROUGH EDUCATION**

We encourage major efforts to strengthen curricula in primary and secondary schools, as well as in colleges and universities, including:

- support of supplemental training for primary school teachers and or midcareer training for secondary school science teachers in evolutionary biology
- greater emphasis on evolution in undergraduate college curricula for biology majors and premedical students, with accessible alternative courses for non-majors
- integration of relevant evolutionary concepts into the postbaccalaureate training of all biologists and of professionals in areas such as medicine, law, agriculture, and environmental sciences

#### **ADVANCING UNDERSTANDING THROUGH COMMUNICATION**

We urge the following roles for evolutionary biologists:

- communicating to federal agencies, and to other institutions that support basic or applied research, the relevance of evolutionary biology to the missions of these organizations
- training the next generation of evolutionary biologists to be aware of the relevance of their field to societal needs
- informing the public about the nature, progress, and implications of evolutionary biology

## PREAMBLE

Three great themes run through the biological sciences: function, unity, and diversity. Much of biology, from molecular biology to behavioral biology, from bacteriology to medicine, is concerned with the mechanisms by which organisms function. Many of these mechanisms are *adaptations* features that enhance survival and reproduction. Some adaptations are found only in certain groups of organisms, but others are shared by almost all living things, reflecting the *unity* of life. At the same time, the *diversity* of characteristics among the earth's millions of species is staggering.

The unity, diversity, and adaptive characteristics of organisms are consequences of evolutionary history, and can be understood fully only in this light. The science of evolutionary biology is the study of the history of life and of the processes that lead to its unity and diversity. Evolutionary biology sheds light on phenomena studied in the fields of molecular biology, developmental biology, physiology, behavior, paleontology, ecology, and biogeography, complementing these disciplines' study of biological mechanisms with explanations based on history and adaptation. Throughout the biological sciences, the evolutionary perspective provides a useful, often indispensable framework for organizing and interpreting observations and for making predictions. As was emphasized in a recent report from the United States National Academy of Sciences (37), biological evolution is "the most important concept in modern biology—a concept essential to understanding key aspects of living things."

Despite its centrality in the life sciences, evolutionary biology does not yet command a priority in educational curricula or in research funding commensurate with its intellectual contributions and its potential for contributing to societal needs. The reasons for this may include the misperception that all important scientific questions about evolution have already been answered, and the controversy among some nonscientists about the reality of evolution and its perceived threat to traditional social values. However, evolutionary biology is an intellectually and technologically dynamic discipline that includes some of the most exciting contemporary discoveries in the biological sciences.

The major purposes of this document are:

- to describe our present understanding of evolution and the major intellectual accomplishments of evolutionary biology;
- to identify major questions and challenges in evolutionary science on which progress can be expected in the near future;
- to describe past and expected future contributions of evolutionary biology, both to other sciences and to social needs in areas such as health science, agriculture, and environmental science; and

- to suggest ways in which progress can be facilitated in basic research, in applications of evolutionary biology to societal needs, and in science education.

This document was prepared for decision-makers responsible for guiding basic and applied scientific research and for developing educational curricula at all levels. Delegates from eight major professional scientific societies in the United States whose subject matter includes evolution have developed the document. Contributions have also been made by other specialists in various topics. A draft of the document was revised in light of feedback elicited from the community of evolutionary biologists in the United States and by making the draft available for public comment at scientific meetings and on the World Wide Web. Although full agreement cannot be expected on every detail and point of emphasis, the major points and conclusions in the following pages represent the opinion of a large majority of professional evolutionary biologists in the United States.

## I. INTRODUCTION

"What a piece of work is man! The beauty of the world, the paragon of animals!" Like Shakespeare's Hamlet, we too marvel at the exquisite features of our species, but after four centuries, we do so in the light of immensely greater knowledge. Reflect, for example, on the human body: a textbook of biology, a lesson in evolution.

We are struck, first, by the innumerable features that enable us to function. Whether we consider our eyes, our brain, or our immune system, we find complex features admirably suited for the functions they perform. Such features that serve our survival and reproduction are called *adaptations*. How did they come to be?

Looking more closely, we also find anomalies that do not make adaptive sense. How do we account for our nonfunctional appendix, for nipples on men, for wisdom teeth that erupt painfully or not at all, or for the peculiar arrangement of our digestive and respiratory tracts, which inconveniently cross each other so that we risk choking on food?

Considering our species at large, we see almost endless variation. Differences among people in size, shape, and pigmentation are just the tip of the iceberg. Almost everyone has unique facial features and unique DNA "fingerprints," there is hereditary variation in susceptibility to infectious diseases, and an unfortunate number of people inherit any of many rare genetic defects. What accounts for all this variation?

If we expand our view and compare ourselves with other organisms, we find a range of features that we share with many other species. We are united with apes and monkeys by our fingernails; with all mammals by hair, milk, and the structure of our teeth and jaws; with reptiles, birds, and amphibians by the basic structure of our arms and legs; and with all vertebrates, including fishes, by our vertebrae and many other features of

our skeleton. Probing more deeply, we find that the structure of our cells unites us with all animals, and that the biochemical functions of our cells are virtually identical across a still wider group of organisms, the eukaryotes: not just animals, but also plants, fungi, and protozoans such as amoebas. Most fundamental of all are DNA, the vehicle of heredity, the variety of amino acids that are the building blocks of proteins, and the specific code in the DNA for each of these amino acids. All these features are the same throughout the living world, from bacteria to mammals. Such commonalities among species demand explanation.

This world of species with which we hold so much in common—how extraordinarily diverse it is, despite its unity! Look at a backyard, a roadside ditch, or even an abandoned city lot, and you will find an astonishing variety of plants, insects, and fungi, and perhaps some birds and mammals. With a lens or microscope you would discover diverse mites, nematode worms, and bacteria. Even you have a thriving community of many kinds of bacteria on your skin, in your mouth, and in your intestines. And this is just the beginning. From the driest deserts to the hot vents on the ocean floor, the world teems with organisms—at least 2 million and perhaps more than 10 million species—that differ in the most amazing ways. They range in size from giant redwoods and whales to viruses that are hardly more than large molecules. They nourish themselves by photosynthesis, by chemical synthesis, and by eating plants, dry wood, hair, or live or dead animals. Some can live almost anywhere; others are so specialized that they can eat only one species of plant, or live only within the cells of a single species of insect. They may reproduce sexually or clonally, have separate sexes or not, outcross or self-fertilize. Their behavior may be as simple as orienting toward light, or complex enough to involve them in networks of cooperation. Among these millions of species are some without which we could not survive, and others, such as the virus that causes AIDS and the protozoan that causes malaria, that are our formidable enemies.

These reflections raise some of the most sweeping and profound questions in biology. How do we account for the unity of life? How can we explain its astonishing diversity? What accounts for the wondrous adaptations of all species, including ourselves, as well as for their nonadaptive features? What accounts for variation, both within and among species?

These are the fundamental questions of the science of evolutionary biology. The endeavor to answer them, and the thousand other questions that grow out of them, has spawned theories and methods that have continually deepened our understanding of the living world—including ourselves. Every subject in the biological sciences has been enriched by an evolutionary perspective. Evolution, which provides an explanatory framework for biological phenomena ranging from genes to ecosystems, is the single unifying theory of biology.

Evolutionary science explains the unity of life by its history, whereby all species have arisen from common ancestors

over the past 4 billion years. It explains the diversity and the characteristics of organisms, both adaptive and nonadaptive, by processes of genetic change, influenced by environmental circumstances. It fashions from general principles specific explanations for the diverse characteristics of organisms, ranging from their molecular and biochemical features to their behavior and ecological attributes. In developing such explanations, evolutionary biologists have honed methods and concepts that are being applied in other fields, such as linguistics, medicine, and even economics. Thus, the perspective developed by evolutionary biology can inform the study of a wide range of phenomena, but the reach of evolutionary thought does not stop there. Attended by controversy, to be sure, the evolutionary perspective that Darwin originated shook the foundations of philosophy, left its imprint on literature and the arts, deeply affected psychology and anthropology, and provided wholly new perspectives on what it means to be human. Few scientific discoveries have had so far-reaching—and challenging—an impact on human thought.

This document addresses the fundamental role that evolutionary science plays in modern biology, its applications to societal concerns and needs, the major future directions of evolutionary research and its applications, and the critical position that evolutionary biology must hold in biological research and in education. To address these issues, it is necessary first to describe the nature of evolutionary research and to highlight its accomplishments, both as basic and applied science.

## II. WHAT IS EVOLUTION?

Biological evolution consists of change in the hereditary characteristics of groups of organisms over the course of generations. Groups of organisms, termed *populations* and *species*, are formed by the division of ancestral populations or species, and the descendant groups then change independently. Hence, from a long-term perspective, evolution is *the descent, with modification, of different lineages from common ancestors*. Thus, the history of evolution has two major components: the branching of lineages, and changes within lineages (including extinction). Initially similar species become ever more different, so that over the course of sufficient time, they may come to differ profoundly.

All forms of life, from viruses to redwoods to humans, are related by unbroken chains of descent. The hierarchically organized patterns of commonality among species—such as the common features of all primates, all mammals, all vertebrates, all eukaryotes, and all living things—reflect a history in which all living species can be traced back through time to fewer and fewer common ancestors. This history can be described by the metaphor of the phylogenetic tree. Some of this history is recorded in the fossil record, which documents simple, bacteria-like life as far back as 3.5 billion years ago, followed by a long history of diversification, modification, and extinction. The

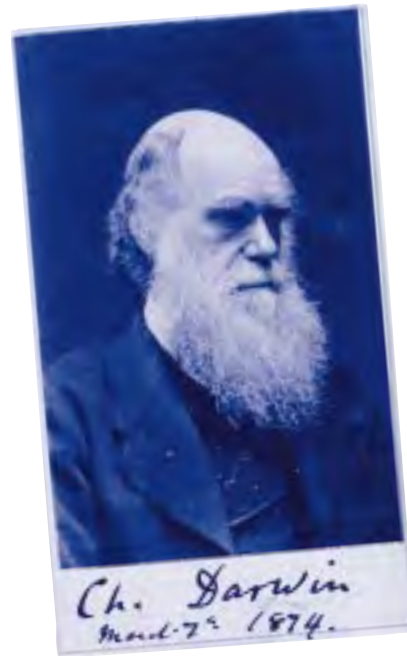
evidence for descent from common ancestors lies also in the common characteristics of living organisms, including their anatomy, embryological development, and DNA. On such grounds, for example, we can conclude that humans and apes had a relatively recent common ancestor; that a more remote common ancestor gave rise to all primates; and that successively more remote ancestors gave rise to all mammals, to all four-legged vertebrates, and to all vertebrates, including fishes.

*Evolutionary theory* is a body of statements about the processes of evolution that are believed to have caused the history of evolutionary events. Biological (or organic) evolution occurs as the consequence of several fundamental processes. These processes are both random and nonrandom.

*Variation* in the characteristics of organisms in a population originates through *random mutation* of DNA sequences (*genes*) that affect the characteristics. “Random” here means that the mutations occur irrespective of their possible consequences for survival or reproduction. Variant forms of a gene that arise by mutation are often called *alleles*. Genetic variation is augmented by *recombination* during sexual reproduction, which results in new combinations of genes. Variation is also augmented by *gene flow*, the input of new genes from other populations.

Evolutionary change within a population consists of a change in the proportions (*frequencies*) of alleles in the population. For example, the proportion of a rare allele may increase so that it completely replaces the formerly common allele. Changes in the proportions of alleles can be due to either of two processes whereby some individuals leave more descendants than others, and therefore bequeath more genes to subsequent generations. One such process, *genetic drift*, results from random variation in the survival and reproduction of different genotypes. In genetic drift, the frequencies of alleles fluctuate by pure chance. Eventually, one allele will replace the others (i.e., it will be *fixed* in the population). Genetic drift is most important when the alleles of a gene are *neutral*—that is, when they do not substantially differ in their effects on survival or reproduction—and it proceeds faster, the smaller the population is. Genetic drift results in evolutionary change, but not in adaptation.

The other major cause of change in the frequencies of alleles is *natural selection*, which is a name for any consistent (nonrandom) difference among organisms bearing different alleles or genotypes in their rate of survival or reproduction (i.e., their fitness) due to differences in one or more characteristics. In most cases, environmental circumstances affect which variant has the higher fitness. The relevant environmental circumstances depend greatly on an organism’s way of life, and they include not only physical factors such as temperature, but also other species, as well as other members of its own species with which the organism competes, mates, or has other social interactions.



## Evolution by Natural Selection

Nineteenth-century biologists Charles Darwin and Alfred Russel Wallace established the foundations for evolutionary theory.

A common consequence of natural selection is *adaptation*, an improvement in the average ability of the population’s members to survive and reproduce in their environment. (The word “adaptation” is also used for a feature that has evolved as a consequence of natural selection.) Natural selection tends to eliminate alleles and characteristics that reduce fitness (such as mutations that cause severe birth defects in humans and other species), and it also acts as a “sieve” that preserves and increases the abundance of *combinations* of genes and characteristics that increase fitness, but which would occur only rarely by chance alone. Thus, selection plays a “creative” role by making the improbable much more probable. Often the effect of selection will be the complete replacement of formerly common genes and characteristics with new ones (a process called *directional selection*), but under some circumstances, “*balancing selection*” can maintain several genetic variants indefinitely in a population (a state called *genetic polymorphism*, as in the case of the sickle-cell and “normal” hemoglobins found in some human populations in Africa).

Natural selection is the ultimate cause of adaptations such as eyes, hormonal controls on development, and courtship behaviors that attract mates, but it cannot produce such adaptations unless mutation and recombination generate genetic variation on which it can act. Over a long enough time, new mutations and recombinations, sorted by genetic drift or natural selection, can alter many characteristics, and can alter each characteristic both quantitatively and qualitatively. The result can be indefinitely great change, so great that a descendant species differs strikingly from its remote ancestor.

The movement of individuals among populations followed by interbreeding (i.e., gene flow) allows new genes and characteristics to spread from their population of origin throughout the species as a whole. If gene flow among different geographically separated populations is slight, different genetic changes can transpire in those populations. Because the populations experience different histories of mutation, genetic drift, and natural selection (the latter being especially likely if their environments differ), they follow different paths of change, diverging in their genetic constitutions and in the individual organisms' characteristics (*geographic variation*). The differences that accumulate eventually cause the different populations to be *reproductively isolated*: that is, if their members should encounter each other, they will not exchange genes because they will not mate with each other, or if they do, the "hybrid" offspring will be inviable or infertile. The different populations are now different *species*. The significance of this process of *speciation* is that the new species are likely to evolve independently from then on. Some may give rise to yet other species, which ultimately may become exceedingly different from one another. Successive speciation events, coupled with divergence, give rise to clusters of branches on the phylogenetic tree of living things.

Although each of the separate processes involved in evolution seems relatively simple, evolution is not as straightforward as this summary might make it appear. The various processes of evolution interact in complex ways, and each of them itself has many nuances and complexities. One gene may affect several characters, several genes may affect one character, natural selection may change in rate or even direction from year to year, or conflicting selection pressures may affect a character. When such complexities are taken into account, it can be quite difficult to predict when and how a character will evolve. Mathematical theory and computer modeling are invaluable tools for understanding how the evolution of a character is likely to proceed. A great deal of evolutionary research consists of formulating precise, often quantitative models, then testing them by experiment or observation.

It is important to distinguish between the history of evolution and the processes held to explain this history. Most biologists regard the *history of evolution*—the proposition that all species have descended, with modification, from common ancestors—as a *fact*—that is, a claim *supported by such overwhelming evidence that it is accepted as true*. The body of principles that describe the causal processes of evolution, such as mutation, genetic drift, and natural selection, constitutes the *theory of evolution*. "Theory" is used here as it is used throughout science, as in "quantum theory" or "atomic theory," to mean not mere speculation, but *a well-established system or body of statements that explain a group of phenomena*. Although most of the details of the history of evolution remain to be described (as is true also of human history), the statement that there has been a history of common ancestry and modification is as fully

confirmed a fact as any in biology. In contrast, the theory of evolution, like all scientific theories, continues to develop as new information and ideas deepen our understanding. Evolutionary biologists have great confidence that the major causes of evolution have been identified. However, views on the relative importance of the various processes continue to change as new information adds detail and modifies our understanding. Yet, to cite evolution as a fact can invite controversy, for probably no claim in all of science evokes as much emotional opposition. Thus we include Appendix I, entitled "Evolution: Fact, Theory, Controversy."

### III. WHAT ARE THE GOALS OF EVOLUTIONARY BIOLOGY?

Evolutionary biology is the discipline that describes the history of life and investigates the processes that account for this history.

Evolutionary biology has two encompassing goals:

- To discover the history of life on earth: that is, (1) to determine the ancestor-descendant relationships among all species that have ever lived—their *phylogeny*; (2) to determine the times at which they originated and became extinct; and (3) to determine the origin of and the rate and course of change in their characteristics.
- To understand the causal processes of evolution: that is, (1) to understand the origins of hereditary variations; (2) to understand how various processes act to affect the fate of those variations; (3) to understand the relative importance of the many co-acting processes of change; (4) to understand how rapidly changes occur; (5) to understand how processes such as mutation, natural selection, and genetic drift have given rise to the diverse molecular, anatomical, behavioral, and other characteristics of different organisms; and (6) to understand how populations become different species. Virtually all of biology bears on this vast project of understanding the causes of evolution, and reciprocally, understanding the processes of evolution informs every area of biology.

#### A. Subdisciplines of Evolutionary Biology

Evolutionary biology includes numerous subdisciplines that differ in their subject matter and methods. Some of the major subdisciplines are:

- **Behavioral evolution.** Behavioral evolutionists study the evolution of adaptations such as mating systems, courtship behavior, foraging behavior, predator escape mechanisms, and cooperation. Behavioral characteristics evolve in much the same way as structural features. Changes in the neural, hormonal, and developmental mechanisms underlying behavior are also objects of evolutionary study, as are the adaptive differences among species in memory, patterns



of learning, and other cognitive processes, some of which are reflected in differences in brain structure. Behavior, physiology, structure, and life history patterns often evolve in concert.

- **Evolutionary developmental biology.** This field seeks to understand evolutionary changes in the processes that translate the genetic information contained in an organism's DNA (its *genotype*) into its anatomical and other characteristics (its *phenotype*). In part, it aims to describe how variation at the genetic level results in variation in the characteristics that affect survival and reproduction. Perhaps its greatest significance lies in its potential to reveal the extent to which developmental processes bias, constrain, or facilitate evolution of the phenotype.
- **Evolutionary ecology.** This field looks at how the life histories, diets, and other ecological features of species evolve, how these processes affect the composition and properties of communities and ecosystems, and how species evolve in response to one another. Its salient questions include: How do we account for the evolution of short or long life spans? Why are some species broadly and others narrowly distributed? Do parasites (including microbial pathogens) evolve to be more benign or more virulent as time passes? How do evolutionary changes and evolutionary history affect the number of species in a community, such as a tropical forest or a temperate forest?
- **Evolutionary genetics.** Evolutionary genetics (which includes population genetics) is a central discipline in the study of evolutionary processes. It uses both molecular and classical genetic methods to understand the origin of variation by mutation and recombination. It describes patterns of genetic variation within and among populations and species, and employs both empirical study and mathematical theory to discover how this variation is affected by processes such as genetic drift, gene flow, and natural selection. The mathematical theory of evolutionary genetics is essential for interpreting genetic variation and for predicting evolutionary changes when many factors interact. It also provides a strong foundation for understanding the evolution of special classes of characteristics, such as genome structure and life histories.
- **Evolutionary paleontology.** This field addresses the large-scale evolutionary patterns of the fossil record. It examines the origins and fates of lineages and major groups, evolutionary trends and other changes in anatomy through time, and geographic and temporal variations in diversity throughout the geologic past. It also seeks to understand the physical and biological processes and the unique historical events that have shaped evolution. Paleontological data

provide a window on deep time, and thus permit the direct study of problems ranging from the change in the form and distribution of species over millions of years to the evolutionary responses of major groups to both catastrophic and gradual environmental changes. These data also allow calibration of rates for such phenomena as mutations in nucleotide sequences.

- **Evolutionary physiology and morphology.** This broad field looks at how the biochemical, physiological, and anatomical features of organisms provide adaptation to their environments and ways of life, and at the history of these adaptations. It is also beginning to define the limits to adaptation—for such limits may restrict a species' distribution or lead to its extinction. Among the questions studied in this field are: How do the form and the function of a feature change in relation to each other during evolution? How and why are some species tolerant of a broad range, and others of only a narrow range, of environmental factors such as temperature? Is there a diversity of mechanisms by which populations may adapt to a new environment?
- **Human evolution.** Many evolutionary biologists draw on the conceptual subdisciplines of evolutionary biology to study particular groups of organisms. Of these groups, one is especially notable: the genus *Homo*. The many anthropologists and biologists who take human evolution as their subject use principles, concepts, methods, and information from evolutionary systematics, paleontology, genetics, ecology, animal behavior—the full panoply of evolutionary disciplines. Other researchers study genetic variation and the processes that affect it in contemporary human populations (a subject intimately related to other areas of human genetics, such as medical genetics). Still others work in the controversial area of human behavior and psychology.
- **Molecular evolution.** Developing hand in hand with the spectacular advance of molecular biology, this field investigates the history and causes of evolutionary changes in the nucleotide sequences of genes (DNA), the structure and number of genes, their physical organization on chromosomes, and many other molecular phenomena. This field also provides tools for investigating numerous questions about the evolution of organisms, ranging from phylogenetic relationships among species to mating patterns within populations.
- **Systematics.** Systematists distinguish and name species, infer phylogenetic relationships among species, and classify species on the basis of their evolutionary relationships. Systematists have contributed greatly to our understanding of variation and the nature of species. Their special knowledge of particular groups of organisms is indispensable

both for inferring the history of evolution and for understanding the detailed workings of evolutionary processes, since each group of organisms presents special, fascinating, and often important questions. Moreover, systematists' knowledge often has unexpected uses. Knowledge of the systematics and biological characteristics of deer mice became invaluable when the novel hantavirus, harbored by these mice, caused fatalities in the United States. Likewise, plants that are related to a species in which a pharmacologically useful compound has been found are likely to contain similar compounds.

## B. Perspectives from Evolutionary Biology

Biological disciplines such as molecular biology and physiology ask “how” questions: How do organisms and their parts work? Evolutionary biology adds “why” questions: Why do specific organisms have particular features rather than others? Thus, while much of biology addresses the proximate causation of observed phenomena, evolutionary biology addresses ultimate causation. Answers to questions about ultimate causation might include “because this species inherited the feature from its distant ancestors,” or “because a history of natural selection favored this feature over others.” That a human embryo has gill slits can be understood only in light of their inheritance from early vertebrate ancestors; that we walk upright can be understood as an adaptation, a trait favored by natural selection in our more recent ancestors. In emphasizing history, we must, at the same time, recognize that evolution is an active, ongoing process that affects humans and all other living organisms.

The study of evolution entails several perspectives that have made important conceptual contributions to biology.

- **Chance and necessity.** A fundamental principle of evolutionary science is that living systems owe their properties to an interplay between *stochastic* (random) events and *deterministic* (consistent, predictable) processes. Random mutations, asteroid impacts, and other such events have greatly influenced the course of species' evolution. Therefore, evolutionary biologists have developed *probabilistic* theories that describe the likelihood of various evolutionary trajectories. An important corollary of random events is historical contingency. Although some adaptations to environmental factors are reasonably predictable, other characteristics of organisms are the consequence of “historical accidents” that launched evolution along one path rather than others. The modifications of the forelimbs for flight, for example, are very different in birds, bats, and pterodactyls, presumably because different mutations presented natural selection with different options in these lineages.
- **Variation.** Whereas physiologists may view variation as undesirable “noise” or experimental error that obscures a “true” value, variation is the all-important object of study for most evolutionary biologists. Probably no lesson from

evolutionary biology is more important than the realization that there are no Platonic “essences,” or fixed, “true,” “normal” properties. Almost every character is somewhat different among the individuals of a population. Evolutionary biologists' emphasis on variation has borne methodological fruit—namely, statistical methods, such as analysis of variance and path analysis, that are widely used in other fields. The evolutionary perspective on variation also has implications for how we think about “normality” and “abnormality,” and about differences in human characteristics. Awareness of variation within populations is a powerful antidote to racism and stereotyping of ethnic and other groups.

- **Biological diversity.** Evolutionary biologists are not only intrigued by the diversity of life, but are also keenly aware of



### An Example of the Uses of Biodiversity Knowledge

CHARLES W. MYERS<sup>1</sup> AND JOHN W. DALY<sup>2</sup>

<sup>1</sup> American Museum of Natural History

<sup>2</sup> National Institute of Diabetes and Digestive and Kidney Diseases

Knowledge of evolutionary (phylogenetic) relationships has helped to guide research scientists to the discovery of natural compounds useful in biomedical research. The poison frogs are a closely related group of New World tropical amphibians found in Central and South America. Their poisons are based on a class of chemical compounds called alkaloids, which the frogs may obtain from small insects and other invertebrates in their diet, and which they later release in defensive skin secretions. Alkaloids from three species of these frogs are used for poisoning the blowgun darts of native forest hunters in western Colombia. *Batrachotoxin*, an alkaloid isolated from one of these poison-dart frogs, *Phyllobates terribilis*,<sup>1</sup> has proved useful in studying the effects of local anesthetics, anticonvulsants, and other drugs. Alkaloids of the *pumiliotoxin* class from a Central American poison frog, *Dendrobates pumilio*, have been shown to have cardiotonic (heart-stimulating) activity. *Epibatidine*, an alkaloid isolated from the skin of a South American poison frog, *Epipedobates tricolor*, is 200 times more powerful than morphine as an analgesic (painkiller), and a commercial synthetic analog is now being widely studied because of its potent nicotine-like activity. These are only a few of the medically useful compounds first discovered in tropical poison frogs. By working closely with evolutionary biologists and systematists who locate, identify, and describe new species of poison frogs, research scientists continue to identify new compounds useful in biomedical research.

Badio, B., H. M. Garraffo, T. F. Spande, and J. W. Daly. 1994. Epibatidine: discovery and definition as a potent analgesic and nicotinic agonist. *Med. Chem. Res.* 4: 440

the contributions to biology that come from studying diverse organisms. To be sure, immense advances in biology have come from in-depth studies of “model” organisms such as yeasts, corn, rats, the bacterium *Escherichia coli*, and the fruit fly *Drosophila melanogaster*; indeed, many evolutionary biologists study these model organisms. However, without examining other species, we cannot know how widely applicable the principles revealed by these model systems are—and, in fact, we know that many such principles apply only with modification, or not at all, to vast numbers of other species. Gene regulation, for example, was first elucidated in bacteria, but is very different in eukaryotes. We need to study diverse organisms in order to learn about physiological adaptations to water shortage in desert plants (including potential crops), the mechanisms by which parasites combat their hosts’ immune systems, or the evolution of social behavior, communication, or learning in animals such as primates. Different organisms present different biological questions, and some species are more suitable than others for addressing each question.

#### IV. HOW IS EVOLUTION STUDIED?

Because evolutionary biology embraces everything from molecular to paleontological studies, a catalogue of its methods would fill several volumes. We can note only a few of the most general, commonly used methods.

- **Phylogenetic inference methods** are used to estimate relationships among species (living and extinct). Recent advances in logical and computational methods have greatly enhanced the confidence with which this can be done. Greatly oversimplified, the underlying principle of these methods is that species that share a greater number of derived (“advanced”) features stem from a more recent common ancestor than species that share fewer such features. It is obvious, then, that rats, whales, apes, and other mammals share a more recent common ancestor with each other than with birds or lizards, since the mammals possess many unique, derived features (e.g., milk, hair, a single lower jawbone). It is less obvious, but nonetheless increasingly likely as new data accumulate, that chimpanzees are more closely related to humans than to gorillas. These conclusions are based not only on improved methods of analyzing data, but also on a virtually inexhaustible trove of new data: long sequences of DNA, which reveal far more similarities and differences among species than can be found readily in their anatomy. The same methods used to infer the genealogy of species can be used to infer the genealogy of the genes themselves. Thus, for example, molecular evolutionary studies can use DNA sequences to estimate how recently variants of a gene carried by different people arose from a single ancestral gene.



#### The Origins of Modern Humans

DOUGLAS J. FUTUYMA

STATE UNIVERSITY OF NEW YORK AT STONY BROOK

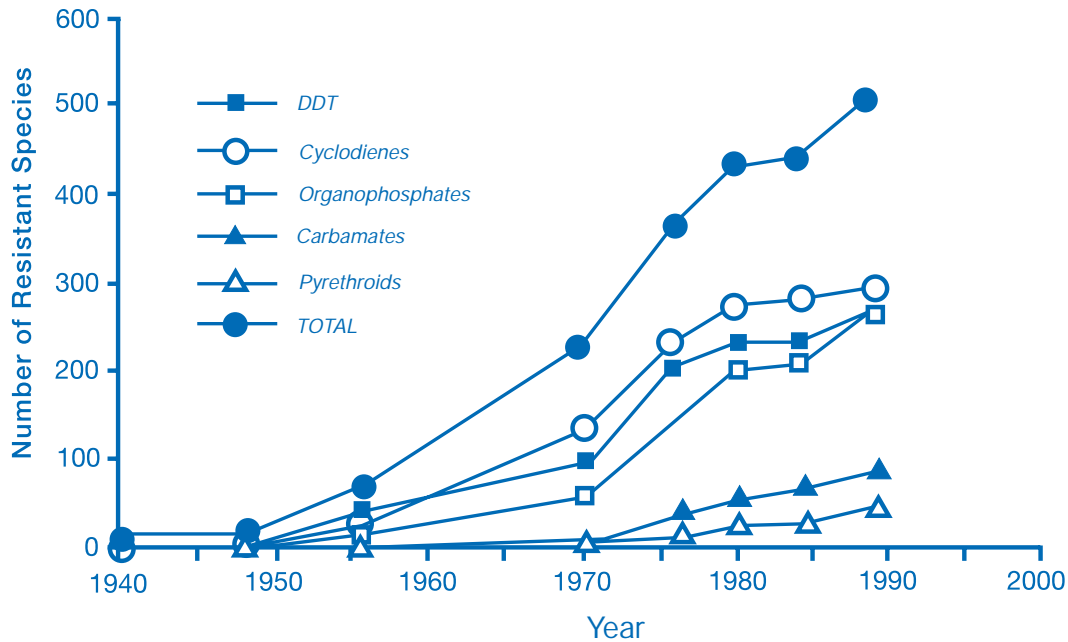
Most hominid fossils from about 1 million to 300,000 years ago are classified as *Homo erectus*, which was widely distributed from Africa to eastern Asia. The skeletal features of *Homo erectus* evolved gradually into those of *Homo sapiens*. An anatomical transition between “archaic” *Homo sapiens*—such as Neanderthals—and “anatomically modern” *Homo sapiens* occurred in Africa about 170,000 years ago, and somewhat later elsewhere. Until recently, it was generally supposed that genes for modern characteristics spread among different populations of “archaic” humans, so that the different archaic populations all evolved into modern humans, but retained some genetic differences that persist among different human populations today. This idea is known as the “multiregional hypothesis.”

The multiregional hypothesis has been challenged by some geneticists, who propose instead that anatomically modern humans evolved first in Africa and then spread through Europe and Asia, replacing indigenous archaic humans without interbreeding with them.<sup>1</sup> According to this “out of Africa” hypothesis, archaic human populations in Europe and Asia have bequeathed few, if any, genes to today’s human populations. This hypothesis is based on studies of variation in the sequence of certain genes, such as mitochondrial genes, from human populations throughout the world. These genes show that DNA sequences from different populations are more similar than we would expect, if they had been accumulating different mutations for 300,000 years or more. Moreover, sequences from African populations differ more from each other than do sequences from Europeans, Asians, and Native Americans—which might indicate that African populations are older and had more time to accumulate mutational differences among their genes.

Analyses of these genes suggest that modern humans spread out of Africa about 150,000 to 160,000 years ago. If this is true, all human beings are more closely related to each other, having descended from more recent common ancestors, than had previously been thought. However, a few genes present a different picture. In these cases, the amount of DNA sequence variation among gene copies is greater in Asian than African populations, and the differences among populations are great enough to suggest that they diverged more than 200,000 years ago—before anatomically modern humans appear in the fossil record. Although many researchers in this field are leaning toward the “out of Africa” hypothesis, the issue has not yet been resolved, and more data will be necessary before a firm conclusion can be reached about the origin of modern humans.

<sup>1</sup>R.L. Cann et al., *Nature* 325:31-36 (1987); D.B. Goldstein et al., *Proc. Natl. Acad. Sci. USA* 92:6723-6727 (1995); N. Takahata, *Annu. Rev. Ecol. Syst.* 26:343-372 (1995); R.M. Harding et al., *Am. J. Hum. Genet.* 60:772-789 (1997).

- **Paleontological databases.** Evolutionary paleontology is founded on systematics, including phylogenetic inference, because it is necessary to classify and determine the relationships of fossilized organisms before anything else can be done with them. Once this is done, fossils can be used for two major kinds of evolutionary study. One is tracing evolutionary changes in the characteristics of lineages through geologic time, such as those that occurred during the descent of mammals from reptilian ancestors. The other is determining the times and rates of origination and extinction of lineages and relating such changes to other events in earth history. For instance, each of five great *mass extinctions*—one of them evidently due to an asteroid impact—was followed by a great increase in the rate of origination of species and higher taxa, providing evidence that diversification of species is stimulated by the availability of vacated resources. Studies of fossil biodiversity rely on computerized databases of the geologic and geographic occurrence of thousands of fossil taxa, data accumulated by thousands of paleontologists throughout the world over the course of two centuries.
- **Characterizing genetic and phenotypic variation.** Characterizing variation is one of evolutionary biology's most important tasks. The statistical methods used to do this can be applied to data of many different kinds. Quantitative genetic analysis, which is also used extensively in the breeding of crops and domestic animals, is an important tool for measuring and distinguishing between genetic and nongenetic variation in phenotypic characteristics. One method of making this distinction involves measuring similarities among relatives, which requires knowledge of the relationships among individuals within natural populations. Molecular genetic markers can often provide such information. Recent advances in DNA-based molecular technologies have made it feasible to construct detailed genetic maps for a wide range of species, and to identify specific DNA regions that control or regulate quantitative characters.
- **Inference from genetic patterns.** Many evolutionary changes (though not all) take immense amounts of time, so the processes involved are often inferred from existing patterns of variation rather than observed directly. Many hypotheses about evolutionary processes can be tested by comparing patterns of genetic and phenotypic variation with those predicted by evolutionary models. For instance, the “neutral theory” of molecular evolution by genetic drift holds that molecular variation within species should be greater, and divergence among species more rapid, for genes in which most mutations have no effect on organisms' fitness than for those in which most mutations have a strong effect. According to this model, genes that encode unimportant proteins or which do not encode functional proteins at all, should display more nucleotide variation than genes that encode functionally important proteins. Studies of DNA variation have abundantly confirmed this model. This model is so powerful that molecular biologists now routinely use the level of sequence variation among species as a clue to whether or not a newly described DNA sequence has an important function.
- **Observing evolutionary change.** Some important evolutionary changes happen fast enough to document within one or a few scientific lifetimes. This is especially likely when, due to human activities or other causes, a population's environment changes, or a species is introduced into a new environment. For example, changes in food supply due to drought in the Galápagos Islands caused substantial, although temporary, evolutionary change in the beak size of a finch, within just a few years; a virus introduced to control rabbits in Australia evolved to be less virulent in less than a decade (and the rabbit population became more resistant to it); rats evolved resistance to the poison warfarin; hundreds of species of crop-infesting and disease-carrying insects have evolved resistance to DDT and other insecticides since World War II (31,54); and the rapid evolution of resistance to antibiotics in pathogenic microorganisms poses one of the most serious problems in public health (4, 42).
- **Experimentation.** Evolutionary studies often involve experiments, such as placing populations in new environments and monitoring changes or selecting directly on a particular character of interest. Among the most common experiments are those that analyze evolutionary change in manipulated populations, either under natural conditions or in the laboratory, using organisms with short generation times that can evolve rapidly. For example, experimenters have used laboratory populations of bacteria to monitor the course of adaptation to high temperatures, novel chemical diets, antibiotics, and bacteriophage (viruses that attack bacteria), and have characterized the new mutations underlying these adaptations (16). One group of researchers predicted the evolutionary changes in life history characteristics (e.g., rate of maturation) that guppies should undergo if they were subjected to a certain species of predatory fish. They introduced guppies into a Trinidad stream where this predator lived, and found that after about six years, the introduced guppies differed from the ancestral population just as they had predicted (50).
- **The comparative method.** *Convergent evolution* is the independent evolution, in different lineages, of similar characteristics that serve the same or similar functions. For example, several unrelated groups of fishes that inhabit turbid waters have independently evolved the capacity to generate a weak electric field that enables them



Increases in the number of pest species resistant to the principal classes of insecticides. (From R. L. Metcalf in R. L. Metcalf and W. H. Luckmann (eds.), *Introduction to Insect Pest Management*. Third Edition, p. 251, copyright 1994 by John Wiley and Sons, N.Y.)

## Insect Pests: Resistance and Management

DOUGLAS J. FUTUYMA

STATE UNIVERSITY OF NEW YORK AT STONY BROOK

Evolution is a dynamic, ongoing process that can have direct, important impacts on human welfare. The evolution of insecticide resistance by pest species of insects and other arthropods provides a spectacular example.<sup>1</sup>

Since World War II, synthetic insecticides have been used to control insects and mites that cause immense crop losses, and by carrying malaria and other diseases, pose major threats to public health. However, many chemical control programs are failing or have failed altogether, because the pest species have evolved resistance.

More than 500 species have evolved resistance to at least one insecticide. Many pest species are now resistant to all, or almost all, of the available insecticides. Moreover, some species that had been uncommon have become serious pests, because insecticide use has extinguished their natural enemies. As insects have become more resistant, farmers have applied ever higher levels of insecticide to their crops, so that more than one billion pounds per year are now applied in the United States. Resistance has made it necessary to develop new insecticides, each at an average cost of 8 to 10 years and \$20 to \$40 million in research and development. Hence insect evolution has imposed a huge economic burden (about \$118 million per year, just in the United States), and an increasing environmental burden of chemicals that can endanger human health and natural ecosystems.

Insect resistance evolves rapidly because natural selection increases the frequency of rare mutations that are not advantageous under normal conditions, but happen to provide protection against harmful chemicals. Entomologists trained in evolutionary genetics have developed strategies for delaying the evolution of resistance. The most effective strategy, based both on evolutionary models and on evidence, is to provide the pest species with pesticide-free “refuges” in which

susceptible genotypes can reproduce, thus preventing resistant genotypes from taking over. The intuitively appealing opposite strategy—trying to overwhelm the insect population with “saturation bombing”—simply hastens the evolution of resistance, because it increases the strength of natural selection.

Although evolution of resistance can be delayed, it is probably inevitable in most cases. Thus modern pest management strategies combine pesticides with other tactics. For example, spider mites in almond orchards have been controlled by applying both a pesticide and predatory mites that had been selected for pesticide resistance in the laboratory. Crop varieties that are genetically resistant to certain insects have been developed both by traditional methods of selection and by genetic engineering. For instance, strains of several crops have been engineered to carry a bacterial gene for a protein (Bt-toxin) that is toxic to certain insects. Pest-resistant crop varieties have often been economically very profitable, but history has shown that if they are planted widely, the insect pest eventually evolves the capacity to attack them, so that it becomes necessary to develop new genetic strains that the pest is not yet adapted to. At least one pest species, the diamondback moth, has already adapted to Bt-toxin. Thus, the “arms race” between the insect evolution and human ingenuity presents a continuing challenge.

<sup>1</sup> National Academy of Sciences (ed.), *Pesticide resistance: Strategies and tactics for management* (National Academy Press, Washington, D.C., 1986); R.L. Metcalf and W. H. Luckmann (eds.), *Introduction to insect pest management*, 3d edition (Wiley, New York, 1994); R.T. Roush and B.E. Tabashnik (eds.), *Pesticide resistance in arthropods* (Chapman and Hall, New York, 1990); B.E. Tabashnik, *Annu. Rev. Entomol.* 39:47-79 (1994); A.L. Knight and G.W. Norton, *Annu. Rev. Entomol.* 34:293-313 (1989).

to sense nearby objects. Convergent evolution is so common that it can often be used to test hypotheses. If we hypothesize a certain function for a feature, then its occurrence or condition should be correlated with specific environments or ways of life. For example, evolutionary ecologists predicted that, irrespective of their phylogenetic relationships, plant species that inhabit environments poor in light, water, or nutrients, and which therefore cannot readily replace tissues lost to herbivores, should contain greater quantities of defensive chemicals than species that grow in richer environments. By comparing many species of plants that grow in different environments, evolutionary ecologists have found considerable evidence supporting this prediction (11).

## V. HOW DOES EVOLUTIONARY BIOLOGY CONTRIBUTE TO SOCIETY?

The many subdisciplines of evolutionary biology have made innumerable contributions to meeting societal needs. Here we mention only a few examples. We focus especially on contributions to human health, agriculture and renewable resources, natural products, environmental management and conservation, and analysis of human diversity. We also mention some extensions of evolutionary biology beyond the realm of the biological sciences.

### A. Human Health and Medicine

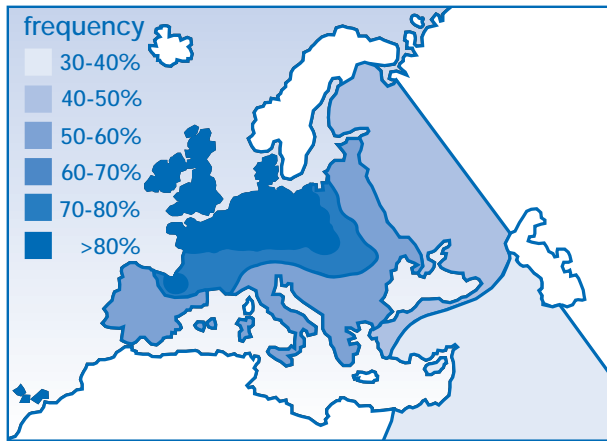
- **Genetic disease.** Genetic diseases are caused by variant genes or chromosomes, although the expression of such conditions often is influenced by environmental (including social and cultural) factors and by an individual's genetic constitution at other loci. To the many medical diseases caused by genetic variants, we can add many common conditions associated with old age, significant components of learning disabilities, and behavioral disorders, all of which contribute to human suffering and demand medical, educational, and social services resources. Each of these genetic disorders is caused by alleles at one or more genetic loci, which range in frequency from very rare to moderately common (such as the alleles for sickle-cell disease and cystic fibrosis, which are rather frequent in some populations). Allele frequencies are the subject of population genetics, which can be readily applied to two tasks: determining the reasons for the frequency of a deleterious allele, and estimating the likelihood that a person will inherit the allele or develop the trait. Thus, for example, the high frequency of alleles for sickle-cell and several other defective hemoglobins in some geographic locations signaled to population geneticists that some agent of natural selection probably maintained these alleles in populations. Their geographic distribution suggested an association with malaria, and subsequent research confirmed that these alleles are prevalent because heterozygous carriers have greater resistance to

malaria. This is a clear illustration of the theory, developed by evolutionary biologists decades before the sickle-cell pattern was described, that a heterozygous fitness advantage can maintain deleterious alleles in populations.

It can be important to couples to know the likelihood that their children will inherit genetic diseases, especially if these have occurred in their family history. Genetic counseling has provided such advice for many decades. Genetic counseling is applied population genetics, for it relies on both pedigree analysis (standard genetics) and knowledge of the frequency of a particular allele in the population at large to calculate the likelihood of inheriting a genetic defect. Likewise, evaluating the health consequences of marriage among related individuals or of increased exposure to ionizing radiation and other environmental mutagens depends critically on theories and methods developed by population geneticists (65).

Molecular biology is revolutionizing medical genetics. The technology now exists to locate genes and determine their sequence in the hope of determining the functional difference between deleterious and normal alleles. Carriers of deleterious alleles can be identified from small samples of DNA (including those obtained by amniocentesis), and genetic therapy, whereby normal alleles can be substituted for defective ones, is a real possibility. Methods and principles developed by evolutionary biologists have contributed to these advances, and are likely to make other contributions in the future. Locating a gene for a particular trait, for instance, is no easy task. The process relies on associations between the gene sought and linked genetic markers (e.g., adjacent genes on the same chromosome). The consistency of association of an allele with such markers—the likelihood that a marker on any one person's chromosome will signal the presence of a deleterious allele in its vicinity—is the degree of “linkage disequilibrium.” Population genetics theory has been developed to predict the degree of linkage disequilibrium as a function of such factors as allele frequencies, recombination rates, and population size. This theory was instrumental in one of the first cases in which a common deleterious allele—the one causing cystic fibrosis—was located and subsequently sequenced. As the effort to realize the promised rewards of the Human Genome Project moves forward, the role played by theories from population genetics will grow (29).

Determining which of the many nucleotide differences between a deleterious allele and a normal allele causes a disease is important for understanding how its effects may be remedied. Molecular evolutionary studies have given rise to several methods that can help to distinguish variation in a gene sequence that strongly affects fitness (by affecting function) from variation that is relatively neutral. These methods employ analyses of DNA sequence variation both within species and among closely related species. We predict



*Gradient of distribution in Europe of the major mutation causing cystic fibrosis relative to overall cf genes.*

## The Nature and Distribution of Human Genetic Disease

ARAVINDA CHAKRAVARTI

CASE WESTERN RESERVE UNIVERSITY

Each human population carries its own unique burden of genetic illnesses. Thus, persons of European ancestry have an increased frequency of cystic fibrosis, Africans and their descendants an increased frequency of sickle-cell disease and many Asian populations have a higher incidence of a blood-anemia called thalassemia. These rare disorders are the result of mutations in individual genes and exhibit simple patterns of inheritance. Modern molecular techniques have led to the identification of many disease genes and the specific changes in the DNA sequence that lead to the illness. A surprising finding is that the high frequency of many of these disorders is not because the underlying genes are highly mutable, but rather because one or more specific mutations have increased in frequency. In many instances, the frequency increase may have occurred by chance (a lottery effect). For example, many genetic diseases are particularly pronounced in social, religious and geographic isolates, such as the Amish, Mennonites and Hutterites in the United States, who owe their ancestry to a small set of

related founders. In other cases, such as cystic fibrosis, sickle-cell disease and thalassemias, there is considerable evidence that the mutations have increased due to a survival advantage to individuals who carry one copy of the mutation, yet who are clinically unaffected and thus can transmit the mutation to future generations.

Knowledge of our ancestry, that is, of the genes and mutations we have received from our forebears and of the evolutionary processes that have shaped their distributions, is crucial to our understanding of human genetic diseases. A major principle to emerge from recent genetic studies in cystic fibrosis, sickle-cell disease, thalassemias and others, is that the numerous patients who carry the most common mutation in each disease do so because they share a common ancestor; that is, they are distant relatives. Consequently, these individuals also share relatively large, contiguous tracts of DNA sequence around the mutation. Geneticists have begun to use this principle of possible evolutionary relatedness of patients as a method for mapping and identifying disease genes. If the culprit gene mutation lies in a segment of DNA shared by most or all patients then disease gene mapping is equivalent to searching for shared DNA segments among patients.

Currently, there is intense interest in genetic analyses of multi-gene disorders, such as cancer, hypertension and the like, since they exact such a large toll in all societies. Evolutionary sharing of mutations among patients, at each gene responsible for these illnesses, is also expected in these common human diseases. Unlike the rare disorders, we expect these mutations to be more common and to share a smaller segment of DNA among patients since they are much older in the human population. Moreover, these common diseases also vary in incidence between different human populations due to variation in both genetic makeup and environment. For these reasons, identifying the genes underlying these diseases is difficult. To accomplish this task, scientists are creating a human gene and sequence map at very high resolution. This map consists of "markers," which are known and ordered segments of human DNA that vary in sequence composition among humans. The mapping principle of finding disease susceptibility and resistance genes by matching patients' DNA for common shared sequence patterns is expected to play a crucial part in these discoveries. In the future, these and other new evolutionary principles will contribute to the identification of new disease genes and to the understanding of the current world distribution of human genetic disease.

that these methods, including comparisons among human genes and their homologues in other primates, will help to identify the variations that cause genetic diseases. In this context, the growing data banks of gene sequences from many species, as well as the Human Genome Project, will provide abundant opportunities for comparisons.

- **Systemic disease.** All genetic diseases collectively affect only about 1% of the human population. In contrast, more and more human disease and death is associated with chronic systemic diseases, such as coronary artery disease, stroke, hypertension, and Alzheimer's disease.

These diseases emerge from a complex set of interactions between genes and environment. This complexity makes it difficult to study the linkage between genes and systemic disease. Evolutionary principles and approaches have already had a major impact on the study of this linkage (65). For example, some genes, because of their known biochemical or physiological functions, can be identified as "candidate genes" for contributing to a systemic disease. However, there is so much molecular genetic variation at these candidate loci in the general human population that

finding the specific variants associated with disease risk is akin to the proverbial search for the needle in the haystack. Evolutionary phylogenetic techniques can be used to estimate a gene tree from this genetic variation. Such a gene tree represents the evolutionary history of the genetic variants of the candidate gene. If any mutation has occurred during evolutionary history that has altered risk for a systemic disease, then the entire branch of the gene tree that bears that mutation should show a similar disease association.

Gene tree analyses have already been successfully used to discover genetic markers that are predictive of risk for coronary artery disease (23), risk for Alzheimer's disease (58), and the response of cholesterol levels to diet (18). Moreover, evolutionary analyses of gene trees can help to identify the mutation that actually causes the significant health effect (23,56)—a critical first step in understanding the etiology of the disease and in designing possible treatments. As more candidate genes for common systemic diseases are identified, there will be a greater need for evolutionary analyses in the future.

■ **Infectious disease.** Infectious diseases are caused by parasitic organisms such as viruses, bacteria, protists, fungi, and helminths (worms). Control and treatment of infectious disease requires not only medical but also ecological research and actions. Critical questions include: What is the disease-causing organism? Where did it come from? Do other host species act as reservoirs for the organism? How is it spread? If it is spread by a carrier agent such as an insect, how far does the carrier typically disperse, and what other ecological properties of the carrier might be exploited to control the spread? How does the organism cause disease, and how might it be treated with drugs or other therapies? How does it reproduce—sexually or asexually or both? Is it likely to evolve resistance to drugs or the body's natural defenses, and if so, how quickly? Is it likely to evolve greater or lesser virulence in the future, and under what conditions will it do so? To each of these questions, evolutionary biology can and does provide answers.

Identifying a disease-causing organism, and its carrier if there is one, is a matter of systematics. If, like HIV, it is a previously unknown organism, phylogenetic systematics can tell us what its closest relatives are, which immediately provides clues to its area of origin, other possible host species, and many of its likely biological characteristics, such as its mode of transmission. If a new species of malaria-causing protozoan (*Plasmodium*) were found, for example, we could confidently predict that it is carried by *Anopheles* mosquitoes, like other *Plasmodium* species. Similarly, identifying disease carriers using the methods of systematics is essential. Progress in controlling malaria in the Mediterranean region was slow until it was discovered that there are six almost identical species of *Anopheles* mosquitoes, differing in habitat and life history, only two of which ordinarily transmit the malarial organism.

The methods of population genetics are indispensable for discovering the mode of reproduction of pathogens and their carriers, as well as their population structure—that is, the sizes of and rates of exchange among local populations. For example, by using multiple genetic markers to study *Salmonella* and *Neisseria meningitidis* (the cause of meningococcal disease), population geneticists have found that both of these pathogenic bacteria reproduce mostly asexually, but do occasionally transfer genes by recombination, even among distantly related strains. The immunological variations that bacteriologists have traditionally used to classify strains of these bacteria are not well correlated with the genetic lineages revealed by multiple genetic markers, nor with variations in pathogenicity or host specificity. Thus, predicting these traits in public health studies will require the use of multiple genetic markers (3, 7). Similarly, population genetic methods can estimate rates and distances of movement of disease-carrying organisms, which affect both disease transmission and potential for

## Human Immunodeficiency Virus

E. C. HOLMES

OXFORD UNIVERSITY

Many viruses, most notably the human immunodeficiency virus (HIV), exhibit enormous genetic diversity—diversity that often arises within the time frame of human observation, and frequently hinders attempts at control and eradication. Evolutionary biology has played an important role in describing the extent of this variation, in determining the factors that have been responsible for its origin and maintenance, and in examining how it may influence the clinical outcome of an infection. It is possible to illustrate the importance of evolutionary analysis in this context—particularly with HIV, for which the most data is available—at three different levels: on a global scale, within infected populations, and in individual patients.<sup>1</sup>

Globally, phylogenetic trees have shown that the two immunodeficiency viruses, HIV-1 and HIV-2, arose separately from simian ancestors, and that within each virus there is considerable genetic variation, which can be organized into distinct “subtypes.” These subtypes differ in their geographic distribution (although most are found in Africa) and possibly in important biological properties. For example, subtype E, from Southeast Asia, appears to be more easily sexually transmissible than other subtypes, and is associated with the recent dramatic spread of the virus through this part of the world. The correct identification of subtypes through phylogenetic analysis will be a critical element in the design of future vaccines.

Within infected populations, evolutionary analyses have led to important epidemiological hypotheses about where different HIV strains have originated, particularly those associated with “low risk” behavioral groups, and whether different risk groups possess characteristic strains. This information will form an important part of behavioral intervention programs, since it will be possible to identify accurately those groups that are most involved with the spread of HIV. An evolutionary approach has also been central to answering questions about whether HIV can be passed to patients by health care workers, as, for example, during surgery.

Evolutionary analyses of genetic variation in HIV have also produced valuable information about changes in the population of viruses within a single patient. Although an individual patient is infected by many viral genotypes, the genetic diversity of the virus soon drops drastically, suggesting that only certain genotypes can successfully invade the host's cells during the early stages of incubation. Later, the virus population within the patient diversifies, producing certain genotypes that are able to invade specific organs, such as the brain. There also appears to be an evolutionary interaction between the virus and the immune system, which may determine when and how HIV eventually causes AIDS. An evolutionary perspective is therefore central to understanding the basic biology of HIV and may help us understand its responses to drug therapy.

<sup>1</sup> A. J. Leigh Brown and E. C. Holmes, *Annu. Rev. Ecol. Syst.* 25: 127-165 (1994).

control. Molecular analysis of a gene in a species of mosquito showed that the gene had recently spread among three continents, evidence of this insect's enormous dispersal capability (49).

The potential rapidity of evolution in natural populations of microorganisms, many of which have short generation times and huge populations, has exceedingly important implications. One, an evolutionary lesson that should have been learned long before it was, is that pathogens may be expected to adapt to consistent, strong selection, such as



that created by widespread, intense use of therapeutic drugs. Resistance to antimicrobial drugs has evolved in HIV, the tuberculosis bacterium, the malarial protozoan, and many other disease-carrying organisms, rendering previously effective therapeutic controls ineffective. Many of these organisms, indeed, are resistant to drugs, partly because antibiotic resistance genes are often transferred between species of bacteria (42). The evolution of drug resistance has greatly increased the cost of therapy, has increased morbidity and mortality, and has raised fears that many infectious diseases will be entirely untreatable in the near future (10). Evolutionary theory suggests that such a grim future may be averted by reducing selection for antibiotic resistance, and the World Health Organization has indeed recommended more judicious, sparing use of antibiotics (67). Further studies of the population genetics of pathogens will be important in future containment efforts.

The virulence of pathogens can also evolve rapidly. The theory of parasite/host coevolution predicts that greater virulence may evolve when opportunities for transmission among hosts increase. Some researchers have postulated that major outbreaks of influenza and other pandemics have been caused by such evolutionary changes that transpired in crowded cities and among mass movements of refugees. Likewise, there is suggestive evidence that HIV has evolved higher virulence due to high rates of transmission by sexual contact and sharing of needles by intravenous drug users (17, 64). It is well established that the population of HIV viruses in an infected person evolves during the course of the infection, and some authors attribute the onset of AIDS—the disease itself—to this genetic change (45).

- **Normal physiological functions.** Understanding the human body's natural defenses against infectious disease is as important as understanding the diseases themselves, and here, too, evolutionary biology can work hand in hand with medical science. For example, genes in the major histocompatibility complex (MHC) play a critical role in cellular immune responses: Their products present foreign proteins to the immune system. The MHC also contributes to rejection of tissue transplants. Some MHC alleles are associated with autoimmune diseases such as juvenile diabetes and a form of crippling arthritis. Genetic variation in the MHC is exceedingly great, which has led population geneticists to seek reasons for this variation. Molecular analyses have revealed that the MHC genes must be under some kind of balancing selection that maintains variation. In fact, some human MHC alleles are genealogically closer to some chimpanzee alleles than to other human alleles, which provides clear evidence that natural selection has maintained variation for at least 5 million years. The variation is almost certainly maintained by the roles different alleles play in combating different pathogens, but its exact role requires further study (39).

## B. Agriculture and Natural Resources

- **Plant and animal breeding.** The relationships among agricultural scientists, geneticists, and evolutionary biologists have been so long and intimate that their fields are sometimes hard to distinguish, especially in the breeding of improved varieties of crops and domestic animals. Darwin opened *On the Origin of Species* with a chapter on domesticated organisms and wrote a two-volume book entitled *Variation in Plants and Animals under Domestication*. One of the founders of population genetics, Sewall Wright, worked for years in animal breeding, and another, R. A. Fisher, contributed importantly to the design and analysis of crop trials. Since then, many geneticists have made equal contributions to evolutionary genetics and to the basic genetics and theory underlying effective selective breeding. In contrast, when the head of the Soviet ministry of agriculture, T. D. Lysenko, rejected evolutionary theory in the 1930s, he ultimately left plant breeding in that country decades behind.

Concepts such as heritability, components of genetic variance, and genetic correlation, as well as experimental elucidation of phenomena such as hybrid vigor, inbreeding depression, and the basics of polygenic (quantitative) variation, play equally central roles in agricultural genetics and evolutionary theory. The most recent example of this mutualistic interaction between fields is the development and application of techniques using molecular markers to locate the multiple genes responsible for continuously varying traits, such as fruit size and sugar content, and to identify the metabolic function of these genes (called quantitative trait loci, or QTL). In the past, only a few model organisms, such as *Drosophila*, were sufficiently well known genetically to provide such information. Now, due to research by crop geneticists, population geneticists, and the Plant Genome Project, it is possible to map genes of interest in virtually any organism, whether it be a domesticated species or a wild species used for evolutionary studies.

Genetic variation, the stock in trade of evolutionary biologists, is the sine qua non of successful agriculture. As any evolutionary biologist knows, a widely planted, genetically uniform crop is a sitting duck for plant pathogens or other pests, which will adapt to it and spread rapidly. The potato blight that caused widespread famine in Ireland in the 1840s is one of many examples of this phenomenon (1). Another spectacular example is the epidemic of southern corn leaf blight in the United States in 1970, which caused an estimated economic loss of \$1 billion (1970 dollars). More than 85% of the nation's acreage of seed corn had been planted with strains carrying a genetic factor (Tcms) that prevents development of male flowers, which was useful for producing uniform hybrid varieties. The Tcms factor, however, made the corn susceptible to a mutant race of the fungus *Phytophthora infestans*, which rapidly spread through

the Corn Belt and beyond. Only a combination of favorable weather and widespread planting of corn with normal genetic makeup prevented an even more devastating blight in 1971 (62).

Despite such lessons, genetically uniform crops are still widely used for reasons of economic efficiency, but it is widely recognized that it is essential to maintain genetic diversity (36). Thus, it is essential to build up “germ plasm” banks of different crop strains, especially strains that differ in characteristics such as drought tolerance and pest resistance. An important source of potentially useful genes is wild species related to the crop—which of course can be recognized only through good systematics. For example, the cultivated tomato, like most crop species, is a self-fertilizing (and therefore genetically homozygous) species that harbors little genetic variation, even among all the available varieties. It originated in Andean South America and made its way to North America via domestication in Europe. Studies of the genetics and evolution of the tomato led to the realization that it has many relatives that are native to Chile and Peru, and that these species carry a wealth of genetic variation.

More than 40 genes for resistance to major diseases have been found among these native species, and 20 of them have been transferred into commercial tomato stock by hybridization. Fruit quality traits have also been improved in this way, and resistance to drought, salinity, and insect pests is expected to be introduced in the next few years, for an estimated four- to five-fold increase in agricultural yield (51).

- **Using biodiversity.** Knowledge of the systematics of tomatoes, together with ecological genetics and an understanding of the plant’s breeding system, formed the foundation for a successful application that is being repeated for many other crops. Genetic engineering, which makes it possible to transfer genes from virtually any species into any other, makes available, for agricultural and other purposes, the vast “genetic library” of the earth’s organisms, which carry a tremendous variety of genes for traits such as heat tolerance, disease and insect resistance, chemicals that impart flavors and odors, and many other potentially useful features. If we are to use this library in the future, it is

### A Lesson from History: The Tragic Fate of Evolutionary Genetics in the Soviet Union

VASSILIKI BETTY SMOCOVITIS  
UNIVERSITY OF FLORIDA

By the 1920s, Soviet scientists had gained international recognition for their pioneering work in many fields of biology. Most notable among these efforts was a unique school of population genetics that synthesized insights from genetics and Darwinian selection theory with knowledge of the structure of wild populations of animals and plants, in order to understand the mechanisms of adaptation and evolution. In the 1920s, Sergei Chetverikov and other Russian population geneticists anticipated the evolutionary synthesis that occurred in the west in the 1930s and the 1940s. Among the contributions of the Russian school of evolutionary theory were the concept of the gene pool, the independent derivation of the concept of genetic drift, and the first genetic studies of wild populations of the fruit fly *Drosophila melanogaster*. The school trained young evolutionists such as N. V. Timofeef-Ressovsky and Theodosius Dobzhansky, who later played key roles in establishing modern evolutionary theory in Germany and the United States. The Russian school affirmed that evolutionary change consists of changes in the frequencies of Mendelian, particulate genes within populations.

This flourishing center of evolutionary research, and most of its scientists, suffered a tragic end. Beginning in the late 1920s, biology in general and genetics in particular was increasingly perceived as dangerous to the political spirit of Stalinist Russia, then pushing to transform itself from an agrarian state into a modern nation. A persecution of genetics and geneticists began in the early 1930s. It was fueled by the rhetoric of Trofim Lysenko (1898–1976), an agronomist with little education and no scientific training, but with grand ambitions for Soviet agriculture based on his mistaken belief in a Lamarckian mechanism of inheritance and organic change. According to Lamarckian and Lysenkoist theory, exposure of parent organisms to an environmental factor such as low temperature directly induces the development of adaptive changes that are inherited by their descendants—a theory of evolution by the inheritance of acquired characteristics, rather than by natural selection of genes.

Western geneticists and evolutionary biologists had already shown that Lamarckian inheritance does not occur. Declaring genetics a capitalist, bourgeois, idealist, and even fascist-supported threat to the state, Lysenko

led a vicious propaganda campaign that culminated in 1948 with the official condemnation of genetics by Stalin and the Central Committee of the Communist Party. Among the casualties of Lysenkoism was Nikolai Vavilov, one of the pioneers of plant breeding, who died of starvation in a prison camp, and the entire school of population geneticists, who were dispersed or destroyed. Lysenkoism quickly led to the wholesale destruction of the very areas of Soviet biology that had gained world prominence in the 1920s.

The Soviet policy against genetics and evolution had disastrous consequences for the Soviet people. In addition to wreaking rural destruction rivaled only by that of Soviet collectivization, Lysenkoism thwarted the development of agricultural science. The Soviet Union was left out of the global agricultural revolution that occurred in the middle decades of this century, fueled in part by genetic innovations such as hybrid corn. Despite rising opposition, Lysenko remained in power until 1965, following Khrushchev’s ouster. Soviet biology was never able to recover effectively from this period. Its earlier promise lived on only in individuals like Dobzhansky, a towering figure in evolutionary biology, who carried insights from Russian population genetics to the west when he immigrated to the United States in 1927.

The full consequences of Lysenkoism and Stalinist biology have yet to be determined, but are now under study by scholars who are gaining access to formerly restricted government sources.<sup>1</sup> Although they debate details, all scholars agree that the reign of Lysenkoism was an especially grim period in the history of science. It is the classic example of the negative consequences of misguided anti-science policies and ideological control of science. The lesson learned is that free inquiry, informed government support of basic and applied sciences, and open debates on scientific subjects—especially those declared threatening or dangerous by special interest groups—are essential for the health and prosperity of nations.

<sup>1</sup> M. Adams, in E. Mayr and W. Provine (eds.), *The Evolutionary Synthesis* (Harvard University Press, Cambridge, MA., 1980), pp. 242–278; D. Joravsky, *The Lysenko Affair* (Harvard University Press, Cambridge, MA, 1979); N. Kremensov, *Stalinist Science* (Princeton University Press, Princeton, NJ, 1997); V. Soyfer, *Lysenko and the Tragedy of Soviet Science* (Rutgers University Press, New Brunswick, NJ, 1994).

necessary both that the library be preserved—that is, that biodiversity not be lost—and that there be librarians—scientists who can provide some guidance toward finding useful “volumes.” These librarians will be evolutionary biologists: those who study systematics and phylogeny, and so know what species exist and which are likely to share similar genes and characteristics, and those who study evolutionary genetics and adaptation, and are able to point the way toward organisms with desirable characteristics.

- **Pest management.** Plant pests, chiefly insects and fungi, take an enormous economic toll in crop losses and control measures annually. Evolutionary biology bears on this problem in many ways. Quite aside from the dangers to public health and the environment resulting from excessive use of chemical pesticides, more than 500 species of insects (including crop pests, pests of stored grains, and disease vectors) have evolved resistance to one or more insecticides in the last 40 years, and some are resistant to all known insecticides. The evolution of pesticide resistance has added \$1.4 billion to the annual cost of crop and forest product protection in the United States (47). Agricultural entomologists trained in evolutionary genetics (31,53) are contributing to efforts to delay or prevent the evolution of resistance, such as rotational use of different control measures and judicious combination of chemical with nonchemical controls. Two nonchemical methods have profited greatly from evolutionary knowledge and theory: use of natural enemies and resistance breeding.

Natural enemies, such as insects that are specialized predators or parasites of pest species, are often sought in the pest's region of origin. So the first question is, where does the pest come from? Finding the answer requires entomologists trained in evolutionary systematics, who may be able to identify the pest using a taxonomy based on evolutionary principles. If the pest is an unknown species, the best clue to its region of origin is the distribution of related species—which can be determined by using evolutionary taxonomy. The search for natural enemies uses the same principles. Once potential enemies such as parasites have been found, it is critical to distinguish among closely related, very similar species, for some may attack the pest and others may attack only its relatives. If an enemy is approved for introduction, large numbers must be bred for release. At this stage, the application of evolutionary genetics is crucial in order to prevent the parasite stock from becoming inbred or unconsciously selected for characteristics that could impair its effectiveness.

Another major pest management strategy is to select for resistance in crop plants by screening for genes that provide resistance in the laboratory or in field plots, and then crossing those genes into crop strains with other desirable characteristics. Knowing the genetic basis of resistance is

important because some kinds of resistance are short-lived. A pest may adapt to a resistant crop strain as readily as it adapts to chemical insecticides. For example, at least six major genes for resistance to the Hessian fly have been successively bred into wheat. In each case, within a few years of widespread planting of the new strain, the fly overcame the resistance: for every resistance mutation in the plant, a corresponding mutation in the fly nullified its effect. Entomologists and plant breeders trained in evolutionary biology are working on methods of engineering multiple resistance to lengthen the effective life of new resistant cultivars.

- **Genetic engineering.** Proposals abound for introducing various traits into crop plants and for broadcasting engineered bacteria that can improve soil fertility or impart frost resistance to certain crops. Questions about their potential risks arise whenever such deliberate introductions are proposed. Evolutionary biologists who study gene interactions have noted the need for tests to be sure that a foreign gene does not unpredictably interact with a crop plant's own genes to generate harmful effects. Perhaps a more likely risk is that such genes could spread by cross-pollination into wild plants related to the crops (e.g., wild mustards related to cabbage) and cause them to become more vigorous weeds. Likewise, because genes are often transferred between species of bacteria, there has been concern that natural bacterial populations could acquire features from engineered bacteria that render them more vigorous and potentially harmful. Thus, methods developed by evolutionary biologists for determining the fitness effects of genes and measuring rates of gene exchange among populations and species will have valuable applications.
- **Forestry and fisheries.** Evolutionary biologists can reveal the genetic structure of populations and species by statistical analyses of genetic markers. These methods have many applications. They enable researchers, for instance, to distinguish among stocks of fish species that migrate from different spawning grounds. Such distinctions have important management and political implications in cases such as the salmon industry, since both the political units that include spawning locations and those where the fish are harvested have an economic interest in the stocks. In forestry, nurseries where commercial stocks of conifers are developed and grown are subject to genetic “contamination” by airborne pollen from wild trees. Methods developed by population geneticists are useful for determining the distance that pollen travels and for measuring levels of contamination, which affect the seed's market value. Evolutionary geneticists have also been active in analyzing the genetic basis of desirable traits, such as growth rate and insect resistance, in conifers. Such knowledge contributes to

hybrid breeding and genetic engineering programs.

### C. Finding Useful Natural Products

Organisms past and present are the source of innumerable natural resources. Almost all pharmaceutical products, many household products, and many industrial applications (starting historically with the manufacture of bread and wine) either use living organisms or originated from biological processes in organisms. Moreover, long-dead organisms provide resources: fossil fuels. The search for fossil fuels is based largely on age correlations among sedimentary deposits—which in turn are based on fossilized protozoans, mollusks, and other organisms studied by paleontologists.

Many living species may prove useful as future crops or, especially, in medical, energy, industrial, or research applications. Indeed, organisms can be considered “living capital” in the words of the President’s Committee of Advisors on Science and Technology (48). Over 20,000 different plants are listed by the World Health Organization as having been used for medicinal purposes by human populations, and a substantial fraction of these really are effective. For example, malaria was treated until very recently by quinine, from the cinchona tree. Recent discoveries of other medicinally useful plant compounds abound. Taxol, a compound found in the Pacific yew, has shown promise in the treatment of breast cancer; the rosy periwinkle of Madagascar contains two chemicals that have proved useful for fighting leukemia (and a variety of other cancers) and which have increased childhood leukemia survival rates from 10% to 95%. Diverse natural plant products are also used as scents, emulsifiers, and food additives in industrial applications. An extract from horseshoe crabs is the basis for the “lysate test,” widely used in the pharmaceutical industry to test for the presence of bacteria.

Microorganisms provide not only products, but also biochemical processes useful in biosyntheses (e.g., of antibiotics, solvents, vitamins, and biopolymers), biodegradations (e.g., in breaking down toxic wastes), and biotransformations (to desired steroids, chiral compounds, and others). Modern molecular biology and biotechnology, for example, rely on the polymerase chain reaction, a method based on an enzyme that is stable at high temperatures, and which was discovered in bacteria that inhabit thermal springs. Pharmaceutical and other industries have initiated programs for screening natural products in the expectation of more such discoveries (see Sidebar 1).

Exploration of biological diversity for new natural products is a major emphasis of the National Research Council’s report, *A Biological Survey for the Nation*, (38) and of the Systematics Agenda 2000 (57), a report on the critical importance of research and training in systematics. Two areas of evolutionary biology are germane—indeed, indispensable—for such targeted exploration. Systematics provides the inventory of organisms, and of their phylogenetic relationships, that is essential for organizing and, in part, predicting the characteristics of

organisms. Evolutionary ecology in the broad sense—the analysis of adaptations—points us toward organisms whose adaptive requirements are likely to produce features that we might use. For example, neurobiologists seeking inhibitors of neurotransmitters for research purposes were led successfully to the venoms of certain snakes and spiders, organisms that have evolved just such inhibitors to overcome their prey. Fungi release antibiotics to control bacterial competitors, and plants harbor many thousands of compounds to ward off their natural enemies. Evolutionary-ecological study of such adaptations has only begun to reveal compounds that merit further attention.

### D. Environment and Conservation

Evolutionary studies have paved the way for new methods of environmental remediation and restoration of degraded land. For example, some grasses and other plants have become adapted to soils highly polluted with nickel and other toxic heavy metals. Extensive studies of the systematics, genetics, and physiology of these plants have laid the foundation for techniques for revegetating and stabilizing soils made barren by mining activities, and even for detoxifying metal-contaminated soil and water. It has been found that some bacteria have the capacity to metabolize mercury to a less toxic form, and their

#### Risk Assessment and Genetically Engineered Organisms

THOMAS R. MEAGHER  
RUTGERS UNIVERSITY

Concern over planned releases of genetically engineered organisms into the environment has prompted a wide range of recommendations for assessing the risks associated with such releases. As transgenic cultivars have come closer to commercial reality, risk assessment issues have shifted from concern over the transgenic organisms themselves to concern over the long-term effects of their possible hybridization with their wild relatives. Introgressive hybridization of modified genes, such as those that confer herbicide resistance, into wild relatives of cultivars could, for example, create problem weeds.<sup>1</sup>

For any transgenic cultivar, the baseline information required to address this concern is the probability of hybrid production with related species. Cultivars of oilseed rape and other cultivated species of *Brassica* have been of particular concern due to economic pressure for the introduction of transgenic oil-seed rape (*Brassica napus*) in close proximity to its wild relatives, some of which are already weeds in crop lands.<sup>2</sup> Empirical data that could form a scientific basis for assessing the risk of this introduction were recently provided by studies on *Brassica napus* and a closely related wild species, *B. campestris*.<sup>3</sup> These studies on *Brassica* will serve as a model on which risk assessment studies of insect-pollinated cultivars can be based.

<sup>1</sup>J. M. Tiedje et al., *Ecology* 70:298-315 (1989); N. C. Ellstrand and C. A. Hoffman, *BioScience* 40:438-442 (1990); L. R. Meagher, Chapter 8 in *A New Technological Era for American Agriculture*, U.S. Congress Office of Technology Assessment, OTA-F-474 (U.S. Government Printing Office, Washington, D.C., 1992)

<sup>2</sup>M. J. Crawford et al., *Nature* 363:620-623 (1993); C. R. Linder and J. Schmitt, *Molecular Ecology* 3:23-30 (1994).

<sup>3</sup>T. R. Mikkelsen et al., *Nature* 380:31 (1996).

genes for this capacity have been transferred into plants in laboratory experiments. In other cases, plants that have evolved the capacity to “hyperaccumulate” heavy metals and thus withstand toxic soils are currently being used commercially as a cleanup technology. Likewise, studies of the evolutionary ecology of seed dispersal and germination are playing a role in the reforestation of overgrazed land in tropical America, and in the revegetation of landfill sites.

Concerns about the environmental impacts of human activity include the consequences of overpopulation, habitat alteration, the prospect of global warming, and documented and projected extinctions of many species. Paleobiological studies of past changes in climate, sea level, and species distributions provide insight into the kinds of organisms that are most likely to be adversely affected by global warming—namely, those with low dispersal powers, narrow geographic ranges, and narrow ecological tolerances. Evidence from populations evolving at different temperatures may also help us to predict the diversity of responses to climate change and the speed with which various populations can adjust to it (61).

As a result of human activity, genetically unique species and populations are becoming extinct at an alarming rate. Our activities threaten not only conspicuous species, such as large mammals and sea turtles, but also innumerable plants, arthropods, and other lesser-known organisms, which collectively are a potential source of natural products, pest control agents, and other useful services (including the recycling of chemical elements that enables the entire ecosystem to operate). Evolutionary biology is playing a major role in addressing this “biodiversity crisis.” An important consideration is which species, ecological communities, or geographic regions merit the most urgent conservation efforts, since there are economic, political, and informational limits on the number of species we can save.

Among the conservation roles of evolutionary biology are:

- Using phylogenetic information to determine which regions contain the greatest variety of biologically different, unique species;
- Using the data and methods of evolutionary biogeography (the study of organisms’ distributions) to identify “hot spots”—regions with high numbers of geographically localized species (Madagascar, New Guinea, and the Apalachicola region of Florida and Alabama are examples);
- Using genetic and other methods to distinguish species and genetically unique populations;
- Using population genetic theory to determine the minimal population size needed to prevent inbreeding depression and to design corridors between preserves to allow gene flow, both of which maintain the ability of populations to adapt to diseases and other threats;

## Heavy Metals and Plants: An Evolutionary Novelty Becomes an Environmental Cleanup Opportunity

THOMAS R. MEAGHER  
RUTGERS UNIVERSITY

The phenomenon of heavy metal tolerance in plants has attracted considerable attention from evolutionary biologists. Heavy metal tolerance was first reported by the Czech scientist S. Prat in 1934, and has since been studied extensively by a number of scientists in Europe and the United States. A. D. Bradshaw and his students, in particular, have conducted extensive experiments on the evolutionary properties of plants growing in contaminated sites, such as mine spoils. Their findings include the following:<sup>1</sup> plants growing in contaminated sites are genetically adapted to be tolerant of heavy metals; metal-tolerant plants do not compete well in noncontaminated sites; selection is so strong that genetic adaptation to contaminated sites takes place even though there is potential for gene flow from nearby nontolerant populations; even relatively low levels of contamination, such as roadside lead pollution from auto exhaust in urban areas, impose selection for metal tolerance. This adaptation of plants to heavy metal contamination has been of particular interest because it is a character that appears to have evolved in part in response to human disturbance.

Evolutionary studies of heavy metal tolerance have contributed to strategies for dealing with contaminated soils on several levels. First, such studies have provided evidence for the toxic effects of heavy metal contamination on nonadapted genotypes. Prior to these evolutionary studies, the presence of plants on some contaminated sites had led to some dangerous misperceptions; as recently as 1972, the National Academy of Sciences concluded that lead had no toxic effects on plants, since plants could grow on contaminated soils! Second, evolutionary studies have contributed to the reclamation and revegetation of contaminated sites.<sup>2</sup> The commercial metal-tolerant variety of the grass *Agrostis tenuis*, known as “Merlin,” was produced directly from natural metal-tolerant populations. Finally, evolutionary studies have shown that the mechanism for metal tolerance is uptake, not exclusion, such that metal-tolerant genotypes are also metal accumulators. This last insight, in conjunction with physiological research on metal-tolerant plants, has led to a growing use of plants as part of a cleanup technology for dealing with contaminated sites. According to the U.S. Environmental Protection Agency, the projected costs of cleaning up metal-contaminated sites will be \$35 billion over the next 5 years in the United States alone. Metal-accumulating plants that will play an important part in this cleanup process are being developed by such private-sector companies as Exxon, DuPont, and Phytotech in cooperation with the U.S. Department of Energy and other agencies.

<sup>1</sup>J. Antonovics et al., *Adv. Ecol. Res.* 7:1-85 (1971); J. Antonovics, in *International Conference on Heavy Metals in the Environment*, pp.169-186 (Toronto, Ontario, 1975); A. D. Bradshaw, *Phil Trans. Roy. Soc. Lond. B.* 333:289-305 (1991).

<sup>2</sup>A.D. Bradshaw and T. McNeilly, *Evolution and Pollution* (Edward Arnold, London, 1981); D.E. Salt et al., *Bio/Technology* 13:468-474 (1995); T. Adler, *Science News* 150:42-43 (1996).

- Using the theory of life histories and other characteristics to predict which species are most vulnerable to extinction;
- Using genetic markers to control traffic in endangered species. (These methods have been used to spot illegal whaling, and are routinely used to distinguish illegally smuggled from legally captive-bred parrots. In fact, these birds have such a high market value that insurance companies are requiring DNA fingerprints of pet parrots.)

## E. Applications beyond Biology

There are reciprocal benefits between evolutionary biology and nonbiological science and technology. Perhaps the oldest such relationship is with economic theory. Darwin's idea of natural selection was inspired by the works of the economist Thomas Malthus, who stressed the effects of competition for scarce resources. In the twentieth century, the development of several evolutionary topics, such as the evolution of life histories and foraging behavior, borrowed from economic theory. But ideas have flowed in the other direction as well. The influence of population genetics on economics began with Sewall Wright's work on path analysis, a statistical technique developed to analyze complex causal systems such as the effects of heredity and environment on phenotypes. This method is now widely used for causal analysis in economics and sociology. More recently, some economists have adopted one of the central principles of evolutionary theory, also given mathematical form by Wright—namely, the effects of historical contingency on subsequent change. Economists such as Douglass North have applied this principle, indicating a shift away from economic theory based on the classic notion that individuals know what it takes to maximize benefits and minimize costs (44).

The need for tools to solve theoretical and practical problems in evolution has stimulated developments in both statistics and mathematics. R.A. Fisher, who devised the analysis of variance, was both population geneticist and statistician. In analyzing random effects in evolution, Wright used diffusion equations that inspired further work on random processes by mathematicians such as William Feller, who was led to develop a large area of probability theory. More recently, the analysis of phylogenetic trees has inspired mathematical research. These methods, suitably modified, will have wide application outside evolutionary biology.

Evolutionary computation and artificial intelligence are among the most active, and potentially useful, subjects in computer science today and are based directly on evolutionary theory. The computer scientist John Holland (25) was profoundly influenced by his colleagues in evolutionary biology and, with his students, pioneered evolutionary computation and genetic algorithms for numerical problem solving. These algorithms, which employ maximization criteria designed to mimic natural selection in biological systems, are currently showing great potential in computer and systems applications. Evolutionary computation is such an active field that two new journals—*Evolutionary Computation* and *Adaptive Behavior*—include many papers on how biological concepts may be applied to computer science and engineering.

## F. Understanding Humanity

Evolutionary data and methods have been used to address many questions about the human species—our history, our variability, our behavior and culture, and indeed, what it means

to be human. Some studies on human variation and evolution are unambiguous and uncontroversial. Other writings about human evolution and its social implications have been extremely controversial—and have evoked as much disagreement among evolutionary biologists as elsewhere. These controversial topics usually have insufficient data to support the claims made, or are instances in which scientific data have been used, without justification, to support social or ethical arguments. Moreover, some popular writers and journalists misinterpret the findings of human evolution and genetics—indicating the need for broader education in these subjects.

- **Human history.** Major topics of study in human history, referred to earlier in this document, are our incontrovertible relationships to African apes, the history of hominid evolution as revealed in the fossil record, and the history of modern human populations, in which evolutionary genetics has played the leading role. Extensive population genetic studies, coupled with phylogenetic methods, have also determined genealogical relationships among human populations. These genetic relationships correspond well to relationships among language groups, which linguists have elucidated with methods modified from evolutionary biology (9). The combination of these disciplines has provided a sounder basis for inferences about major population migrations and the spread of important cultural systems such as agriculture and the domestication of animals.
- **Variation within and among populations.** Genetic differences among human populations are small compared with the great amount of variation within them. Moreover, geographic patterns often differ from one gene to another, which implies that a difference between populations in one characteristic is not likely to be useful for predicting differences in other characteristics. These data and principles have supported the vigorous arguments that many evolutionary biologists have made against racism and other kinds of stereotyping (13, 35).
- **Human nature.** One of the most controversial of all subjects is what is “natural” to the human species. This topic evokes enormous interest among people in all walks of life, whatever their beliefs about evolution may be. In contrast to other species, it is evidently “natural” for us to learn and use language, for example. The issue comes down to which human behavior patterns are products of evolutionary history, which are products of cultural environment, and which result from an interaction between the two. Evolutionary behaviorists have documented evolved differences in many behavioral traits among other animal species and have successfully used principles such as kin selection to explain how these behaviors are adaptive. Many evolutionary biologists, anthropologists, and psychologists are optimistic

that such principles can be applied to human behavior, and have offered evolutionary explanations for some intriguing behaviors that are widely distributed among human populations, such as incest taboos and gender roles. Other evolutionary biologists, anthropologists, and psychologists are skeptical of these interpretations, and stress the effects of learning and culture. The challenge will be to devise definitive tests of the hypotheses.

- **Models of cultural change.** Analogies between cultural change and biological evolution have often been drawn, and at times have influenced models in cultural anthropology. Some past analogies were naive and erroneous, such as the supposition that complexity necessarily increases in both biological and cultural evolution. Even the best such analogies have severe limitations because some mechanisms of cultural “evolution” differ importantly from those of biological evolution. Nevertheless, the form and content of evolutionary models have been used, with suitable modifications, to develop models of cultural change (8). Some of these models take into account the interplay between cultural and genetic change, since there is evidence that each can influence the other. The most promising models are quite recent and have not yet been adequately tested with data.

- **Evolution in popular and intellectual culture.** No one, from the most dedicated biologist to the most impassioned creationist, would deny that the idea of evolution has had a huge influence on modern thought. Innumerable books have been written about the impact of Darwinism on philosophy, anthropology, psychology, literature, and political history. Evolution has been used (abused, we would say) to justify both communism and capitalism, both racism and egalitarianism. Such is the grip of the evolutionary concept on the imagination.

Fascination with evolution, though, is not limited to ethereal realms of intellectual discourse. An unmeasured, but probably large, economic benefit flows indirectly from the role of evolutionary biology in educating children and adults in scientific concepts and also in providing popular entertainment. Books and television productions on biodiversity, natural history, human origins, and prehistoric life (including dinosaurs) are extremely popular and provide a readily accessible entry into abstract scientific thinking. Many children first become interested in science, engineering, and environmental affairs through exposure to natural history and then through introduction to the evolutionary principles that explain life’s unity, diversity, and adaptations. Even among people who do not pursue careers in science and engineering, an interest in natural history and evolution enhances critical thought (the basis of the Jeffersonian ideal of an educated citizenry). This interest is also a considerable economic force, through purchases of books and magazines, toys for children,

and attendance at museums and even the cinema. (The popular movie *Jurassic Park* could not have been made without the new understanding of dinosaurs developed by evolutionary biologists in the preceding 20 years.) The throngs of visitors to dinosaur exhibits in museums, the popularity of science fiction that employs evolutionary themes, the news coverage of every major hominid fossil discovery and every major new idea about human evolution, the widespread public concern about genetic theories of human behavior and about the possibility of cloning—all attest to the fascination, foreboding, and hope that people feel about the evolutionary history and future of humanity and the world.

## VI. HOW DOES EVOLUTIONARY BIOLOGY CONTRIBUTE TO BASIC SCIENCE?

### A. Accomplishments in the Study of Evolution

A full list of the accomplishments of evolutionary biology—some spectacular and others modest—would be very long. Here are capsule descriptions of a few of the most important advances.

- Many lines of evidence unequivocally demonstrate that evolution has occurred. It is currently believed that all known organisms are descended from a common ancestor that existed more than 3.5 billion years ago. The evidence for the relatedness of all life includes commonalities such as cell structure, the amino acid composition of proteins, the almost universal genetic code, and the near-identity of nucleotide sequences in many genes that play similar functional roles in very different organisms. For example, the genes that govern the first steps in embryonic development, specifying the axes and major body regions of the embryo-to-be, are similar in sequence, organization, and basic function in insects and vertebrates; in fact, some mouse genes, implanted in a fly’s genome, can “instruct” the fly genes to perform their normal developmental functions. Evidence of common ancestry is also provided by nonfunctional DNA sequences called *pseudogenes*: “dead” genes that have lost their function, but are shared by many species. Morphological characteristics, such as the rudimentary wings of many flightless insects that are descended from flying ancestors, also attest to evolution. Inferences of common ancestry based on comparisons among living species have been abundantly supported by direct fossil evidence of evolutionary transitions. The evolution of terrestrial amphibians from fishes, of reptiles from amphibians, of birds from dinosaurs, of mammals from reptiles, and of whales from terrestrial mammals can all be traced in the fossil record.

- Methods of phylogenetic, or genealogical, inference have been successfully developed, and many relationships among organisms have been established (although much remains to be done). Phylogenetic inference methods provide evidence on relationships among organisms, and this, in turn, provides a foundation for innumerable other studies. The history of evolutionary change in particular characteristics, for instance, can be inferred from their distribution on a phylogenetic tree. Among insects, we can safely say that social behavior has evolved independently at least 15 times, since each of the 15 groups of social species is most closely related to a different nonsocial group. Moreover, comparisons among closely related social insect species have shown that increasingly intricate sociality has evolved in steps.

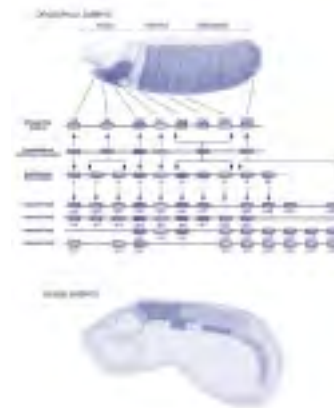
Phylogenetic studies have revealed or confirmed some remarkable events in the history of life. Perhaps the most stunning of these discoveries is that some important parts of eukaryotes' cells, such as mitochondria and chloroplasts, are descended from free-living bacteria that became intracellular symbionts. Phylogenetic inference methods also yield "gene trees," diagrams of the relationships among variant genes within a species and among species. When analyzed in the light of population genetic models, gene trees can reveal a great deal about the history of populations, such as their age, their former size, and their history of subdivision.

- The tempo and mode of evolution has been documented. Phylogenetic and paleontological data show that different characteristics evolve at different rates within a lineage (a pattern called *mosaic evolution*), so that every organism is a patchwork of characteristics that have changed substantially in the recent past and others that have changed little over many millions of years. This is true of both DNA sequences and phenotypic features. Individual anatomical features and clusters of features usually seem to evolve quite rapidly at some times in the history of a lineage, and hardly at all at other times. In the fossil record, this pattern is recorded as "*stasis*" interrupted occasionally by short periods of rapid change—a pattern that has been termed "*punctuated equilibrium*." There are several recent competing explanations for this pattern. Another common pattern is *evolutionary radiation*, in which many distinct lineages diverge from a common ancestor within a short time. These bursts of diversification are often associated with the evolution of a new adaptation that provides access to new resources or a new way of life (e.g., flight), or with the extinction of taxa that had previously dominated the ecosystem.

- Patterns of diversification and extinction have been described from the fossil record. Early marine organisms, for example, increased rapidly in diversity, then remained at a roughly stable level for much of the Paleozoic era (545–248 million years ago). Their diversity then dropped sharply, to perhaps 4% of their previous diversity, during the greatest mass extinction that life has yet suffered. Diversity then rebounded rapidly, and has more or less increased ever since. The separation of the continents, creating separate platforms for diversification, has contributed to the global increase in diversity, as has the ascendancy of "modern" groups that can utilize a broader array of

## Homeobox Genes

SEAN B. CARROLL  
UNIVERSITY OF WISCONSIN



*Hox* gene organization and expression. Top, the A-P domains of *Drosophila Hox* gene expression correspond to the order of the genes within the *Hox* complex. Middle, the evolutionary relationship between the *Drosophila*, *Amphioxus* and mouse *Hox* clusters, and the deduced complement of *Hox* genes in the presumed common ancestor of arthropods and chordates. Bottom, the A-P domains of mouse *Hox* genes within the developing mouse also correspond to gene order in the *Hox* complexes. Adapted from ref. 50, 52, and 75.

The evolution of animals has long been approached through systematics and paleontology. However, the genetic basis for the morphological diversity of any animal group has, until recently, been beyond the reach of biology. How do body plans and body parts evolve? One of the most important discoveries of the past decade is that most or all animals share a special family of genes, the *Hox* genes, which are important for determining body pattern. The diversity of *Hox*-related features in arthropods (segment morphology, appendage number and pattern) and vertebrates (vertebral morphology, limb and central nervous system pattern) suggests that *Hox* genes have played an important role in morphological evolution. Recent studies of many different types of animals suggest that much of animal diversity has evolved around a common set of *Hox* genes that are deployed in different ways and regulate different genes in specific groups.<sup>1</sup>

<sup>1</sup> S.B. Carroll, *Nature*, 376: 479-485 (1995); R.A. Raff, *The Shape of Life: Genes, Development, and the Evolution of Animal Form* (University of Chicago Press, Chicago, 1996).





## Transitions in the Fossil Record: Whales from Ungulates

J. JOHN SEPKOSKI, JR.  
UNIVERSITY OF CHICAGO

Whales and dolphins (cetaceans) are definitely mammals: they are warm-blooded, they suckle their young, they have three bones in the middle ear. They even have partial vestigial hindlimbs within the body wall. Exactly how cetaceans are related to other mammals, however, has been elucidated only since the 1960s, through a combination of good phylogenetic analysis and spectacular paleontological discoveries.

It is now known, through a seamless series of transitions found in the fossil record, that cetaceans evolved during the Early Eocene from a primitive group of carnivorous ungulates (hoofed mammals) called mesonychids. This group had unusually large heads for their body size and had teeth adapted for crushing turtles. Thus, some mesonychids must have been living near water inhabited by turtles.

The oldest fossil included in the Cetacea is *Pakicetus*, a skull from Lower Eocene riverine strata in Pakistan. The structure of the skull is cetacean, but the teeth are more like those of mesonychids than those of modern toothed whales. A more complete fossil, also from Pakistan but from shallow marine deposits, is the early Middle Eocene *Ambulocetus*. This animal's front forelimbs and powerful hind legs had large (and still hoofed) feet suitable for paddling, which were capable of being turned

backward like those of a sea lion. *Ambulocetus* would have been capable of moving between sea and land. More importantly, however, the vertebrae in the lower back of *Ambulocetus* had a highly flexible articulation, making the back capable of strong up-and-down motion, the method modern cetaceans use to swim and dive.

In slightly younger marine deposits in Pakistan, two more fossil cetaceans, *Indocetus* and *Rodhocetus*, have been found. These animals had hind limbs that were probably functional, but *Rodhocetus* had lost fusion of the vertebrae where the pelvis articulates to the backbone in terrestrial mammals. This loss of fusion permitted yet greater flexibility in dorsoventral movement for swimming, and suggests that the animal did not venture onto land often, if at all.

*Basilosaurus*, from Upper Eocene rocks of Egypt and the United States, is a more modern whale, with front flippers for steering and a completely flexible backbone. Still, along this backbone are vestiges of *Basilosaurus's* terrestrial ancestry: complete hind limbs though now small, not articulated to the backbone, and probably nonfunctional. In the later evolution of the cetaceans, these hind limbs became further reduced, losing the toes and kneecap needed for terrestrial locomotion.

resources or habitats (e.g., flowering plants). Throughout the fossil record, there has been turnover-extinction and origination of taxa. The causes of extinction are poorly understood, but knowledge of the biological characteristics of groups that were prone to extinction in the past may help us to predict vulnerability to extinction among present-day species. The pattern of extinctions in coastal marine invertebrates over geologic time, for example, suggests that tropical reef dwellers are most vulnerable.

- A quantitative theory of fundamental evolutionary processes has been devised and validated. The mathematical theory of population genetics—of genetic change within and among populations—describes the interplay and relative importance, under various conditions, of mutation rate, recombination, genetic drift, gene flow versus isolation, and various forms of natural selection. These processes have been well documented and quantified in both experimental and natural populations of many species. Thus, for instance, it is possible to say confidently that natural selection exerts so much stronger a force than mutation on many phenotypic characters that the direction and rate of evolution is ordinarily driven by selection even though mutation is ultimately necessary for any evolution to occur. Population genetic models also show how several factors, such as certain

forms of natural selection and population structure, maintain genetic variation instead of eroding it.

- The theory of evolutionary processes has been successfully extended to molecular data. For example, the neutral theory of molecular evolution, an extension of the theory of genetic drift developed in the 1930s, predicts that the greatest variation should occur in the functionally less critical parts of a gene. In one of many confirmations of this theory, mutations were experimentally induced in various parts of a gene of the bacterium *Escherichia coli*. As predicted, mutations in those regions that differ little among different species of bacteria proved to impair enzyme function, whereas mutations in regions that vary widely among species had little effect (15).
- Populations have been found to be highly variable genetically. Both classic and molecular techniques have revealed extensive genetic variation within and among populations. Certainly no two humans that have ever lived, except for identical twins, have been genetically identical. The tasks remain of explaining more fully why this variation exists, of determining why some features are more genetically variable than others, and of finding out how readily natural selection can shape this variation into new adaptations to various environmental challenges.

- These high levels of genetic variation have several implications. Most important, they may allow populations to evolve rapidly when environments change, rather than having to wait for just the right mutations to occur. The reservoir of genetic variation has contributed to the success of *artificial selection* (deliberate selection by humans) of desirable traits in crops and domestic animals, and accounts for other instances of rapid evolution, such as the development of insecticide resistance in many species of insects.
- The process of evolution can be observed and studied directly. The existence of genetic variation, and the continual origin of new genetic variation by mutation and recombination, enable us to study many evolutionary processes as they occur. Studies of bacteria, for example, have shown that adaptive evolution can be based on new mutations, not just on preexisting variation (22). Observed adaptive changes often have deleterious side effects, which, if sufficiently great, can limit further adaptation. But subsequent genetic changes sometimes occur that remedy these side effects. For example, populations of a blowfly that attacks sheep evolved resistance to the insecticide diazinon. The resistant populations initially showed retarded development and physical abnormalities, but these traits later diminished due to selection of other genes that ameliorated the deleterious effects (32).
- The mechanisms by which new species arise have been clarified. Although much remains to be learned about speciation, a great deal has been learned about the genetic changes that underlie this process. In animals, it appears that speciation typically involves divergence between geographically separated populations, as the genes that come to predominate in one population are incompatible with those in the other. Genetic studies have shown that in some instances, this incompatibility is caused by a small number of genes, suggesting that speciation has occurred rapidly, while in other cases, interactions among a large number of genes are responsible, implying that speciation has occurred slowly and gradually. Certain modes of speciation are more prevalent in plants than in animals, such as speciation by *polyploidy* (multiplication of whole sets of chromosomes). Some wild species of plants that evolved by polyploidy have been directly “re-created” in laboratory experiments.
- Many forms of natural selection have been documented. For example, selection operates not only through differences in survival and female reproduction, but also through differences in male mating success, termed *sexual selection*. This process entails competition among males or preference by females for males with certain traits. Experiments have shown that sexual selection is responsible for many elaborate, even bizarre, male behaviors and anatomical traits, such as huge antlers in deer and the bright plumes and elaborate displays of many male birds.

Traditionally, natural selection was defined as differences in survival or reproduction among phenotypically different individuals within populations of a species. We now know that selection can also reside in differences in survival or reproduction among genes as such (genetic selection), among whole groups of individuals (group selection), and among species or higher taxa (taxon selection). Genetic selection can be especially potent. “Selfish genes” are genes that, by various mechanisms, spread more copies of themselves through a population than other genes do. For example, transposable elements are DNA sequences that replicate and spread throughout the genome. Such genes may not benefit, and may even harm, the organism or the species as a whole.

- Theories based on natural selection have explained the evolution of many puzzling characteristics. From a long list, we mention two examples: cooperative behavior and senescence.
  - Cooperative behavior. Altruistic behavior, such as adult animals failing to breed and instead helping other individuals to rear offspring, seems difficult to explain, because such “altruistic” genotypes divert energy that they could otherwise use for their own reproduction or survival. How, then, can we account for the cooperative behavior of many animals? A major answer to this question is kin selection. An individual who aids others may bequeath fewer of its own genes to subsequent generations, but it may more than compensate for this by enhancing the survival and reproduction of its relatives, which carry many of the same genes. Most cooperative behavior, it turns out on close study, is indeed directed toward relatives, not toward the species at large.
  - Senescence. Why, if natural selection consists in part of differences in survival, do organisms undergo senescence and have a limited life span, shorter or longer depending on the species? The mathematical theory of life histories shows that offspring born late in a parent’s life contribute less to future population numbers than offspring born earlier. Consequently, reproducing late in life contributes fewer genes to the population than early reproduction. Therefore, the genetic advantage of surviving to reproduce declines with age. If, therefore, genes that enhance survival or reproduction early in life have deleterious side effects later in life, they may be selected because of their effect on early reproduction, but cause senescence as a side effect. This hypothesis has been supported by studies again also of experimental populations of *Drosophila* (53).
- Processes of coevolution have been elucidated. Evolutionary ecologists are developing and testing hypotheses about how interacting species affect each other’s evolution. For instance,

the antagonism between prey and predators, and between hosts and parasites or pathogens, can lead to evolutionary “arms races” in which each changes in response to changes in the other. The adaptations that result can be intricate: plants, for example, have evolved diverse chemical defenses against herbivores and pathogens, including compounds such as nicotine, caffeine, and salicylic acid (aspirin) that humans have used for diverse purposes. Each such defense, however, has been overcome by some insect species, which have evolved physiological mechanisms to neutralize it.

- Greater understanding of the developmental basis of the evolution of complex characters has been achieved. A long-standing question is how complex anatomical characteristics, especially novel ones such as the feathers of the first birds, evolve. To answer this question, we will need to understand how the normal pathways of development of morphological features can change. The recent spectacular advances in developmental biology are paralleled by studies of evolutionary change in developmental mechanisms. In salamanders, for example, evolutionary changes in genes that affect the production of hormones, or the responses of various tissues to those hormones, have influenced the rate and timing of development, resulting in species that retain many juvenile characteristics throughout their adult life. Such changes may have important, widespread effects; for instance, some salamanders that grow only to a miniature size fail to develop certain bones and have greatly altered skulls. Molecular developmental studies in *Drosophila* fruit flies have discovered “master” switch genes, which regulate the action of other genes lower in the command hierarchy, that determine the identity and features of the segments of the insect’s body. Comparative evolutionary studies show that homologues of these genes exist in mammals and other animals as well. These master genes all regulate lower-level genes that differ from one group of organisms to another, and so generate different characteristics. Likewise, genes have been found that may regulate flower development in all flowering plants. Remarkably, “master” genes that regulate the development of flowers have some similarities in DNA sequence to animals’ master genes. Most of the advances in evolutionary developmental biology are very recent; the field is undergoing rapid growth.
- Many aspects of human evolution have been elucidated by recent research in paleoanthropology, phylogenetic systematics, and molecular population genetics. DNA sequences show that humans are closely related to the African apes, especially to chimpanzees. The more than 98% DNA sequence similarity of humans and chimpanzees implies that they diverged from a common ancestor about 6 to 8 million years ago. Discoveries of early hominids with many apelike features (such as a small brain, curved finger and toe bones,

and dental features) are being made almost yearly in eastern Africa. The oldest hominid fossils so far discovered are about 4.4 million years old, approaching the time of common ancestry suggested by the DNA data. Some fossil hominid populations grade into each other.

Considerable controversy surrounds the hypothesis, based on studies of variation in DNA, that all contemporary human populations are descended from a single African population that spread into Eurasia about 100,000 to 200,000 years ago, replacing populations of *Homo sapiens* that had previously occupied this region. According to this hypothesis, genetic differences among modern human populations in different parts of the globe have had little time (on an evolutionary scale) in which to develop. In fact, although there are some regional genetic differences in characteristics such as facial features and the frequencies of blood groups, all human populations are, overall, genetically very similar. Most human genetic variation is found within, rather than among, populations. Thus, if all humans were to become extinct except for a single tribe somewhere on earth, at least 85% of the genetic variation that exists today would still be present in the future population that grew from that surviving tribe (40).

## B. Contributions to Other Biological Disciplines

Early in the twentieth century, most biologists were broadly trained, so that many brought both a mechanistic and an evolutionary perspective to their research. Many geneticists, for example, were motivated by evolutionary questions, and contributed to evolutionary theory as well as to our understanding of genetic mechanisms. Hermann Muller, for instance, made many important contributions to evolutionary genetics and also won a Nobel Prize for discovering that radiation causes mutations.

With the growth in science and the explosive growth in information, however, biology has become increasingly fragmented into specialized subdisciplines, and biologists have become increasingly narrowly trained. Hence many biologists who work in areas such as molecular biology and neurobiology have little background in evolutionary biology and are unaware of its potential contributions to their disciplines. Nevertheless, mutual influences between evolutionary biology and the other biological disciplines have continued, and in some areas have grown. We can sketch only a few examples of the contributions of evolutionary data and approaches to other biological sciences.

- **Molecular Biology.** Evolutionary approaches have contributed insight into the structure of ribosomal RNA, the chemical medium responsible for translating the genetic information in DNA into protein structure. Ribosomal RNA has a secondary structure composed of loops of unpaired nucleotide sequences and stems of base pairs that

are matched in a manner similar to the double-stranded structure of DNA (Watson-Crick base pairing). Chemical and biophysical methods, such as X-ray crystallography, provided some information on the structure of small RNAs, but were ineffective in resolving the structure of larger RNAs such as ribosomal RNA. However, phylogenetic analyses of ribosomal RNA sequences from diverse species identified the evolutionarily conserved regions of the molecule, providing the basis for specifying those portions that maintain its secondary structure by Watson-Crick pairing. Thus, inference from evolutionary analysis provided fundamental data on the structure of these ubiquitous, critical components of the protein-synthesizing machinery (43). In another application of phylogenetic analysis, molecular biologists have inferred the sequence of ancestral proteins, synthesized them, and examined their properties (2, 26).

The genomes of eukaryotic organisms, including mammals, vary greatly in size, due to variation in the often huge numbers of repeated sequences of DNA. These repeats, moreover, vary greatly in sequence and organization. For many years, they were accounted for by the “selfish DNA hypothesis” (12, 14, 46) which states that the repeated DNA serves no function for the organism, but is propagated because any DNA sequence that can successfully replicate itself and be transmitted to subsequent generations has a selective advantage over sequences that are less capable of doing so. This theory has prompted further work on repetitive DNA, and there is growing evidence that such DNA may sometimes play more of a functional role than previously thought.

The genetic code is redundant. Many of the amino acids that compose proteins are encoded in DNA by several nucleotide triplets (codons) that differ in the third nucleotide position. The several synonymous codons for a particular amino acid might be expected to be equally frequent in the DNA, but very often one is far more frequent than the others, a pattern called “codon bias.” Molecular evolutionary biologists have reasoned that natural selection may be responsible for such patterns. Such selection would have to be weak, since synonymous codons do not differ in their effects on the protein products that carry out the biochemical functions on which the survival of the organism depends. Population genetic theory predicts that weak selection should be more effective in large than in small populations. As this theory predicts, codon bias is more pronounced in organisms such as bacteria and yeasts, which have huge populations, than in mammals, which have much smaller ones. Thus, it is indeed likely that natural selection chooses among synonymous codons, and the remaining question is what the mechanistic differences are among synonymous codons that might affect survival or

reproduction. A leading hypothesis is that the translation of messenger RNA into protein may be more efficient if a common codon, rather than a variety of different codons, interacts with the transfer RNAs involved in protein synthesis (5). Evolutionary research thus points the way to research on fundamental molecular mechanisms.

- **Developmental Biology.** Similarities among the embryos of species that differ radically as adults were among Darwin's chief sources of evidence for evolution. Much of embryology in the decades after Darwin was concerned with differences among organisms in development and with development as a source of evidence for phylogenetic relationships. Early in the twentieth century, however, attention shifted to the mechanisms of development, and embryology became an experimental science, largely divorced from evolutionary studies. Nevertheless, a few developmental biologists acknowledged that some embryological phenomena could be understood only in the light of evolutionary history. The notochord, for example, makes only a brief appearance in the development of mammals, after which it disappears. It plays an essential role, for it induces the development of the nervous system; but that it should exist at all is explicable only by the fact that it is a functionally important structural feature throughout life in primitive vertebrates. The developmental role of the notochord evolved early in vertebrate history, and because of this role, it has been retained in the embryos of mammals long after its structural function in their ancestors was replaced by the evolution of the bony spinal column.

A resurgence in interaction between developmental and evolutionary biology is now under way, in part because of a renewed focus on development by evolutionary biologists and in part because comparisons among species of genes that play critical roles in development. For example, the comparative approach has provided critical insights into the function of genes involved in eye development and into the mechanisms of eye morphogenesis. Walter Gehring and his research group in Switzerland have recently discovered that a similar system of genetic control of eye development prevails in insects and mammals, and may apply to all animals. In fact, they found that a gene that controls eye development in mammals can induce development of the very different eyes of insects when it is transplanted into *Drosophila* fruit flies. The key feature of this genetic system is a single “master control” gene that initiates eye formation and appears to regulate the activity of the many other genes that contribute to eye development (21). This commonality has a practical benefit: insects and other animal species, which are easier and less costly to study than humans, can be used as models for improving our understanding of the developmental and genetic bases of congenital and hereditary eye malformations, as well as their diagnosis and possible

treatment, with the confidence that knowledge derived from these species can be applied meaningfully to humans.

- **Physiology and Morphology.** Evolutionary biology has long influenced the study of physiology in animals and plants, and can make many other contributions that are only now being developed. Some of these contributions will influence the field of human physiology, including related areas such as sports medicine and clinical psychology; others will advance our understanding of basic physiological mechanisms and their applications to areas such as medicine, agriculture, and veterinary science (20).

Evolutionary physiology includes the study of physiological functions in species that occupy different environments. Many interesting mechanisms for coping with extreme environments have been discovered that have deepened our understanding of physiology and biochemistry. Proteins have been discovered that prevent the formation of ice crystals in the cells of Antarctic fishes that live in waters near the freezing point. Studies of diving mammals such as seals have provided insight into how these animals can function without breathing for long periods at high pressures—data that bear on the physiology of human divers. Another example bears on the regulation of blood pH during open-heart surgery (66). Usually, such surgery is facilitated by cooling the body and thus slowing the heart rate. Cooling the body raises blood pH, and clinicians have seen this as a “problem” to be solved by adjusting the pH to the level found at the body’s normal temperature (37°C). However, comparative physiologists have pointed out that blood pH normally rises as body temperature declines in ectothermic animals such as reptiles, with no adverse effects. This recognition has led to changes in the way surgical hypothermia is managed.

The theory and methods of evolutionary genetics can contribute to our understanding of the basis of variation in physiological functions within species. These methods, for example, have been widely used to describe the extent to which physiological differences among individual organisms are due to genetic differences (“nature”) versus individual adjustments to environmental variables (“nurture”). One such method is artificial selection on physiological characteristics. Human-induced evolutionary changes in experimental populations have shown that genes influence characteristics such as alcohol tolerance, temperature tolerance, and learning ability. In populations that have been altered by artificial selection, a search for characteristics that have undergone a correlated change can then reveal candidates for physiological mechanisms underlying the variation. Traits that may affect senescence are being sought in experimental populations of *Drosophila* and the nematode *Caenorhabditis elegans*, in which delayed maturity has been achieved by artificial selection (27, 53). In other studies,

mouse populations are being selected for differences in activity levels, with the aim of determining whether or not such differences affect health, life span, or female reproduction (as may occur in humans). Because such data on humans are nonexperimental and difficult to interpret, such studies of animal models have much to contribute.

- **Neurobiology and Behavior.** Behavioral traits evolve just as morphological characteristics do, and like morphological traits, they are often most similar among closely related species. Phylogenetic studies of behavior have provided examples of how complex behaviors such as the courtship displays of some birds have evolved from simpler ancestral behaviors.

Evolutionary biologists have worked extensively on the relative contributions of genes and experience (learning, in the broad sense) to variation in behavior, and have shown that these differ depending on the trait and the species. In an effort to understand how natural selection has acted on the genetic component of variation to shape adaptively important behaviors, evolutionary biologists have developed a wide range of mathematical models that predict the behaviors that may evolve, depending on a species’ ecological and social environment. Some of these are related to economic models. For instance, models of foraging behavior have successfully predicted the foraging “decisions” made by birds and other animals in the face of variation in the quality and spatial distribution of food.

The evolutionary study of animal behavior has joined with comparative psychology in several research areas, such as the study of learning. It is now clear that natural selection has fostered the ability to learn different tasks in different species, and that such adaptations can be studied in much the same way as morphological adaptations. Species of birds, for instance, differ markedly in their ability to remember sites in which food has been stored; this ability is extremely high in those species that typically cache seeds or other food.

Although neurobiologists recognize that the mechanisms they study are adaptations, they generally do not study behavioral mechanisms in expressly evolutionary terms. So far, evolutionary biology has contributed little to the understanding of molecular processes in neurobiology, and the points of contact between neurobiology and evolutionary biology have been rather few. There are some notable exceptions, however, especially in comparative and evolutionary studies of sensory mechanisms and neuroanatomy. For instance, the size of the song-controlling region in the brain of songbirds differs among populations and species that vary in the number of different songs they sing. In some species of owls that can locate prey in total darkness, clusters of brain cells that process information on sound are spatially organized so that they form a literal map of the three-dimensional environment from which sounds are

received. Comparative studies of this kind, based on an understanding of the adaptive requirements of different species, can thus lead to new understanding of behavioral mechanisms.

## VII. WHAT DOES THE FUTURE HOLD FOR EVOLUTIONARY BIOLOGY?

### A. Applied Science

As discussed above, evolutionary biology has made diverse contributions to societal needs. However, its potential contributions greatly exceed those made to date. In contrast to some other biological disciplines such as biochemistry and ecology, in which applications to health or environmental science are emphasized in training and research, the development of an explicit field of “applied evolutionary biology” is only beginning (19, 33, 41).

The history of evolutionary biology shows that beneficial interactions between basic and applied research can flow in both directions. Evolutionary genetics has profited from genetic research aimed at improving crops and domesticated animals. Studies of mutational changes in the metabolic capacities of microorganisms, pursued in part because of their industrial applications, have shed light on the evolution of biochemical pathways. Genetic and phylogenetic studies of corn and other crops have provided insight into rates of evolution and changes in developmental pathways. The study of sickle-cell hemoglobin and other polymorphisms in humans has provided some of the best analyses of modes of natural selection. The evolution of pesticide and drug resistance in insect pests, weeds, rats, and pathogenic bacteria, the evolution of life history characteristics in overexploited fish populations and introduced insect pests, the evolution of virulence in viruses and bacteria, and coevolution between insects and plants have been subjects of some of the best case studies of evolutionary dynamics.

This background shows that evolutionary biologists can often address basic questions by working on systems that are directly relevant to societal needs. To be sure, the ideal systems for addressing certain basic intellectual problems will often not be those with immediate social utility, although it is often hard to predict in advance what questions in basic science will lead to useful breakthroughs. Moreover, we reiterate the importance of exploring and understanding the diversity of organisms as an intellectual goal, in light of some of the payoffs discussed above. But in many cases, research on a socially relevant organism or system can both advance basic science and contribute to societal needs. We anticipate that evolutionary biologists will increasingly play these dual roles.

It is important to emphasize that much of the expected progress in applied evolutionary biology will require, and be inseparable from, progress in basic research. As in other biological disciplines, studies of model organisms and systems

(including not only standard laboratory species such as yeasts, *Drosophila*, and *Arabidopsis*, but also a variety of wild species) will provide insights that can be applied to societal needs. Likewise, conceptual and theoretical advances in basic evolutionary biology will contribute to progress in applied evolutionary biology. Important progress will be made in the areas of health science, agriculture, natural products, environment and conservation, technology development, and educational and intellectual interchange with other scholarly disciplines and with the general public.

**Health science.** Advances in applying evolutionary disciplines to human health fall into several categories.

- **Human genetic diversity.** Research on human genetic diversity will complement the Human Genome Project, which ultimately will sequence the entire human genome. Such research will provide data, at the molecular level, on the immense genetic diversity that exists within and among human populations. The techniques of population genetics and phylogenetic analysis will be applied to the exploding information on human genetic variation to determine the history of populations (e.g., their past sizes, movements, and interchanges), and will continue to provide tools for identifying the genetic lesions associated with inherited diseases and defects (as in the case of cystic fibrosis, breast cancer, and others). Evolutionary comparisons of human DNA sequences with those of other species will provide insight into gene functions. Population geneticists will analyze the genetic bases of interesting variable traits, such as reactions to allergens. Genes that provide adaptations to environmental factors such as pathogens and diet will be identified by studying genetic differences among and within populations. The methods used by evolutionary geneticists will be applied to human diversity in order to elucidate cases of complex inheritance of disease (e.g., those due to interactions among multiple genes) and to study genotype/environment interactions—the differential expression of traits such as disease resistance under different environmental conditions.
- **Genetic identification.** Population genetics has developed, and is continuing to improve, analytical methods for identifying individuals and relationships among individuals from a profile of genetically variable markers. This methodology also uses linked genetic markers to determine the likelihood that an individual carries genes of particular interest (e.g., those causing a genetic disease). As evolutionary geneticists improve these methods and apply them to data on human genetic diversity, it will be possible to use molecular markers more confidently and accurately for such purposes as counseling individuals on the likelihood that they or their children will carry a genetic disease, determining paternity, and forensic analysis.

- **Evolutionary developmental genetics.** Comparative data on the genetic and mechanistic bases of development in diverse vertebrates and other organisms will shed much light on the mechanisms of human development. Such studies will contribute to our understanding of the bases of hereditary and other congenital defects in humans, and may ultimately be useful in developing gene therapies.
- **Mechanisms and evolution of antibiotic resistance.** Genetic, phylogenetic, and comparative biochemical studies of bacteria, protists, fungi, helminths, and other parasites will help to identify targets for antibiotics. The rapid evolution of antibiotic resistance in previously susceptible pathogens presents a critical need for evolutionary study, aimed at understanding the mechanisms of resistance, its rate of evolution, factors that may limit such evolution, and ways of preventing or counteracting it.
- **Parasite virulence and host resistance.** Evolutionary studies of parasite/host interactions, using both model systems and human parasites and pathogens, are only beginning to determine the conditions that lead parasites to become more virulent or more benign. Evolutionary geneticists and evolutionary ecologists need to develop a general, predictive theory of the evolution and population dynamics of pathogens and their hosts, especially for rapidly evolving organisms such as HIV and for rapidly migrating host species like modern humans. Analyses of genetic variation in resistance to pathogens in humans and other hosts are also needed.
- **Epidemiology and evolutionary ecology of pathogens and parasites.** New and resurgent diseases have emerged as major threats to public health, and more will probably do so in the future. Evolutionary biologists can aid in the effort to counter these threats in several ways. Screening for and studying the phylogeny of organisms related to known pathogens (e.g., viruses of other primates and vertebrates) may allow researchers to identify pathogens with the potential to enter the human population. Genetic, ecological, and phylogenetic studies of new and emergent pathogens (e.g., hantavirus and the Lyme disease spirochete) can elucidate their origins, their rates and modes of transmission, and the ecological circumstances leading to outbreaks or to the evolution of greater virulence. Experimental studies of model systems, including organisms related to known pathogens, can identify mechanisms of virulence and the genetic and environmental factors that influence drug resistance. (Such studies will also have relevance, of course, to crops and domestic animals as well as economically important wild populations, such as fish.)

**Agriculture and biological resources.** We noted above the many ways in which evolutionary biology has had an intimate relationship with agriculture and the management of biological resources such as forests and fisheries. The scope for further contributions in these areas is enormous. We highlight only a few of the most important topics to be pursued.

- **Pesticide resistance.** Despite new alternative methods of pest management, judicious use of pesticides will undoubtedly remain indispensable. The evolution of pesticide resistance in insects, nematodes, fungi, and weeds is a serious economic problem that should receive major attention. This will require studies of the genetics and physiological mechanisms of resistance, population dynamic studies, and modeling of methods to limit or delay the evolution of resistance.
- **Alternatives in pest management.** Evolutionary considerations will be important in evaluating many alternative methods of pest management, such as mixing different crops or crop varieties (intercropping), or developing transgenic crops that carry resistance factors protecting them against insects or other pests. Experiments have shown, for example, that tobacco pests can adapt to transgenic tobacco carrying a bacterial toxin, highlighting the need for studies of genetic variation in insect responses to transgenic crops. There is enormous potential for transgenic use of the innumerable secondary compounds and other properties of wild plants that protect them against insects and pathogens. Experimental and phylogenetic screening of these natural resistance factors should prove rewarding. The large field of evolutionary ecology concerned with secondary plant compounds and the interactions between plants and their insect and fungal enemies is relevant to this effort. It will be important to analyze the physiological effects of natural resistance factors on pest organisms, the mechanisms by which some insects and fungi overcome their effects, and genetic variation in the responses of target species to natural resistance factors.
- **Genetic diversity in economically important organisms.** Production of food, fiber, and forest products has historically been greatly improved by exploiting genetic variation, and the methods for doing so have been deeply informed by evolutionary biology. Evolutionary and agricultural scientists together will use QTL (quantitative trait loci) mapping and other methods to locate the genes for, and elucidate the mechanistic bases of, important plant traits, such as resistance to pathogens and to environmental stresses. Such studies will also serve the interests of basic scientists interested in the adaptations of plants to environmental factors. Similar studies on wild plants will locate genes for useful traits that can be genetically engineered into crops. Research programs of this kind will use principles and information from studies of plant phylogeny and adapta-

tion. The critically important task of developing and maintaining germ plasm banks (i.e., storing genetic diversity of crop plants and their relatives for future needs) will continue to depend on studies of variation within and among populations.

- **Fisheries.** Several kinds of evolutionary studies have been and will continue to be important in managing commercial and sport fisheries. Molecular genetic markers will aid researchers in distinguishing breeding populations and migration routes of species such as cod and salmon. Studying the evolution of life history characteristics such as growth rate and age at maturity will enable managers to evaluate the genetic and demographic effects of harvesting on fish populations. For certain fish species that are widely stocked, genetic and physiological studies of adaptation to and fitness in different environments will be useful. Stocking plans will also include the use of transgenic fish, which are in the early stages of development.

**Natural products and processes.** Pharmaceutical and other industries are actively searching for novel products and processes by screening plants, animals, and microorganisms (33). Because of its commercial implications, the search for and development of novel products and processes raises serious issues in patent law, international law, and the publication of scientific data that are beyond the scope of this report, but which will affect the engagement and activities of research scientists. Evolutionary studies will greatly contribute to research and development, resulting in many novel products and processes.

- **Systematics and phylogeny.** Documenting the diversity of potentially useful organisms is the foundation for all further work. This has been recognized, for example, by the President's Committee of Advisors on Science and Technology (48) and by the pharmaceutical companies that have funded biodiversity inventories in Costa Rica and elsewhere. The phylogenetic aspect of systematics is crucial for pointing researchers toward species that are related to those in which potentially useful compounds or metabolic pathways have been found, since related species may have similar, perhaps even more efficacious, properties. The systematics of bacteria, protists, fungi, and other inconspicuous organisms are very poorly known and require extensive investigation.
- **Studies of adaptation.** Antibiotics, resistance factors for use in transgenic crops, and other useful natural products are likely to be found by studying the chemical mechanisms of competition among fungi and microorganisms, the defenses of plants against their natural enemies, and the waxes, steroids, terpenes, hormones, and innumerable other compounds that organisms use for diverse adaptive ends.

- **Genetic and physiological studies.** Bacteria, yeasts, and other microorganisms have exceedingly diverse metabolic capacities. They have been the source of penicillin, of the polymerase enzyme used in DNA sequencing, and of important industrial processes of fermentation, biosynthesis, and biodegradation. Industry anticipates that "great advances in bio-processing can be expected from future exploration of the yet unexplored biodiversity of the land and sea" (30). Yet most microorganisms have not yet been described and characterized, the physiological capacities of most of them are unknown, and there is little information available on their genetic diversity, or on what kinds of novel metabolic capacities can arise by mutation. Researchers trained in evolutionary genetics, physiology, and systematics will make important contributions to this area.

**Environment and conservation.** Evolutionary principles are immediately applicable to the conservation of rare and endangered species and ecosystems; in fact, many leading conservation biologists have done research in basic evolutionary biology. Evolutionary biology can also shed light on environmental management issues that bear directly on human health and welfare. Here we highlight only a few of the needs for evolutionary study in the fields of environmental management and conservation.

- **Bioremediation.** *Bioremediation* refers primarily to the use of organisms (especially bacteria and plants) in cleaning up spills and toxins, treating sludge, and restoring degraded soils. Evolutionary biology can contribute to bioremediation by identifying species or genetic strains with desirable properties, by understanding the agents of natural selection that give rise to such properties, and by identifying the conditions that favor the persistence of useful organisms. Bacteria that can degrade polychlorinated biphenyls (PCBs) and other persistent contaminants are known, but it is not known whether this capability is characteristic of certain species or evolves in situ due to selection of new mutations. The community of bacteria involved in wastewater treatment undergoes a change in composition during the process, but the roles of turnover of species versus genetic change in the metabolism of persistent species are not known. Evolutionary genetics and systematics, together with microbial ecology and physiology, should continue to make important contributions to these and other questions in bioremediation.
- **Unplanned introductions.** Many of our most serious pests, including weeds, insects, red-tide dinoflagellates, and zebra mussels, do the most damage in regions to which they are not native. Quarantine procedures instituted by the U.S. Department of Agriculture are intended to prevent such introductions. The advent of genetic engineering has caused concern about the escape of vigorous, genetically novel microorganisms, plants, fishes, or other organisms, and



about the possibility that genes for novel capacities could spread by hybridization from transgenic organisms into wild ones, transforming benign species into novel pests. Evolutionary biologists have been active in assessing such risks (60). Studies of gene flow between and within species and evaluations of the fitness effects of genes must complement ecological studies of the relevant organisms if we are to predict the possible unintended effects of transgenic releases. The traditional role of systematics in identifying introduced organisms will continue to be important.

■ **Predicting effects of environmental change.** Of the many effects human activities have on the environment, the most universal possible effect is global warming. Many other environmental alterations, such as desertification, salinization of fresh water, and acid rain, have more local, but still profound, effects on both wild species and biological resources. Predicting and possibly forestalling the effects of such changes is an important goal for ecological studies, but evolutionary biology also faces major challenges. In particular, we need to understand far better the conditions under which populations adapt to environmental changes versus migrating or becoming extinct, and what kinds of species will follow these courses. We also need to understand the conditions favoring “breakouts,” in which species adapt to and disperse rapidly into novel environments. Agriculture and urbanization have produced many novel environments, and such breakout species may not be benign. Evolutionary biologists have documented many examples of species that have adapted rapidly, and many that have not, but a fuller theory of vulnerability versus potential for rapid adaptation is needed (28). Paleobiological studies can complement genetic and ecological studies by providing detailed histories of changes in the composition of communities and the distributions of species under past environmental changes. Paleobiology can also help us to develop generalizations about the kinds of species and communities that are most vulnerable.

■ **Conservation of biodiversity.** Alteration of habitats, intentional and unintentional harvesting of natural populations, and other human activities constitute a grave threat to the persistence of many species. Inevitably, difficult choices will be necessary in the allocation of resources, and not all threatened species and ecosystems will be safeguarded.

Evolutionary biology and ecology work hand-in-hand in addressing these issues (34). There is a need for intense efforts to describe the diversity, distribution, and ecological requirements of organisms, especially those in regions where natural habitats are most rapidly being lost.

Evolutionary systematics, biogeography, and ecological genetics provide the information needed in order to develop guidelines for conserving the greatest genetic diversity.

Previous crises in biodiversity can be seen in the fossil record, and evolutionary paleontologists can use these records as natural experiments on the consequences of biodiversity loss, the characteristics of species most at risk, and the nature and time scale of biotic recovery. For example, many extinction events in the geologic past were followed immediately by outbreaks of weedy “disaster species.” Much more needs to be learned about this process, since there is no guarantee that disaster species that might arise in modern regions that have suffered extensive losses of biodiversity would be benign (55). Similarly, past biodiversity crises are associated with marked declines in primary productivity. This fact is relevant to future human welfare, in that humans now consume an estimated 25% of global primary productivity.

Evolutionary biologists are also studying such relevant problems as the minimal population sizes necessary for species to retain sufficient genetic variation to avoid inbreeding depression and to adapt to diseases, climate change, and other perturbations; the factors that cause extinction; the role of multiple populations in the long-term genetic and ecological dynamics of species; the role of interactions among species in maintaining viable populations; and the effects of coevolution among interacting species on dynamic processes in ecosystems. Conservation biology will be strengthened by further research on these poorly understood problems.

Some conservation efforts rely on germ plasm banks (for plants) and captive propagation (for animals). Population genetic theory plays a crucial role in these efforts. For example, inbreeding depression in small captive populations can be avoided by applying population genetic principles (59).

**Technology development.** In all sciences, the need to solve problems stimulates the development of new techniques and technologies. As noted earlier, most of the broadly applicable technologies that have been developed at least partly due to the need to solve evolutionary problems have been in the areas of statistics, computation, and data management. We anticipate that as evolutionary biology addresses ever more complex problems and richer data sets, collaborations among evolutionary biologists will lead to further technical innovations in these areas. Some likely areas of progress will be the analysis of the dynamics of complex, nonlinear systems; optimal search routines—e.g., for phylogenetic tree structures; evolutionary computation—i.e., development of “evolving” algorithms for efficient problem solving; and applications in computer-based artificial intelligence and artificial life.

**Public understanding of science.** Important challenges for evolutionary biology lie not only in the domain of research, but also in the domain of public understanding and appreciation of science, which is necessary both for the support of research and for the awareness and understanding an educated citizenry requires in an increasingly scientific and technological age. Many surveys of students and the general public have shown that the United States ranks relatively low among industrial nations in their command of science and mathematics. This is a matter of serious concern to all scientific disciplines and, indeed, to all agencies and organizations concerned with the future of the country's human resources for technical and economic development.

Evolutionary biologists are keenly aware of the need for increased education in and understanding of science. The subject matter of evolutionary biology includes topics that directly impinge on individuals' health and welfare, such as inherited disease, gene therapy, infectious disease, and the evolution of antibiotic resistance by pathogens, food production, agricultural pest management, genetic engineering, bioremediation, conservation, and the effects of global warming. Issues related to evolution, such as genetic differences among human populations, the fossil history of life, and indeed, the reality of evolution itself, are frequent topics of public discourse. Yet much of the public does not understand basic genetics or evolutionary biology. Incredible as it may seem in an age of spacecraft and supercomputers, polls find that more than half of the American public does not even believe in the scientific veracity of evolution, the unifying principle of all of biology.

Although some professional biologists have devoted great efforts to educating the public, the greatest efforts in public outreach in the United States have been made by organizations such as the National Center for Science Education, and the largest educational role has been played by secondary school teachers. Professional biologists should devote more effort to public education, availing themselves of opportunities such as press releases, engagement with the media, and museum exhibits. They should take every opportunity to point out the evolutionary dimensions of biological phenomena that capture the public's attention; for instance, pests and disease organisms do not merely "mutate" or "develop" resistance to drugs—they *evolve* resistance. Heightened efforts to teach about evolution and related subjects are also required at both the college and secondary levels.

## B. Basic Science

Evolutionary research is progressing on many fronts, but the unknown still greatly exceeds the known. In some areas we simply have less information than we should (for example, the history of diversity in the fossil record is very incompletely known.) In other cases, questions have been tentatively

answered using only one or a few study systems, and we do not know how widely those answers can be generalized. (For example, the numbers of genes contributing to reproductive isolation between species have been estimated for some *Drosophila* species, but for few other kinds of organisms.) In many cases, evidence has been obtained for or against one of several competing hypotheses, but the full range of hypotheses has not been tested adequately. (Of the several hypotheses that may explain the advantages of sexual reproduction, only a few have been tested.) Some long-standing questions have resisted analysis until recently, but new techniques offer great promise. (The question of how developmental pathways evolve is a conspicuous example.) Especially in molecular biology, entirely new phenomena have been discovered that call for evolutionary explanation and understanding.

We anticipate virtually unprecedented progress in basic evolutionary biology in the next decade or two, if there is adequate support for research and the training of young researchers. In this section, we list some of the areas in which progress is especially desirable and feasible, given present techniques and technical advances that may be anticipated in the near future. Although many evolutionary biologists would undoubtedly add to this list, the following high-priority questions and challenges represent a consensus of evolutionary biologists with diverse specialties and approaches. We group these research questions into several categories, which are equal in importance and priority.

**Theory and technique.** Much of evolutionary research has been guided by theory (often mathematical), which frames hypotheses, provides precise predictions or expectations, constrains the interpretation of data, and often specifies the kind of data required to test hypotheses. The training of evolutionary theoreticians continues to be highly important. Among the many areas requiring further theoretical work are:

- the continuing development of coalescent theory, used for inferring evolutionary processes from "gene trees";
- development of the theory of the relationship between phylogenies of genes and phylogenies of species and populations;
- further theoretical work on phylogenetic trees, for example, methods to compare and evaluate trees, to infer the history of character evolution from the phylogenetic distribution of characters, and to infer evolutionary processes from tree structure;
- the development of population genetic theory for application to underexplored topics, such as the nature and evolutionary consequences of gene interactions, gene-environment interactions, and the evolution of polygenic traits with different genetic architectures;

- development of optimization models for analyzing the evolution of behavior, life histories, and other phenotypic traits;
- models of evolutionary change in developmental pathways; and
- predictive models of the coevolution of interacting species.

All research depends on advances in techniques. Molecular and other experimental methods have greatly influenced evolutionary research, but evolutionary biology is also, and perhaps uniquely, dependent on analytical, statistical, and numerical (computational) methods. In the future, evolutionary research will particularly require progress in:

- methods for searching and manipulating massive amounts of data, such as DNA sequences;
- improvement of methods of maximum likelihood and other statistical procedures for analyzing population genetic data (e.g., molecular markers of mating systems);
- methods of aligning different DNA sequences;
- improvement of methods of phylogenetic analysis (as noted above); and
- improvement of methods for fine-scale mapping of quantitative trait loci.

**Evolutionary history.** Describing and explaining the history of evolution is one of the major goals of evolutionary biology. This is achieved mostly through phylogenetic methods, which are discussed below, and paleobiological study. Priority goals in paleobiology include:

- a more complete history of the diversity of life through time, especially of bacteria and other forms of life during the earliest five-sixths of life's history (the Precambrian era);
- improved data and methods for testing hypotheses about the causes of variation (among time periods and among taxa) in rates of speciation, extinction, and diversification (which includes accounting for both mass and background extinctions, the latter being particularly poorly understood);
- a better understanding of the constraints on and mechanisms of adaptation during unique historical events, such as the apparently explosive origin of animal diversity and the colonization of land by plants and arthropods;
- explaining differences among taxa in their susceptibility to and recovery from mass extinctions;
- a better understanding of common sequences of evolutionary events in the wake of mass extinctions, including massive expansions of weedy species and characteristic time

scales of ecosystem recovery—both of which relate to the contemporary biodiversity crisis; and

- tracing more fully the history and rate of evolution of characters, and of correlations among characters, in evolving lineages (such data are required to test many hypotheses, such as “punctuated equilibrium”).

**Systematics.** Systematic studies contribute to our knowledge of evolutionary history. They can also be used to test hypotheses about evolutionary processes by inferring the sequence and time of branching of lineages and the sequence and rate of change in their characteristics. Improved analytical methods and data have recently made systematics a far more vibrant, rigorous field than it had been, but much remains to be done. Among the important challenges are:

- Documenting the diversity of living organisms. Estimates of the number of living species vary widely. Among bacteria, protists, fungi, nematodes, mites, and many groups of insects, the majority of species probably have not yet been described, although these groups play exceedingly important roles in ecosystems and include many forms that directly impinge on human welfare. A full inventory of living organisms and their biological characteristics will provide the same kind of foundation for ecology, evolutionary biology, and other biological sciences that geologic surveys provide for earth science and the extractive industries. Recognizing biodiversity as “living capital,” a panel of the President’s Committee of Advisors on Science and Technology recommended a substantial increase of investment in the discovery of species, in phylogenetic and genetic analysis of diversity, and in museum collections, herbaria, and the other infrastructure of systematics (48).
- “Growing the tree of life.” Estimates of phylogeny have been developed for a small minority of taxa, but even these few estimates have already been used extensively for testing hypotheses in many areas of evolutionary biology and ecology. A high priority for evolutionary systematics should be more (and more robust) phylogenetic trees, embracing the full panoply of living and extinct organisms. These trees can be successively joined to build a phylogeny of all life. The more complete this tree of life, the better it will serve as an organizing framework for biological data of all kinds and as a basis for testing innumerable hypotheses. In order to accomplish this, widely accessible databases for storing phylogenetic estimates will be indispensable.
- Improving methods for inferring, evaluating, and using phylogenies to test hypotheses. For example, existing statistical methods for assessing the confidence to be placed in a phylogenetic tree will probably be superseded. Methods for using tree structure to determine differences among groups in rates of diversification are still being developed.

- Developing theoretical and empirical bases for integrating phylogenetic history with evolutionary processes. Researchers must find ways of bridging the gulf between theory and data on evolutionary processes and the procedures of phylogenetic inference in order to create a fully integrated theory of evolutionary biology.

**Speciation.** Possibly no major topic in evolutionary biology is as difficult and controversial as speciation, in part because it generally proceeds too fast to be fully documented in the fossil record, but too slowly to be observed within an investigator's lifetime. New approaches are needed, and are on the horizon, for answering some major questions about this process, the fount of biological diversity.

- Character differences between newly formed species, especially those that can prevent gene exchange between them, must be characterized, genetically and mechanistically. That is, we need to know not only the number and location of the genes involved (estimated in only a few cases), but also the developmental or biochemical effects by which gene differences cause reproductive isolation and other character differences.
- The processes that cause speciation must be determined. Whether selection, genetic drift, or a combination of the two are generally responsible for speciation is a major, unresolved question. If selection is generally the cause, the agents of selection will need to be identified.
- The rapidity and predictability of speciation must be determined. We do not know whether isolated populations inevitably become different species, at what speed speciation occurs, or if the rates depend on taxa or environmental conditions. We also need to know the degree to which geographic isolation is required for speciation.

**Evolutionary genetics.** Evolutionary genetics, including population genetics, plays a major role in the theory and analysis of character evolution and speciation. Among the major challenges for evolutionary genetics, we include the following:

- New theory on inadequately explored topics. Such topics include the nature of gene interactions (epistasis) and their evolutionary consequences; genetic processes in metapopulations, clusters of local populations that are subject to extinction and recolonization; and the genetic processes leading to speciation.
- Explaining levels of genetic variation in natural populations. New methods, especially analysis of DNA sequence variation, are giving us much more precise information on and insight into this old problem. In addition, greater understanding of evolutionary processes will arise as studies of DNA sequence variation are integrated into population-level studies.

- Describing "mutational landscapes"—that is, characterizing the variation that arises through mutation. Whether or not there are "forbidden" character states that can never arise, whether mutations act synergistically, and what their pleiotropic effects might be are among the many questions with important implications.
- Characterizing the genetic basis of character variation within and among species. Identifying the loci responsible for character variation, and their mechanistic effects on development, morphology, and physiology, will become feasible as methods of mapping (quantitative trait loci) are improved. Once such candidate genes have been identified, it will be possible to integrate studies of their developmental function with studies of their variation and evolution.
- Developing a predictive theory of adaptability and response to environmental change. Global warming and other environmental changes make it imperative that we understand when populations are likely to succeed or fail in adapting to new or changed environments. This will require an understanding of what governs rates of evolution.
- Understanding the population genetics of extinction. Comparatively little is known about the roles of such factors as cessation of gene flow and inbreeding depression in shrinking populations, yet this knowledge will be essential in preserving biodiversity and designing refugia for endangered species.

**Evolution of genes and genomes.** The intensely active interface between evolutionary biology and molecular genetics will continue to provide insight into the evolution of the structure of genes and genomes. New molecular phenomena may well be revealed that will invite evolutionary interpretations. From the standpoint of our present knowledge, subjects that require further study include the following:

- Further analysis of the evolution of rates of mutation and recombination. Important questions include whether or not "optimal" rates evolve, what evolutionary processes lead to variation in recombination rates among and within genomes, and what the mechanisms of such variation might be.
- Documentation and assessment of the evolutionary consequences of novel sources of genetic variation, such as lateral gene transfer among species, transposable elements, and unequal recombinational exchange.
- A deeper understanding of the evolution of linkage relationships among genes, and of changes in the number and the structure of chromosomes.
- Analysis of the roles of selection and other factors in the evolution of coding and noncoding DNA.

- Analysis of the evolution of the information content of genomes from both phylogenetic and mechanistic perspectives, as well as evolutionary analysis of the packaging of information in genomes, large-scale patterns in DNA, and the processes whereby new gene functions evolve.
- Analysis of genic selection and of conflict within genomes (e.g., segregation distortion, evolution of gene expression, etc.).

**Evolution and development.** The processes by which developmental pathways evolve, and conversely, the effects of developmental processes on the paths evolution may take, hold profound interest not only for developmental biologists but also for paleobiologists, systematists, and all biologists concerned with the evolution of phenotypic characters. Due to molecular and other technical advances in developmental biology, unprecedented progress in this area may be anticipated, and in fact is well under way. Almost every aspect of development will reward study, but several approaches and topics will be especially important:

- Theoretical analysis of how phenotypes may be altered or constrained by developmental pathways.
  - Analysis of the relationship between development and the genetic basis of variation in characters, both within and among species. This will require comparative and experimental studies of developmental differences among genotypes and among closely related taxa, complementing the broad taxonomic comparisons that are traditional in developmental biology.
  - Understanding the genetic bases of phenotypic differences, and how genes acquire new developmental roles.
  - Analysis of the developmental basis of complex and evolutionarily novel characters.
  - Identifying developmental constraints on evolution and the mechanisms that underlie them.
  - Understanding the relationships between phylogenetic and biological homology. Phylogenetically homologous characters (i.e., characters possessed by several different taxa and by their common ancestor) sometimes have remarkably different developmental pathways. A major challenge for developmental evolutionary biologists is to understand how the genetic foundation of a character may change even though its mature form remains relatively constant. Conversely, it is important to understand how the developmental roles of conserved genes come to differ among taxa (6, 63).
- Analysis of developmental mechanisms in modular organisms, such as plants and corals, compared with nonmodular forms, such as arthropods and vertebrates.
  - Understanding the evolution of self-recognition and non-self-recognition systems. The compatibility or incompatibility of cells, mediated largely by cell surface factors, governs such phenomena as the union of eggs and sperm, pollen/stigma interactions (e.g., self-incompatibility), immune system processes, and the migration and adhesion of cells in animal development. A better understanding of these phenomena will have broad implications for subjects such as speciation, plant breeding systems, character evolution, and disease resistance.

**Evolution of phenotypic characters.** The several subdisciplines of evolutionary biology that take specific classes of phenotypic characteristics as their subject will continue to address important problems, some of which are in the early stages of analysis. The following sample of challenges is by no means exhaustive.

- Develop criteria for evaluating differences between theoretical optimal values and observed values for phenotypic characters.
- Account for variation in the rate of evolution among characters and among taxa. The most pressing need is to develop methods of distinguishing the relative roles that “external” (e.g., ecological sources of selection) and “internal” factors (e.g., genetic correlations, developmental constraints) play in determining evolutionary rates.
- Develop and test theories about the evolution of suites of characters that are correlated either by function or by their genetic and developmental foundations. How do we determine which characters will evolve in concert, or how the degree of correlation changes over evolutionary time?
- Develop and empirically test theories about the evolution of a large class of interesting characters, such as:
  - sexual versus asexual reproduction, variations in sex determination mechanisms, inbreeding versus outcrossing, and other aspects of breeding systems;
  - sexually selected characters;
  - the mechanisms of behavior, including neural substrates and hormonal controls;
  - the mechanisms by which organisms respond to varying environments, such as phenotypic plasticity, learning, dispersal, and physiological acclimation;
  - physiological tolerances of environmental variables such as temperature, water availability, and environmental and dietary toxins;

- complex morphological structures and biochemical pathways; and
- the breadth of species' diets, habitat use, and geographic distributions.

### **Evolution of ecological interactions and communities.**

About 30 years ago, evolutionary ecologists hoped to explain major features of ecological communities, such as species diversity and food web structure, by developing a theory of interactions among species based on both evolution and demography. Progress toward that goal has been modest for several reasons, including the complexity of communities and failure, in the past, to take sufficient account of the effects of evolutionary and geologic history. A more pluralistic community ecology seems to be emerging (52), in which evolutionary history and processes will play essential roles. Priority research areas include:

- development of methods for identifying and quantifying the effects of evolutionary and environmental history on community composition and on dynamic changes in communities;
- development and testing of theories of the effects of genetic variation and evolutionary change on the stability of species interactions and on extinction vs. persistence in the face of biological and environmental change;
- development and testing of hypotheses to account for the limits to the ecological and geographic distributions of species;
- development of methods for distinguishing the effects of coevolution and species assembly on the composition and structure of communities;
- development and testing of predictive theories on the coevolution of interacting species, including:
  - host/parasite interactions and the evolution of virulence and resistance in pathogens and their hosts;
  - mutualistic interactions, especially those involving microbial symbionts, including the stability of mutualisms and their role in community structure;
  - competition among species, including its importance and evolutionary consequences; and
  - diffuse coevolution—i.e., the evolutionary dynamics of complex interactions among multiple species.
- development and testing of theories on the effects of evolution on properties of ecosystems (e.g., productivity, nutrient turnover) and the effects of those properties on the physical environment.

## **VIII. MECHANISMS FOR MEETING THE CHALLENGES OF THE FUTURE**

If we are to realize the great promise that evolutionary biology holds for both basic and applied science and for education, we will need enhanced research funding, structural mechanisms, and educational foundations. The following suggestions and recommendations in each of these areas should speed progress toward the goals described in the preceding section.

### **A. Advancing Understanding through Research**

The rate of progress and the accomplishments of a science are fundamentally dependent on the level of funding for rigorous research and on the policies and mechanisms that govern its disposition. These include research initiatives, allocations to large collaborative efforts versus investigator-based programs, and permanent positions at universities and colleges, institutes, agencies, and corporations. Development of new directions in research needs to be deliberately fostered in order to overcome limitations of traditional sources of research funding to keep up with the potential for progress on both basic and applied fronts. These considerations lead to the following recommendations for promoting evolutionary research.

- **Interdisciplinary research.** Because evolutionary biology is inherently interdisciplinary, exchange of ideas, information, and techniques is important, both among the subdisciplines of evolutionary biology and between evolutionary biologists and researchers in other biological and nonbiological disciplines. We strongly urge that mechanisms be established for encouraging evolution as a central theme in interdisciplinary research, perhaps by sponsorship of annual workshops addressing interdisciplinary themes coordinated by appropriate national agencies or scientific societies. These workshops would be structured to provide for exchange of ideas and demonstration of techniques, and would be intended to foster research collaborations that might otherwise not develop. We would envision bringing evolutionary biologists together with researchers in such fields as developmental biology, neurobiology, endocrinology, microbiology, computer science, and many others.
- **Intensive training workshops.** Because of the rapid progress taking place in molecular technology, computing, data analysis, and other areas of evolutionary and other biological sciences, researchers can look forward to extended productive careers only by keeping abreast of new developments. We recommend the establishment of annual workshops devoted to intensive training in new techniques. Again, these workshops would be coordinated through appropriate funding agencies or scientific societies. The intent of these workshops differs from the explicit development of interdisciplinary research described in the previous item.

- **Maintain funding for individual-based research programs.** Considerable discussion has focused on the value of diverse research programs in individual laboratories, funded at a relatively modest scale, compared with large projects that require collaboration among numerous laboratories. In some fields of science, large-scale projects are the most effective, even essential. In evolutionary biology, certain large, coordinated efforts may indeed play important roles. Examples of such efforts include the development of databases for paleontologic, phylogenetic, and other data on biodiversity, data on human diversity and the like.  
 However, evolutionary biology, reflecting the diversity of its subject matter, has progressed due to the interplay of ideas, principles, and data issuing from individual researchers in each of its subdisciplines. We therefore affirm the preeminent value of individual-based research programs.
- **Recognize the contributions of both well-studied model systems and diverse systems.** Some fields of biology progress largely by focusing primarily on a few model systems, such as *E. coli* bacteria, *Caenorhabditis* nematodes, and *Arabidopsis* plants. Likewise, certain areas of evolutionary biology, such as population genetics, have achieved great progress by utilizing the voluminous information and techniques available for model systems such as *Drosophila*. Many other subdisciplines of evolutionary biology can likewise profit from research on model systems; for instance, evolutionary developmental biology will be furthered by comparative studies of the groups of organisms that include model organisms such as *Drosophila*, *Caenorhabditis*, and *Arabidopsis*. However, it is inherent in evolutionary biology, which aims to describe and understand the full history and diversity of organisms, that it cannot be restricted to a few model species. In order to understand the diversity of life and its implications for human endeavor, creative tension must be maintained between studies of well-understood models and explorations of the broader diversity of organisms.
- **Databases.** Much progress in evolutionary biology depends on analyzing data collected by numerous researchers. For example, databases of DNA sequences are extensively used not only by molecular but also by evolutionary biologists, and data on fossil occurrences are used not only by paleobiologists, but also by other biologists and even physicists interested in nonlinear dynamics. The evolutionary dimensions of environmental management, conservation, and the search for economically useful species will be greatly aided by accessible, widely shared databases on biodiversity, including information on geographic and ecological distributions, phylogenies, fossil occurrences, and museum and herbarium holdings. We support the development of such databases.
- **ILTER sites.** Ecologists have obtained important data from the Long-Term Ecological Research (ILTER) sites situated in several biomes in the United States through infrastructural and research support from NSF. In addition to providing data on long-term ecological and environmental changes, these sites are potential resources for researchers studying long-term genetic changes in populations, including changes in characteristics that mediate organisms' responses to climate change. Evolutionary biologists should be encouraged to take advantage of the special funding opportunities associated with ILTER sites to conduct carefully framed evolutionary studies.
- **Research centers for evolutionary biology.** We suggest that the community of evolutionary biologists discuss the advisability and feasibility of establishing one or more research centers for evolutionary biology. The major functions of such centers would be to (1) organize workshops of the kinds described above; (2) provide work space for visiting scientists in order to support data analysis, publication, and interaction among subdisciplines; (3) manage databases and electronic communication networks for evolutionary scientists; and (4) foster cross-disciplinary communication among the many subdisciplines of evolutionary biology.
- **Identifying a more explicit role for evolutionary biology in the missions of diverse federal agencies.** A large proportion of basic research in evolutionary biology in the United States is supported by the National Science Foundation. Without denying the legitimate need of other disciplines for greater funding commensurate with increasing costs and enhanced prospects for progress in those fields, we emphatically support efforts by NSF to obtain increased budgets for basic research in those biological sciences, including evolutionary biology, that are progressing to unprecedented levels of understanding. Basic and applied evolutionary research is intimately related to the missions of many funding agencies, because of its applications in health, agriculture, natural resources, and other social needs. We urge agencies to review the ways in which various subjects studied by evolutionary biologists may contribute to those agencies' missions. Appendix IV suggests research areas that are directly relevant to the goals of some federal agencies in the United States, as well as industry, private foundations, and some international agencies.

## B. Advancing Understanding through Education

Formal education both trains the nation's work force in each of the areas of specialized knowledge and methodology on which society depends and trains an informed citizenry that can make reasoned decisions and adapt to change. As science and technology change our world at an ever-increasing pace, it becomes steadily more important for people to understand and use information from the sciences, including biology. However, a report from the United States National Academy of Science (37) noted with concern that "teaching of science in the nation's public schools often is marred by [the] serious omission" of evolution. Because, as the report noted, evolution plays a central role in modern biological science and its applications to societal need, we provide the following recommendations for education, including both formal schooling and dissemination of information to the public:

- **Training of K–12 school teachers.** Excellent education at the elementary, middle, and high school levels is critical for all students. The inadequate preparation of elementary, middle, and high school students in the sciences is a widely recognized cause for national concern. The level of understanding of evolution and related subjects such as genetics is especially poor. Evolution is frequently given little or no coverage in high school biology curricula. Furthermore, many well-meaning, overworked teachers are unable to keep abreast of some of the most important progress in the field, and consequently provide inadequate coverage of the topic. We therefore recommend that agencies responsible for education increase their efforts toward the continuing education of teachers in evolutionary biology and related subjects by supporting summer courses and workshops that will be rewarded with professional advancement. We urge professional biologists to contribute to such efforts. Such courses should emphasize the process of scientific inquiry and critical thinking, the progress in concepts and information that the field has enjoyed, and the relevance of evolution to human life and societal needs. A variety of teaching materials are available for such programs.
- **College and university curricula.** Our comments concern course offerings for both biology majors and nonmajors. In many or most colleges and universities, a course on evolution is an elective, taken by a minority of biology majors, most of whom do not think it relevant to their medical or other careers. The majority of biology majors may have little exposure to evolution beyond a few weeks (or less) in an introductory biology course. This does not prepare them to recognize or understand the relevance of evolutionary concepts and information to human health, agriculture, environmental science, or even to research in molecular biology or other biological disciplines. Biology

departments in some leading universities (e.g., Cornell University, the University of Colorado, and the University of California) have recognized that evolutionary concepts are as fundamental and integral to the biological sciences as genetics and molecular biology, and have established a course on evolution as a requirement for biology majors. Because of the unifying role that evolution plays in biology, its relevance to the interpretation of data in all biological disciplines, its many demonstrated and potential applications to societal needs, and its position as one of the more important intellectual developments in the history of Western ideas, we strongly urge other colleges and universities to include a course on evolution among the requirements for biology majors.

Many biology departments offer nonmajors courses in critically important subjects such as genetics and ecology. For the reasons described above, evolution is an equally important element in an educated person's understanding of biology. Well taught, such a course will intrigue and excite students, and will provide them not only with a technical understanding of issues that affect their lives, but also with an enlightened perspective on social and philosophical issues and a heightened understanding of the living history of ideas. We urge, in the strongest terms, that a nonmajors course in evolution be made available in every college and university.

- **Inclusion of evolutionary science in specialized advanced training.** As this document has already made clear, elements of evolutionary biology are profoundly relevant to fields such as medicine, public health, law, agronomy, forestry, natural products chemistry, and environmental science. However, postbaccalaureate training in most of these fields often is devoid of coverage of even the simplest, most relevant evolutionary concepts, such as the nature and importance of genetic variation. Moreover, we have already noted that most students receive almost no education on evolution as undergraduates. We urge that professional schools and graduate programs in these fields incorporate relevant evolutionary material into their curricula.
- **Enhanced graduate training in evolutionary biology and its applications.** We noted above that training grants can contribute immeasurably to preparing graduate students for excellent, innovative research careers. Grants for doctoral research are equally important. In evolutionary biology, it is customary for Ph.D. students to do dissertation research that is thematically related to their advisor's research, but is not an integral part of the advisor's research projects and cannot be supported by the advisor's grants. This custom fosters independent thought, innovation, self-reliance, and learning beyond the advisor's sphere of knowledge, and it is



suitable for a field that takes biological diversity as its subject. There exist funding programs for Ph.D. research in NSF and some other agencies, but in a quantity incommensurate with the need and the prospective returns. We urge the establishment of dissertation support by agencies that presently do not provide it.

- **College and university faculty positions.** For both educational reasons and to promote the development of research excellence in modern biology, it is essential that biology departments of colleges and universities include faculty in several of the evolutionary subdisciplines. Faculty in evolutionary biology typically have a broad, interdisciplinary outlook that enhances communication with colleagues in other disciplines, and they very frequently attract some of the most outstanding graduate students in biology Ph.D. programs. Most importantly, evolutionary biology is an intellectually dynamic discipline that unifies biology and extends beyond it. Because it encompasses a variety of subdisciplines from molecular evolution to systematics and paleobiology, no one faculty member can have sufficient expertise to represent the entire discipline. Indeed, many universities harbor departments or programs with names such as “Ecology and Evolutionary Biology” that include specialists in several or many evolutionary subdisciplines. Emerging disciplines such as evolutionary developmental biology and evolutionary neurobiology need to be complemented by more traditional disciplines such as systematics and population genetics, which despite their maturity are addressing new questions with new methods and techniques.

### C. Advancing Understanding through Communication

- **Communication between the scientific community and federal agencies.** Evolutionary biologists need to communicate to federal agencies, and to other institutions that support basic or applied research, the relevance of evolutionary biology to the missions of those agencies.
- **A National Committee on Evolutionary Biology.** The exponential increase of research on many fronts has been accompanied by growth in the number of specialized societies, journals, and annual meetings, and by a tendency toward increased specialization in students’ research and perspectives. Efforts to counter these trends, such as joint meetings of the Society for the Study of Evolution, the Society of Systematic Biologists, the American Society of Naturalists, and the Society for Molecular Biology and Evolution, and symposia organized by the Paleontological Society, have been enthusiastically received, indicating broad interest in mechanisms that can unite the field. Moreover, evolutionary biologists recognize that it will be important

to be visible in their interactions with the public, with educators, and with governmental and private agencies that support research. We therefore suggest that the professional societies explore the desirability and feasibility of a jointly sponsored steering or advisory committee on evolutionary biology. The membership of this committee could be appointed and structured in much the same way as existing journal editorial boards. Its potential roles might include (1) establishing and maintaining an Internet site, linked to the sites of relevant scientific societies, for disseminating information of broad interest; (2) responding to queries from funding agencies about trends and needs in research, and communicating generally held views to such agencies; (3) helping to coordinate workshops and other mechanisms for advancing training and research; (4) making university administrators and other educators aware of educational and training needs; (5) communicating important advances to the media; (6) coordinating efforts to educate the public on evolutionary aspects of topics such as racism, genetic engineering, and the conflict between creationism and evolutionary science; and (7) keeping scientists aware of legislation relevant to evolutionary biology, and educating legislators and their staffs about evolutionary issues relevant to pending legislation. Such a Committee could be developed through a consortium of scientific societies, possibly initiated by a specific society, such as the American Society of Naturalists or the Society for the Study of Evolution.

- **Reorganization of foundational support for evolutionary research.** The largest share of basic research in evolutionary biology in the United States is supported by the National Science Foundation. Research grants in the several subdisciplines of evolutionary biology are awarded by numerous divisions and panels within NSF. This structure is suitable for funding research that lies squarely within many of the subdisciplines, but interdisciplinary proposals often face difficulty because some reviewers on the relevant panels are unfamiliar with the context into which the proposals fit. For example, research on the borders between paleobiology and evolutionary developmental biology, between molecular genetics and evolutionary ecology, or between population genetics and systematics may face “double jeopardy” in finding funding. On the other hand, recent success rates for NSF proposals jointly reviewed by Systematic Biology and Population Biology suggest that this problem is being addressed. Recent initiatives by NSF on “Integrative Research Challenges in Environmental Biology” and “Biocomplexity” are also directed toward providing more funding opportunities for interdisciplinary initiatives. We suggest that NSF consider follow up on such initiatives by establishing a more permanent unit, perhaps on “Biodiversity and Biotic Change,” that could comprehen-

sively address the spectrum of evolutionary research, including the interdisciplinary research that makes such conspicuous contributions to scientific progress.

- **Training grants for graduate education and research.** The health and progress of any discipline depends on the training of the graduate students who will be the next generation of researchers. To this end, there is need for an increase in grant opportunities for graduate student training and research to foster the broad basic and applied perspectives discussed here. Basic and applied research will most profit from training grants in interdisciplinary areas, applied evolutionary biology, and theoretical evolutionary biology. Training a generation of researchers at the interface between basic and applied evolutionary biology will have the added benefit of exporting evolutionary thinking into some applied disciplines in which the evolutionary perspective can enhance understanding.
- **Postdoctoral and mid-career opportunities.** Postdoctoral positions and mid-career research leaves are critical for enabling researchers to learn or develop new techniques or to initiate new research programs, especially those with an interdisciplinary or applied dimension. Support for postdoctoral and mid-career research positions currently falls far short of the need. Increasing the sources of such support will be important for progress in both basic and applied evolutionary biology.
- **Training in underdeveloped subjects.** In several important areas of evolutionary biology, the number of young scientists who will become the future corps of researchers is sorely inadequate. Perhaps the most conspicuous of these areas are (1) mathematical and statistical evolutionary biology, including modeling and data analysis; (2) systematic biology of groups of organisms that have been inadequately studied and/or include species of importance to human society (e.g., microorganisms, protists, algae, fungi, plants, insects, nematodes); and (3) evolutionary paleobiology, focusing on speciation and biodiversity. To address this critical need, Ph.D. students must be trained in these areas, and employment opportunities, such as positions in university and college biology departments, must be made available to them.
- **Public outreach and education.** The greatest challenge to evolutionary biologists, and to all scientists, is to communicate new and interesting information and concepts to the public at large. Evolutionary biology faces the additional challenge of reaching and convincing a portion of the public that is skeptical about, or even hostile to, the very concept of evolution. Although evolution is hardly controversial in many other countries, it is a politically and educationally

volatile issue in the United States (see Appendix I, “Evolution: Fact, Theory, Controversy”). Yet without its evolutionary foundation, biology cannot be a modern science, for however fully we describe biological phenomena, we cannot fully understand their causes except with reference to evolutionary processes and history. Without evolution, many of the potential applications of biology to societal needs will remain undeveloped and even unexplored. No issue in public education about biological matters holds greater urgency or importance than communicating the nature, implications, and applications of evolution.

In the strongest possible terms, we urge evolutionary scientists to become engaged with public education, and urge educational institutions to communicate the reality, vitality, and societal importance of evolution to the public. Possible vehicles for doing so include:

- Public talks to local school and citizens’ groups;
- Museum exhibits on modern evolutionary biology and the evidence for evolution;
- Press releases on exciting advances in evolutionary research;
- Letters to newspapers and magazines, and urging coverage of evolution in science columns;
- Monitoring textbooks and communicating reactions to publishers and school boards;
- Addressing television and radio audiences; and
- Supporting organizations that contribute to public education in biology.

## IX. CONCLUSION

Researchers in molecular and developmental biology, physiology, ecology, animal behavior, psychology, anthropology, and other disciplines continue to adopt the methods, principles, and concepts of evolutionary biology as a framework. Likewise, applied research in forestry, agriculture, fisheries, human genetics, medicine, and other areas increasingly attracts scientists trained in evolutionary biology. Evolutionary biologists have expanded their vision, addressing both basic questions throughout the biological disciplines and problems posed by society’s needs. As a result of both the rapid growth of this “evolutionary work force” and technological advances in areas such as molecular methodology, computing, and information processing, progress in evolutionary biology and related areas is more rapid now than ever before. With the appropriate and necessary support in education and research, the evolutionary disciplines will make ever greater contributions to applied and basic knowledge.

In the applied realm, evolutionary biologists are embracing their social responsibilities. There are many ways in which their discipline can help humanity:

- to understand and combat genetic, systemic, and infectious disease
- to understand human physiological adaptations to stresses, pathogens, and other causes of ill health
- to improve crops and mitigate damage by pathogens, insects, and weeds
- to develop tools for analyzing human genetic diversity as it applies to health, law, and the understanding of human behavior
- to use and develop biological resources in a responsible manner
- to remedy damage to the environment
- to predict the consequences of global and regional environmental change, and
- to conserve biodiversity and discover its uses.

In basic science, we stand at the threshold of:

- fully documenting biodiversity and describing the phylogenetic relationships among all organisms
- more completely understanding of the causes of major changes in the history of life
- discovering and explaining processes of evolution at the molecular level

- understanding how developmental mechanisms evolve and give rise to new anatomical structures
- elucidating the processes that both cause and constrain adaptations in physiology, endocrinology, and anatomy
- deriving a deeper understanding of the adaptive meaning and mechanisms of behavior, and
- developing a predictive theory of coevolution between species, such as pathogens, parasites, and their hosts, and of the effects of coevolution on populations and ecological communities.

Evolutionary biology plays a central role in the complexity of biological systems. Evolution is the source of biocomplexity. The continued and enhanced support of this field is critical to maximizing the nation's research progress in both basic and applied arenas. In terms of societal needs for the twenty-first century, the time to make the investment in evolutionary biology is now, while there is still time either to change current trends or to better prepare us to deal with their consequences. Current and projected population levels will result in increasing environmental impacts, increasing pressure on food production, ever greater challenges to biological diversity, and enhanced opportunities for the emergence of new diseases. A healthy scientific base in evolutionary biology is an essential element in preparing us to meet these issues. Evolutionary biology must be at the heart of the nation's research agenda in biology, just as it is at the heart of the field of biology.

## BIBLIOGRAPHY

1. Adams, M. W., A. H. Ellingboe, and E. C. Rossman. 1971. Biological uniformity and disease epidemics. *BioScience* 21:1067-1070.
2. Adey, N. B., T. O. Tollefsbol, A. B. Sparks, M. H. Edgell, and C. A. Hutchison III. 1994. Molecular resurrection of an extinct ancestral promoter for mouse L1. *Proc. Natl. Acad. Sci. U.S.A.* 91:1569-1573.
3. Beltran, P., and 10 others. 1988. Toward a population genetic analysis of *Salmonella*: genetic diversity and relationships among strains of serotypes of *S. choleraesuis*, *S. derby*, *S. dublin*, *S. enteridis*, *S. heidelberg*, *S. infantis*, *S. newport*, and *S. typhimurium*. *Proc. Natl. Acad. Sci. U.S.A.* 85:7753-7757.
4. Bishop, J. A., and L. M. Cook (eds.). 1981. *Genetic Consequences of Man Made Change*. Academic Press, London.
5. Bulmer, M. 1988. Evolutionary aspects of protein synthesis. *Oxford Surveys in Evolutionary Biology* 5:1-40.
6. Carroll, S. B. 1995. Homeotic genes and the evolution of arthropods and chordates. *Nature* 376:479-485.
7. Caugant, D., L. Mocco, C. Frasch, L. Froholm, W. Zollinger, and R. Selander. 1987. Genetic structure of *Neisseria meningitidis* populations in relation to serogroup, serotype, and outer membrane protein pattern. *J. Bacteriol.* 169:2781-2792.
8. Cavalli-Sforza, L. L., and M. W. Feldman. 1981. *Cultural Transmission and Evolution*. Princeton University Press, Princeton, NJ.
9. Cavalli-Sforza, L. L., P. Menozzi, and A. Piazza. 1994. *The History and Geography of Human Genes*. Princeton University Press, Princeton, NJ.
10. Cohen, M. L. 1992. Epidemiology of drug resistance: implications for a post-antimicrobial era. *Science* 257:1050-1055.
11. Coley, P. D., J. P. Bryant, and F. S. Chapin III. 1985. Resource availability and antiherbivore defense. *Science* 230:895-899.
12. Dawkins, R. 1976. *The Selfish Gene*. Oxford University Press, Oxford.
13. Dobzhansky, Th. 1962. *Mankind Evolving*. Yale University Press, New Haven, CT.
14. Doolittle, W. F., and C. Sapienza. 1980. Selfish genes, the phenotypic paradigm and genomic evolution. *Nature* 284:601-603.
15. Dubose, R. F., and D. L. Hartl. 1991. Evolutionary and structural constraints in the alkaline phosphatase of *Escherichia coli*. In R. K. Selander, A. G. Clark, and T. S. Whittam (eds.), *Evolution at the Molecular Level*, pp. 58-76. Sinauer, Sunderland, MA.
16. Dykhuizen, D. E. 1990. Experimental studies of natural selection in bacteria. *Annu. Rev. Ecol. Syst.* 21:393-398.
17. Ewald, P. W. 1994. *Evolution of Infectious Disease*. Oxford University Press, Oxford.
18. Friedlander, Y, E. M. Berry, S. Eisenberg, Y. Stein, and E. Leitersdorf, 1995. Plasma lipids and lipoproteins response to a dietary challenge - Analysis of four candidate genes. *Clinical Genetics* 47:1-12.
19. Futuyma, D. J. 1995. The uses of evolutionary biology. *Science* 267:41-42.
20. Garland, T., Jr., and P. A. Carter. 1994. Evolutionary physiology. *Annu. Rev. Physiol.* 56:579-621.
21. Halder, G., P. Callaerts, and W. J. Gehring. 1995. Induction of ectopic eyes by targeted expression of the eyeless gene in *Drosophila*. *Science* 267:1788-1792.
22. Hall, B. G. 1983. Evolution of new metabolic functions in laboratory organisms. In M. Nei and R. K. Koehn (eds.), *Evolution of Genes and Proteins*, pp. 234-257. Sinauer, Sunderland, MA.
23. Haviland, M. B., R. E. Ferrell, and C. F. Sing. 1997. Association between common alleles of the low-density lipoprotein receptor gene region and interindividual variation in plasma lipid and apolipoprotein levels in a population-based sample from Rochester, Minnesota. *Human Genetics* 99:108-114.
24. Heywood, V. H. (ed.). 1995. *Global Biodiversity Assessment*. United Nations Environmental Programme. Cambridge University Press, Cambridge.
25. Holland, J. 1992. *Adaptation in Natural and Artificial Systems*. MIT Press, Cambridge, MA.
26. Jermann, T.M., J. G. Opitz, J. Stackhouse, and S. A. Benner. 1995. Reconstructing the evolutionary history of the artiodactyl ribonuclease superfamily. *Nature* 374:56-59.
27. Johnson, T. E. 1990. Increased life-span of age-1 mutants in *Caenorhabditis elegans* and lower Gompertz rate of aging. *Science* 249:908-912.
28. Kareiva, P. M., J. G. Kingsolver, and R. M. Huey (eds.). 1993. *Biotic Interactions and Global Change*. Sinauer, Sunderland, MA.
29. Lander, E. 1996. The new genomics: global views of biology. *Science* 274:536-539.
30. Laskin, A. 1994. P 14 in L. R. Meagher and T. R. Meagher (eds.), *Leaping into the Future with Evolutionary Biology*. Rutgers University, New Brunswick, NJ.
31. McKenzie, J. A. 1996. *Ecological and Evolutionary Aspects of Insecticide Resistance*. Academic Press, San Diego.
32. McKenzie, J. A., and G. M. Clarke. 1988. Diazinon resistance, fluctuating asymmetry, and fitness in the Australian sheep blowfly. *Genetics* 120:213-220.
33. Meagher, L. R., and T. R. Meagher. (eds.) 1994. *Leaping into the Future with Evolutionary Biology: The Emerging Relevance of Evolutionary Biology to Applied Problems and Opportunities* [Report of a workshop.] Rutgers University, New Brunswick, NJ.
34. Meffe, G. K., and R. M. Carroll. 1997. *Principles of Conservation Biology*. Second edition. Sinauer, Sunderland, MA.
35. Montagu, A. 1974. *Man's Most Dangerous Myth: The Fallacy of Race*. Oxford University Press, London.
36. National Academy of Sciences - National Research Council. 1972. *Genetic Vulnerability of Major Crops*. National Academy Press, Washington, D.C.
37. National Academy of Sciences, Working Group on Teaching Evolution. 1998. *Teaching About Evolution and the Nature of Science*. National Academy Press, Washington, D.C.
38. National Research Council. 1993. *A Biological Survey for the Nation*. National Academy Press, Washington, D.C.
39. Nei, M., and A. L. Hughes. 1991. Polymorphism and evolution of the major histocompatibility complex loci in mammals. In R. K. Selander, A. G. Clark, and T. S. Whittam (eds.), *Evolution at the Molecular Level*, pp. 222-247. Sinauer, Sunderland, MA.
40. Nei, M., and A. K. Roychoudhury. 1982. Genetic relationship and evolution of human races. *Evolutionary Biology* 14:1-59.
41. Nesse, R. M., and G. C. Williams. 1994. *Why We Get Sick: The New Science of Darwinian Medicine*. Times Books, NY.
42. Neu, H. C. 1992. The crisis in antibiotic resistance. *Science* 257:1064-1073.
43. Nollar, H. F. 1984. Structure of ribosomal RNA. *Annu. Rev. Biochem.* 53:119-162.
44. North, D. C. 1990. *Institutions, Institutional Change, and Economic Performance*. New York: Cambridge University Press.
45. Nowak, M. A., R. M. May, and R. M. Anderson. 1990. The evolutionary dynamics of HIV-1 quasiespecies and the development of immunodeficiency disease. *AIDS* 4:1095-1103.
46. Orgel, L. E., and F. H. C. Crick. 1980. Selfish DNA: the ultimate parasite. *Nature* 284:604-606.
47. Pimentel, D., and nine others. 1992. Environmental and economic costs of pesticide use. *BioScience* 42:750-760.

48. President's Committee of Advisors on Science and Technology. 1998. *Teaming with Life: Investing in Science to Understand and Use America's Living Capital*.
49. Raymond, M., A. Callaghan, P. Fort, and N. Pasteur. 1991. World-wide migration of amplified insecticide resistance gene in mosquitoes. *Nature* 350:151-153.
50. Reznick, D., H. Bryga, and J. A. Endler. 1990. Experimentally induced life-history evolution in a natural population. *Nature* 346:357-359.
51. Rick, C. M., and R. T. Chetelat. 1995. Utilization of related wild species for tomato improvement. *Acta Horticulturae* 412:21-38.
52. Ricklefs, R. E., and D. Schluter (eds.). 1993. *Species Diversity in Ecological Communities*. University of Chicago Press, Chicago.
53. Rose, M. R. 1991. *The Evolutionary Biology of Aging*. Oxford University Press, Oxford.
54. Roush, R. T., and B. E. Tabashnik (eds.). 1990. *Pesticide Resistance in Arthropods*. Chapman and Hall, NY.
55. Sepkoski, J. J., Jr. 1997. Biodiversity: past, present, and future. *Journal of Paleontology* 71:533-539.
56. Sing, C. F., M. B. Haviland, A. R. Templeton, and S. L. Reilly. 1995. Alternative genetic strategies for predicting risk of atherosclerosis. In F. P. Woodford, J. Davignon and A. D. Sniderman (eds.), *Atherosclerosis X. Excerpta Medica International Congress Series*, pp. 638-644. Elsevier, Amsterdam.
57. Systematics Agenda 2000: Charting the Biosphere. 1994. Dept. of Ornithology, American Museum of Natural History, New York.
58. Templeton, A. R. 1995. A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping or DNA sequencing. V. Analysis of case/control sampling designs: Alzheimer's disease and the apolipoprotein E locus. *Genetics* 140:403-409.
59. Templeton, A. R., and B. Read. 1983. The elimination of inbreeding depression in a captive herd of Speke's gazelle. In C. M. Schonewald-Cox et al. (eds.), *Genetics and Conservation*, pp. 241-261. Benjamin Cummings, Menlo Park, CA.
60. Tiedje, J. M., R. K. Colwell, Y. L. Grossman, R. E. Hudson, R. E. Lenski, R. N. Mack, and P. J. Regal. 1989. The planned introduction of genetically engineered organisms: ecological considerations and recommendations. *Ecology* 70:298-315.
61. Travis, J., and D. J. Futuyma. 1993. Global change: lessons from and for evolutionary biology. In P. M. Kareiva, J. G. Kingsolver, and R. M. Huey (eds.), *Biotic Interactions and Global Change*, pp. 251-263. Sinauer, Sunderland, MA.
62. Ullstrup, A. J. 1972. The impacts of the southern corn leaf blight epidemics of 1970-1971. *Annu. Rev. Phytopathol.* 10:37-50.
63. Wagner, G. P. 1996. Homologues, natural kinds, and the evolution of modularity. *Am. Zool.* 36:36-43.
64. Ward, J. W., and 14 others. 1989. The natural history of transfusion-associated infection with human immunodeficiency virus: factors influencing the rate of progression to disease. *New England J. Med.* 321:947-952.
65. Weiss, K. M. 1993. *Genetic Variation and Human Disease*. Cambridge University Press, Cambridge.
66. White, F. N. 1989. Temperature and acid-base regulation. *Adv. Anesth.* 6:67-96.
67. Williams, R. J., and D. L. Heymann. 1998. Containment of antibiotic resistance. *Science* 279:1153-1154.

## APPENDIX I

### EVOLUTION: FACT, THEORY, CONTROVERSY

When biologists refer to the theory of evolution, they use the word “theory” as it is used throughout science. It does not mean a mere speculation or an unsupported hypothesis. Rather, as *The Oxford English Dictionary* puts it, “a hypothesis that has been *confirmed* or *established* by observation or experiment, and is propounded or accepted as accounting for the known facts; a statement of the *general laws, principles, or causes* of something known or observed” (our italics). The complex body of principles that explain evolutionary change is a theory in the same sense as “quantum theory” in physics or “atomic theory” in chemistry: it has been developed from evidence, tested, and refined, and it accounts for literally thousands of observations made throughout the entirety of biological science and paleontology.

Like *all* scientific theories, the theory of evolution is a *current best explanation*. It has withstood innumerable tests and attempts to disprove it, but it is still being refined, modified in the light of new knowledge, and extended to account for newly discovered phenomena. The theory of genetics has had such a history, progressing from Mendel’s simple early principles to the complex body of molecular principles that constitute today’s theory of inheritance, and it is constantly being refined and modified, even though its core principles have remained valid for a century. So it is with the theory of evolution.

Is evolution also a fact? All but the most trivial facts begin as untested hypotheses—such as the hypothesis that the earth revolves around the sun. They acquire “facthood” as more and more evidence accrues in their favor, and as they withstand attempts to refute them. The evidence and attempt at refutation may take many forms besides simple observations; indeed, the most powerful evidence is not mere observations, but conformity to predictions that the hypothesis makes about what we should see if the hypothesis is true or false. We do not observe the earth making a circuit around the sun; we accept this hypothesis because of the numerous, verified astronomical observations—and more recently observations from spacecraft—that conform to the predictions of the hypothesis. So Copernicus’s hypothesis is now a fact—a statement supported by so much evidence that we use it as if it were true.

Biologists accept as fact that all organisms, living and extinct, have descended, with innumerable changes, from one or at most a few original forms of life. For Darwin in 1859, this was a hypothesis, for which he provided abundant evidence from comparative anatomy, embryology, behavior, agriculture, paleontology, and the geographic distributions of organisms. Since that time, all of the many thousands of observations in each of these areas have supported Darwin’s core hypothesis. To these observations has been added copious evidence that Darwin could hardly have dreamed of, especially from paleontology and molecular biology. A century’s accumulation of such evidence establishes *descent, with modification, from common ancestors* as a fact of science. How we explain this fact—what the principles and causes of it may be—is the *theory* of evolutionary process, parts of which are subject to various amounts of scientific debate, modification, and extension.

To claim evolution as a fact is to confront controversy, for probably no claim in all of science evokes as much emotional opposition as biological evolution. Nonetheless, no scientific hypothesis other than common descent with modification can account for and make predictions about the unity, diversity, and properties of living organisms. No other hypothesis of the origin of biological diversity is supported by such overwhelming evidence, and no competing hypothesis spawns such richness of scientific study and has as many implications for the biological sciences and their applications to societal needs.

### EVOLUTION AND SPIRITUAL BELIEF: A NECESSARY CONFLICT?

The theory of evolution is controversial because it is perceived by some people to be incompatible with religious beliefs, especially about human nature and origins. The so-called creationist opposition to evolution is so vocal in the United States that it has threatened federal funding of evolutionary research, despite its basic scientific value and numerous applications. Equally importantly, it has driven public school systems to minimize education in evolutionary science, contributing to widespread scientific illiteracy. (A 1988 study of teenagers’ command of science worldwide ranked Americans in the lowest 25 percent, behind students in countries such as Japan, England, and Hungary.) More than half of Americans believe that humans were created in their present form about 10,000 years ago, even though the reality of evolution—including human evolution—has not been seriously controversial among scientists for almost a century (37).

Priests, ministers, rabbis, and Pope John Paul II have affirmed the validity of evolutionary science while also affirming the spiritual validity of the Bible’s teachings. Some clergy indeed teach about evolution and even do evolutionary research. Evolutionary biologists themselves include atheists, agnostics, and devout participants in various religions. Most theologians seem to agree that whether or not belief in God and acceptance of evolution are compatible is a matter of individual decision. Most evolutionary biologists agree that issues of spiritual belief cannot be decided by science, which by its nature is limited to determining natural observable causes, cannot pronounce on supernatural matters, and cannot provide answers to ultimate philosophical or ethical questions.

This last point needs emphasis. Anti-evolutionists have charged that evolution robs society of any foundation for morality and ethics, and that it teaches a materialistic world view, which would justify the principle that might makes right. But evolutionary science has never taught any such thing, and if properly exercised, cannot teach any such thing, for science in itself has no moral or ethical content, for good or ill. Whether the science be physics or evolutionary biology, it teaches us only what the observable world is like and how it works. Such sciences as physics, chemistry, geology, physiology, and neurobiology, exactly like evolutionary biology, admit no supernatural causes for the actions of atoms, the sun’s energy, the health or ills of the human body, or the powers of the human brain. These sciences recognize only natural, material causes, and we rely on their naturalistic theories when we build airplanes, synthesize new plastics, listen to weather reports, or consult our doctors. We would no more apply religious principles to these activities than we would seek moral guidance from medical doctors, engineers, or chemists. So it is with evolutionary science: no more nor less materialistic than any other science, it offers no moral guidance, only dispassionate analysis of how biological systems function and came to be. What use we make of such information is for individuals and society to decide.

## APPENDIX II

### HOW THIS DOCUMENT WAS PRODUCED

At the invitation of their respective society presidents, representatives\* from the American Society of Naturalists (ASN), the Society for the Study of Evolution (SSE), the Society for Molecular Biology and Evolution (SMBE), the Ecological Society of America (ESA), the Society of Systematic Biologists (SSB), the Genetics Society of America (GSA), the Animal Behavior Society (ABS), and the Paleontological Society (PS) met in Indianapolis, Indiana, on April 22-23, 1995, to discuss the need for preparation of a report defining the challenges and opportunities facing the science of evolution. The purpose of this document would be to serve as a statement of the nature and importance of the field for use by policymakers, educators, and scientists alike.

A working committee representing the major disciplines in evolutionary biology was convened to draft a working document to be presented to the memberships of our respective societies. Co-chairs D. Futuyma (editorial) and T. Meagher (organizational) were elected at the April 1995 workshop to draft proposals to seek funding to support workshops to develop the report and to coordinate and oversee its writing and publication. The project has been supported by the A. P. Sloan Foundation and the National Science Foundation. Announcements of the existence of the working committee and its charges were made in *The American Naturalist*, *Ecology*, *Evolution*, *Genetics*, *Molecular Biology and Evolution*, and *Science*.

The working committee met in October 1995 (in Lawrenceville, NJ) and March 1996 (in Chicago, IL) to discuss the content of the report and to distribute writing and research assignments. Between meetings, regular contact was maintained among working group members via email. The report has been distributed to the executive councils of the relevant scientific societies for feedback in 1996–1997, and a copy of the document was posted on the World Wide Web in 1997 for inspection and feedback by the scientific community at large, with announcements and access information placed in several of the above-mentioned journals. A final meeting of the working group took place in April 1997 (in Palo Alto, CA) to address issues of overall balance in the final document and to appoint a smaller working group to oversee final publication of the report.

## APPENDIX III

### GLOSSARY OF FREQUENTLY USED TERMS

**Allele:** One of several alternative forms of a gene, differing from other forms in nucleotide sequence, and usually in its effect on some character.

**Allele frequency:** The proportion of gene copies in a population that are a specific allele. If the population has  $N$  individuals, each with 2 gene copies, the total number of genes in the population is  $2N$ .

**Biodiversity:** The number of alleles or taxa in a specified geographic area (ranging from a local region to the whole earth). The number of taxa is often referred to as “*taxonomic diversity*” or, simply, “*diversity*.”

**Character:** A specific feature, e.g., “molar teeth.” A *character state* is one of several alternative conditions of a feature, e.g., the specific number of molars. A *quantitative character* varies continuously (e.g., weight) rather than discretely, usually because of the effects of both the environment and the action of several or many genes, hence the term “*polygenic*” character.

**Coalescent theory:** A body of population genetics theory that uses relationships among DNA sequences to infer the evolutionary processes that have affected genes and populations.

**Development:** The changes that an individual organism undergoes during its lifetime, from egg, seed, etc., through maturity to death.

**Extinction:** The death of all individuals in a local population, a species, or a higher taxon.

**Fitness:** The contribution to the next generation of a genotype, relative to that of other genotypes, reflecting its probability of survival and its reproductive output.

**Fixation:** The state of an allele that replaces all other alleles in a population, so that its frequency is 1 (i.e., 100%).

**Fossil:** Any recognizable trace of an ancient organism preserved in a geologic deposit.

**Gamete:** A cell, such as an egg or sperm, that unites with another cell to form a new organism.

**Gene:** A unit of heredity, usually a sequence of DNA that encodes a protein or other product that influences the development of one or more characters. Each amino acid in a protein chain is encoded by one or more specific triplets made up of four kinds of nucleotide bases.

**Gene flow:** The movement of genes from one population into another (usually of the same species) resulting from movement of individuals or their gametes.

**Genetic drift:** Random changes in the frequencies of alleles within a population due to random sampling of genes.

**Genotype:** A specific combination of alleles at one or more loci. Organisms such as humans carry two copies of each gene at each of most loci (one from the mother and one from the father); the genotype at a given locus is *homozygous* if the two copies are the same allele, and *heterozygous* if they are different alleles.

**Locus (pl., loci):** The site on a chromosome occupied by a gene; this term is often used to refer to the gene itself.

**Mass extinction:** A large increase in the number of extinctions (with a concomitant decline in diversity) over a geologically short interval of time (years to many thousands of years).

**Mutation:** Alteration of the DNA sequence of a gene; hence, the origin of a new allele.

**Neutral alleles:** Two or more alleles that do not differ in their effect on fitness. Such alleles are said to be “*selectively neutral*.”

**Phenotype:** An observable characteristic(s) of an organism, e.g., eye color, respiration rate, number of offspring produced. Both genetic and environmental factors often determine the phenotype.

**Phylogeny:** The historical pattern of branching, produced by speciation or population isolation, that has resulted in a diversity of taxa or differentiated populations.

**Pleiotropy:** The effects of a single gene on more than one character.

**Polymorphism:** The presence in a population of two or more alleles at a given genetic locus.

**Population:** A local group of individuals of a species; in sexually reproducing organisms, the members of a population interbreed with each other more frequently than they do with members of other populations.

**Selection:** Shorthand for “*natural selection*,” i.e., consistent differences in the rate of survival or reproduction between different genotypes or alleles due to differences in the phenotypes they produce.

**Species:** As used by most evolutionary biologists, a species is a population of organisms that actually or potentially exchange genes by interbreeding, and which are reproductively isolated from other such populations by biological differences that reduce or prevent gene exchange. *Speciation* is the origin of two or more species by the division of an ancestral species into reproductively isolated populations.

**Taxon (pl., taxa):** A named entity in biological classification, such as a species (e.g., *Homo sapiens*) or an order (e.g., Primates). A *higher taxon* is one above the species level (e.g., a genus or family), and ideally represents a group of species that have descended from their most recent common ancestor.

\* Douglas Futuyma (ASN), Leslie Real (ASN, ESA), Thomas Meagher (SSE), Walter Fitch (SMBE), Carol Lynch (SSE), Linda Maxson (SMBE), Charles Langley (GSA), J. John Sepkoski, Jr. (PS), Zuleyma Tang-Martinez (ABS) and Michael Donoghue (SSB), Mark Courtney observing for NSF.

## APPENDIX IV.

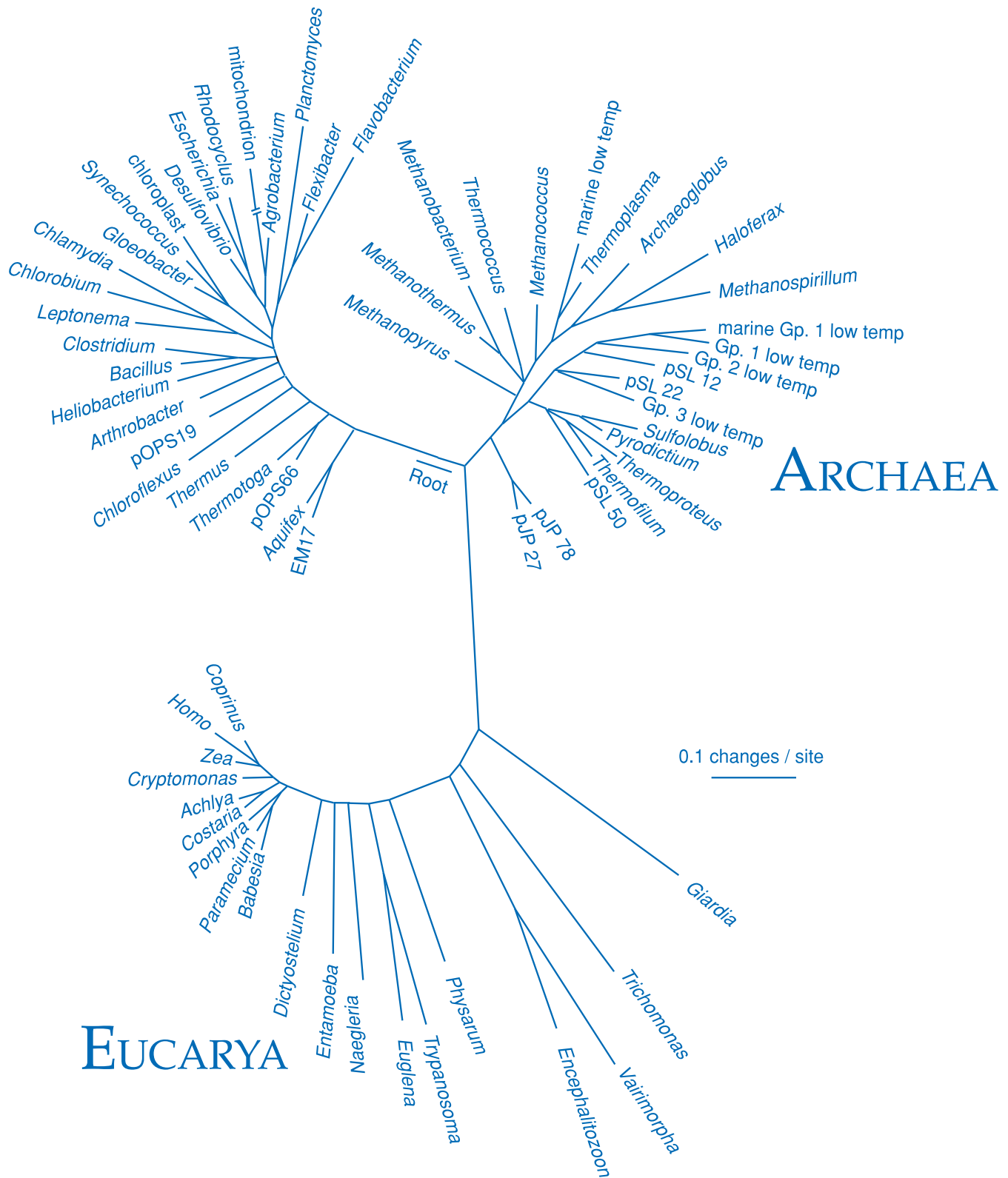
### MATCHING EVOLUTIONARY RESEARCH TO AGENCY MISSIONS

We have described the emergence of a field of applied evolutionary biology, which includes research that is immediately directed toward societal needs as well as basic research that is clearly prerequisite to developing applications. Progress in these areas is closely related to the missions of diverse agencies, and will clearly contribute to their needs and goals. Certain agencies, such as the National Science Foundation, indeed do support research in some of the subdisciplines of evolutionary biology. However, many of those listed below have funded little of the evolutionary research that could advance their goals. Examples of possible matches between agencies and evolutionary research areas relevant to their missions include:

- **National Institutes of Health (NIH):** Evolution and diversity of genome organization; molecular evolution; population genetic theory; QTL (quantitative trait loci) mapping; evolution of developmental mechanisms; evolutionary morphology and physiology; mechanisms of adaptation to environmental stresses; coevolution (of pathogens or parasites and hosts); numerical and analytical techniques for using molecular data; genetic epidemiology; genetic diagnostics; evolution of drug resistance in microorganisms; human variation; evolutionary approaches to the biological basis of human behavior; mechanisms of behavior related to cognitive function; hormonal function and its effects on behavior.
- **U.S. Department of Justice:** Genetic identification; population genetics of molecular polymorphisms; analytical methods.
- **U.S. Department of Agriculture (USDA):** Genetic variation and QTL mapping of characters of plants; molecular evolution and developmental evolution in plants; plant breeding systems; evolutionary physiology of plants, domesticated animals, and insects; natural pest resistance in wild plants; genetics, ecology, behavior, and systematics of plants, insects, nematodes, fungi, and other plant pathogens; parasite/host coevolution; genetics and evolutionary ecology of soil organisms; evolution of resistance to natural toxins and synthetic pesticides and herbicides; statistical and numerical data analysis.
- **Environmental Protection Agency (EPA):** Genetics, ecology, and evolution as applied to bioremediation; microbial evolution; adaptation to global and local environmental change; genetics and adaptability of small and/or threatened populations; biodiversity (including systematics, biogeography, evolution of species interactions, and paleobiology of community change).
- **U.S. Department of the Interior:** Bioremediation of damaged environments; evolutionary genetics and physiology of forest and fishery resources; adaptation to global and local environmental change; genetics and adaptability of small and/or threatened populations; evolution of life histories and breeding systems of harvested populations; biodiversity analysis (e.g., inventory, systematics, biogeography, remote habitat sensing, species interactions); theoretical, statistical, and numerical methods.
- **Department of Defense (DOD):** Systematics, genetics, and evolutionary ecology of parasites, pathogens, and disease vectors; systematics and evolutionary ecology of marine organisms; adaptation to global change, past and present; genetic characterization of individuals via DNA fingerprinting.
- **National Air and Space Administration (NASA); National Oceanographic and Atmospheric Administration (NOAA):** Biodiversity analysis of vegetation and marine systems (including systematics, biogeography, evolutionary ecology); effects of species composition, species interactions, and genetic variation on ecosystem processes; adaptation to global and local environmental change; paleobiological studies of communities and environments; statistical and analytical methods; origins of life and exobiology; adaptation to extreme environments.
- **World Health Organization:** Epidemiology and biogeography of disease; evolution of disease resistance; emergence of new diseases; ecological and evolutionary relationships between diseases and their vectors.
- **UNESCO (UNEP-United Nations Environmental Programme):** UNEP's support of biodiversity surveys can be strengthened by basic research into the origin and stability of biodiversity at levels from gene frequencies within populations to numbers of species to variation in habitats and ecosystems. The UNEP *Global Biodiversity Assessment* cites the importance of paleobiological studies of biological responses to global change, and it outlines the importance of evolutionary biology to our understanding of biodiversity and its management (24).
- **Industry:** The descriptions above of past and potential applications of evolutionary science to such goals as bioremediation, natural products development, and biotechnology make it clear that various industries will find it useful to support research in such areas as comparative analysis of genes and genomes; QTL mapping of microorganisms; evolutionary genetics of transgenic organisms and their interactions with wild species; coevolution in microbial systems; adaptability and evolutionary ecology of soil organisms, weeds, and pest species; evolution of resistance to antibiotics, pesticides, and herbicides; adaptive analyses of the chemical properties of plants and other species; systematics and biodiversity of microorganisms, plants, and other species.
- **Private foundations:** Private foundations can play a critical role in launching research in directions that may not be readily funded by federal agencies. Within this category, proposals for research that is truly innovative and therefore "high risk/high gain" in nature; that is interdisciplinary, and likely to fall between the traditional areas funded by public agencies; or that is out of fashion (perhaps because it entails amassing more data on traditional subjects) are especially likely to benefit from the flexibility that private foundations often can exercise.



# BACTERIA



Universal phylogenetic tree showing the relationships among Bacteria (e.g., most bacteria and blue-green algae), Archaea (e.g., methanogens and halophiles) and Eucarya (e.g., protists, plants, animals, and fungi).



Cover

Mark Spencer/Auscape. Reef scene of sea fans, crinoids, and soft corals, Coral Sea, Australia

Deane Bowers, University of Colorado–Boulder. Baltimore Checkerspot butterfly (*Euphydryas phaeton*), Eastern United States

DNA, Rutgers University photo archives

Jonathan Adrain, Natural History Museum, London. Whiterock fauna (Lower Silurian Period) fossil trilobite (*Exallaspis coronata*), W. Midlands, England

Mary E. Eaton/NGS Image Collection. Devil's bit (*Chamaelirium luteum*). Reproduced with permission from *The Book of Wild Flowers*. ©1924, National Geographic Society

Inside Covers

John Weinstein, Field Museum of Natural History, and David Jablonski, University of Chicago. Fossil crinoids, Cretaceous Period (85 million years old), Kansas GEO85594c

Page 4

Julie Margaret Cameron, c/o Clements Museum, University of Michigan. *Carte de visite* photograph of Charles Darwin (1874)

Page 7

Charles W. Myers, American Museum of Natural History. Poison-dart frog (*Phyllobates terribilis*), Colombia, South America

Page 8

National Museum of Kenya, c/o Craig S. Feibel, Rutgers University. 1.9-million-year-old hominid skull (*Homo habilis*), Koobi Fora, Rift Valley, Africa

Page 10

Drawn by R.L. Lampman. Reprinted with permission from R.L. Metcalf in R.L. Metcalf and W.H. Luckman (eds.), *Introduction to Insect Pest Management*. Third Edition, p. 251, copyright 1994 by John Wiley and Sons, N.Y.

Page 12

Aravinda Chakravarti, Case Western Reserve University. Cystic fibrosis gene frequency map

Page 21

Sean B. Carroll, University of Wisconsin. *Hox* gene organization and expression in *Drosophila* and mouse embryos. Reproduced with permission from S.B. Carroll et al., 1995. *Homeotic genes and the evolution of arthropods and chordates*. *Nature* 376:479-485. ©1995, Macmillan Magazines Ltd.

Page 22

R. Kellogg, c/o Annalisa Berta, San Diego State University. Line drawing of archaeocete (fossil whale) skeleton. Abstracted with permission from A. Berta, 1994. *What Is a Whale?* *Science* 263:180. ©1994, American Association for the Advancement of Science

Page 46

Norman R. Pace, University of California–Berkeley. Universal phylogenetic tree based on ribosomal RNA sequence differences. reproduced with permission from N.R. Pace, 1997. *A Molecular View of Microbial Diversity and the Biosphere*. *Science* 276:734-740. ©1997, American Association for the Advancement of Science

