

# EVOLUTIONARY BIOLOGY IN BIODIVERSITY SCIENCE, CONSERVATION, AND POLICY: A CALL TO ACTION

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Evolutionary biologists have long endeavored to document how many species exist on Earth, to understand the processes by which biodiversity waxes and wanes, to document and interpret spatial patterns of biodiversity, and to infer evolutionary relationships. Despite the great potential of this knowledge to improve biodiversity science, conservation, and policy, evolutionary biologists have generally devoted limited attention to these broader implications. Likewise, many workers in biodiversity science have underappreciated the fundamental relevance of evolutionary biology. The aim of this article is to summarize and illustrate some ways in which evolutionary biology is directly relevant. We do so in the context of four broad areas: (1) discovering and documenting biodiversity, (2) understanding the causes of diversification, (3) evaluating evolutionary responses to human disturbances, and (4) implications for ecological communities, ecosystems, and humans. We also introduce bioGENESIS, a new project within DIVERSITAS launched to explore the potential practical contributions of evolutionary biology. In addition to fostering the integration of evolutionary thinking into biodiversity science, bioGENESIS provides practical recommendations to policy makers for incorporating evolutionary perspectives into biodiversity agendas and conservation. We solicit your involvement in developing innovative ways of using evolutionary biology to better comprehend and stem the loss of biodiversity.

**KEY WORDS:** Contemporary evolution, eco-evolutionary dynamics, evolutionary applications, rapid evolution, systematics, taxonomy.

Evolutionary biologists should be predisposed to the idea that evolutionary biology is directly relevant to biodiversity science, and that it can have enormous practical value in guiding conservation efforts, enhancing sustainability, and improving human welfare (Futuyma 1995; Palumbi 2002; Stockwell et al. 2003; Meagher 2007; Bell and Collins 2008; Neese and Stearns 2008; Smith and Bernatchez 2008). Evolution, after all, provides the fundamental context and framework for comparative analyses of biodiversity, and its implications, across all levels of biological organization. Outside our discipline, however, the practical relevance of evolutionary biology is apparently not so obvious. Indeed, evolutionary biologists are increasingly compelled to defend the strategic value of their discipline to the public and to government agencies, not to mention many of their ecologically oriented colleagues. At present, however, we may be on the cusp of a dramatic change in this perspective.

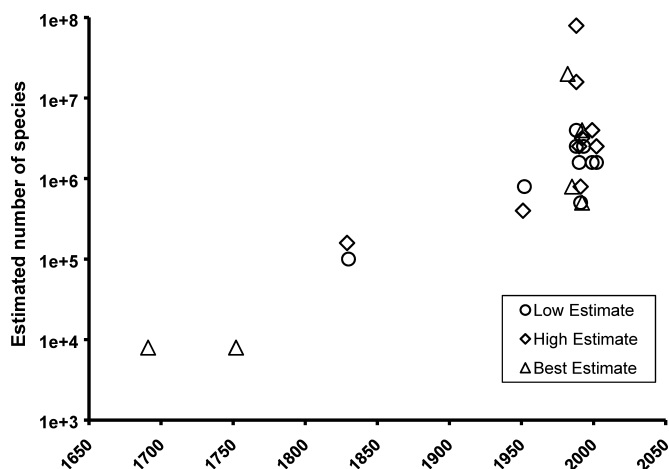
Some of the first and most important conservation biologists were also evolutionary biologists: starting with Darwin and Wallace and accelerating with Ed Wilson, Peter Raven, and Michael Soulé. Presently, however, evolutionary biology has comparatively little impact on conservation planning and sustainable development. This deficiency might simply reflect the limited participation of evolutionary biologists—as compared to, for example, ecologists and environmental economists—in ongoing discussions about conserving and managing biodiversity. For example, relatively few evolutionary biologists are involved in national delegations to the Convention on Biological Diversity (CBD). Similarly, few of us contributed to the recently completed Millennium Ecosystem Assessment (MEA), or are aware of the ongoing effort to establish an Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES; Loreau et al. 2006; www.ipbes.net). Meanwhile, our ecological colleagues have not only been actively engaged in such policy-science developments,

but have also succeeded in mainstreaming ecological concepts such as sustainability and ecosystem services, whereas environmental economists are busy putting monetary values on these services. The authors of the present article believe that evolutionary biologists can, and must, become more broadly and effectively engaged in the ongoing biodiversity dialogue—not just for the sake of our discipline, but for the benefit of society.

The main purpose of this article is to summarize and illustrate some of the ways in which evolutionary biology is directly relevant to biodiversity science, conservation, and policy. Our discussion is organized into four areas: (1) discovering and documenting biodiversity, (2) understanding the causes of diversification, (3) evaluating evolutionary responses to human disturbances, and (4) implications for communities, ecosystems, and humans. In each case, we highlight the past, present, and potential future contributions of evolutionary biologists. In closing, we invite participation in bioGENESIS (Yahara and Donoghue 2007; Donoghue et al. 2009; www.diversitas-international.org/biogenesis), a new Core Project launched recently within the International Programme of Biodiversity Science, DIVERSITAS. bioGENESIS is designed to build an international network of evolutionary biologists promoting relevant evolutionary research, improving the integration of evolutionary thinking into biodiversity science, and providing concrete recommendations to policy makers.

## *Discovering and Documenting Biodiversity*

By the end of the 18th century, Linnaeus and his followers had described some 20,000 species. This was a remarkable achievement for the time and an extraordinary advance in human comprehension of Earth's biodiversity. And yet, since then, more than 1,700,000 additional species have been discovered and



**Figure 1.** Various estimates of the number of species on Earth in relation to the year in which the estimate was made (redrawn from Dobson et al. 2008).

described—and this is still only the tip of the biodiversity iceberg, with many millions of species awaiting discovery and description (Fig. 1). The majority of these undescribed organisms comprise the bacteria, archaea, and microeukaryotes (fungi, nematodes, various algae, and others), many of which could be of great practical importance for humans (e.g., Curtis et al. 2006; Dobson et al. 2008). This great variety of organisms, both described and undescribed, must be accurately documented if they are to be preserved and used sustainably (Cracraft and Wheeler 1997; Wheeler 2004). Tragically, at the present rate of discovery and description, many (perhaps most) species will vanish before they are even discovered. And it is not enough to just identify and enumerate these species—the evolutionary relationships among them must be understood—as much of the rest of this article will illustrate.

The documentation and organization of biodiversity remains largely the task of the systematics community (taxonomists, systematists, phylogeneticists) of evolutionary biologists, whose work governs the rate of discovery and description on which biodiversity inventories and conservation efforts depend. The tasks of this community range from identifying the intraspecific taxonomic units that are important for conservation (Waples 1991; Moritz 1994; Crandall et al. 2000) all the way to disentangling branches of the tree of life that orient all biological knowledge (Cracraft and Donoghue 2004). Some concrete examples of the direct application of these efforts include the identification of cryptic species within critically endangered taxa (Daugherty et al. 1990; Gentile et al. 2009) and the use of phylogenetic diversity indices to identify biodiversity hotspots (Petit et al. 2003; Forest et al. 2007).

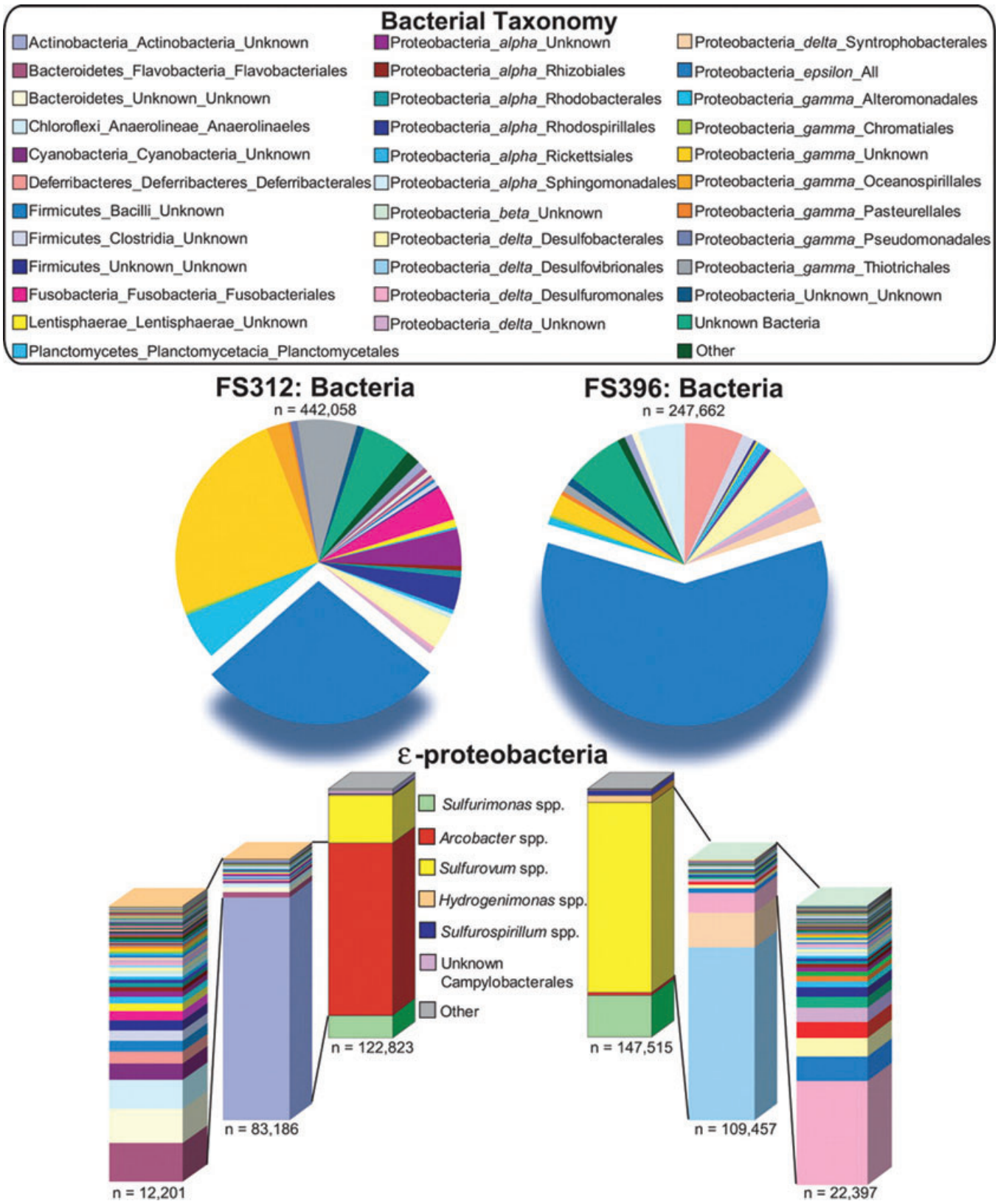
Activities of the systematics community also underpin the rapidly expanding and increasingly accessible knowledge-base on which biodiversity science has come to depend. Examples include the compilation and organization of DNA sequences in

GenBank ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)) and EMBL ([www.ebi.ac.uk](http://www.ebi.ac.uk)), specimen locality data in GBIF ([www.gbif.org](http://www.gbif.org)), digital images in MorphBank ([www.morphbank.net](http://www.morphbank.net)), DNA barcodes in CBOL ([www.barcoding.si.edu](http://www.barcoding.si.edu)), and phylogenetic trees in TreeBASE ([www.treebase.org](http://www.treebase.org)). These databases facilitate regional portals to biodiversity data, such as CONABIO in Mexico ([www.conabio.gob.mx](http://www.conabio.gob.mx)) and BIOTA in Brazil ([www.biota.org.br](http://www.biota.org.br)), which then provide an evidential basis for sound local and regional conservation planning and policy. Likewise, these databases underpin global monitoring efforts, such as the emerging Biodiversity Observation Network (GEO BON; Scholes et al. 2008; [www.earthobservations.org/cop\\_bi\\_geobon.shtml](http://www.earthobservations.org/cop_bi_geobon.shtml)).

This crucial baseline information provided by the systematics community does not come easily, and, if current trends continue, the future will see a marked decrease in the number of scientists with taxonomic expertise (Hopkins and Freckleton 2002; Wheeler 2004). This disturbing prospect underscores the importance of achieving far greater efficiencies throughout the workflow of biodiversity documentation, including the field collection of specimens, the discovery and rapid description of taxonomic units, and the deposition and curation of biodiversity information in relevant and accessible databases. These efforts thus include not only species descriptions, but also the improved provision of information for decision-makers who need to compare biodiversity across space and time.

Fortunately, new approaches are greatly accelerating the rate of biodiversity discovery. Examples range from rapid biodiversity assessments in critical areas ([www.biosurvey.conservation.org](http://www.biosurvey.conservation.org)) to metagenomic surveys of microbial communities (Venter et al. 2004; Lambais et al. 2006; [www.dels.nas.edu/metagenomics](http://www.dels.nas.edu/metagenomics)). For example, ICoMM (International Census of Marine Microbes, [www.icomm.mbl.edu](http://www.icomm.mbl.edu)) has adopted a tag sequencing strategy to document marine microbial diversity (Sogin et al. 2006). In October 2007, this group reported more than 20,000 types of bacteria and archaea at just two hydrothermal vents (Fig. 2; Huber et al. 2007). Even without formal species descriptions, this type of metagenomic data can be used in quantitative measures of phylogenetic beta diversity (Lozupone et al. 2007), which can help identify the environmental drivers of diversity and reveal areas of high diversity or endemism.

Also essential will be an accelerated rate of data capture, synthesis, and accessibility, primarily through the development of new IT and cyberinfrastructure solutions. Encouraging efforts in this direction include new tools to increase the efficiency of taxonomic work flows (e.g., the EDIT Internet Platform for Cybertaxonomy; [www.e-taxonomy.eu/platform](http://www.e-taxonomy.eu/platform)) and the automated capture of label data from museum specimens (e.g., HERBIS, [www.herbis.org](http://www.herbis.org)). Moreover, synthetic outputs, along the lines of the Encyclopedia of Life ([www.eol.org](http://www.eol.org)) and the Tree of Life Web Project ([www.tolweb.org](http://www.tolweb.org)), will play increasingly important roles



**Figure 2.** Taxonomic breakdown of bacterial V6 tags from each or two hydrothermal vents (FS312 and FS396) revealed by tag sequencing (from Huber, J. A., D. B. M. Welch, H. G. Morrison, S. M. Huse, P. R. Neal, D. A. Butterfield, and M. L. Sogin. 2007. Microbial population structures in the deep marine biosphere. *Science* 318:97–100. Reprinted with permission from AAAS.) The taxonomic distribution of e-proteobacterial genera is shown in normalized histograms for each site, with each color in the histograms representing a unique tag sequence.

in organizing and providing the biodiversity information on which an integrated biodiversity science depends. Open-source Internet solutions are particularly valuable because they dramatically increase accessibility to researchers and managers across the globe, regardless of their institutional affiliation or financial resources.

Finally, exciting advances can be made by formally linking phylogenetic data to explicit geographical information. For example, the connection of phylogenetic trees to geographic maps, such as in Google Earth ([www.earth.google.com](http://www.earth.google.com)), can help identify the origin and track the spread of invasive species and (re)emerging diseases. Recent examples include analyses of avian influenza (Janies et al. 2007) and SARS (Janies et al. 2008; [www.supramap.osu.edu/cov/janiesetal2008covsars.kmz](http://www.supramap.osu.edu/cov/janiesetal2008covsars.kmz)). Likewise, the integration of phylogenies into ecological niche modeling can help explain the history and rate of niche evolution, thus enhancing our ability to predict geographic range shifts as a function of climate change (Pearman et al. 2008; Evans et al. 2009).

As this section has sought to illustrate, evolutionary biologists are making key contributions to the development of improved tools for discovering, describing, and organizing biodiversity. Many of these improvements have involved collaborations between evolutionary biologists and statisticians, bioinformaticists, geographers, and ecologists. These collaborations are building a template for understanding, visualizing, and making accessible the staggering wealth of biodiversity information.

## *Understanding the Causes of Diversification*

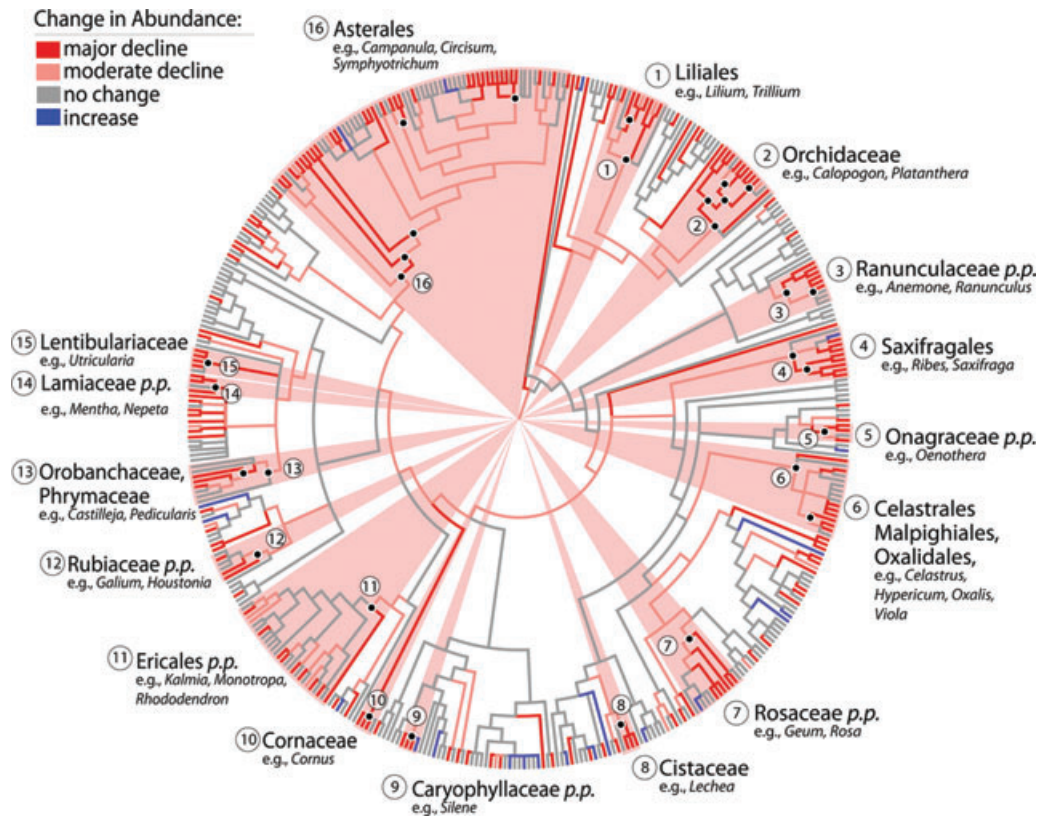
Current biodiversity is the product of past evolution, just as future biodiversity will be a product of contemporary evolution. Evolutionary biologists can therefore help provide a basis for predicting biodiversity responses to environmental change, whether local or global. For example, phylogeneticists are analyzing the extent to which evolutionary radiations in the past have been spurred by character changes (e.g., key innovations), climate changes, or the spread of lineages into new areas (Moore and Donoghue 2007). They are also studying how biotas have been assembled, and the factors that have shaped the composition of regional species pools and local communities (Ackerly 2003; Gillespie 2004). Recent studies have, for example, assessed patterns of phylogenetic relatedness in communities to infer the relative importance of habitat filtering, competitive interactions, shared diseases, and facilitation in community assembly (Cavender-Bares et al. 2004; Webb et al. 2006; Cavender-Bares et al. 2009). Similar processes will surely influence the structure of future communities following environmental perturbations, including climate change, habitat loss, and invasive species.

The role of evolution during past environmental change is also being revealed through the work of paleobiologists (Prentice

et al. 1991; Roy et al. 2001; Jaramillo et al. 2006). In some cases, it is even possible to infer evolutionary dynamics and the drivers of morphological change with great precision. One example is the 21,500-year time series (at 250 year intervals) of fossil stickleback fish, a sequence revealing likely interactions between immigration, natural selection, and genetic constraints (Hunt et al. 2008). At larger spatial and temporal scales, paleobiologists are identifying factors that account for the vulnerability or resilience of lineages and ecosystems through mass extinctions, and how these systems do or do not rebound following such events (Jablonski 2008). Given that we are experiencing a new wave of extinction, these historical analyses help us understand how the history of existing lineages and communities might influence their future dynamics (Jablonski 2001, 2008).

Also of direct relevance to predicting patterns of future biodiversity are historical studies of biogeography and phylogeography. For instance, studies of biotic interchanges in the past, such as the great American interchange (Marshall et al. 1982; Vermeij 1991), bear on the likely impacts of invasive species—although not without caveats (Ricciardi 2007). Molecular studies, in particular, have helped to reconstruct historical patterns of species movement and colonization (Taberlet et al. 1998; Schneider and Moritz 1999; Guggisberg et al. 2009), and have contributed to a better understanding of how barriers and corridors structure biodiversity (Young et al. 1996; Mansion et al. 2008). Increasingly, historical reasoning is also being employed to explain spatial biodiversity gradients, such as the latitudinal gradient in species richness (Wiens and Donoghue 2004; Jablonski et al. 2006; Wiens et al. 2006). Along these lines, several analyses have sought to explain the composition of species within particular regions, such as biodiversity hotspots, as a function of phylogenetic history (niche conservatism) and migration (habitat tracking) versus in situ speciation and extinction (Goldberg et al. 2005; Rangel et al. 2007; Donoghue 2008; Crisp et al. 2009). With this framework, and with knowledge of the distribution of barriers and corridors, we may be able to predict the relative importance of immigration versus in situ adaptation to community composition following environmental perturbations.

A growing concern in biodiversity science is how to identify and maintain the key functional traits on which ecosystem services depend. Evolutionary analyses have an important bearing on this issue—because seemingly convergent traits (e.g.,  $C_4$  photosynthesis in different lineages) might function quite differently (Kellogg et al. 1999), whereas seemingly divergent traits or lineages might function similarly (e.g., some related  $C_3$  and  $C_4$  plants show similar levels of carbonic anhydrase activity; Edwards et al. 2007). Knowledge of these connections between phylogeny and function can help build better predictive models of biological responses to climate change (Edwards et al. 2007), and may prove crucial in assessing the risk to ecosystem services of



**Figure 3.** Changes in the abundance of flowering plants from the Concord Woods of New Hampshire (1900 vs. 2007) superimposed on a composite phylogeny. Species declines are not randomly distributed across the phylogeny, instead being mostly concentrated in clades where flowering times do not closely track temperature (from Willis et al. 2008). Used with permission—Copyright (2008) National Academy of Sciences, USA.

losing particular species or lineages. For example, Rezende et al. (2007) demonstrated the possibility of cascading extinction events within communities as a function of the phylogenetic distribution of flower forms and pollinators. Phylogenetic analyses also can be useful in identifying clades marked by traits that render their species particularly susceptible to extirpation or extinction (Fig. 3; Willis et al. 2008). Conservation efforts can then be focused on these vulnerable and important clades.

The key point of this section is that evolutionary biologists can tell us much about how current and past biodiversity patterns have been influenced by past evolutionary processes, and the interaction between evolution and past geographical and climatological processes. In turn, these studies can help predict what might happen to biodiversity patterns in the face of future changes in geography (e.g., barriers or conduits to movement) and climate.

### Evaluating Evolutionary Responses to Human Disturbances

Evolutionary biologists are increasingly turning their attention to the phenomenon of “rapid” or “contemporary” evolution; that is, ongoing evolution on relatively short time frames such as years

or decades (Hendry and Kinnison 1999; Stockwell et al. 2003; Hendry et al. 2008). One appeal of this phenomenon is that evolution is most easily studied when it is most rapid, which tends to be the case when humans perturb the environment (Stockwell et al. 2003; Hendry et al. 2008; Darimont et al. 2009). Moreover, the nature of some human-caused environmental change is such that we can predict its spatial and temporal occurrence, which then allows focused sampling, before-to-after time series, and reference to control populations. Studies of human-disturbed populations can thus yield fundamental evolutionary insights that would not otherwise be possible (Smith and Bernatchez 2008).

Contemporary evolution might often prove crucial to the conservation of biodiversity (Stockwell et al. 2003), including climate change (Bradshaw and Holzapfel 2008). For example, theoretical models have shown how altered environments cause maladaptation that compromises individual fitness, population size, and the probability of persistence (Bürger and Lynch 1995; Gomulkiewicz and Holt 1995; Orr and Unckless 2008). Empirical confirmation has been slower but some nice examples have been advanced (Both et al. 2006). The same theoretical models have then illuminated the circumstances under which populations might be able to adapt to these environmental changes. Supporting

some of these expectations, studies of natural populations have shown that short-term changes in adaptive traits can indeed improve individual fitness (Gordon et al. 2009), enhance population productivity (Kinnison et al. 2008), and increase population size (Pelletier et al. 2007).

However, evolution will not always save populations facing environmental change. It is therefore important to closely examine how contemporary evolution is influenced by a variety of factors, including genetic variation (Etterson and Shaw 2001; Hoffmann et al. 2003; Lavergne and Molofsky 2007), gene flow (Hedrick 1995; Garant et al. 2007), population size and stochasticity (Fagan and Holmes 2006), and phenotypic plasticity (Price et al. 2003; Ghalambor et al. 2007). All of these factors can be directly and indirectly modified by human activities, thus establishing direct ties between evolutionary insights and management decisions. And, of course, some species might have insurmountable genetic, physiological, or life-history limits to certain types of adaptation (Both and Visser 2001; Bernardo et al. 2007)—these need to be clarified for the proper management of endangered species.

Human activities can thus cause considerable contemporary evolution within populations, and these activities can alter the very course of evolutionary diversification (Hendry et al. 2006; Seehausen et al. 2008). As one example, human-caused eutrophication in Lake Victoria reduced the quality of sexual signals that maintained reproductive isolation between species, thus precipitating a hybrid swarm (Seehausen et al. 1997). Likewise, human-mediated introductions can create opportunities for hybridization between exotic and native species, which under some circumstances can result in the origin of new aggressive species that do further harm to ecosystems (Ayers et al. 2009).

This section has summarized some of the evidence that human disturbances cause contemporary evolution in natural populations. These changes can make the difference between population persistence versus extirpation, and the outcome will depend on various ecological, demographic, and evolutionary opportunities and constraints. This realization points to the importance of understanding not only the causes of current biodiversity, and of conserving the resulting biodiversity patterns, but also of understanding and conserving evolutionary processes that will influence future biodiversity.

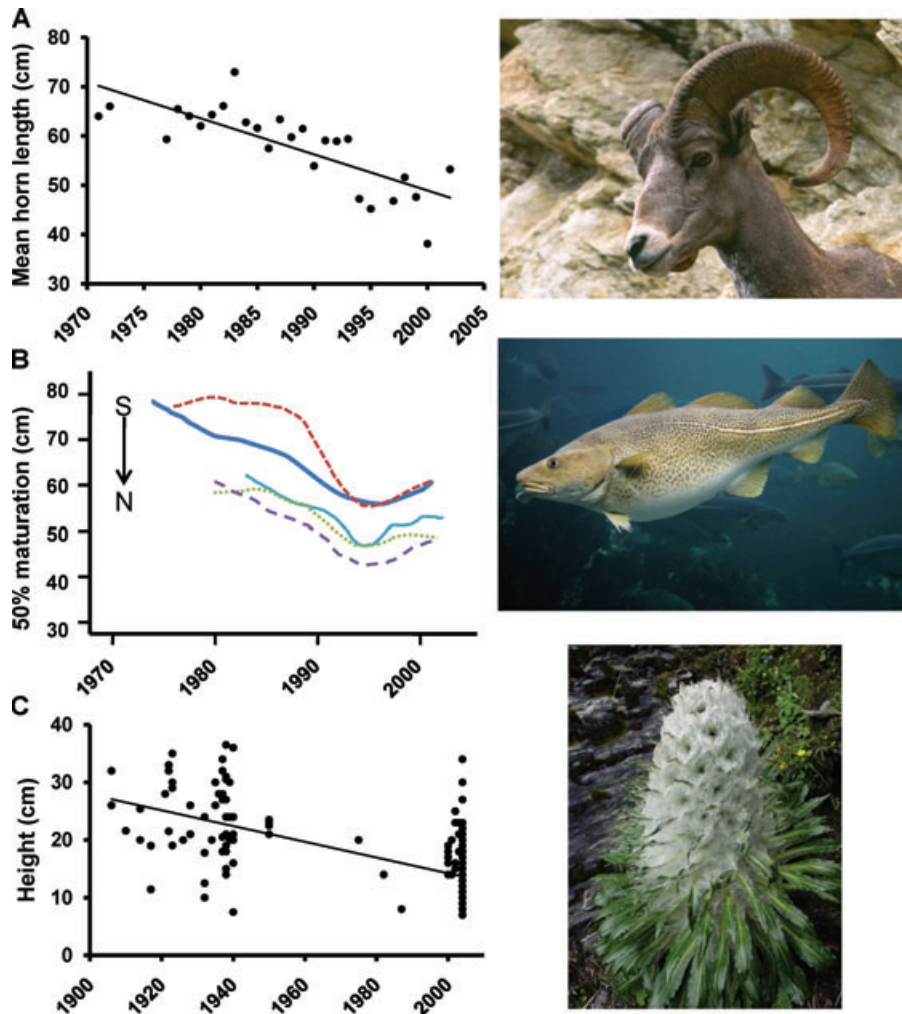
### *Implications for Communities, Ecosystems, and Humans*

We now extend ideas from the previous section into a consideration of how contemporary evolution can have broad impacts on ecological parameters, including community dynamics and ecosystem functioning, as well as potential consequences for human health and welfare. Particularly dramatic and well-known

examples relate to the evolution of resistance by viruses, bacteria, insects, and weedy plants in the face of our chemical attempts to control them (Palumbi 2002). The resulting effects on our health and prosperity are a constant reminder of the dramatic importance of evolution in our daily lives. Here, however, we focus on emerging insights into other evolutionary effects that might initially be less obvious but ultimately prove just as important.

“Eco-evolutionary dynamics” refers to interactions and feedbacks between ecology and evolution on contemporary time scales (Thompson 1998; Hairston Jr. et al. 2005; Carroll et al. 2007; Pelletier et al. 2009; Post and Palkovacs 2009). One example of research in this area is the demonstration that genetic diversity within plant populations influences arthropod diversity, primary productivity, decomposition rates, and nutrient cycling (Zhu et al. 2000; Whitham et al. 2006; Bailey et al. 2009; Johnson et al. 2009). Another example is the demonstration of how functional trait differences among closely related fish populations can substantially alter the structure of aquatic invertebrate communities (Palkovacs and Post 2008; Palkovacs et al. 2009). These results show that standing genetic variation can influence ecological processes, which leads to the prediction that contemporary changes in this genetic variation can influence important ecological processes. Experimental confirmation of this prediction has come from evidence that predator–prey oscillations in rotifer–algal laboratory microcosms are dramatically altered by ongoing evolutionary change (Yoshida et al. 2003).

The existence of eco-evolutionary dynamics means that evolutionary principles should be integrated into the concepts of sustainability, ecosystem services, and biosecurity. The examples are manifold—although only a few will have to suffice here. First, overharvested populations often show phenotypic changes that reduce the value of those resources for stakeholders, including the evolution of smaller size in intensively harvested ungulate, fish, and plant populations (Fig. 4). In some cases, these changes then hamper population recovery because smaller individuals often have lower reproductive rates. Second, evolutionary changes in invasive species can increase their impact on native species (Mooney and Cleland 2001; Strayer et al. 2006), as well as their geographical spread (Phillips et al. 2006; Urban et al. 2007). Third, as has already been noted, hybridization between exotic and native species can lead to new invasive species that have particularly dramatic effects on their environment (Schierenbeck and Ellstrand 2009). Fourth, the evolution of photosynthetic properties in algae might influence future climate change (Bell and Collins 2008). Fifth, human-manipulated populations (hatchery fish, crop plants, genetically modified organisms [GMOs]) can show dramatically reduced genetic variation, which can have devastating consequences for susceptibility to pathogens (Zhu et al. 2000). Sixth, evolution in human-manipulated populations can negatively impact the adaptation and productivity of nearby wild



**Figure 4.** Examples of changes in adult body size for harvested wild populations. Panel (A) shows trophy-hunting induced decreases in horn length for 4-year-old bighorn sheep (*Ovis canadensis*) rams on Ram Mountain Alberta (redrawn from Coltman et al. 2004). Panel (B) shows commercial-fishing induced decreases in mean size at maturity for 5-year-old female Atlantic cod (*Gadus morhua*) from five sites (different lines) in the Northwest Atlantic (redrawn from Olsen et al. 2005). Panel (C) shows harvesting-induced changes in the height of snow lotus (*Saussurea laniceps*) plants at flowering (redrawn from Law and Salick 2005). Photos used with permission of Andrew Hendry (bighorn sheep), Dieter Craasmann (Atlantic cod), and Wayne Law (snow lotus).

populations with which they interbreed (Ellstrand et al. 1999; Ford 2002; Araki et al. 2007).

As the foregoing examples illustrate, human-induced evolutionary change can cause major problems for society. Understanding these possibilities then provides opportunities for avoidance or mitigation, or perhaps even to turn evolution to our advantage. Some applications come from understanding the (re)emergence, spread, and control of pathogens (Morens et al. 2004). For example, evolutionary knowledge has been used to locate the Middle East source of West Nile Virus (Petersen and Roehrig 2001), and to monitor its spread across North America (Bertolotti et al. 2007). Similarly, an explicit evolutionary approach has informed the time of origin, rate of diversification, global spread, and likely chimeric molecular constitution of the A(H1N1) 2009 influenza virus

(Smith et al. 2009). Other applications relate to invasive species. For example, evolutionary principles have been used to identify and eradicate the invasive alga *Caulerpa taxifolia* in California (Jousson et al. 2000) and to document the spread of *Phragmites* in the New World (Saltonstall 2002). Evolutionary principles have also been used to (1) assess the benefits of manipulating gene flow for endangered species (Hedrick 1995; Pimm et al. 2006), (2) consider the best designs for marine reserves (Baskett et al. 2005), and (3) evaluate the risks of GMOs (Kelly et al. 2005). And, to return to the outset of this section, evolutionary principles are now routinely adopted in strategies to prevent the evolution of drug resistance in human pathogens (Neese and Stearns 2008).

A clear conclusion inescapably emerging from the above examples is that evolutionary thinking should be an integral part



of ecology, conservation, natural resource management, and human health care. Evolutionary biologists should increasingly take advantage of opportunities to make contributions in these areas, because these serve the dual purpose of addressing societal concerns about biodiversity while also providing basic insights into evolution.

### *Evolutionary Biology within DIVERSITAS: The bioGENESIS Project*

Evolutionary biologists can aid biodiversity science, conservation, and policy by (1) focusing their research on questions relevant to these topics, perhaps along the lines described above; and (2) becoming actively involved in transmitting the resulting insights to other scientific disciplines and to policy makers. These goals fall within the purview of DIVERSITAS, an international research programme of biodiversity science under the auspices of ICSU (International Council for Science), IUBS (International Union of Biological Sciences), SCOPE (Scientific Committee on Problems of the Environment), and UNESCO (United Nations Educational, Scientific and Cultural Organization). DIVERSITAS was formed to “understand, conserve, and sustainably use biodiversity,” and is initially organized around a set of three “Core Projects” entitled bioDISCOVERY, ecoSERVICES, and bioSUSTAINABILITY. More recently, an explicit evolutionary Core Project, bioGENESIS, has been formed (Yahara and Donoghue 2007; Donoghue et al. 2009). bioGENESIS aims to provide an evolutionary framework for biodiversity science, conservation, and policy, and thus seeks to address the broad topics, and accomplish some of the specific goals, that have been outlined above.

bioGENESIS focuses on an evolutionary framework, and the necessary integration with other aspects of biodiversity science is achieved through the links with the other Core Projects and the broader DIVERSITAS programme. For example, we referred above to the use of phylogenetic diversity measures (Faith 1992; Forest et al. 2007) to set regional biodiversity conservation priorities. Evidence so far suggests that alternative regional priorities, based on conventional species-level analyses, or ecosystem services, might not capture these phylogenetic or evolutionary values (Forest et al. 2007). The bioGENESIS Core Project not only promotes these evolutionary aspects of biodiversity, but, as a broader part of DIVERSITAS, helps to integrate these aspects with ecosystem services and other values to society. Decision-makers can thus be provided with a more complete range of values on which to base policy.

A Science Plan for the first stages of bioGENESIS has now been produced ([www.diversitas-international.org/biogeneration](http://www.diversitas-international.org/biogeneration); Donoghue et al. 2009), and we are moving forward with the implementation of its objectives. We now hope to advance these

objectives, broaden the scope and reach of bioGENESIS, and bring more evolutionary biologists and their ideas into the project. There are many ways to participate in DIVERSITAS and to foster the aims of the bioGENESIS Core Project. In particular, we encourage evolutionary biologists to propose activities that support the goals outlined above and in the bioGENESIS Science Plan. This will help us achieve a better understanding of the contributions that evolutionary biology can make to a truly integrative and relevant biodiversity science.

### *Conclusions*

A major impediment to reducing biodiversity loss around the globe is our limited knowledge of the true extent of biodiversity, its evolutionary history, and the forces that shape responses to environmental change. We are thus currently underprepared to recognize contemporary changes and to implement appropriate responses. Although much fundamental work remains to be done, the information currently available already allows some inferences and predictions about the future. It also allows us to formulate broad areas of evolutionary investigation that are of direct relevance to the discovery, documentation, sustainable use, and protection of biodiversity. In short, evolutionary biologists can make crucial contributions to combating the loss of diversity and improving the health of our planet.

Despite the great significance of evolutionary biology to a broad range of issues surrounding biodiversity, these insights seem only rarely to reach other relevant fields, not to mention the general public and policy makers. We therefore urge the evolutionary biology community to engage in activities that are of direct relevance to current environmental issues, and, more generally, to help to foster a better understanding of the societal contributions of our discipline.

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