The Best and the Worst of Times for Evolutionary Biology

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The 21st century will offer great opportunities, but also challenges, for the field of evolutionary biology, particularly in areas related to molecular genetic technologies, the environment, biodiversity, and public education. The coming decades promise to be both the best and the worst of times for the evolutionary disciplines.

Keywords: biodiversity, environment, genetic engineering, education, natural history

It was the best of times, it was the worst of times, it was the age of wisdom, it was the age of foolishness, it was the epoch of belief, it was the epoch of incredulity, it was the season of Light, it was the season of Darkness, it was the spring of hope, it was the winter of despair....

—Charles Dickens, *A Tale of Two Cities*

These evocative sentiments from Charles Dickens's classic (1859) appeared in the same year as Charles Darwin's *On the Origin of Species.* They also encapsulate the feelings of many natural historians about the state of evolutionary biology at the beginning of the 21st century (Avise 2001a, Wilson EO 1994, 2002). My intent here is to explain how there can be such conflicting emotions about the current state of biology and to elaborate on some glorious opportunities as well as daunting challenges for the science of evolutionary genetics in the coming years. I will concentrate on recent discoveries and technological breakthroughs in molecular biology and on how these affect humankind's capability to describe, understand, and in some cases even manipulate evolutionary genetic processes.

An example of how this is the best of times for evolutionary biology is provided by the recent elucidation of a draft sequence of all 3-billion-plus nucleotide pairs in the human genome (Lander et al. 2001, Venter et al. 2001). This achievement, which will stand forever as a milestone in the history of science, is a crucial step toward someday deciphering the metabolic and physiological functions of proteins and RNA molecules encoded by the approximately 40,000 human genes. If even a modest fraction of the scientific and media hoopla surrounding the genome project proves justified, not only will medical breakthroughs accrue rapidly, but so too will conceptual revelations about how evolution has forged intra- and intergenomic processes. I discuss some of these processes later in this article.

Large-scale genetic profiling (such as by microarray techniques and comparative genomic sequencing) will help to identify and characterize the genes that influence traits at the levels of metabolism, physiology, and morphology. From such approaches the long-sought Holy Grail of evolutionary biology—a fuller understanding of the causal links from genotype to phenotype—will gradually be achieved. In the first century following Darwin and Mendel, the basic driving forces of evolution were elucidated through observations on natural history, and the fundamental principles of heredity were uncovered by monitoring patterns of genetic transmission of traits in a few species that could be bred readily under controlled conditions. In this, the second post-Darwin, post-Mendel century, which could be characterized as the age of molecular biology, scientists finally have obtained direct access to the genetic mechanisms of evolutionary change in all species.

Editor's note: This article is based on a speech given by the author to a public education colloquium on evolution held in Otzenhausen, Germany, during the week of 18 March 2002.

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In the 1968 science fiction film *2001: A Space Odyssey,* by Stanley Kubrick and Arthur C. Clarke, several astronauts and a supercomputer named HAL were sent on a grand mission to explore the solar system. In real life in the 1960s, some of the earliest molecular genetic approaches were introduced to evolutionary studies (Margoliash 1963, Harris 1966, Lewontin and Hubby 1966, Avise 1994), and in 2001 the first complete sequence of the human genome was analyzed (with extensive computer assistance). These achievements ushered in an exploratory era of science nonfiction (it could be named *2001: An Inner Space Odyssey)* that is turning out to be as intellectually fascinating as the outer space odyssey envisioned by Kubrick and Clarke.

Another source of promise (but also trepidation) began in the early 1970s when researchers constructed the first recombinant DNA molecules *in vitro* (Jackson et al. 1972). Building on this technological breakthrough, molecular geneticists have gained unprecedented powers to reshape life. Now researchers routinely identify genes for a variety of biological functions, modify and reassemble these genes in test tubes, insert the recombinant DNA molecules into living cells, and thereby swap genetic material freely among any living species. Hundreds of plant, animal, and microbial species have been engineered to carry designer genes from foreign sources, and many of these transgenic organisms already have played or soon will play huge roles in medicine, pharmacology, environmental bioremediation (e.g., cleaning up toxic wastes), animal husbandry, and agriculture (Avise 2004).

Some prognosticators believe that the application of recombinant DNA methods to gene therapy and gene replacement (the repair or replacement of defective genes in the body) soon may lead to a revolution in the history of medicine comparable to the introductions of sanitation, anesthesia, and antibiotics and vaccines. If the new recombinant gene technologies live up to their early billing, we or our children might see a day when gene therapy can alleviate sickle cell anemia, heart disease, cancer, or various other human genetic disorders. Just as we may marvel at our forebears' fortitude in the dark ages before the advent of our modern medicine, our grandchildren may look back with marvel at our fortitude in the era preceding the wide availability of gene therapies. Nonetheless, the technical hurdles remain daunting. Although more than 400 experimental gene-replacement trials have been conducted within the last decade (involving a total of about 4000 human subjects), there are few if any definitive medical success stories to date, and the entire discipline is under intense scrutiny by advocates and critics alike (Lyon and Gorner 1995, Anderson 2000, Pfeifer and Verma 2001).

Even more daring is the proposal that genetic engineering soon might be extended to cells in the human germ line (Stock and Campbell 2000). In contrast to somatic gene therapy, which directly affects only the individuals receiving the procedure, the intent of germ-line engineering is to alter the human gene pool in subsequent generations as well. Obvious candidates for germ-line engineering are alleles that produce terrible genetic disorders such as cystic fibrosis or Huntington's disease. Who will object if molecular means can be found to reduce human suffering by correcting such conditions? But also, who will favor efforts to engineer in one's children germ-line genes for cosmetic features, such as height or athletic ability, or for higher IQ?

In the first half of the 20th century, several eugenics movements around the world exalted the notion that *Homo sapiens* could be bettered by selective breeding. Such efforts came to a nadir in Nazi Germany, where racial extermination was the purported means to improve humanity's gene pool. Purposeful germ-line manipulation must therefore be preceded by extensive ethical discussion by a broad cross section of society. Such initiatives will have to also distance themselves from ill-conceived eugenics movements of the past.

Experts agree that we currently find ourselves in the midst of one of the largest mass extinction sagas in the history of life.

Recombinant DNA technologies are a double-edged sword in other arenas as well. One dangerous possibility is the production of biological weapons (Fraser and Dando 2001, Knobler et al. 2002). In principle, it would be quite easy for someone with nefarious motives to mix and match genes from different species and thereby engineer deadly microbes invulnerable to conventional drugs. Even well-meaning scientists might create ghastly strains accidentally. This sobering prospect recently became more plausible after a poliovirus was (deliberately) synthesized chemically *ex nihilo,* using genetic information from a publicly available database (Cello et al. 2002). Another frightening viral strain was engineered to contain a mixture of genes from the dengue fever and hepatitis viruses (Pickrell 2001). In yet one more instance of alarming use of recombinant DNA methods, pathenogenicity was inadvertently enhanced experimentally in a mouse analogue of the human smallpox virus (Finkel 2001). Any release or escape of such deadly organisms could have grave consequences.

There are other reasons to fear that the 21st century could be the worst of times for biology. Ecologists and natural historians are painfully aware that the subject matter of their devotion—biodiversity—is under assault worldwide as the continents fill with people. The collective weight of human activities is leading to the disappearance of wilderness. Atmosphere and oceans are being polluted, marine fisheries are collapsing worldwide, and wetlands and freshwater aquifers have shrunk dramatically. In short, Earth's renewable and nonrenewable resources are being tragically squandered. In the Amazon Basin, for example, which is famous for its rich biota, slash-and-burn fires are so numerous that their light is visible to astronauts in the space shuttle. Some of these astronauts have felt moved to speak in a deeply spiritual tenor about the beauty of the "blue planet" and to bemoan how we are despoiling this special, fragile place.

Experts agree that we currently find ourselves in the midst of one of the largest mass extinction sagas in the history of life. Species are being lost at rates at least 100-fold higher than they were before the coming of humanity, with total losses by century's end projected to be somewhere between 10 and 50 percent of Earth's now-living biota. This biological holocaust has been unrivaled since the time, 65 million years ago, an asteroid struck the planet and precipitated a global winter. Biologists affected by biophilia (Wilson EO 1984)—a deep emotional attachment to nature—grieve that biodiversity is now entering another winter of despair.

Where can evolutionary science help?

Against this backdrop of conflicting emotions about the state of modern biology, I want to describe four broad fronts where evolutionary science and its sister discipline of genetics face near-term societal, as well as scientific, challenges and opportunities.

Biotechnology. During the industrial revolution that began two and a half centuries ago, advances in technology, in concert with wasteful consumptive practices, enabled humans to dominate the planet (and foul its life-support systems). Some might argue that this is a sufficient ground to reject new biotechnologies in the offing. Others, however, might agree with E. O. Wilson's (2002) recent assessment of the biodiversity crisis: "Science and technology led us into this bottleneck. Now science and technology must help us find our way through and out" (p. xxiv).

Whatever one's sentiments about recombinant DNA methods, this genetic genie is already well out of the bottle. In the early 1970s, fewer than 20 years after the discovery of the structure of deoxyribonucleic acid (DNA), scientists first transferred foreign genes into *Escherichia coli* and coaxed these genetically modified (GM) bacteria into producing valuable medical compounds, such as human insulin. These scientists thereby established a path to commercial genetic engineering. A decade later, researchers created the first GM crop (transgenic tobacco), a feat that led to an ongoing revolution in plant genetic engineering. Today, patents are issued routinely for GM products and technologies in a wide variety of lucrative pharmaceutical and agricultural enterprises around the globe.

About 10,000 years ago, our ancestors invented agriculture. By sowing the seeds of edible wild plants, harvesting the resulting foods or fibers, and retaining seeds from the best specimens for subsequent planting, they began to transform native plant varieties into the bountiful domestic fruits and vegetables of today. Such artificial selection over the centuries required no cognizance of evolutionary processes—just a keen eye for desirable plants, strong arms to tend the crops, and patience. Today's agricultural engineers still need a keen eye for their subject, but patience no longer is necessary. Through recombinant DNA techniques, the genes of crop plants (and animals) can be manipulated directly and nearly overnight. Some people see an ethical imperative for such efforts, pointing out the burgeoning number of human mouths to feed. Others are outraged by such manipulations and caution scientists not to interfere with their food.

The first GM crops were approved for commercial planting in the United States in the early 1990s, and within a decade roughly 50 percent of the corn, soybean, and cotton planted across the United States was genetically modified for one trait or another. At least 70 percent of the processed foods on American grocery shelves now contain ingredients derived from transgenic sources. Most GM crops in cultivation today were intended to improve food quality or to display resistance to disease microbes, insect pests, or herbicides (NRC 2000, Pew 2001). Consumers in the United States generally have accepted this transition, but public outcries against transgenic "frankenfoods" and agricultural "farmageddons" have been loud in much of Europe, causing those governments to block the spread of GM technologies. The different public reactions serve notice that societal attitudes as well as science play a huge role in the success or failure of commercial GM enterprises.

The available scientific evidence often leaves ample room for polarized opinions on GM crops, especially with regard to environmental issues. Among the potential blessings of GM crops are increased yields per acre, nutritional and health benefits to people and domestic animals, and ecological payoffs such as a rapid phaseout of dangerous chemical pesticides (for example, when GM crops genetically engineered for pest resistance are planted widely). Proponents of agricultural engineering argue that transgenic crops soon will usher in a "Gene Revolution" that will do even more to alleviate world hunger than did the Green Revolution that began in the 1950s, when new varieties of high-yield crops were generated by more traditional plant-breeding methods.

There are, however, important scientific concerns too. Transgenes in some GM plants could pose human health risks, for example, by inducing allergies. Another risk is that transgenes might escape to nontarget plants and precipitate ecological or agricultural disasters. Consider, for example, if transgenes for herbicide tolerance or insect resistance were to transfer from engineered crops into related weed species. Social implications must also not be forgotten. Notably, the widespread deployment of GM crops most likely will be attended by a further shift toward monocultural farming practices, a diminution in the number of indigenous crop varieties, and greater reliance by farmers on large agribusinesses. Thus, agricultural shifts prompted by the gene revolution will entail profound economic and social as well as ecological consequences, and these may not always be for the good.

The most widely planted GM crops to date have been engineered to carry *Bt*-toxin genes, named for the bacterium from which they are derived—*Bacillus thuringiensis*. These microbial genes confer resistance against particular insect pests. Ideally, these GM crops should alleviate much of the need for synthetic chemical insecticides, such as DDT, that were a hallmark of the Green Revolution but also poisoned the land and wildlife (Carson 1962). On the other hand, potential biological downsides to *Bt*-engineered crops include the

possibility that (a) transgenes might leak into nontarget populations via pollen or seed flow or into other species via introgressive hybridization, (b) the toxic *Bt*-proteins could harm beneficial or other nontarget insects that feed on the transgenic crops (but see Pimentel and Raven 2000), or (c) populations of some targeted insect pests might evolve genetic resistance to the transgenic *Bt*-toxins and thereby render them ineffective.

It seems clear that the ecological and evolutionary–genetic sciences can constructively inform the ongoing efforts of the high-tech agriculture industry. For example, appropriate experimental and theoretical research could answer questions such as these: How far and where do the pollen and seeds of particular transgenic crops move? With what wild species might GM plants hybridize? Which nontarget insect species are affected by the plant-expressed *Bt*-toxins, how severely, and with what ecological consequences? What are the molecular and evolutionary–genetic routes to *Bt*-toxin resistance in pest populations, and how likely is such genetic resistance to evolve under the novel selection pressures stemming from widely planted GM crops? How and where might crop plants best be engineered to prevent the evolution of pest resistance? How might GM crops best be deployed to mitigate potential ecological dangers?

Seldom are such scientific issues seriously addressed by the industries that stand to profit from the genetic engineering projects or by government agencies mandated to oversee and license the commercial operations. As a net result of this lack of input from the ecological and evolutionary sciences, societies unnecessarily court too many biological disasters.

Another prime example comes from medicine, where a frightening development in recent years is the widespread evolution of microbial resistance to powerful antibiotics such as penicillin (Palumbi 2001). For decades, these compounds were disseminated all too readily by a medical profession that failed to foresee predictable evolutionary responses by the microbes. Antibiotic supplements in commercial animal feeds have been another source of selection favoring the evolution of microbial drug resistance. Now, a desperate and costly scramble is under way to identify new generations of antibiotic drugs that can offer people renewed protection against the resistant "superbugs." Even a rudimentary understanding of evolutionary genetic principles by the medical and agricultural industries might well have prompted wiser antibiotic practices and thereby avoided this crisis.

Understanding life's operations. Quite apart from biotechnological applications per se, the molecular revolution in biology is also yielding unprecedented conceptual insights into basic evolutionary processes. A good example comes from transposable or mobile elements. In the early 1950s, Barbara McClintock discovered these "jumping genes" as they moved about the genome of corn plants, hopping routinely from one chromosomal site to another, often replicatively. The significance of these observations went mostly unappreciated at the time, but jumping genes later were found to be important and nearly ubiquitous features of eukaryotic cells. In 1983, McClintock was awarded a Nobel Prize for her work.

Various classes of jumping genes and their less-frisky evolutionary descendants and relatives have proved to be astonishingly abundant in most plant and animal species. They often make up more than 50 percent of the genome (Brosius 1999). In humans, for example, each cell contains more than 500,000 copies of one class of 300-base-pair sequences (known as Alu) and about 100,000 copies of a longer family of sequences that accounts for about 5 percent of our total DNA. Such nucleotide sequences generally have no known function apart from their own self-perpetuation. Most stem from "master copy" sequences that over time have given rise to vast numbers of derivative sequences. By replicatively dispersing themselves across the genome, transposable elements enhance their own prospects for transmission to the next generation.

Jumping genes are thus prototypical selfish genetic elements. They also can be described as miniature intracellular parasites. Through their tendency to induce mutations, and also, perhaps, from the sheer metabolic burden of their vast numbers, jumping genes commonly damage their hosts. The analogy to parasites is apt in another regard: Phylogenetic discoveries based on DNA sequence analyses (e.g., Xiong and Eickbush 1990) indicate that some jumping genes—the retrotransposable elements—have close evolutionary ties to the family of infectious viruses that includes the causal agent of AIDS.

Like any association between host and parasite, however, selection-mediated evolution sometimes works out symbiotic relationships between the participants. Growing evidence indicates that at least some former jumping genes have even been recruited over evolutionary time into activities beneficial to their host (McDonald 1990, 1998). These include the sponsorship of recombinational variation of immune-response genes, the formation of centromeric regions that help direct chromosome movements during cell divisions, the repair of chromosomal ends (telomeres) whose decay otherwise is associated with the aging process, and the promotion of gene duplications and other genetic alterations that in general provide important (albeit fortuitous) fodder for evolutionary innovation.

Jumping genes are merely one among several "nontraditional" types of genetic elements whose presence could scarcely have been imagined in the premolecular era. Also inhabiting the human genome are vast armies of noncoding DNA sequences known as introns that stand like sentinels between the coding regions of protein-specifying genes; battalions of repetitive DNA sequences, each composed of nearly identical DNA sequences aligned in closed rank; active promoters and regulator sequences that act like field sergeants, ordering around the squadrons of proteins and nucleic acid molecules that do the grunt work of cellular metabolism; and legions of pseudogenes, former genes that are no longer functional but clutter the genome like corpses on a battlefield.

Thus, the traditional image of a genome densely packed with DNA that benefits the cell has turned out upon close molecular inspection to be a mirage. The protein-coding genes that prescribe much of our genetic health are scattered about the genome like tiny desert oases embedded in long linear stretches of what appears at first sight to be a noncoding genomic wasteland. The noncoding regions make up the vast majority of our total DNA. Protein-coding genes have been the traditional focus of medical research on inborn errors of human metabolism, but they constitute just a tiny fraction (about 2 percent) of our species' genetic heritage.

Not that the rest of the human genome is mere junk. What was formerly termed "junk DNA" is actually a treasure chest of information about the evolutionary process. An analogy to garbage is appropriate. In recent decades, anthropologists have come to view ancient garbage dumps near human settlements as wonderful sources of historical information. Likewise, biologists are beginning to appreciate that by rummaging through the junk DNA in our cells, they can unearth information about genes' evolutionary lifestyles. To fully catalogue such historical genomic information is a major research challenge for the coming decades.

An emerging view is that the genome is in many ways like an extended intracellular society of interacting genetic elements. Within each such microecosystem are multitudinous quasi-independent DNA sequences with elaborate divisions of labor and functional collaborations. Such sequences can also engage in evolutionary feuds stemming from hereditary conflicts of interest (Avise 2001b). Such intergenic conflicts are nearly inevitable in any species that engages in sexual reproduction, because unlinked genes in such species are partially autonomous (as a result of the vagaries of Mendelian transmission). Genes are not all inherited together but instead are segregated and re-sorted in sexual reproduction. Thus, genes tend to evolve replication tactics that enhance their individual prospects for survival and transmission.

The net result is that different pieces of DNA within an extended lineage continually play coevolutionary games. Their strategies often bear striking analogy to those observed among people partially bound in social arrangements. These can include collaborative efforts but also individual opportunism, group alliances but also cheating, and societal strictures against any unduly egoistic tendencies of the individual (Avise 1998). Such societal metaphors for gene-by-gene interactions in evolutionary as well as in contemporary time are less than perfect, but they do evoke a more realistic and powerful image of molecular affairs than does the image of genes as relatively inert beads strung along the chromosomes.

I will describe one example that illustrates the beauty and complexity of intragenomic interactions. Recent phylogenetic analyses of DNA sequences have demonstrated that genes in the living cells of all advanced organisms ultimately trace back to several (and perhaps many; Margulis and Sagan 2002) endosymbiotic marriages between unrelated microbes early in the history of life (Golding and Gupta 1995, Hedges et al. 2001, Hartman and Fedorov 2002). The most famous of these nuptial occasions, which occurred more than a billion years ago, was the formation of an intimate cellular union between a purple bacterium and another microbe that bore the precursors of many of the genes now housed in each cell's nucleus.

Following this intercellular wedding, some of the purple bacterium's genes gave rise to the genome of mitochondria. Most, however, were incorporated into the evolving nucleus of a primordial eukaryotic cell. These genes continue to collaborate today with DNA stemming from other ancient microbes that likewise participated in early endosymbiotic amalgamations.

These are well-documented evolutionary happenings. Other molecular events that are legacies of the original endosymbioses still occur within the cells of individuals. For example, a multitude of proteins encoded by nuclear genes continually migrate to the mitochondria, where they engage in exquisite molecular ballets with the protein products of mitochondrial genes to mediate production of chemical energy.

Ancient microbial matrimonies left other legacies. In any zygote or fertilized oocyte, most of the cytoplasm comes from the egg rather than the sperm, so mitochondrial DNA (mtDNA) is transmitted to offspring almost exclusively via females. This makes mtDNA a valuable genealogical marker for deciphering the matrilineal component of any animal pedigree, much as surnames provide markers of patrilines in many human societies. Data of mtDNA show that all modern human matrilines trace to expansions of our species that occurred when our forebears left Africa in fairly recent evolutionary times (Cann et al. 1987, Templeton 2002).

Being maternally inherited, the modern mitochondrial genome also retains a quasi autonomy that can bring it into evolutionary conflicts of interest with biparentally inherited nuclear genes (Eberhard 1980, Hurst 1993). For example, from the selfish perspective of a cytoplasmic gene, it matters little if males are sterile or debilitated, because males are not a viable avenue for cytoplasmic transmission (Frank and Hurst 1996). From this evolutionary vantage, it is no coincidence that a disproportionate fraction of genes contributing to male sterility in many plant and animal species are housed in the cytoplasm. Because cytoplasmic genes are transmitted maternally, they behave as if they are rather indifferent to male well-being. They may even jeopardize the longer-term evolutionary health of a species by biasing families toward producing daughters rather than sons, sometimes dramatically (e.g., Rigaud et al. 1999).

We are coming to realize that Darwinian processes operate not only at the traditionally understood levels of the organism and kinship group but also on DNA sequences engaged in the evolutionary struggle for existence (Dawkins 1976). These molecular-level Darwinian processes are intimately tied to sexual reproduction, because under Mendelian rules of heredity, unlinked genes have noncoincident transmission routes and, thus, quasi-independent evolutionary fates. Different pieces of DNA tend to evolve individualized

fitness strategies as they collaborate but also jostle for successful passage through an extended organismal pedigree.

Genes may be considered to resemble miniature intracellular deities in their dominion over human affairs (Avise 1998), yet they provide mechanistic as opposed to otherworldly explanations. Genes are physical rather than metaphysical entities, natural rather than supernatural, real rather than ethereal. They give every indication of having been fashioned not by the loving hands of a conscious engineer, but by an amoral (not immoral) evolutionary process—natural selection—that shapes life at several hierarchical levels, including that of the DNA sequences themselves. Like other evolutionary genetic forces such as mutation and recombination, natural selection has no consciousness, no code of conduct, no reflective concern about the consequences of its actions. Selection is a powerfully creative and directive force in biology, but it is as uncaring as gravity or lightning about organismal well-being.

The often-surprising consequences of natural selection are also being explored now in many other contexts, including aging and death. Why, from an evolutionary perspective, should genes ever dictate senescence and mortality for the individual?

Theoretical population biologists have shown that senescence and death are virtually inevitable evolutionary repercussions of organismal reproduction (Hamilton 1966, Rose 1991, Austad 1997). Natural selection tends to act more forcibly on genes transmitted through young rather than old reproducers (Medawar 1952). As a long-term evolutionary consequence, older age classes in any population tend to become developmental repositories for genes with age-delayed deleterious somatic effects. In part, such genes accumulate simply because of weak selection against their loss. A related realization is that genes for aging are favored by natural selection whenever their beneficial effects at early stages of life outweigh deleterious effects later on (Medawar 1952, Williams 1957). For example, any genes that predispose for bone calcification in adolescents might improve an individual's genetic fitness by strengthening limbs. Under the action of natural selection over the generations, these calcification genes would increase in frequency, even if they also happened to harden artery walls and thereby promote heart disease later in life. The net effect of such age-related natural selection is that there tends to evolve a marked acceleration of death probabilities with advancing age.

In short, aging and death do not violate some rule of evolution by natural selection. Rather, they exist because natural selection fails to prevent the accumulation of disabling genes in the elderly. These are just a few examples of how the field of evolutionary genetics can yield objective insights into human conditions that in prior ages fell under the purview of mythology, theology, and religion (Avise 1998, Wilson DS 2002).

Coming years will see a further elaboration of both the workings and the outcomes of selection-mediated evolution at biological levels ranging from molecules to organisms and beyond. An important challenge will be to establish firmer scientific connections across these hierarchical planes. For example, it will be interesting to discover how selection has shaped genes that mechanistically underlie the aging process.

Fundamental research of this type may well lead the field of evolutionary genetics further into realms that some philosophers and theologians might prefer science left unexplored. Such is the paradoxical state of affairs in the modern world where scientific rationalism and religious revelation struggle to coexist as powerful but opposing means of knowing. To parrot again Charles Dickens, it is indeed both an age of wisdom and an epoch of belief.

Natural history and phylogeny. A quarter-century ago, Carl Woese and George Fox (1977) used DNA sequences from a small ribosomal RNA gene to infer that life on Earth is divided into three primary historical kingdoms or domains: the Archaebacteria (archaea), the Eubacteria (bacteria), and the Eukaryota (eucarya). This early glimpse at deep branches in the tree of life demonstrated the astonishing power of molecular data for reconstructing phylogeny. Since then, the volume of genetic information has grown exponentially, and systematists now routinely employ nucleotide sequences to estimate the relatedness of species of any degree of evolutionary separation. For example, a recent meta-analysis of DNA sequences from more than 5000 genes was used to infer the approximate dates of the most recent common ancestors of more than 300 species representing the major groups of placental mammals (Kumar and Subramanian 2002).

Within the next decade or two, scientists almost certainly will complete a near-exact reconstruction of the tree of life, including inferred phylogenies of all the major taxonomic groups recognized among the 1.7 million described living species. These genealogical histories will have been mostly derived from inheritance from parent to offspring, but instances of genetic transfer between organismal lineages (Bushman 2002), as mediated by retroviruses or other means, will also be documented.

Some classes of DNA evolve so rapidly that they illuminate historical relationships even among individuals within a species (Avise 2000). The applications range from paternity and maternity assignments to analysis of population separations often dating to the Ice Ages. Apart from the historical reconstructions per se, the molecular genetic appraisals also will reveal a wealth of behavioral and natural history information. Thus, this century will also see a further flowering of molecule-based natural history (Avise 2002).

This assembly of the tree of life will stand as another of the grand achievements in the history of biology, at least comparable in importance to the human genome project. It will provide the historical backdrop necessary for virtually all studies in comparative biology, from the basic to the applied. For example, details of the tree of life will enable researchers to chart the phylogenetic origins and evolutionary transitions of any anatomical or physiological feature. More practically,

the tree will enable scientists to describe how biodiversity has changed over time, which will aid conservation efforts, and it will assist bioprospectors in their searches for pharmaceutical or other valuable compounds from nature. In short, the tree of life will serve as a comprehensive road map for nearly all exploratory research in biology.

Education, religion, and the appreciation of biodiversity. A report from the National Research Council (1998) concluded that the United States is conferring too many graduate degrees in biology for current societal demands. The report likened the fates of many recent biology graduates to planes circling an airport: Postdoctoral students typically enter a long holding pattern before gaining clearance to land a job in their chosen profession, and having landed, still face daunting hurdles before they secure research funding. This description speaks very poorly of our nation's priorities. We live in an era when there is a need for *more* biologists and earth scientists to help inform decisions on the complex challenges that are of utmost concern in agriculture, medicine, and the environment. Well-trained biologists are essential, as are science-literate religious and political leaders and a scientifically informed public. A compelling challenge for government is to structure legislation and economic incentives in ways that will promote the biological sciences.

In a popular article published in a 1973 issue of the *American Biology Teacher,* the evolutionary geneticist Theodosius Dobzhansky penned a famous phrase. "Nothing in biology," he wrote, "makes sense except in the light of evolution." Dobzhansky was referring not merely to the genealogical history of life. He was also alluding to how the evolutionary sciences explain biological phenomena using dispassionate reasoning and objective evidence. They are thus expressly divorced from faith in metaphysical causation. It is a great irony that in this age of genetics and biotechnology most people are grossly ignorant about evolution and genetics or openly hostile to their implications. For example, only about 10 percent of Americans believe that evolution occurs as an entirely natural phenomenon, and about one-third of high school biology teachers reject the concept of evolution altogether (Pigliucci 2002). This is, indeed, both the season of light and the age of foolishness.

In Ohio, fundamentalist Christian groups have been hard at work lobbying legislators and school boards to water down or even squelch the teaching of evolution in public schools. In Georgia, the Cobb County school board recently directed that biology textbooks include a sticker that in essence disclaims evolution. Similar attacks on evolutionary biology are initiated almost every year. These creationist salvos are much like those launched by William Jennings Bryan during the infamous 1925 "monkey trial" in Dayton, Tennessee (Larson 1997). There, defense attorney Clarence Darrow staunchly but unsuccessfully defended the right of John Scopes to teach evolution in public schools, a right that was denied in a state law sponsored by Protestant fundamentalists.

Some creationists would have us believe that Earth is only 10,000 years old, that all species were forged from nothing in 6 days by supernatural means, and that fossils are the traces of creatures trapped during a recent global flood. These mythologies, reflecting one literal reading of a Bronze Age religious text, might be educational if included in courses on comparative religion, history, or sociology. In fact they have numerous harmful consequences.

Why are the creationists so committed to erasing evolution from the blackboards of science classrooms? Analysts suggest that the creation–evolution debate in America has its roots in three quintessential aspects of US culture: a prevalence of religious notions in politics, a core value of equal time for all points of view in public discourse, and pervasive scientific illiteracy (Antolin and Herbers 2001). Behind these proximate causes is a deeper philosophical objection (Futuyma 1983, Alters and Alters 2001). Following Darwin's elucidation of natural selection as the primary force shaping evolution, no compelling justification remained for invoking the direct hand of an omnipotent God to account for life's origins and diversity. Nor were there any longer grounds for assuming unique genealogical status for *Homo sapiens.* The apparent hegemony of evolutionary causation in previously sacred realms was more than many fundamentalists could tolerate.

Such views are not confined to Christian extremists. Dobzhansky opened his 1973 article by quoting from a letter to the king of Saudi Arabia from one of that country's leading sheikhs, who wrote: "The Holy Koran, the Prophet's teachings, the majority of Islamic scientists, and the actual facts all prove that the sun is running in its orbit...and that the earth is fixed and stable, spread out by God for his mankind.... Anyone who professed otherwise would utter a charge of falsehood toward God, the Koran, and the Prophet" (p. 125). These sentiments, of course, are strikingly reminiscent of those expressed by the Catholic Church when, in 1633, it found the scholar Galileo guilty of heresy for suggesting that Earth is neither flat nor the center of the universe.

The physical and biological sciences have given us a very different perspective on the world and its biota in space and time. No longer can humanity rationally see itself as the center of all creation, nor can we any longer rationalize continued abuse of the biosphere. Likewise, the evolutionary sciences have given us a grand temporal perspective on life. Humans have inhabited Earth for only the last few seconds of the cosmic calendar, yet already we threaten to squeeze from the planet much of the exuberant biodiversity that traces in ancestry back across 4 billion years. Aldo Leopold (1949) worded the ramifications thus: "We know now what was unknown to all the preceding caravan of generations: that men are only fellow-voyagers with other creatures in the odyssey of evolution. This new knowledge should have given us, by this time, a sense of kinship with fellow-creatures; a wish to live and let live; a sense of wonder over the magnitude and duration of the biotic enterprise" (p. 109).

I have argued that an expanded literacy in the evolutionary and genetic sciences will be crucial in the coming decades

if societies are to address the growing technical challenges in biology. Nonetheless, I want to suggest that with respect to the most critical and urgent challenge of all—shepherding Earth's biodiversity through this critical bottleneck century—science and religion can and must put aside their philosophical differences, at least for now, and join forces in a crusade to save the planet.

Organized churches and religious leaders have a tremendous opportunity to play key moral as well as orchestrational roles. For example, the Koran encourages Muslims to examine the beauty of their natural surroundings with curiosity and attentiveness. The Bible encourages Christians to act as responsible stewards of God's creation. The teachings of Buddhism emphasize personal ethics and wise restraint. Indeed, every major world religion encourages appreciation and respect for our surroundings and for life. Organized religions can offer both moral authority for preserving biodiversity and logistical expertise to convey that imperative to their congregations. Yet sadly, most religious leaders have spurned this calling.

In his 1973 article, Dobzhansky wrote: "I am a creationist *and* an evolutionist. Evolution is God's, or Nature's method of creation" (p. 127). Naturalists of earlier times typically were deeply spiritual also. Consider the natural theologians. When William Bartram roamed the southeastern United States 200 years ago, he sought through his naturalist studies to glorify the works of God. On nearly every page of his diary (see Van Doren 1955), Bartram expressed a sense of wonderment: "This world, as a glorious apartment of the boundless palace of the sovereign Creator, is furnished with an infinite variety of animated scenes, inexpressibly beautiful and pleasing, equally free to the inspection and enjoyment of all his creatures" (p. 15). When John Muir, another famous natural theologian, explored the western United States a century later, he often wrote of God's bounty as well: "every crystal, every flower a window opening into heaven, a mirror reflecting the Creator" (Muir 1911, p. 153).

When Darwin set out on his voyage of discovery in the early 1800s, he was a natural theologian seeking to understand the nature of creation. He had no idea that his discoveries soon would revolutionize rational thought about nature and humanity's place within it. Yet, like Bartram and Muir, he also retained a sense of its magnificence, as illustrated by the famous closing paragraph in *The Origin of Species* (1859): "It is interesting to contemplate a tangled bank, clothed with plants of many kinds, with birds singing on the bushes, with various insects flitting about, and with worms crawling through the damp earth, and to reflect that these elaborately constructed forms, so different from each other, and dependent upon each other in so complex a manner, have all been produced by laws acting around us.... There is grandeur in this view of life, with its several powers, having been originally breathed by the Creator into a few forms or into one" (p. 490).

In the 21st century, it will be an urgent challenge to instill in our collective psyche a moral commitment to Earth and its remaining biodiversity. Like the natural theologians and the early evolutionists, societies must find a way to integrate the emotive power of religion with the rational insights of science. They could thus promote a deeper respect for nature and engender a passion to preserve it.

A closing hope

With the grave responsibility to protect biodiversity from human impacts also comes a magnificent opportunity. Consider a future world in which human societies universally seek to attain a sustainable relationship with nature. Imagine that this planetary ethos eventually becomes so deeply ingrained within our collective psyche that it becomes one of mankind's defining legacies. Although the shift would be huge, it is within the realm of possibility. Perhaps the sciences of evolutionary biology, genetics, and ecology (hopefully with encouragement from organized religions) can help point the way toward such a new environmental ethic. Perhaps humanity can rise to this opportunity to save the biosphere, and with it ourselves.

Acknowledgments

Thanks go to DeEtte Walker and an anonymous reviewer for helpful suggestions that improved the manuscript. Recent support for the author's work has come from a Pew Foundation Fellowship in marine conservation.

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