11

ECOLOGY AND EVOLUTION OF INFECTIOUS DISEASE

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CENTRAL ISSUES

Two leading challenges in environmental sciences are understanding the causes and consequences of earth's diminishing biodiversity and understanding the ecology and evolution of infectious diseases. At the intersection of these challenges is the global decline of amphibians. Emerging infectious diseases are among the suspected causes of many declines (Daszak et al. 1999; Carey et al. 2002a; Chapter 10, this volume). Emerging infectious diseases are diseases that are newly recognized, novel in a population, or rapidly increasing in incidence, virulence, or geographic range (Daszak et al. 2000). Although infectious diseases are suspected of causing the extinction of some species (McCallum and Dobson 1995), basic epidemiological theory suggests that pathogens are unlikely to cause extinction (Dobson and May 1986). A key to understanding the role of pathogens in amphibian declines is reconciling this discrepancy, which will require understanding pathogen emergence, host susceptibility, and the joint population dynamics of host and pathogen.

Host–pathogen interactions must be understood at several scales—the individual organism, local population, metapopulation, and region—and the outcome at one scale does not extrapolate simply to another. For example, contrary to what we might expect, a pathogen that kills individual hosts rapidly does not invariably drive a population or species to extinction, because a high transmission rate is necessary for pathogens to exert significant population-level effects. In theory, high transmission favors more virulent pathogens, at least as long as the incidence of disease is increasing in the population (Ebert 1999), but as hosts die, population density declines and transmission decreases. Eventually, the host population reaches a low density where trans-

mission ceases; hence, we expect that disease alone will not cause extinction in a one host–one pathogen system.

The chytrid fungus *Batrachochytrium dendrobatidis* and ranaviruses are among the leading suspected causes of many amphibian declines (Daszak et al. 1999; Carey et al. 2002a; and Chapter 10, this volume). Chytrids and ranaviruses have wide host ranges (Appendix 11.1), and our best evidence indicates that they differ in how each affects amphibian population dynamics. Viruses generally cause host populations to fluctuate, whereas declines, even extinctions, attributed to chytridiomycosis are reported from Big Tableland, Queensland, Australia (Berger et al. 1998); Fortuna Forest Reserve, Panama (Berger et al. 1998); Peñalara Natural Park, Spain (Bosch et al. 2001); and Rocky Mountain National Park, Colorado (Muths et al., in press). *B. dendrobatidis* infects 46 of the Australian frog species analyzed to date; 13 species appear to have declined, three are extinct, and many of these occurred at high elevation. Three-quarters of frog species surveyed in Costa Rica and Panama have declined (Lips 1999; Young et al. 2001; Lips and Donnelly 2002); chytrids are associated in almost every instance. Four Central American sites show similar patterns of susceptibility among frog species: the most susceptible species have restricted elevation ranges, large body sizes, and breed in streams (K. Lips, J. Reeve, and L. Witters, Southern Illinois University, unpublished data). Although there are chytrid-associated declines and extinctions, frogs infected with *B. dendrobatidis* also occur at sites without apparent evidence of host population declines in Canada (Quebec: M. Ouellet, personal communication; British Columbia: Raverty and Reynolds 2001) and in the United States (Maine: J. Longcore, University of Maine, personal communication; Georgia: P. Daszak and D. Porter, Consortium for Conservation Medicine, Lamont-Doherty Earth Observatory, Columbia University, personal communication; and Arizona: V. Miera and E. Davidson, Arizona State University, personal observation).

In this chapter, we review amphibian host–pathogen dynamics at the local, metapopulation, and regional scales; Carey and colleagues in Chapter 10 focus on the individual level of analysis. We use two disease models, the tiger salamander–ranavirus system and the amphibian–chytrid system. At each scale we focus on life history variation and genetic variability of hosts and pathogens.

HOST–PATHOGEN DYNAMICS AT THE LOCAL POPULATION SCALE

At the local scale, infected hosts transmit a pathogen to susceptible hosts, which then spread the infection to others before recovering or dying. Depending on conditions, transmission among hosts either causes an epidemic or the disease dissipates. Most simple epidemic models account for disease dynamics at the local scale, and analyses at other levels, especially the metapopulation level, are often extrapolations of the

host–pathogen dynamics of local populations. Ranavirus epidemics in tiger salamanders (*Ambystoma tigrinum*) illustrate host–pathogen dynamics at the local scale.

A breeding pond, marsh, or earthen stock tank is the central point of activity for a tiger salamander population. Eggs are laid in such aquatic habitats in late winter, spring, or summer and develop into quickly growing aquatic larvae that usually metamorphose in the same season. Metamorphosed salamanders overwinter in terrestrial refugia; some larvae and neotenic adults overwinter in the water (Sexton and Bizer 1978; Collins 1981). In several subspecies, hatchlings may develop into either a typical larva that feeds on invertebrates or a cannibalistic phenotype that preys on invertebrates and conspecifics (Collins et al. 1993). Epidemics kill larvae and metamorphosed animals, and usually occur during late summer or early fall when host densities are high, but after the peak densities (Pfennig et al. 1991; personal observation). Ambystoma tigrinum virus (ATV) and the closely related Regina ranavirus (RRV) are virulent pathogens that spread by close contact between infected and susceptible tiger salamanders (Jancovich et al. 1997; Bollinger et al. 1999). The viral life cycle appears to be confined to tiger salamanders—no syntopic alternate hosts are known (Jancovich et al. 2001)—and ATV is infectious for only about 2 weeks outside a host. ATV epidemics progress on a much shorter time scale than larval tiger salamander development rates. Infections are generally lethal within 2 or 3 weeks. Salamander reproduction and recruitment occurs annually, so within a season, dead or recovered salamanders generally are not replaced with additional susceptible animals. This phenology supports host–pathogen dynamics that result in epidemics. The disease dissipates within a season as fewer and fewer of the original larvae remain to be infected.

Disease may alter life history trajectories, potentially affecting amphibian fitness components such as timing of and size at metamorphosis (Wilbur and Collins 1973; Alford and Harris 1988). Disease increases risk in aquatic habitats; therefore, selection should favor early metamorphosis by amphibian larvae in ephemeral aquatic habitats. Death need not be caused directly by a pathogen; rather, in an ephemeral pond, a pathogen could slow larval growth and development to the point that host death would result from drying of the aquatic habitat before metamorphosis is possible. This hypothesis was tested by rearing larval salamanders from two areas of Arizona (White Mountains and San Rafael Valley) in mesocosms with and without ATV. Survival and growth rates were lowest in viral treatments and in animals from the San Rafael Valley, a region with low genetic variability (Jones et al. 1988; M. Parris, E. Davidson, and J. Collins, University of Memphis, unpublished data). A second laboratory study reinforced the result of delayed metamorphosis in disease environments (J. Brunner, D. Schock, J. Collins, and E. Davidson, Arizona State University, unpublished data). However, although infected animals had slower growth rates, they were not exposed to a drying regime. It is possible that larvae in desiccating environments may facultatively reduce their larval period to metamorphose quickly.

Because the experiments thus far have not challenged infected larvae with a desiccating environment, it remains to be tested how larvae respond developmentally to such conditions. Nevertheless, longer larval periods increase the time exposed to aquatic predators, which may have important fitness consequences for salamanders (Wilbur and Collins 1973; Alford and Harris 1988).

How does ATV persist between years? Animals that survive exposure to ATV may harbor transmissible infections for more than six months (J. Brunner, D. Schock, J. Collins, and E. Davidson, Arizona State University, unpublished data). We have also recorded dispersing metamorphosed animals carrying virus at the end of an epidemic, and we have indirect evidence that metamorphosed animals return infected. Persistence between epidemics is apparently due to long-lived, transmissible, sublethal infection; however, we acknowledge the possibility that the virus is sequestered in a still-unidentified, aquatic reservoir. Larvae and metamorphosed animals that survive infection with no clinical signs of disease can transmit infections to naïve individuals seven months after exposure, suggesting that animals with subclinical infections could transmit virus among populations or between years (J. Brunner, D. Schock, J. Collins, and E. Davidson, Arizona State University, unpublished data). The complex salamander life history alone may provide a reservoir (i.e., metamorphosed animals) that explains viral persistence and transmission. Laboratory experiments show that larvae are approximately 10 times more likely to recover from ATV infection than are metamorphosed animals (J. Brunner, D. Schock, J. Collins, and E. Davidson, Arizona State University, unpublished data). Infected, metamorphosed salamanders returning to a pond to breed may reinitiate an epidemic.

Chytrid fungus dynamics differ from viral dynamics in key ways. *Batrachochytrium dendrobatidis* has a wide host range (Appendix 11.1), and may have an independent saprophytic stage. Pathogenicity varies widely by host species, life stage, and environmental conditions. For example, American bullfrogs (*Rana catesbeiana;* E. Davidson, J. Jancovich, Arizona State University, unpublished data) and tiger salamanders (E. Davidson, M. Parris, J. Collins, J. E. Longcore, A. Pessier, J. Brunner, R. Medville, Arizona State University, unpublished data) are resistant carriers, at least in the laboratory; the Australian frog *Litoria caerulea* (White's treefrog) is susceptible in the laboratory (Pessier et al. 1999). Interspecific variation in susceptibility means that host–pathogen dynamics may differ among amphibian community types. An amphibian community with a resistant reservoir host could allow chytridiomycosis to persist in one or more species while driving other susceptible host species to extinction.

Pathogenicity also varies intraspecifically by life stage. Chytrids only infect keratinized epithelial tissue (Fellers et al. 2001). In tadpoles, mouthparts are the only keratinized tissue, whereas in metamorphosed animals keratin is distributed throughout the epidermis. Therefore, frogs with overlapping generations of larval and metamorphosed stages may act as their own pathogen reservoir. There is no evidence that the fungus is lethal in tadpoles, but infected larvae have slower growth and development

rates than uninfected larvae. M. Parris, E. Davidson, and J. Collins (University of Memphis, unpublished data) varied intraspecific density, predation, and presence of chytrids in gray treefrog (*Hyla versicolor;* Figure 11.1) larvae in mesocosms. Larvae reared with chytrids were smaller at metamorphosis and had longer larval periods when reared with predators. In a second experiment, F_1 hybrids of plains and southern leopard frogs (*Rana blairi* and *R. sphenocephala*) had smaller body masses at metamorphosis than parents when exposed to chytrids, suggesting disease resistance may be reduced via genetic recombination inherent in hybridization. These experiments indicate that chytrid effects on host life history may be complex and indirect.

Environmental cofactors can significantly alter growth and transmission of a pathogen and/or ability of its host to respond. This is particularly true for external pathogens like chytrid fungi and environmentally sensitive amphibian hosts. For example, different thermal and hydric environments, which tend to cycle together, may affect development of chytridiomycosis. *Litoria chloris* continually exposed to mist, characteristic of natural rainforest habitat in Australia, developed clinical disease and died significantly faster than animals exposed to either continual rain or dry air with access to standing water (R. Alford, James Cook University, unpublished data).

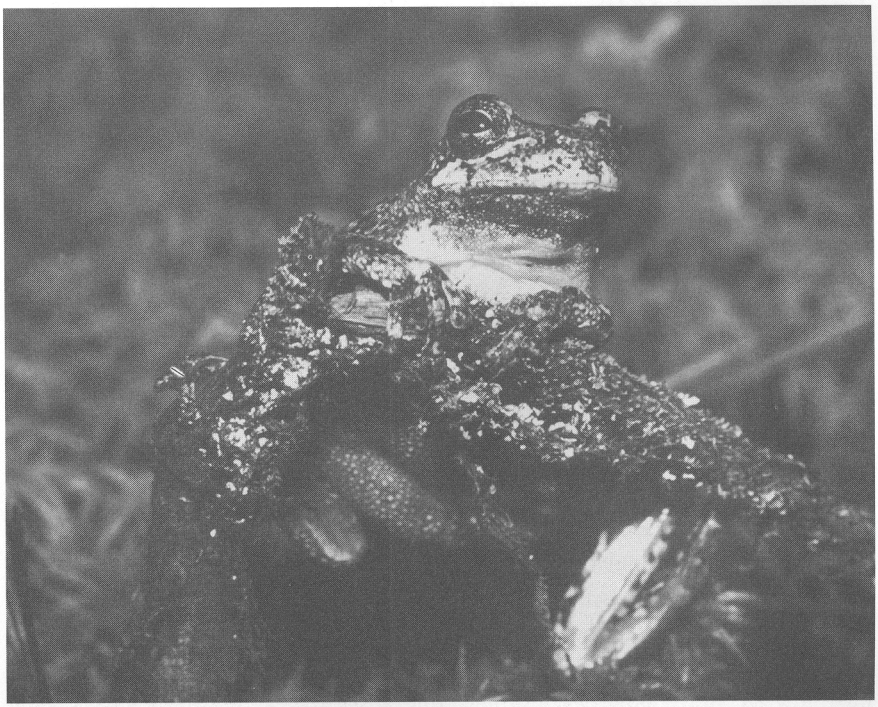

Figure 11.1. Gray treefrog (*Hyla versicolor*). (Photo by David Scott, Savannah River Ecology Laboratory)

Several additional lines of evidence suggest that microenvironment affects infectivity of the chytrid fungus *Batrachochytrium dendrobatidis*. In culture, the fungus grows between 4°C and 28°C, with optimal growth between 15°C and 28°C. Infected western toads (*Bufo boreas*) in Colorado held at either 12°C or 23°C had high mortality, but toads kept on a 5°C/30°C diel temperature regime for 42 days survived, suggesting that a natural daily range of body temperatures could keep the fungus in check (C. Carey, University of Colorado, unpublished data). Thus, frogs that exhibit different basking behaviors may be differentially susceptible to chytrid infection; short periods of high environmental temperature can halt disease progression and may clear animals of chytrid infections (R. Alford, James Cook University, personal communication).

There is no simple, general relationship between ultraviolet (UV)-B radiation and chytridiomycosis in amphibians. UV-B radiation may stress amphibians, making them more susceptible to infection (Carey 1993; Blaustein et al. 1994a). In a multifactorial mesocosm experiment in Oregon, chytrids had no effect on tadpole survivorship; tadpoles exposed to ambient UV-B levels had lower survival than those shielded from UV regardless of chytrid treatment (A. Hatch and A. Blaustein, Oregon State University, unpublished data). UV-B levels have increased about 4% in Central America over the past 20 years (B. Middleton, NASA, unpublished data), but present levels of ambient UV-B may decrease chytrid susceptibility of amphibians in Panama (P. Murphy and K. Lips, Southern Illinois University, unpublished data). Low pH (Harte and Hoffman 1989; Long et al. 1995) and fungal pathogens other than chytrids can also damage amphibians at various life stages (Kiesecker and Blaustein 1995; Berger et al. 1998; Pessier et al. 1999).

HOST–PATHOGEN DYNAMICS AT THE METAPOPULATION SCALE

Naturalists have long known that amphibian population sizes can fluctuate greatly from natural causes. A two- or three-fold increase or decrease in the number of adults from one reproductive season to the next is possible (Wilbur 1980), and even without epidemics, local extinctions are expected. But while a local population, or deme, may go extinct, recolonization from neighboring populations will "rescue" it, and so the regional population size remains relatively stable. However, rare species are statistically more likely to go extinct than common species because rare species generally have some combination of narrow geographic range, specialized habitat, and low abundance (Rabinowitz et al. 1986). Certain life-history traits (e.g., long lifespan, low fecundity, slow development, migratory stages, or complex life cycles) may also make species more vulnerable. K. Lips, J. Reeve, and L. Witters (Southern

Illinois University, unpublished data) found that some amphibian populations in Central America are declining because of ecological factors associated with rarity, although the best predictor was degree of association with stream habitats.

While some amphibian species are exceptions and do not fit the metapopulation pattern (e.g., even pond-breeding amphibians may not necessarily act as metapopulations; Marsh and Trenham 2001), metapopulation models are generally useful for understanding the spatial and temporal dynamics of many amphibian populations. Tiger salamander populations in the western United States are often closely associated with ponds (Collins 1981), and dispersal between breeding sites may be limited by distance such that local ponds/populations are somewhat independent (but see Trenham et al. 2001). In Arizona, we know of local populations that disappear, sometimes for several years, to be recolonized later, and all of the tiger salamander metapopulations that we monitor are apparently stable.

The metapopulation dynamics that maintain these salamander populations could also maintain their pathogens. If an occasional metamorphosed immigrant were infected sublethally by ATV, for example, the metamorph could initiate an epidemic on arrival at a susceptible host population. As noted above, salamanders can harbor transmissible, sublethal infections for more than 6 months. At the end of one fall die-off on the Kaibab Plateau, about 90% of the recently metamorphosed salamanders dispersing from a pond were infected. It is also the case that from the point of view of ATV, since salamanders are a major viral vector, the virus also has a metapopulation structure.

If dispersing amphibians bring pathogens with them, then human alteration of metapopulation structure can alter host–pathogen dynamics. Draining wetlands and similar activities that eliminate aquatic habitats/patches for amphibians increase the probability of metapopulation extinction, but also increase the prevalence of disease among populations such that pathogens go extinct within a local population. Increasing the availability of aquatic habitats, such as new farm ponds and stocktanks, should have the opposite effect. Since the pathogen also exists in this same metapopulation structure, facilitating movement between patches by adding or creating habitats, a common management tool, may make local host populations less independent. Theoretically, this can increase the probability of metapopulation extinction by facilitating the spread of contagious, virulent diseases (Hess 1996). The increased transmission between local populations achieved by easing movement between them might also select for enhanced viral pathogenicity, and increased probability of extirpating all demes.

The metapopulation dynamics of host and pathogen will be overwhelmed when the parasite is a host generalist or has a reservoir, as appears to be the case with chytridiomycosis. Numerous amphibian species are susceptible to infection, but they differ markedly in disease and mortality. The widely distributed American bullfrog

(*Rana catesbeiana*) for example, appears unaffected by chytrid infection so that the prevalence of infections may be very high. Karen Lips found that sentinel, uninfected frogs in Central America contracted lethal infections. The fungus apparently remains viable in the environment, probably in streams, increasing the chance of exposure to the pathogen. Susceptible species, therefore, even though patchily distributed in the landscape, may never be free from exposure to chytrids. Reservoirs are thought to make even metapopulation-level extinction far more likely.

As mentioned previously, the development of lethal chytridiomycosis also depends heavily on abiotic or environmental conditions, such as low temperatures, high moisture, and a nearly neutral pH. These conditions, however, are distributed patchily in space and time, and will conceivably affect disease dynamics among patches. Epidemics associated with chytrids occur in the cooler months in Arizona (Sredl 2000) and at higher, cooler elevations in tropical Australia and Central America where temperatures fall within chytrid tolerance (Berger et al. 1998; Lips 1998, 1999). Declines due to chytridiomycosis are most common at higher elevations in the tropics (Alford et al. 2001; Young et al. 2001). Low-elevation sites have temperatures typically above the limit for chytrid growth (e.g., >29°C; Longcore et al. 1999). Cloud forest stream water is often characterized by shaded, low UV conditions, and is consistently buffered between pH 6.8 and 7.5, a range favorable for chytrid growth; chytrid-susceptible anurans are declining in these habitats. Laboratory studies in Panama indicated that high water temperatures, even for short periods, might slow or even allow clearance of chytrid infections. Temperature, pH, and UV-B radiation, acting alone or synergistically, may ultimately determine the degree of chytrid infection in stream anurans (P. Murphy and K. Lips, Southern Illinois University, unpublished data).

Movement of amphibians into patches of habitat that are optimal for growth of chytrids is important for sustaining disease. Lips and colleagues found that mid-elevation populations of the emerald glassfrog (*Centrolene prosoblepon*) at El Copé, Panama, have declined but still persist. Genetic analyses indicate a bias toward upstream movement and suggest that these populations survive because of migration from downstream sites. Although a means for frog persistence, this recolonization may also provide the transmission necessary for long-term chytrid persistence at the site, and thereby inhibit reestablishment of susceptible species. Immigrants coming from lower elevations may also carry sublethal infections that are expressed as lethal infections when the host reaches a locality with environmental conditions that support disease progression.

The relationship between disease dynamics and metapopulation structure is not well understood. Considerable work is needed to unite the theories for metapopulations, epidemiology, and host–pathogen coevolution in ways that support generalizations and predictions. Relative gene flow rates of pathogens and their hosts, and the resulting population genetic structures, are likely important in determining disease dynamics. These variables influence where and when local adaptation may

arise; factors like relative virulence of pathogens and whether diseases are endemic or epidemic are also affected (Gandon et al. 1996; Thrall and Burdon 1997; Gandon and Van Zandt 1998; Otto and Michalakis 1998; Lively 1999).

HOST–PATHOGEN DYNAMICS AT THE REGIONAL SCALE

To understand chytrids and ranaviruses at the regional level, we must understand how they spread and become established. We know that chytrids are in frog populations spanning the United States, but is the distribution of these pathogens continuous with Central American strains (Appendix 11.1)? Amphibian dispersal alone is unlikely to explain pathogen movement on the regional scale, and thus, without the aid of humans or alternative long-distance carriers like birds, we expect the movement of amphibian pathogens between regions to be low. Metapopulations within regions, and regions themselves, should be relatively independent host–pathogen systems. This should result in pathogens from different regions being genetically divergent and locally adapted host–pathogen systems (see below). For example, cannibalistic tiger salamander larvae are rare in the Kaibab Plateau region of northern Arizona where epidemics are common (Pfennig et al. 1991; Jancovich et al. 1997), and cannibals are almost never found in the San Rafael Valley in southern Arizona where epidemics are very common. Cannibalism is most frequent in regions where ranaviral disease is infrequent. Regional variation in epidemics may explain regional variation in occurrence of cannibals because they are more likely to contract disease by eating infected conspecifics.

Despite a priori reasons to expect genetic variability between sites, there are several possible modes of pathogen dispersal that may explain the lack of genetic variability we are finding among virus and chytrid isolates (see below). For example, we are investigating the possibility that birds move sufficient amounts of virus to initiate epidemics in regions separated by thousands of kilometers, as many tiger salamander epidemics occur along migratory bird routes (D. Schock, Arizona State University, personal communication). Game fish such as walleye, which are stocked in many areas, could also act as vectors of salamander viruses on a regional scale (D. Schock, T. Bollinger, and J. Collins, Arizona State University, unpublished data).

Human dispersal of pathogens may have a role in defining the geographic distribution of ranaviruses and chytrids around the world. The pet trade, aquaculture, movement of bait animals, transportation of water and mud, and inadvertent and deliberate movement of species may easily introduce pathogens into naïve populations (Appendix 11.1). Humans moving salamanders, especially as fishing bait, can disperse infected salamanders between normally isolated populations. In the United States, tens of thousands of salamanders are moved between ponds and as far as

from Nebraska to Arizona (Collins et al. 1988), and ATV has been isolated from salamanders obtained from a bait supplier in Phoenix, Arizona (A. Storfer, J. Jancovich, D. Schock, and J. Collins, Washington State University, unpublished data).

Genetic variation in host and pathogen can provide important information, such as estimates of time since divergence in pathogens and resulting coevolutionary patterns. About 80 chytrid isolates are now in culture, and 50 are being analyzed with amplified fragment length polymorphisms (James et al. 2000; Bradley et al. 2002). In addition, P. Daszak and D. Porter (University of Georgia, unpublished data) analyzed 613 bases of internally transcribed spacer region portions (ITS1 and ITS2) of 18S and 28S ribosomal DNA and a portion of the 5.8S gene of 39 chytrid strains. There is a maximum of 5% sequence divergence among all isolates (low for fungi) despite their global distribution, and some Australian and Central American chytrid isolates are identical (P. Daszak and D. Porter, Consortium for Conservation Medicine, Lamont-Doherty Earth Observatory, Columbia University, unpublished data). Multilocus sequence typing showed only five variable nucleotides of 5,918 total bases at 10 loci among 32 globally distributed chytrid strains, suggesting recent emergence (E. Morehouse, T. James, A. Ganley, R. Vilgalys, L. Berger, and J. Longcore, Duke University, unpublished data). Collectively, the data support the conclusion that amphibian chytridiomycosis is an emerging infectious disease whose spread was possibly facilitated by humans (Daszak et al. 1999).

Viral phylogeographic analyses also show shallow sequence divergence and likely recent spread. Genome-level comparisons between ATV (J. Jancovich, E. Davidson, N. Parameswaran, J. Mao, V. Chinchar, A. Storfer, J. Collins, and B. Jacobs, Arizona State University, unpublished data) and RRV (Mao et al. 1999) show low sequence divergence at three conserved genetic markers. The major capsid protein shows less than 1% sequence divergence among isolates from Arizona to Saskatchewan and no variation within sites; the methyltransferase gene also shows no variability (J. Jancovich, E. Davidson, N. Parameswaran, J. Mao, V. Chinchar, A. Storfer, J. Collins, and B. Jacobs, Arizona State University, unpublished data). These data suggest that we are investigating several strains of one viral species, and in concert with infected salamanders from bait shops, support the possibility of human-enhanced viral spread (J. Jancovich, E. Davidson, H. Weimann, S. Kumar, J. Collins, A. Storfer, and B. Jacobs, Arizona State University, unpublished data). Despite little genetic differentiation among viral strains, tiger salamanders crossinfected with viral isolates from Arizona, Saskatchewan, and Manitoba differed in survivorship, time to death, and temperature tolerance, providing evidence of local adaptation (D. Schock, Arizona State University, unpublished data). An eIF-2α homolog, one of several genes found during sequencing of ATV and RRV (J. Jancovich, E. Davidson, N. Parameswaran, J. Mao, V. Chinchar, A. Storfer, J. Collins, and B. Jacobs, Arizona State University, unpublished data), is particularly interesting because it modulates host immune response (especially antiapoptosis function) in other viruses. When this homolog was inserted

in place of a vaccinia (pox virus) gene, it restored wild-type phenotype (i.e., inhibition of host protein synthesis, coupled with the selective translation of viral mRNAs). These results are the first to suggest that ranaviruses are capable of immune evasion and that their hosts may have an interferon-like activity (B. Jacobs, Arizona State University, unpublished data). Ongoing studies will test the hypothesis that genetic variability in this homolog explains regional variation in viral virulence.

Variation in viral effects on amphibian populations could also be explained by the extent to which viruses and hosts have coevolved. To investigate coevolutionary patterns, A. Storfer (Washington State University, unpublished data) sequenced 900 bp of mtDNA in tiger salamanders from sites with ranavirus epidemics from southern Arizona to southern Canada. Salamanders show little sequence divergence among all sites despite the large geographic area, and the resulting gene genealogy is being reconciled with that of ranavirus isolates from the same regions to test for concordance and local adaptation. Genetic variability in other loci (e.g., MHC) is being investigated to test for a correlation between variation and resistance.

Both viruses and chytrids have shorter generation times than their amphibian hosts, so we expect higher fitness on sympatric versus allopatric hosts. Preliminary support for this prediction comes from cross-infection experiments that exposed tiger salamanders from three widely separated regions in Canada and the United States to ranaviruses collected from the same regions (D. Schock, Arizona State University, unpublished data). As predicted by theory, virus isolates were most effective at evading the defenses of their native host population (estimated by several criteria including percentage of hosts surviving and percentage of hosts sublethally infected), indicating ranavirus isolates are locally adapted. Further, the results of novel host–pathogen pairings were unpredictable; that is, the outcome could not be inferred from knowing how the ranavirus isolate performed in its native host population. Given the increasing ease with which pathogens are moved on a global scale, these findings have important implications for wildlife conservation and epidemiology in general.

POTENTIAL SOLUTIONS

The interaction of environmental factors and population dynamics at the local, metapopulation, and regional levels governs both a pathogen's virulence and its possible emergence as an infectious disease. Amphibians and their pathogens offer ideal, if sometimes unfortunate, cases for studying these forces because there is a continuum from host–parasite coexistence to declines and extinctions of amphibian populations. We have discussed variables that might trigger epidemics and the spread of disease within and among populations. The spatial pattern of habitats dictates dispersal rates among populations, facilitating or slowing an epidemic. Pathogens can

alter host life history, and life history stages within the same host may vary in their capacity to serve as a pathogen reservoir. Explaining the emergence and spread of amphibian diseases means understanding the complex interaction of virulence, susceptibility to infection, and the population dynamics of host and pathogen. Each contributes individually and collectively to host–pathogen coexistence or extinction, and each operates at several scales.

Increased education, especially for those involved in protecting and restoring wetlands, is important. If infectious diseases are not considered in habitat conservation, there can be serious, unintended, and unexpected results. The guidelines of the Declining Amphibian Population Task Force (DAPTF) should be followed (available online at http://www.mpm.edu/collect/vertzo/herp/Daptf/fcode_e.html). The possibility of pathogen translocation must be incorporated into legislation and regulations for commercial activities such as the pet trade, bait trade, and aquaculture.

Further research is needed at the scale of the metapopulation. The key questions center on three areas related to how disease affects the likelihood of local population extinction, the probability of successful recolonization, and the source–sink status of subpopulations making up the metapopulation.

1. Dispersal rates and dispersal mechanisms of host and pathogen: How does fidelity to the breeding site vary among species? Are juveniles or adults more likely to disperse? What factors determine dispersal success and disease prevalence of dispersing animals? Will sublethal infections hinder dispersal by reducing the likelihood that infected animals will reach a new site?
2. Effect of disease on local population dynamics: How do epidemics interact with other phenomena (e.g., drought) to affect juvenile recruitment and the likelihood local populations will go extinct? Are there environmental or other factors (e.g., population density) that make some local populations experience epidemics more often than others?
3. Variation in the spatial and temporal patterns of disease outbreaks: Do local populations vary in susceptibility or resistance to disease? Do spatial patterns of disease outbreak vary with distance such that the spread of disease is consistent with transmission by dispersing, infected animals? Or, is the timing and occurrence of new outbreaks independent of epidemics at nearby sites? The latter might suggest human or other modes of disease introduction, or perhaps interactions with other stressors at the local population scale are responsible for epidemics.

The complexity of host–pathogen systems means that solving the problem of how we might minimize or eliminate disease as a contributor to global amphibian declines will not be easy. It seems clear, however, that at the very least we need a much better understanding of how humans might deliberately or inadvertently dis-

perse infected hosts and/or pathogens through commerce—pet trade, bait trade, aquaculture (Appendix 11.1)—and even ecotourism. If we can identify the sources of disease and control pathogen reservoirs, we might forestall the progress of epidemics and prevent susceptible amphibian species from being driven to extinction, perhaps by resistant, carrier species of amphibians. Metapopulation structure offers another way to manage disease. An important element in any effort to restore amphibian populations by constructing or rehabilitating aquatic habitats will be distributing habitats across a landscape in ways that minimize the spread of disease and the evolution of virulent pathogens while still allowing for successful colonization/recolonization of sites (e.g., Hess 1996). Finally, we need a better understanding of the environmental cofactors that might facilitate or inhibit the spread of disease or the susceptibility of amphibians to pathogens. Here again, the complexity of the interactions means that reaching answers and instituting solutions are likely to be difficult, but the alternative—simply watching and describing the loss of amphibian biodiversity—is unacceptable.

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