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Editorial

Infectious disease: Inextricable linkages between human and ecosystem health

1. Introduction

Intellectual ghettos are passé. There was a time when the control of wildlife diseases was the domain of veterinarians while conservation was that of biologists. That false dichotomy has long since passed as infectious disease has become a central issue in biological conservation, which itself has become enmeshed in an inter-disciplinary web that embraces the health of ecosystems and people (e.g. Riordan et al., 2006). Indeed, these issues are set to become more entwined, as globalisation, climate change, human population expansion and the natural and unnatural movements of species interact to catapult emergent and mobile diseases to prominence beyond either the public health or conservation agendas, to land firmly on the global political table. Infectious diseases have passed in both directions between people and wildlife since time immemorial, but today the enormous rise in human populations, their penetration to every corner of wilderness with concomitant land-use changes, and their transportation of organisms around the world creates an explosive mix of risks.

Is infectious disease generally a matter for concern by conservation biologists? One general answer might be that infectious diseases are hazards to ecosystems when they affect keystone species such as top predators, or when they undermine ecosystem support systems (Foresight, 2006). However, infectious disease is a natural phenomenon, and a general tenet of biological conservation might be not to meddle where natural processes operate naturally. Compassion might prompt the rescue, or even euthanasia, of a sick animal, but such an intervention could be said to have little relevance to conservation, much of which is focused on the viability of populations and ecological communities. Of course, even before since it was formalised in the models of Anderson and May (1978), ecologists have realised not only that parasites (in the widest sense of pathogens) were not merely a source of morbidity and mortality in Nature, but could also limit, even regulate, some populations. In that sense, pathogens are clearly relevant to conservation biologists, as part of natural processes, but that certainly does not qualify them as a problem, nor does it constitute a justification for meddling in population processes insofar as these processes are natural. This line of thought and it has merit, leads to the

conclusion that infectious diseases may often not be of concern to conservation. It also leads sometimes to conservationists being disquieted by a too ready eagerness to intervene when disease afflicts wildlife. On the other hand, there are clear and pressing cases where infectious disease in wildlife conspicuously affects, or is affected or caused by, humans, and human involvement is an operational definition of topics within the ambit of conservation (Cleaveland et al., 2002). So, as is characteristic of conservation issues, the decision of when an infectious disease justifies intervention is not always straightforward, and indeed the position of infectious disease within conservation is both technically and philosophically challenging. It was discussions of such topics that prompted us to convene a conference to explore the diverse ways in which infectious disease threaded through issues in mammalian conservation.

To say that this Special Issue of Biological Conservation is merely the proceedings of a conference would not be correct. Nonetheless, it was catalysed by a two-day event held on 21st–22nd May 2005: The Mammals Trust UK's International Conference on Wild Mammals and Disease, and the ensuing Think Tank hosted at Tubney House by Oxford University's Wildlife Conservation Research Unit. From these events grew the papers that comprise this volume. Our starting point was that infectious diseases can have profoundly damaging consequences for mammal populations, particularly those that are already small or isolated. Some of the diseases affecting wildlife also pose potential threats to human health. Of 1415 known pathogens that have infected humans historically, 62% had zoonotic origin (Taylor et al., 2001). Furthermore, emergence of human pathogens is associated with the ability to infect wildlife for bacteria, fungi and viruses (Cleaveland et al., 2001). It is estimated that 75% of all diseases emerging over the last two decades have been zoonoses; these include SARS, avian influenza, Ebola, monkey pox, and the West Nile Virus (Brown, 1999; Hart et al., 1999).

A brief scan of the major issues in conservation biology worldwide reveals infectious disease as a recurrent linking thread between them. For example, alien species bring with them a host of other, less obvious, creatures that can cause disease: ticks and fleas, intestinal worms and protozoans, viruses and bacteria. In Britain, an obvious case is the grey

squirrel, *Sciurus carolinensis*; more than half a century of research and puzzlement passed before the breakthrough that their impact on native red squirrels, *Sciurus vulgaris*, was mediated by a virus. Habitat loss and modification, the most important issue for biodiversity conservation, which is also due to the expansion of human populations and activities, has widespread ramifications for infectious disease transmission to and from wildlife. Worldwide, the expansion, both in range and density, of domestic dogs and cat populations with their human masters has led to an apparent increase in incidence of outbreaks in wild carnivores, particularly canids (Woodroffe et al., 2004). For example, rabies spread by dogs threatens canids around the world, including highly endangered Ethiopian wolves, *Canis simensis*, and African wild dogs, *Lycaon pictus* (Laurenson et al., 2004). The few recent isolated cases of rabies transmitted to humans by Daubenton's bats, *M. daubentonii*, have given a new impetus to studies of the prevalence of this group of viruses in bat populations in the UK and its implications for human health (Harris et al., 2006).

These were some of the issues we sought to explore as we began planning the weekend of brain-storming that gathered together experts from the cutting-edge of wildlife disease studies from around the world. And from their energetic deliberations we identified a series of seven themes which we propose as the key topics in this field of conservation biology, and around which this Special Issue is constructed.

2. Infectious diseases and extinction risk

While biological conservation is not solely about rarity, and seeks to solve problems involving species that span the pestilential to the imperilled, extinction risk is the ultimate indicator. Our first theme, therefore, was to explore the circumstances in which infectious diseases can threaten extinction. Several papers, including those on rabies in Ethiopian wolves, *Canis simensis* (Randall et al., 2006), and African wild dogs, *Lycaon pictus* (Vial et al., 2006), disease in Island foxes, *Urocyon littoralis* (Clifford et al., 2006), squirrel parapox virus (SQPV) in red squirrels, *Sciurus vulgaris* (Gurnell et al., 2006), and devil facial tumour disease (DFTD) in Tasmanian devils, *Sarcophilus harrisii* (Hawkins et al., 2006) examine this theme.

Wild canids are particularly susceptible to generalist pathogens transmitted from domestic dog reservoirs, such as rabies and canine distemper virus (Woodroffe et al., 2004). The three papers on canids, case reports and population viability analyses, illustrate how dramatic die-offs of around 70% can threaten the persistence of such rare populations, particularly when combined with other causes of population decline, as in the case of Island foxes. As canids generally exhibit rapid population growth rates, only population viability analyses can estimate population persistence and determine the effectiveness of disease control strategies.

Pathogen-mediated competition, which can lead to unviable populations, is starkly illustrated by analyses of the dynamics of SQPV in red and grey squirrels. Gurnell et al. (2006) describe how SQPV causes disease with high mortality in red squirrels but appears non-pathogenic in grey squirrels.

However, not all populations of introduced grey squirrels carry the virus – those in Scotland and Italy do not – but the rate of red squirrel replacement by grey squirrels is some twenty times faster in those areas where grey squirrels carry the virus. The conservation of red squirrels will depend on minimising contact between these species.

These examples illustrate that diseases has the potential drive extinction when a pathogen infects a variety of host species and is maintained, often with low pathogenicity, in a more numerous reservoir host, spilling over into a less numerous and sometimes isolated threatened host (Lyles and Dobson, 1993). Yet diseases can also decimate large populations of endemic species. Hawkins et al. (2006) record the extraordinary case of devil facial tumour disease (DFTD) that now constitutes a serious threat to the Tasmanian devil *Sarcophilus harrisii*. The Tasmanian devil is the world's largest extant marsupial carnivore. DFTD is a cancerous disease found exclusively in wild devil populations, and Hawkins et al. report that it is consistently fatal to afflicted individuals. The tumours were first reported in 1996 and have subsequently been histologically confirmed in individuals from 41 separate sites, covering 51% of Tasmania (with a maximum of 83% of individuals infected). On the basis of the threat posed by DFTD, the devil has been listed as a threatened species in Tasmania.

3. Identification of pathogen reservoirs

A recurring issue in infectious disease epidemiology, from public health, conservation and livestock management perspectives, is the difficulty in identifying the reservoir of infection for multi-host pathogens (e.g. Courtenay et al., 1994; Haydon et al., 2002; Mathews et al., 2005). Reservoir identification can aid disease management, ensuring that the correct host is targeted with appropriate and effective disease control tools. When disease control measures in wild species of conservation concern are difficult to implement, due to complicated logistics or limited finances, identification of a reservoir domestic host may offer potential control measures that might be both effective and feasible. The importance of reservoir identification is classically illustrated by a range of papers in this Special Issue, for example the ongoing dilemma facing bovine tuberculosis control (Macdonald et al., 2006), the diseases emerging from bats (Breed et al., 2006), phocine distemper virus (PDV) in northern seal population (Hall et al., 2006) and the canid pathogens threatening Island foxes (Clifford et al., 2006).

In the southwest of England bovine tuberculosis has proved increasingly recalcitrant and is currently increasing in cattle at an annual rate of 18%. Macdonald et al. report on studies of the possible role of various wild mammals and conclude that if any wildlife species plays a significant role in the epidemiology of bTB in cattle, it is likely to be badgers, *Meles meles*, although the role of deer, particularly Fallow deer, *Dama dama*, in a local context is still unclear. Other species simply do not occur in sufficiently large numbers or transmission does not appear sufficiently frequent to allow *M. tuberculosis* persistence and thus constitute potential reservoirs.

Identifying the reservoirs of the emergent Henipaviruses, which caused mortality in humans and domestic animals (Hendra virus in horses, Nipah virus in pigs) in the 1990s has been challenging, but these viruses have now both been identified in fruit bat species (Breed et al., 2006). This paper highlights the role of bats as reservoirs of these and other emerging diseases. Behavioural and physiological characteristics of species such as the fruit bats, including the ability to cover long distances between islands and continents, close association at roosts and their mammalian physiology, ensure a large effective population size for pathogen persistence and adaptation. Identification of fruit bats as reservoirs for Henipaviruses means that control can be directed at minimising their contact with domestic species.

Ecological communities are complex and elucidating the reservoir host, when situations cannot be experimentally manipulated is challenging. Hall et al. (2006) illustrate this with the case histories of two outbreaks of phocine distemper that have severely affected harbour seal (*Phoca vitulina*) populations in European and UK waters. Both outbreaks were detected on the Danish Island of Anholt, the first in 1988 and the second in 2002. Harbour seals were highly susceptible to infection while sympatric grey seals are more resistant. In this phocid community the most likely reservoir of the virus are Arctic species of seals, but grey seals, *Halichoerus grypus*, could be important asymptomatic carriers that link these reservoir hosts to the harbour seal populations further south. Hall et al. emphasise that understanding of the determinants of the host range remains poor, and that development of more realistic epidemiological models should be combined with studies into the factors controlling species and individual susceptibility. Only then will further understanding of reservoirs hosts and transmission routes be built up.

Clifford et al. (2006) paper on Island foxes also illustrates the approach that must be taken when reservoirs cannot be identified. Serological studies suggest that feral cats are not putative reservoirs for the canid pathogens under study, but have not revealed whether the pathogens can be maintained in the small Island fox populations or are introduced from domestic dogs. In this situation, the practical solution seems to be targeted vaccination programs against the most virulent pathogens and continued intensive disease surveillance.

4. Using models to improve disease management for conservation

It is clear from this Special Issue that modelling is a powerful tool for understanding and planning the management of infectious disease. Recent stochastic, mixed models offer novel predictions about the role of culling, fertility control, and oral rabies vaccination in rabies control and are reviewed by Sterner and Smith (2006). Furthermore, both Vial et al. (2006) and Randall et al. (2006) illustrate how alternative management strategies might affect disease persistence and spread in African wild dogs and Ethiopian wolves, respectively. Targeting only a viable minimal 'core' of the population, through oral or even parenteral vaccination, is likely to be effective as well as more affordable and logistically less

demanding. Even if only 40% of animals were protected with a vaccine lasting only two years, this would ensure persistence of even small populations through suppression of the largest outbreaks of disease, that reduce populations to below minimum viable population sizes.

Similarly, modelling of the spread of both grey squirrels and their SQPV, by Gurnell et al. (2006) has identified four main corridors whereby grey squirrels will reach Kielder Forest (one of the red squirrel's last strongholds in England), initially within two years and in large numbers within 10 years. Assuming that greys will not settle within Kielder because of the unfavourable nature of the spruce habitat, the authors predict that SQPV disease will burn out at the edges of the forest, although many red squirrels will die. This burn-out is unlikely to be the scenario in other refuge areas where the habitat is more favourable to greys. Gurnell et al. conclude that the conservation of red squirrels will therefore depend on minimising contact between red and grey squirrel populations. This will necessitate monitoring grey squirrels as they approach refuge areas, and removing them.

Morgan et al. (2006) illustrate both the power and the limitations of a modelling approach, through their study of the pathogens of the Saiga antelope (*Saiga tatarica*) and domestic ruminants in Central Asia. For both foot and mouth disease and gastrointestinal nematodes, they reveal that the main risk is associated with infection of saigas from livestock, the putative reservoir host and subsequent geographical dissemination of infection through saiga migration. Their discussion on the trade-off between adding biological reality to models, and thereby increasing mathematical complexity and intractability, highlights that the main contribution of modelling is probably to force researchers to formalise understanding in a logical way, highlighting the areas in which too little is known. These areas of uncertainty can then be made the focus of further research, and sound a warning not to accept too readily the predictions of simpler models.

Sterner and Smith (2006) go on to adopt a further multidisciplinary approach and integrate models of disease spread with economic analyses of medical, public health, and veterinary costs. This reveals how post-exposure prophylaxis and increased pet vaccinations have been major costs during and after epizootics in North America. They recommend that this approach should be expanded when considering disease control options in biodiversity conservation.

5. Disease surveillance as a cornerstone in disease and conservation management

Disease surveillance and monitoring self-evidently provide crucial evidence to underpin management decisions. The advances in recent years in molecular techniques have been rapid and have provided powerful tools for the investigation of wildlife disease. This is forcefully illustrated by Leendertz et al. (2006) who describe approaches and techniques that can be used in the field when investigating baseline health status and disease outbreaks in great apes, focusing in particular on non-invasive sample collection and mortality investigations. This provides the very basis for diagnosis and

surveillance and can be extrapolated to other species. This paper also demonstrates how synergies can also be obtained through close collaboration between the fields of public health and conservation (see below).

Harris et al. (2006), also report on exemplary programmes of both passive and active surveillance in the United Kingdom to investigate the prevalence of European Bat LyssaViruses (EBLV) a rabies-related virus, in bats. Since 1977, 784 cases of EBLV have been recorded in 12 bat species in Europe. Some 5000 bats have been tested for lyssaviruses for surveillance, and an antibody prevalence level of 3–8% of EBLV-2 has been found in Daubenton's bat. However no cases of live lyssavirus infection or lyssavirus viral RNA have been detected through active surveillance. The authors emphasise how research and monitoring regarding prevalence, transmission, pathogenesis and immunity is required to ensure that integrated bat conservation continues throughout Europe, whilst enabling informed policy decision regarding both human and wildlife health issues.

Disease surveillance is also a cornerstone of diagnosis and control when considering the effect of reintroductions and translocations. However, as Mathews et al. (2006b) argue, despite guidelines recommending health-screening and surveillance of translocated individuals and in re-established populations, few reports are available and best practice is rarely observed. These authors present two case studies of health surveillance in wildlife reintroduction programmes – in water voles (*Arvicola terrestris*) in the UK, and in marsupial dibblers (*Parantechinus apicalis*) in Australia. These illustrate the potential importance of even basic screening strategies in helping to avoid disease transfer and identifying predictors of survival.

6. Synergies between human biomedical research and conservation biology

Building on improved techniques for surveillance, one would expect strong parallels between disease in humans and wildlife, and hence that advances in new research fields such as comparative genomics and molecular genetics would hold lessons for conservation biology. O'Brien et al., 2006 argue exactly this case, using examples drawn from wild species of the cat family, Felidae. They conclude that resolving the interaction of host and pathogen genomes can shed new light on the process of disease outbreak in wildlife and in people, by reviewing a highly virulent feline coronavirus epidemic in African cheetahs and a disease model for human SARS, which illustrate the critical role of ancestral population genetic variation. Furthermore, widespread prevalence of species specific feline immunodeficiency virus (FIV), a relative of HIV-AIDS, occurs with little pathogenesis in felid species, except in domestic cats, suggesting immunological adaptation in species where FIV is endemic. O'Brien et al. conclude that conservation management may benefit greatly from advances in molecular genetic tools developed for human biomedical research to assay the biodiversity of both species host and emerging pathogens.

Leendertz et al. (2006) provide a further illustration of how these synergies can be built up, by demonstrating how collaboration between human laboratories, veterinarians and field

biologists can successfully tackle emerging diseases in great ape and human populations. Successful pathogen detection in wild great apes has been achieved several times thanks to approaches and techniques that have been developed for human pathogen detection, focusing in particular on investigation of deaths and non-invasive sample collection.

7. Wildlife and emerging diseases of humans

Most of the host–pathogen systems reported in this Special Issue concern situations where pathogens have been defined as 'emerging', that is they have recently increased in incidence, impact or geographic range; have recently moved into new populations; or are caused by recently-evolved pathogens (Morse, 1995; Dazak et al., 2000; Lederberg et al., 1992). A variety of reviews have highlighted the situations and risk factors for emergence in human and domestic animals populations (Morse, 2004; Taylor et al., 2001; Cleaveland et al., 2001). The expansion of human populations is paramount, influencing agricultural development, urbanisation, deforestation and habitat fragmentation. This in turn influences disease emergence by changing the densities and ecology of disease hosts and pathogens, and altering human interaction with them (McMichael, 2004). For example, the penetration of remote forest areas through logging or bushmeat hunting is rapidly escalating the contacts between people and primates (Zommers and Macdonald, 2006). Not only does this have important implications for direct persecution through the harvest of bushmeat, but it also raises sinister opportunities for disease transmission as described by Leendertz et al. (2006). They describe recent outbreaks of disease in great apes, including Ebola, and indications of cross-transmission of Ebola and other viruses between primates and humans. There is no doubt that research that integrates infectious disease with primate ecology provides insights to emerging diseases in humans and the role of disease in primate evolution.

International travel and global trade hugely increase the capacity for disease spread and are thus other factors that determine disease emergence. A prime example was apparently rabbit haemorrhagic disease virus (RHDV) which was first identified after thousands of domestic rabbits died suddenly in China in 1984. Similar epidemics subsequently occurred in other regions of Asia, the Middle East, Europe and North America, suggesting that the virus had dispersed widely following its emergence in China. However, Forrester et al. (2006) report that RHDV had circulated apparently harmlessly for many years before the first recognised epidemic in China. They have therefore studied the evolution, emergence and dispersal of this virus in relation to its impact on conservation of wildlife species. Using phylogenetic analysis they show that the Chinese epidemic virus represents a relatively recent lineage derived from more divergent European viruses that circulated for many years prior to 1984. They show that the genetic lineages of the pathogenic viruses that emerged in the UK in the early 1990s, are distinct from and pre-date those of the 1984 Chinese virus. In short, several other divergent pathogenic European strains of RHDV emerged from apparently harmless strains to cause epidemic outbreaks,

independently of the Chinese 1984 epidemic virus. Forrester et al. also illustrate the complexity of conservation issues surrounding the rabbit in the UK – originally an invasive species, now an agricultural pest, yet a source of food for rare native predators and an important tool for habitat conservation.

Contact with wildlife has also been identified as a risk factor for emerging human pathogens (Taylor et al., 2001). This is illustrated in this Special Issue by papers describing high profile emerging viruses that have caused significant disease in domestic animals and humans from wild fruit bats in Asia and Australia (Breed et al.) and European bats (Harris et al.) Hendra virus has caused disease in horses and/or humans in Australia every five years since it first emerged in 1994. Nipah virus has caused a major outbreak of disease in pigs and humans in Malaysia the late 1990s and has also caused human mortalities in Bangladesh annually since 2001. Emergence may have been precipitated by unsustainable hunting of fruit bats and deforestation which have changed the distribution and thus contact rates between fruit bats and humans or their domestic animals, combined with an increase in domestic pig production in Asian countries.

8. Social behaviour and disease transmission

Animal behaviour, as the central factor, more often than not, in determining transmission of infectious disease between infected and susceptible individuals, is unquestionably important in wildlife epidemiology and conservation. This point was originally made in the context of failing attempts to control rabies in European red foxes, *Vulpes vulpes*, which largely ignored their behavioural ecology (Macdonald, 1980), and in this volume it is made stridently by Randall et al. and Vial et al., who illustrate how knowledge of, respectively, Ethiopian wolf and African wild dog social systems is important to understanding and managing the extinction threat they both face from rabies. Macdonald et al. (2006) further emphasise this in the context of attempted control of bovine tuberculosis (bTB) in cattle. The worsening situation of bTB in cattle has occurred despite a succession of government schemes involving killing badgers with the intention of reducing transmission of bTB to cattle. Macdonald et al. discuss the perturbation hypothesis which postulates that killing individuals may affect the survivors in ways (behavioural, physiological, immunological) that cause a disproportionate, and perhaps counter-productive, effect. They conclude that the Perturbation Hypothesis is supported by the data and does provide one plausible mechanism to explain why culling badgers has not generally achieved control of bTB in cattle. Macdonald et al. draw on various studies to argue that to have any prospect of contributing significantly to controlling bTB in cattle, a badger cull would have to be undertaken over a very large area. Considering the likely very important role of cattle-to-cattle transmission, and the opportunities for solutions in terms of farm management and surveillance, they judge it would be inappropriate (and probably impractical) to undertake such a cull now (especially in the context of revised agricultural payments which increasingly put a premium on custody of the countryside and its biodiversity (Mathews et al., 2006a)).

Remarkable satellite tracking studies have revealed long distance migrations by the fruit bats (Breed et al., 2006). This behaviour clearly has far-reaching implications for disease transmission within and across continents, particularly for migratory species. Saiga movements, that determine the timing and scale of contacts with domestic animals, also crucially affect disease transmission and persistence. Morgan et al. (2006) explain how for both foot and mouth disease and gastrointestinal nematodes, the main risk is associated with infection of saigas from livestock, and subsequent geographical dissemination of infection through saiga migration. The chance of this occurring for foot and mouth disease is predicted to be highly dependent on saiga population size and on the time of viral introduction. For nematodes, the level of risk and predicted direction of transmission are affected by key parasite life history traits, such that prolonged off-host survival of *Marshallagia* in autumn enables infection of saigas and transfer northwards in spring.

9. Discussion

These seven themes have been in the news regularly FZS1 since our weekend workshop, as the world anxiously watches the progress of H5N7 avian flu, West Nile virus and SARS on the front-pages. SARS, appearing in southern China in late 2002, illustrates that issues at the heart of biodiversity conservation and ecosystem health are fundamental to human well-being. SARS may have emerged in humans from SARS-like coronaviruses (CoV) in Himalayan palm civets (*Paguna larvata*) and other small carnivores in the wet markets of Asia. Specimens collected from animals found in live wild-game markets in Guangdong China have yielded a SARS CoV-like virus and several of the early SARS patients in Guangdong Province worked in the sale or preparation of wildlife for food (Bell et al., 2004; Peiris et al., 2004) and half of 10 civet dealers at the market were found to have antibodies that cross reacted to SARS (Bell et al., 2004). Recent research suggests that the disease may have jumped to civets from Rhinolophid bats in the marketplace, since SARS-like coronavirus has been detected in three species from China, Australia and the USA (Li et al., 2005 and Lau et al., 2005). Greater genetic variation between these bat strains (as revealed by nucleocapsid protein sequences) than seen in the human or civet SARS indicates that the viruses and bats have had time to co-adapt, and hence that bats are probably the origin of SARS. Bats find themselves along with civets and people in wildlife markets, to which live mammals are brought from increasingly remote areas into contact with an increasingly large human population with global links. Bats are also important pollinators and dispersal agents, and many are endangered species and thus their conservation is a priority for the continuing function of many ecosystems. This blend of factors links the concerns of public health, agriculture, biodiversity conservation, animal welfare, third world development and global economics.

A salient reality shrieks from the SARS story and is touched on elsewhere in this volume: the inter-connectedness of global populations of humans and wildlife. Hunters,

farmers, market vendors and consumers experience direct risk of zoonotic disease transmission from bushmeat and animals (Karesh et al., 2005). However, human to human transmission then spreads the risk to other individuals around the world and can turn a local outbreak into a global crisis. The local SARS outbreak in Hong Kong and Southern China, quickly spread to 25 countries across five continents, through human air travel (Peiris et al., 2004). The fact that over 700 million people travel by air annually (Karesh et al., 2005) means that the risk of global epidemics has never been higher and is the factor that could accelerate the spread of a global flu pandemic, ahead of vaccine production, should the mutations for human–human transmission occur.

All these studies bring repeatedly to the fore the inextricable linkages that ensure that no wildlife disease issue is the preserve of any one discipline. Ecologists to economists, virologists to veterinarians, philosophers to politicians, are all enmeshed in understanding the linkages, and in working together to find solutions. The need for an interdisciplinary approach has been reiterated widely in recent years and is highlighted again in the recently published UK Office of Science and Innovation Foresight Report “Infectious Disease: preparing for the future”. This report brought together diverse experts to consider the threats from disease for wildlife and for humans. Their conclusions emphasise the pressing nature of the issue, not least because of advancing climate change which may affect host and vector abundance and distribution and thus contact networks and transmission rates, but also because of the huge costs of disease outbreaks that affect human or livestock health. For example, BSE in the United Kingdom in 1996–1997 is estimated to have cost £2.3 billion whereas avian influenza in Vietnam in 2003/2004 is costed at £0.32 billion (Foresight, 2006). Against this background, progress forward must be made.

But which way is forward? Whilst evidence-based policy is surely essential, and thus science must underpin disease management, we live in a rapidly changing, unpredictable world where a complex web of risk factors can give rise to new disease-related problems at any turn. Science thus may not always have complete answers prepared in anticipation but, with investment, it can prudently look ahead. One Delphic circle of the wise recently identified the following priority areas (Foresight, 2006) for investment (i) novel information technology for capture, analysis and modelling of data for the early detection of infectious diseases, (ii) early detection and characterisation of new or newly resistant/virulent pathogens using genomics, (iii) improving technology for the rapid identification and characterisation of infectious diseases in the field and (iv) high-throughput screening for infectious diseases of people, animals and plants using surrogate, non-invasive markers in airports, sea/road containers and livestock markets. Others could add to this list. For example, this, and all other branches of conservation biology, must urgently develop inter-disciplinary syntheses, must achieve alignment with other major guests around the table of environment, sustainability and development, and must not forget the underpinning importance of a deep understanding of natural history (Macdonald et al., 2006).

Some of the roads leading to these new initiatives are charted in the papers gathered in this Special Issue. Biological

conservation stands to benefit from the anticipated advances in new diagnostic, monitoring and control tools. Given that the vast majority of endangered species occur in the developing world, these tools and technologies must also be cheap and practical to use in areas where infrastructure is poor. Moreover, although we are easily seduced by the new technology, we must keep an eye on the fact that old, lo-tech methods might frequently be best in the developing world and we must keep an eye on the fact that new technology is seductive and that in many instances, old methods might still be best.

Several spectres loom as infectious diseases, the exploding human population and the biodiversity and extinction crises travel together into the 21 century. Some wild populations that were once sufficiently abundant to withstand epizootic disease are now so reduced that an outbreak could tip the balance towards extinction. Many of these find themselves encircled and infiltrated by burgeoning hoards of infectious domestic species. Some wildlife diseases that once smouldered in isolated wilderness now challenge people that have penetrated their isolation and, through remarkably few links, populate a transmission chain that spans the globe. On the bright side, however, the papers in this volume reveal how the problems are starting to be understood, in some cases sufficiently to achieve solutions. Furthermore, biodiversity conservation has taken its place, along with others concerned with infectious diseases, at the table where environmental futures will be decided. One conservation truth is particularly, and perilously, clear when it comes to infectious disease: biodiversity and humanity are in it together.

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