Chapter 13
Disease Ecology

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Introduction

In his 2008 strategic vision for the National Institutes of Health of the United States, Director Elias Zerhouni argued that medical care in the twenty-first century needs to be redirected (Zerhouni 2008). Despite progress in the practice of preventive medicine, he stated, most treatment still focuses on late intervention, once a patient's symptoms are already apparent. We need, he argued, to move instead toward "preemptive medicine" in which the development of symptoms is prevented altogether. Zerhouni illustrated this new approach by describing the discovery of genes that predispose certain individuals to particular diseases. With this knowledge, he argued, public health care providers could focus on prevention and early diagnosis in high-risk patients, rather than just on treatment.

We suggest that the full development of preemptive medicine must incorporate another type of strategy as well: the mitigation of disease by environmental monitoring and management. The pathogens that cause infectious diseases interact not just with their hosts to cause disease; they are also embedded within a web of interactions among organisms in ecological communities. Recent research in the ecology of disease has demonstrated that knowledge of these interactions can be used to predict, prevent, and mitigate the transmission of infectious diseases.

In this chapter, we describe this emerging understanding by defining four key principles of disease ecology. We begin by describing the important role of the density of disease organisms such as pathogens, hosts, and vectors (see Box 13.1) in the transmission of infectious diseases. But we also describe how in some situations, the behavior of organisms, including humans, can override density's importance. Further, we describe how disease outbreaks can often be anticipated well in advance

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by looking at the chain of ecological interactions that precede them. We then explore two examples of types of cryptic, indirect interactions that may occur in a wide variety of diseases of humans, their livestock, and their crops. In conclusion, we argue that recent research in disease ecology tightly links human health with environmental conservation and that a critical understanding of disease ecology is essential for establishing a preemptive medicine. This need is particularly strong for people in impoverished rural communities who are more vulnerable to infectious diseases, and who may have greater interaction with the natural environment.

Box 13.1 Disease Terms

Diseases are typically grouped into two categories: infectious and non-infectious. Non-infectious diseases are those caused by genetic disorders, by food, or by the environment (e.g. ultraviolet radiation which can lead to skin cancer). Infectious diseases are caused by infection of a *host* with an organism – a *pathogen*. Pathogens have traditionally been divided into two groups – *microparasites*, which include the smallest organisms (viruses, bacteria, fungi, and some protists); and *macroparasites*, which include organisms that can be seen with the unaided eye (e.g. helminths). Pathogens can be transmitted from one host to another in a variety of ways. Some pathogens are transmitted through sexual contact, others through contact with respiratory droplets, blood, or feces, and still more in other ways. Some pathogens require another organism (e.g. a mosquito, a tick, a fly – a *vector*) to transport them from host to host; these are the *vector-borne diseases*.

The Importance of Density

The chapter on land use by Myers in this volume has described myriad ways in which the environment can influence the transmission of infectious diseases. Conceptually, the examples so far have generally been quite straightforward. For example, the clearing of a forest for agriculture can increase habitat quality for a mosquito that serves as a disease vector (Singer and DeCastro 2001). Implicitly, these types of examples recognize the importance of population density in disease transmission – the more abundant a pathogen or vector or host is, the more frequently infectious diseases should be transmitted. For the past 30 years, the study of the ecology of diseases has been similarly focused on population density as a determinant of disease risk or severity.

Density is at the core of mathematical models that ecologists use to explore the effects of different factors on disease transmission. The simplest, and best-known, of these models is conceptually very simple. Imagine a pathogen, like a cold virus, that's transmitted directly between hosts. Within this model, hosts can be either infected or susceptible, meaning that they're capable of being infected.

Transmission between infected and susceptible hosts occurs at a particular rate, called the rate of transmission. In such simple models, the number of individuals who get infected during a given time is determined by the product of the rate of transmission, how many susceptible hosts there are (because they're the ones available to become infected), and how many infected hosts there are (because they're the ones who can transmit the infection). So in this model, the densities of susceptible and infected hosts, combined with the rate of transmission, entirely determine how many hosts will be infected in the future.

Models such as this simple susceptible-infected (or S-I) one and its extensions have been very useful. For example, derivations from this model can be used to determine what fraction of a population needs to be immunized to prevent the spread of an infectious disease, such as measles or mumps, and this information can then be used to guide public health efforts. Models can also estimate how small a host population needs to be to prevent a disease from spreading, and this information, too, can be used to determine effective public health strategies (for an excellent introduction to basic epidemiological models, see Allman and Rhodes 2004). A recent study using sophisticated density-based models identified the ecological causes of ongoing epidemics of measles in Niger, and suggested that a combination of sustained and reactive vaccination, coupled with stringent surveillance early during seasonal outbreak periods, could reduce mortality and morbidity substantially (Ferrari et al. 2008).

Despite the enormous utility of density-based models, however, the densities of hosts, pathogens, and vectors do not always tell the whole story. In the following sections, we focus on more complex ways in which organisms, including people, interact to affect human health directly, by influencing transmission of human pathogens, or indirectly, by affecting the health of crops or livestock. In many of these examples, ecological interactions can lead to surprising effects on health that could not be predicted from the density of hosts or vectors.

Density Isn't Everything

Bovine tuberculosis (BTb) is a serious disease that causes progressive emaciation in cattle and other mammals, including humans. The disease is caused by infection with the bacterium *Mycobacterium bovis*, a close relative of the bacterium that causes the more familiar human Tb. *M. bovis* is passed from host to host primarily through respiratory secretions and through milk (Cosivi et al. 1999). Humans can become infected from drinking infected milk that has not been sterilized.

To control BTb, public health professionals typically concentrate on reducing the density of infected cattle by closely monitoring herds and euthanizing cattle that show symptoms (Woodroffe et al. 2006). In some areas of the world, this approach has been effective, because the density of infected cattle is the critical factor in transmission. In Great Britain, however, BTb has repeatedly been a problem, despite efforts to solve the problem by culling infected cattle. One reason BTb has been hard to control in Britain is that cattle are not the only host species that can transmit

the disease. In the 1970s, scientists discovered that European badgers, *Meles meles*, are also effective hosts for *M. bovis* and they often live in proximity to cattle (Krebs et al. 1997). When this wildlife reservoir for the bacterium was discovered, farmers were given license to cull badgers to reduce badger densities and thus make them less likely to transmit infection to susceptible cattle (Griffin et al. 2005).

But reducing badger density through culling did not reduce transmission either. In fact, BTb incidence was 27% *greater* in areas that had been culled to reduce badger density compared to areas that hadn't been culled (Donnelly et al. 2003). Why? Because badgers are social animals that defend group territories. Culling disrupts their tightly knit social groups, causing them to increase movement distances and the sizes of their home ranges (Woodroffe et al. 2006). The result of this increased level of movement is to increase badger contact rates with cattle, and thus the transmission of tuberculosis.

Culling of badgers in Britain has pitted conservationists, who want to protect badger populations, against farmers, who want to protect their cattle (Krebs et al. 1998). But it turns out that both groups should be on the same side, at least on this issue. It's important to note that while BTb remains a huge *economic* issue in Britain, it is not a prominent issue for human health directly because of the widespread sterilization of milk for human consumption. But in other parts of the world, particularly in Africa, BTb is a major human health issue (Cosivi et al. 1999); we return to BTb in Africa later in this chapter.

The key underlying feature of the badger example is that social behaviors affect the number of interactions that can cause BTb; behavior trumps density. This might be an unusual, or even a unique example that makes an interesting story but isn't broadly applicable. But it turns out that the critical importance of behavior is a feature of many diseases, including a number that are particularly relevant to human health, as we describe below.

For certain kinds of diseases, the number of contacts between susceptible and infected hosts is relatively constant; it doesn't increase as the density of hosts increases. The classic examples are sexually transmitted diseases like HIV/AIDS (Lloyd-Smith et al. 2004). The number of sexual contacts that an individual person has is limited at a relatively constant level; people generally don't have a greater number of sexual contacts just because they live among a higher-density population. The transmission of sexually transmitted diseases depends, then, on the *percentage* of hosts that are infected, because this represents the chance that a particular sexual encounter includes an infected host (Fig. 13.1). A similar situation is thought to exist for diseases transmitted by arthropod vectors such as mosquitoes and ticks. The number of blood meals taken by a vector on a host species tends to be fixed at a relatively constant level. For example, ticks tend to feed once per life stage and female mosquitoes tend to feed once per egg-laying event, with roughly constant intervals between such events[1]. Therefore, the probability that a particular vector

[1]Important exceptions to this general rule occur, for example, when environmental factors such as climate warming accelerate biting rates of some vectors.

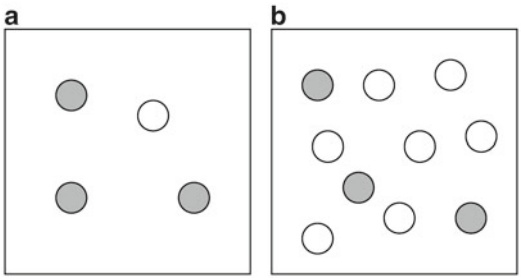

Fig. 13.1 Frequency-dependent versus density-dependent transmission for a sexually-transmitted infectious disease. In density-dependent transmission, the density of infected hosts (*gray circles*) is equal in both panels. Thus, an uninfected host is at equal risk in both cases. However, the situation changes for frequency dependent transmission. If people have relatively constant rates of sexual encounters regardless of density, a particular person will have a sexual encounter with, for example, one other person in a certain time interval, regardless of how many people there are in total. So if this person has a sexual encounter with a person in panel (**a**), he or she is more likely to encounter an infected host (*gray circles*) than an uninfected one (*white circles*), because infected hosts represent 75% of the population. In panel (**b**), this person is much less likely to encounter an infected host, even though there are many more total hosts, because infected hosts represent only 30% of the population. This is an example of frequency-dependent transmission, and it is thought to be common for sexually-transmitted diseases of humans and other animals

individual will acquire an infection depends less on the population density of hosts than on the percentage of hosts that are infected (the frequency).[2] In disease ecology jargon, sexually transmitted and many vector-borne diseases are said to have *frequency-dependent* rather than *density-dependent* transmission.

One interesting side note is that in some situations, density might be correlated with the frequency of infection. In the case of HIV/AIDS, infection is more likely among promiscuous people, intravenous drug users, and men who have sex with men (Fan et al. 2007). If people with those characteristics tend to choose to live in more dense populations, as in urban areas, then there will be a correlation between high density and high frequency of incidence of HIV/AIDS.

Look Upstream

In the previous section, we emphasized that density doesn't always predict infectious disease transmission. But of course in many cases, it does, and mitigation efforts are frequently aimed at reducing the density of hosts or vectors. Disease ecologists are increasingly recognizing that it is often possible to predict when and where hosts or vectors will be at high density, often well in advance.

[2]The probability that a human being will become infected by this vector depends on the likelihood that the vector is infected (which is frequency dependent) and the number of times infected vectors feed on the human (which is related to the density of vectors). In this way, transmission of vector-borne diseases can be both frequency and density dependent.

This potentially allows disease transmission to be dramatically reduced. The trick is to look upstream, sometimes literally.

In Belize, the growth of plants in wetland habitats is limited by the availability of phosphorus. Where phosphorus is in short supply, the wetlands are dominated by sparse, short vegetation interspersed with floating mats of cyanobacteria (Rejkmankova et al. 2006). But when phosphorus is abundant, this sparse vegetation is replaced over time with dense growth of cattails (*Typha* spp.) and other large, dense plants (Rejkmankova et al. 2006). Both types of plant communities harbor larvae of mosquitoes that serve as vectors of malaria. The female of a particular mosquito species, *Anopheles albimanus*, prefers to lay eggs in sparsely vegetated marshes with cyanobacterial mats. The other species, *A. vestitipennis*, prefers the densely vegetated marshes.

When phosphorus runs off from agricultural areas, it fertilizes sparsely vegetated areas, resulting in increased growth. This in turn appears to turn habitat for *A. albimanus* into habitat for *A. vestitipennis*, the species more likely to transmit malaria (Grieco et al. 2002). So the over-use of phosphorus in agricultural fertilizers in Belize leads to a delayed increase in malaria risk because it causes an increase in the density of malaria vectors through a chain of interactions. This discovery leads to several obvious interventions. Increasing the local use of bednets would deal directly with the problem of higher densities of highly competent malaria vectors. Managers could also try to reduce the abundance of *Typha* and other dense vegetation in wetlands (Rejkmankova et al. 2006) to prevent the mosquito increases earlier in the chain. And finally, farmers could reduce phosphorus use, or runoff into wetlands, to prevent the problem in the first place. None of these solutions is easy, but all would have valuable, pre-emptive benefits for human health.

Another example of a chain of direct interactions, although perhaps a more surprising one, comes from the northeastern USA, which is an area of high incidence of Lyme disease. Lyme disease is caused by a bacterium, *Borrelia burgdorferi*, that is passed from host to host by a tick vector. In the northeastern USA, the vector is the blacklegged tick, *Ixodes scapularis.* These ticks feed on a variety of mammals, birds, and reptiles (Keirans et al. 1996). When uninfected ticks feed on infected hosts, they can pick up the infection; once ticks become infected, they can pass the infection on to humans (Ostfeld 1997). But it turns out that not all host species are equally likely to transmit infection to ticks. If ticks feed on skunks or opossums or squirrels, the ticks are relatively unlikely to acquire an infection, even if the hosts are infected with the bacterium (LoGiudice et al. 2003). But if ticks feed on white-footed mice (*Peromyscus leucopus*), they have more than a 90% chance of becoming infected. For this reason, the white-footed mouse is called the most competent reservoir for the Lyme bacterium.

Given that mice are much more likely to infect ticks than any other species is, it is not surprising that the abundance of white-footed mice in a habitat is a good predictor of the number of infected ticks (Ostfeld et al. 2006). If we could predict the number of mice in a habitat, then, we should be able to predict when Lyme disease risk will be high. But what predicts when mouse abundance will be high? In some areas, the answer turns out to be simple: acorns (the fruit of oak trees of the genus *Quercus*). Acorns are rich in protein and lipids, and, perhaps most importantly, some species of acorns store well over the winter when other food is scarce.

In years when mice have acorns to eat, they survive the winter at much higher numbers and begin spring breeding earlier than in years when they don't. In fact, acorns are such a good food for mice that the number of acorns in the fall predicts the number of mice the following summer (Ostfeld et al. 2006). Acorns also predict the number of infected ticks 2 years later, with a time lag that results from the long life cycle of the tick. So based on acorn abundance in 1 year, we can predict with fairly high accuracy what Lyme disease risk will be like almost 2 years later. Unusually high acorn crops occur only every few years and they affect large regions in synchrony (Ostfeld et al. 2006), so there are distinct times and areas of high Lyme disease risk. Two years is plenty of lead-time to inform local health care providers and the public when to be most vigilant, and education has been shown to be effective at reducing the severity of Lyme disease cases (A. Evans, unpublished data).

In summary, in situations in which density is an important determinant of disease risk, knowing the ecology of the organisms involved can often make it possible to predict well in advance the times and locations when disease risk will be greatest. The challenge is to identify the chain of events leading to high abundance. In both the wetland and acorn examples, what leads to high abundance of a vector or host is, not surprisingly, a flush of resources, although the resources in both cases were several steps removed from the disease organisms (Ostfeld and Keesing 2000).

Interestingly, a recent review found that such links between resource pulses and increases in disease transmission are strikingly common (McKenzie and Townsend 2007), occurring in 54 of 55 examples surveyed. Why disease transmission should be exacerbated, rather than inhibited or unaffected by nutrient pulses is not immediately evident. One possibility is that negative or neutral results are less likely to lead to publication, resulting in a publication bias that does not reflect reality (McKenzie and Townsend 2007). Another possibility is that there is a biological reason why organisms that are involved in disease transmission are likely to respond positively to pulses of nutrients. Perhaps the very traits that tend to make organisms good hosts or vectors for pathogens (e.g. being widespread and able to achieve high abundance in a diversity of habitats) make them capable of responding positively to nutrient or other resource availability. Indeed, for a number of diseases, the most competent reservoir for pathogens is highly likely to be a habitat generalist, based on our observations of Lyme disease, West Nile virus encephalitis, babesiosis, various hantaviruses, Junin virus, and others. Habitat generalists are likely to be able to respond opportunistically to resources, and they are also ideal habitats themselves for pathogens because they are widespread, abundant, and resilient to disturbance. These hypotheses remain to be fully explored.

Cryptic Interactions

The examples in the preceding section illustrated chains of direct interactions that could influence the abundance of hosts or vectors for diseases. But interactions that affect transmission can also be much less direct; in fact, they can be so indirect that they are almost hidden.

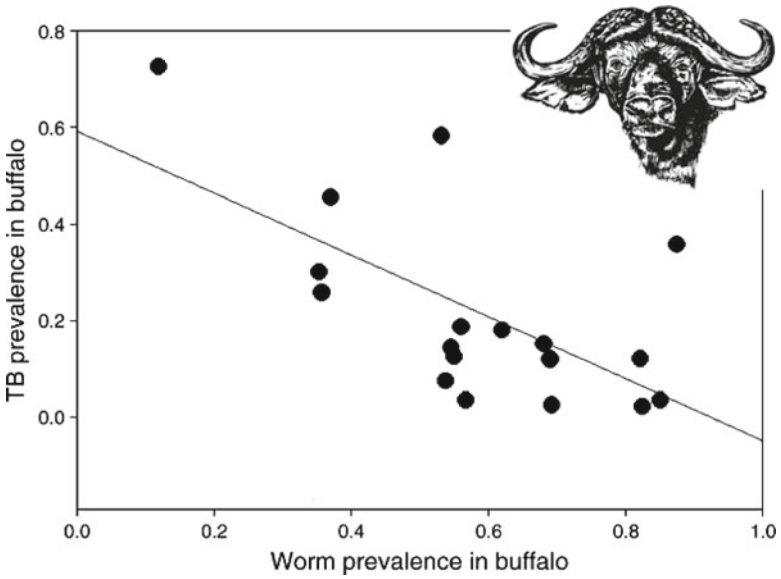

Fig. 13.2 Negative correlation between TB prevalence and worm infection prevalence in African buffalo (Adapted and reprinted from Jolles et al. 2008)

One recent example of a disease system with complex, cryptic, and indirect interactions comes from studies of bovine tuberculosis again, but this time in South Africa. Wild African buffalos (*Syncerus caffer*) can be infected with *Mycobacterium bovis*, just as domestic cattle can be. They can also be infected with other organisms, including gastrointestinal roundworms (Jolles et al. 2008). Jolles, Ezenwa, and colleagues asked whether infection with *M. bovis* is affected by infection with roundworms. They found that buffalos with high numbers of roundworms were unlikely to be infected with *M. bovis*, whereas those with low numbers of roundworms were likely to be infected (Fig. 13.2). What could cause this negative correlation? One possibility is that buffalo that are infected with both pathogens die at a higher rate, and they found evidence that this is indeed the case. For example, buffalos infected with Tb had significantly worse body condition only if they were also infected with worms; infection with worms alone had no effect on body condition.

Another possible explanation for the pattern in Fig. 13.2 is that the animals' immune systems might not be able to simultaneously mount effective immune responses to both pathogens. The immune system of mammals uses two distinct pathways to combat pathogens, depending on whether the pathogens are intracellular, like *M. bovis*, or extracellular, like roundworms (Jolles et al. 2008). The immune system also cross-regulates the two responses: when one pathway is activated, the other is actively suppressed (Jolles et al. 2008). Jolles et al. found that worm-free buffalos had the highest levels of activity of the immunological pathway that combats extracellular pathogens. Thus, buffalos that mount a strong immune response to worm infection may be more susceptible to infection with Tb because

their immune systems are suppressing the intracellular response in favor of the extracellular response.

Jolles and her colleagues developed analytical models to assess whether either increased mortality or cross-reactivity could account for the patterns of co-infection that they observed in buffalo herds. Their analyses suggest that neither effect alone is sufficient to cause the pattern they observed; both increased mortality and immunological cross-reactivity must be occurring.

Of course, the health of buffalos is not directly connected to human health, but in many parts of Africa, buffalos and domestic cattle can come into close enough contact for transmission to occur (Cosivi et al. 1999). And, of course, the health of cattle is intimately connected to human well-being as is discussed in the chapters on hunger in this volume. But perhaps more importantly, the buffalo Tb system may serve as a model of how interactions between pathogens occur within hosts, and suggest ways that this knowledge could be used in effective treatment. For example, the buffalo example suggests that treating gastrointestinal worms could reduce Tb infection: if buffalos don't have to activate an immune response to worms, their immune system is freer to tackle Tb infection. Similar patterns have already been observed in a number of human diseases and treatment of parasitic infections is recommended for reducing the severity of Tb and HIV/AIDS in humans (Hotez et al. 2006).

Complex interactions can also occur outside of hosts. We return to our discussion of Lyme disease for an example. We mentioned previously that different host species have different probabilities of infecting ticks that are feeding on them, with the white-footed mouse infecting 92% of feeding ticks with the Lyme bacterium. Recent research has demonstrated that mice are also the hosts from which ticks are most likely to successfully take a blood meal (Keesing et al. 2009). More than half of ticks that are experimentally placed on mice manage to feed successfully, and almost all of those become infected with the Lyme bacterium (Fig. 13.3). In contrast, ticks are much less likely to be able to feed successfully on other host species, and those that do feed successfully are much less likely to become infected with the Lyme bacterium. Of 100 ticks that are placed on an opossum to elicit feeding, for example, only about four manage to feed successfully; the rest are groomed off and killed (Keesing et al. 2009). And of those that feed successfully, only 3% are likely to become infected with the Lyme bacterium (LoGiudice et al. 2003). Remarkably, when we find opossums in the forest, they have hundreds of ticks feeding successfully on them at any one time (LoGiudice et al. 2003). That means that opossums serve as an ecological trap for ticks: it must be the case that thousands of ticks attempt to feed, but 96% of those are killed by the opossum. And then of those few hundred that survive, only a handful become infected, because opossums are also poor reservoirs for the Lyme bacterium (LoGiudice et al. 2003). Having opossums, and other similar hosts, around is a good way to reduce Lyme disease risk, because they remove a huge number of ticks from the environment, while only infecting a small number of them. In contrast, having a lot of white-footed mice around increases risk, because they successfully feed lots of ticks and the ones they feed are highly likely to become infected.

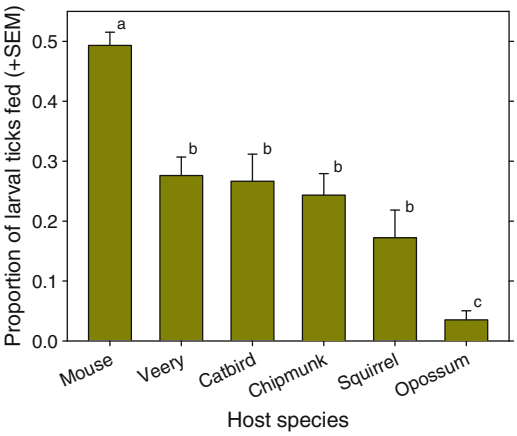

Fig. 13.3 The proportion of larval ticks that fed successfully (+ standard error of the mean) on six species that are common hosts for larval blacklegged ticks (*Ixodes scapularis*) in upstate New York, USA. Hosts were captured in the field and held in the laboratory until ticks naturally feeding on them had fed to repletion and dropped off. Hosts were then reinfested with 100 larval ticks and monitored to determine the proportion of those ticks that fed successfully. Lowercase letters indicate results that were significantly different (Data from Keesing et al. 2009)

Creating habitats with few mice is actually not that difficult, at least conceptually. As described earlier, mice are more abundant after big acorn crops, so acorns largely determine abundance through time. But from place to place, mice are found at high densities in habitats that have lost most of their vertebrate biodiversity (Nupp and Swihart 1998; LoGiudice et al. 2008). This is apparently because in these habitats, mice have lost both competitors, like squirrels and chipmunks, and predators, like foxes and weasels (Rosenblatt et al. 1999). Not surprisingly, habitats with higher predator diversity have lower mouse densities, and lower Lyme disease risk (Logiudice et al. 1998) because of an abundance of alternative hosts like opossums that siphon tick meals away from mice and then don't infect many of those ticks. This is an example of a phenomenon called the "dilution effect" in which high diversity reduces disease risk. The dilution effect has been described for a variety of diseases of plants and animals (Keesing et al. 2006; Keesing et al. 2010) including a number of human diseases such as West Nile virus encephalitis (Allan et al. 2008; Swaddle and Calos 2008; Ezenwa et al. 2006, 2007), hantavirus pulmonary syndrome (Dizney and Ruedas, in litt.), bartonellosis (Telfer et al. 2005), and of course Lyme disease (LoGiudice et al. 2003).

To protect human health, then, we should, it seems, create or preserve habitats with high vertebrate biodiversity. But how is that done? The only way we know of, at least in temperate forests, is to prevent forest fragmentation. Diversity is highest in continuous forest and large forest patches, presumably because bigger animals have larger requirements for space to maintain viable populations and can't survive in small fragments. In fact, small patches of fragmented forests in the eastern USA have the highest abundance of mice (Nupp and Swihart 1998), the lowest vertebrate diversity (Rosenblatt et al. 1999), and the highest Lyme disease risk (Allan et al. 2003).

Higher diversity is correlated with larger habitat areas in ecosystems throughout the world, an ecological phenomenon called the species-area relationship (Lomolino et al. 2006). If the dilution effect is as widespread as it appears to be, then preserving large, intact habitats would be a good strategy for conserving wildlife and, not coincidentally, might also be a good strategy for protecting human health, at least in some disease systems. Of course, the relationship between disease and habitat fragments occurs for Lyme disease because the best host for the pathogen is also an ecologically resilient host that is present in – and reaches high abundance in – degraded habitats such as forest fragments. If this is unique to the Lyme disease system, then the dilution effect might not occur for other diseases. But the same phenomenon does occur for a number of other diseases, as we have already noted. The most competent reservoirs for West Nile virus, for example, are birds such as house sparrows, house finches, American robins, and bluejays that live in degraded human habitats. Perhaps, then, it's not only a coincidence that the most competent reservoirs for pathogens are frequently those generalist species that survive best in a wide range of habitats. Perhaps successful pathogens have evolved to be best adapted to hosts that are ecologically resilient, and therefore most likely to respond positively to human-caused disturbances. An alternative, but not mutually exclusive, hypothesis is that ecologically resilient hosts have evolved life history strategies in which allocation of resources to particular types of immune defense is minimized. Such a strategy could be advantageous if disease rarely kills these animals before predators do. The result would be that these resilient species that are permissive to vectors and pathogens tend to dominate in human-degraded environments. These questions remain to be explored both theoretically and empirically.

Both the Lyme disease and buffalo tuberculosis examples illustrate that complex and indirect interactions among pathogens, hosts, and, in some cases, vectors, can lead to surprising outcomes. Just because interactions are complex, however, does not mean they are intractable. Both examples suggest general principles that might occur in a wide variety of disease systems, allowing us to make educated guesses about complex interactions in previously unstudied disease systems.

Summary and Conclusions

Throughout this chapter, we have emphasized features of disease transmission that appear to be broadly applicable. The densities of pathogens, hosts, and vectors are clearly important in many disease systems. So, too, though, are other things. Social behavior, in some circumstances, can override the effects of density, as in the badger example. So when social interactions are changing, for humans or for other animals involved in transmission of infectious diseases, we should not be surprised if disease transmission is affected. Diseases that are sexually-transmitted or vector-borne, and those that involve animals with a highly structured social organization, like that of badgers, would be most likely to be affected this way.

When density is the major factor determining disease transmission, we might be able to predict disease risk well in advance by keeping in mind the chain reactions that can lead to high densities. If we can, then we should be able to initiate public health interventions, including education, in time to reduce transmission. We must also be mindful of less direct interactions that might nevertheless be crucial. As the buffalo Tb example illustrates so well, when hosts are infected with both extracellular and intracellular pathogens, mitigation focused on one pathogen might reduce infection or severity of the other. Not surprisingly, given their shared mammalian ancestry, humans and buffalos appear to share responses to co-infection, so this strategy could apply to human health both directly and indirectly, though much on this topic remains to be explored.

Finally, lessons from Lyme disease suggest that the preservation of natural habitats might have direct bearing on human health because those habitats are likely to harbor high diversity and this diversity protects humans from disease transmission. The generality of the dilution effect is currently being explored by a number of research groups and their results should provide a great deal of insight into this intriguing possibility that aligns the goals of conservation with those of public health.

Collectively, the examples in this chapter demonstrate the many ways in which ecological interactions among organisms can influence the transmission of infectious diseases. The infectious diseases whose ecological complexities we understand in the most detail are not those that inflict the highest burden of disease on humans, such as tuberculosis, malaria, and dengue. However, there is no reason to believe that other pathogens should be any less sensitive to the types of interactions we have described in this chapter. As these examples have demonstrated, the integration of ecology with public health and sustainable development could improve the lives of people throughout the world.

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