POLICY PERSPECTIVES

Alien Pathogens on the Horizon: Opportunities for Predicting their Threat to Wildlife

Helen E. Roy[1], Helen Hesketh[1], Bethan V. Purse[1], Jørgen Eilenberg[2], Alberto Santini[3], Riccardo Scalera[4], Grant D. Stentiford[5], Tim Adriaens[6], Karolina Bacela-Spychalska[7], David Bass[5,8], Katie M. Beckmann[9], Paul Bessell[10], Jamie Bojko[5,11], Olaf Booy[12,13], Ana Cristina Cardoso[14], Franz Essl[15,16], Quentin Groom[17], Colin Harrower[1], Regina Kleespies[18], Angeliki F. Martinou[19], Monique M. van Oers[20], Edmund J. Peeler[5], Jan Pergl[21], Wolfgang Rabitsch[15], Alain Roques[22], Francis Schaffner[23], Stefan Schindler[15,16], Benedikt R. Schmidt[24,25], Karsten Schönrogge[1], Jonathan Smith[26], Wojciech Solarz[27], Alan Stewart[28], Arjan Stroo[29], Elena Tricarico[30], Katharine M.A. Turvey[1], Andrea Vannini[31], Montserrat Vilà[32], Stephen Woodward[33], Anja Amtoft Wynns[2], & Alison M. Dunn[11]

[1] Centre for Ecology & Hydrology, Maclean Building, Benson Lane, Crowmarsh Gifford, Wallingford, Oxfordshire OX10 8BB, UK
[2] Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark
[3] Institute for Sustainable Plant Protection - C.N.R, Via Madonna del Piano, 10, I-50019 Sesto Fiorentino, Italy
[4] IUCN SSC Invasive Species Specialist Group, Via Valentino Mazzola 38 T2 B 10, I-00142 Roma, Italy
[5] Centre for Environment, Fisheries and Aquaculture Science (Cefas), Barrack Road, Weymouth, Dorset DT4 8UB, UK
[6] Research Institute for Nature and Forest (INBO), Kliniekstraat 25, B-1070 Brussels, Belgium
[7] Department of Invertebrate Zoology & Hydrobiology, University of Lodz, Banacha 12/16, 90–237 Lodz, Poland
[8] Department of Life Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, UK
[9] Wildfowl & Wetlands Trust (WWT), Slimbridge, Gloucestershire GL2 7BT, UK
[10] The Roslin Institute, University of Edinburgh, Easter Bush, Midlothian, EH25 9RG, Scotland, UK
[11] School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds LS2 9JT, UK
[12] Animal and Plant Health Agency, Sand Hutton, York YO41 1LZ, UK
[13] Centre for Wildlife Management, School of Biology, Newcastle University, Newcastle-upon-Tyne NE1 7RU, UK
[14] European Commission, DG Joint Research Centre, Directorate D- Sustainable Resources, 21027 Italy
[15] Environment Agency Austria, Department of Biodiversity and Nature Conservation, Spittelauer Lände 5, 1090 Vienna, Austria
[16] Division of Conservation, Vegetation and Landscape Ecology, Department of Botany and Biodiversity Research, University Vienna, Rennweg 14, 1030 Vienna, Austria
[17] Botanic Garden Meise, Domein van Bouchout, B-1860 Meise, Belgium
[18] Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Institute for Biological Control, Heinrichstrasse 243, Darmstadt D-64287, Germany
[19] Joint Services Health Unit, BFC RAF Akrotiri BFPO 57, Cyprus
[20] Laboratory of Virology, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands
[21] Department of Invasion Ecology, Institute of Botany, The Czech Academy of Sciences, CZ-252 43 Průhonice, Czech Republic
[22] Institut National de la Recherche Agronomique, INRA UR0633, Zoologie Forestière, 45075 Orléans, France
[23] Avia-GIS, Risschotlei 33, 2980 Zoersel, Belgium
[24] Department of Evolutionary Biology and Environmental Studies, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland
[25] KARCH, Passage Maximilien-de-Meuron 6, 2000 Neuchâtel, Switzerland
[26] Animal and Plant Health Agency (APHA), Exotics and Risk Team, Area 5A, Nobel House, 17 Smith Square, London, SW1P 3JR UK
[27] Institute of Nature Conservation, Polish Academy of Sciences, Al. Mickiewicza 33, 31–120 Kraków, Poland
[28] School of Life Sciences, University of Sussex, Falmer, Brighton BN1 9QG, UK
[29] Centre for Monitoring of Vectors, Netherlands Food and Consumer Product Safety Authority, P.O. Box 9102, 6700 HC Wageningen, The Netherlands
[30] Università degli Studi di Firenze, via Romana 17, I-50125 Firenze, Italy
[31] DIBAF-University of Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
[32] Estación Biológica de Doñana (EBD-CSIC), Avda, Américo Vespucio, s/n, Isla de la Cartuja, 41092 Sevilla, Spain
[33] Department of Plant and Soil Science, University of Aberdeen, Institute of Biological and Environmental Sciences, Cruickshank Building, Aberdeen AB24 3UU, Scotland, UK

Abstract

According to the Convention on Biological Diversity, by 2020 invasive alien species (IAS) should be identified and their impacts assessed, so that species can be prioritized for implementation of appropriate control strategies and measures put in place to manage invasion pathways. For one quarter of the IAS listed as the "100 of the world's worst" environmental impacts are linked to diseases of wildlife (undomesticated plants and animals). Moreover, IAS are

Gifford, Wallingford, Oxfordshire OX10 8BB, UK.
E-mail: hele@ceh.ac.uk

a significant source of "pathogen pollution" defined as the human-mediated introduction of a pathogen to a new host or region. Despite this, little is known about the biology of alien pathogens and their biodiversity impacts after introduction into new regions. We argue that the threats posed by alien pathogens to endangered species, ecosystems, and ecosystem services should receive greater attention through legislation, policy, and management. We identify 10 key areas for research and action, including those relevant to the processes of introduction and establishment of an alien pathogen and to prediction of the spread and associated impact of an alien pathogen on native biota and ecosystems. The development of interdisciplinary capacity, expertise, and coordination to identify and manage threats was seen as critical to address knowledge gaps.

Introduction

Invasive alien species (IAS) are defined by the Convention on Biological Diversity (CBD) as *"species whose introduction and/or spread outside their natural past or present distribution threatens biodiversity."* The CBD requires its Parties to ensure that by 2020 IAS are identified and their impacts assessed, so that priority species can be controlled or eradicated and measures put in place to manage invasion pathways (Aichi Target 9; https://www.cbd.int/sp/targets/). For one quarter of IAS listed by the International Union for Conservation of Nature as the "100 of the world's worst" environmental impacts are linked to diseases of wildlife (Hatcher *et al.* 2006, 2012). Moreover, IAS represent a significant source of "pathogen pollution" defined as the human-mediated introduction (often unintentional) of a pathogen to a new host or region. Despite current advances in our understanding of biological invasions, little is known about the biology of alien pathogens, disease-causing parasites including viruses, bacteria, fungi, protists, and nematodes, and their impacts on biodiversity after introduction into new regions (Roy *et al.* 2016). To date, attention has largely focused on major diseases of humans, domesticated livestock, and cultivated plant species. The spread of alien pathogens, which affect wildlife, undomesticated plants, and animals living in the "wild" (Usher 2012), has received less attention despite the magnitude of their known and potential effects on endangered species, ecosystems, and ecosystem services (Peeler *et al.* 2011; Fisher *et al.* 2012).

Species inventories inform horizon scanning and surveillance, while additionally underpinning prevention, control, and elimination of IAS (Roy *et al.* 2014). There are now databases providing high-quality data on IAS to inform science, policy, and ultimately conservation (Roy *et al.* 2014; Essl *et al.* 2015). However, only a few alien pathogens are included, notably those with devastating effects on biodiversity, for example,

species such as *Aphanomyces astaci*, an oomycete and causal agent of crayfish plague that has devastated native crayfish populations in Europe for more than 150 years (Filipová *et al.* 2013), *Batrachochytrium dendrobatidis*, a chytrid fungus infecting over 350 species of amphibian worldwide (Fisher *et al.* 2009), and the emerging and closely related pathogen of salamanders, *Batrachochytrium salamandrivorans* (Martel *et al.* 2014). Even known high-risk pathogens are underrepresented or absent from these databases, for example, the beetle-vectored fungus *Raffaelea quercivora* and *Raffaelea quercus-mongolicae* (Kim *et al.*, 2009), responsible for oak (*Quercus* spp.) wilt diseases in East Asia, or the Oriental eye worm *Thelazia callipaeda* transmitted by *Phortica variegata* (Diptera: Drosophillidae) to cats, dogs, wild carnivores, and occasionally to humans (Roggero *et al.* 2010).

We argue that the threats posed by alien pathogens should receive greater attention by CBD Parties through legislation, policy, and management, to allow competent authorities of Member States and transnational organizations to address the requirements of the Aichi Target 9. Additionally, key areas for research should be identified to help scientists, wildlife managers, and conservation practitioners bridge the knowledge gaps, which affect the opportunities to take action, and hence inform policy and decision makers. Here, we describe a collaborative prioritization exercise used to identify knowledge gaps, research priorities, and policy recommendations with respect to alien pathogens threatening wildlife within natural and seminatural systems.

Advancing the understanding of alien pathogens threatening wildlife

Horizon scanning, the systematic examination of future potential threats and opportunities, is a useful approach for prioritizing IAS for action and identification of knowledge gaps (Roy *et al.* 2014). A horizon scanning

workshop "Enhancing the understanding of invasive alien pathogens" was held on 18–19 March 2015 at the Centre for Ecology & Hydrology (Wallingford, UK). A total of 39 experts from 13 European countries, including pathologists and ecologists (with expertise ranging from conservation biology and invasion ecology to wildlife epidemiology and disease management), were invited to address the overarching aim of advancing understanding of alien pathogens which pose a threat to wildlife within natural and seminatural systems. Due to the attention already received, including regulations and other legislation in place, we did not consider primary pathogens affecting cultivated plants, livestock, and humans. Nevertheless, we recognized the opportunities to learn from the plant, animal, and human health sectors given parallels in the processes of pathogen introduction, establishment, spread, and management.

The primary output of the workshop was unanimous recognition of how little is known about the epidemiology of almost all alien pathogens (and other parasites) in association with vectors and wildlife hosts. A list of 10 key research priorities was produced by standard consensus methods (Roy *et al.* 2014) (Figure 1). These included those relevant to the processes of introduction and establishment of an alien pathogen (Figure 1; 1–9); and to prediction of the spread and associated biodiversity and ecosystem impacts of an alien pathogen (Figure 1; 4–10). There was unanimous acceptance that invasion events by pathogens, and particularly epidemiological events, are very difficult to predict. The development of interdisciplinary capacity, expertise, and coordination to identify and manage threats was seen as critical to address knowledge gaps.

Knowledge gaps constrain our ability to undertake a risk assessment

Risk assessment is essential for underpinning many components of IAS management and policy, including prevention (informing legislation and justification of restrictions, as well as horizon scanning for potential threats), early warning and rapid response (prioritizing action and guiding surveillance), and long-term control (prioritizing species and areas for control). However, our ability to determine the environmental risk of alien pathogens is constrained at all stages (EFSA 2006) of an environmental risk assessment, for example:

(1) **Problem formulation**, in which broad consideration is given to the potential hazards. This step requires identification of potential alien pathogens (at species or strain level) in the source range that are likely to arrive within a new region (Figure 1; priorities 1–4) alongside likely routes of introduction (Figure 2). It is also necessary to consider the ecological and evolutionary factors that determine the likelihood that an introduced pathogen might infect, and have high impact, on new host species in the invaded range (Figure 1; priorities 4–9). Many recognized invasive alien pathogens were previously unknown to science, or at best scarcely known, prior to introduction, therefore the ability to undertake a risk assessment can falter at this early stage. Implementation of both traditional (e.g., histopathology) and modern (e.g., molecular tools such as eDNA) technologies (Schmidt *et al.* 2013; Bass *et al.* 2015) is required to screen for putative pathogen groups and to better inform risk management. However, the movement of alien species drives disease emergence by creating conditions whereby putative pathogens can infect new hosts; thus, invasive alien pathogens may not be highlighted because impacts may not be reliably predicted from assessing previously known associations (Peeler *et al.* 2011). Such lack of knowledge is even evident for pathogens relevant to livestock and humans (such as Schmallenberg virus and Zika virus) prior to invasion beyond the native range.

(2) **Hazard characterization**, in which the impacts of the pathogen are quantified. Predicting the impact of an alien pathogen requires data on its prevalence, pathogenicity, and virulence in the new range (i.e., impact on individuals or existing pathogens of the novel host strain/species; Figure 1; priority 8), as well as data on pathogen transmission dynamics (including spillover, spillback, and dilution) and distribution in the new range that will influence the extent of the impact (Figure 1; priorities 9–10) (Tompkins *et al.* 2011).

(3) **Exposure characterization**, in which the likelihood of a given hazard occurring is determined, for example, an alien pathogen emerging in the wild. The ability to characterize the likelihood of an alien pathogen emerging is constrained, in particular, by key knowledge gaps on the distribution of pathogens in their source range and their likelihood of introduction (Figure 1; priorities 1–4). Concurrently, there is also a lack of information on life history, host specificity, adaptive potential, and transmission dynamics, which are needed to assess the potential for an introduced pathogen to infect species/populations in a newly invaded geographical range (Figure 1; priorities 5–7).

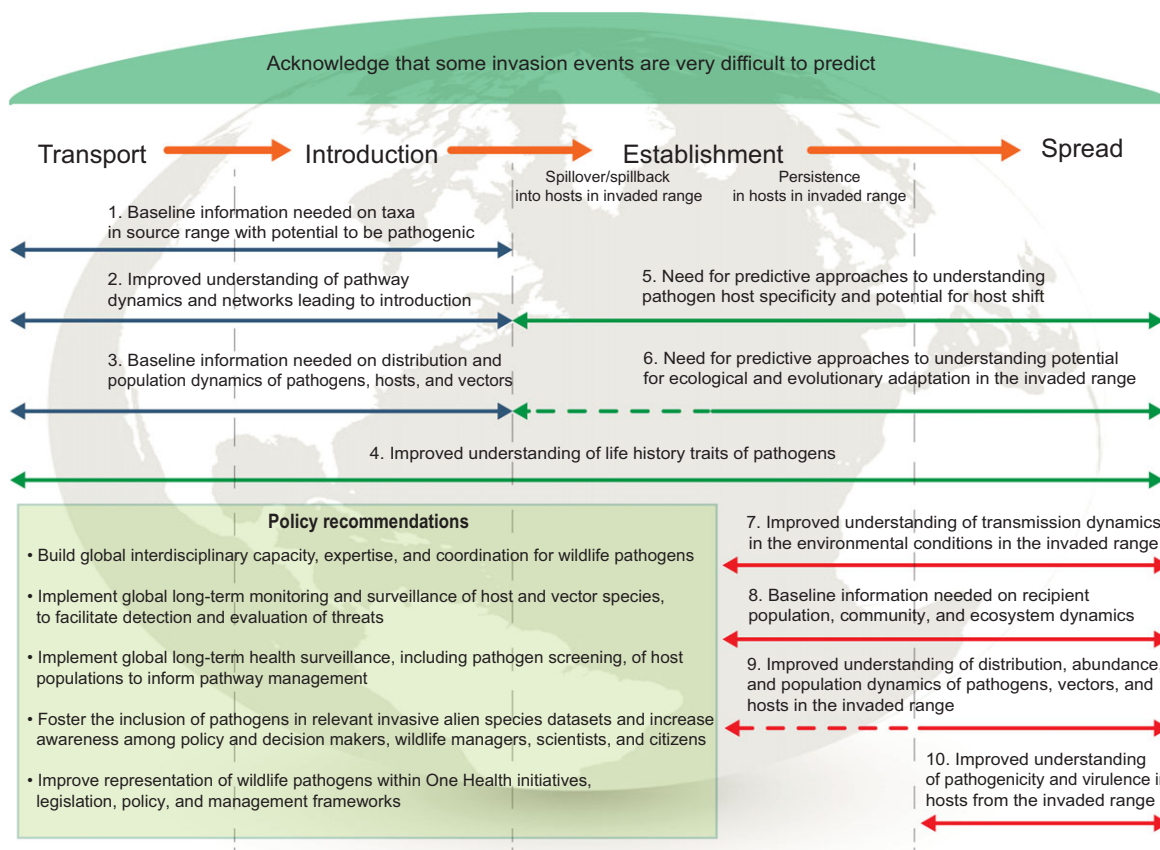(4) Stages A–C inform risk management strategies, and taken together produce an **overall risk evaluation**.

Figure 1 Alien pathogens represent a major threat to biodiversity; however, there are important gaps in understanding these threats that hinder management at every stage of the invasion process: transport, introduction, establishment, and spread. A horizon scanning workshop "Enhancing the understanding of invasive alien pathogens" including 39 experts (pathologists and ecologists with expertise ranging from conservation biology and invasion ecology to wildlife epidemiology and disease management) from 13 European countries addressed the overarching aim to advance the understanding of alien pathogens threatening wildlife. Experts identified and agreed on 10 research priorities that would not only increase understanding of the role of alien pathogens in invasion biology, but could also inform risk assessment frameworks and ultimately, One Health initiatives.

Invasion events are difficult to predict

It is important to note the unpredictable nature of invasion events and to recognize the imperfect nature of horizon scanning exercises (Roy *et al.* 2014). This unpredictability is particularly pronounced for pathogen invasions and perhaps represents the greatest challenge to managing their threat. The introduction of alien pathogens can lead to novel host–pathogen or indeed novel pathogen–pathogen combinations with no previous coevolutionary history (Dunn & Hatcher 2015). The disease outcomes of these novel combinations may be extremely complex as demonstrated by a few key examples.

The pine wood nematode, *Bursaphelenchus xylophilus*, a native of North America, is responsible for a devastating epidemic of wilt disease in Asia and Europe (Kikuchi *et al.* 2011). *B. xylophilus* has a complex life cycle that includes fungal feeding, plant parasitism, and an association with an insect vector (Kikuchi *et al.*

2011). In the invaded areas, the nematode utilizes novel hosts as vectors (long-horn beetles, *Monochamus* sp.) and novel food sources (Ophiostomatoid fungi) (Haran *et al.* 2015).

Culicoides vector species provide further insights into the complexity of novel host–pathogen combinations (Purse & Golding 2015). Reciprocal laboratory experiments indicate that African and American *Culicoides* vector species are susceptible to infection with viruses from different continents; demonstrating that coevolution between vectors and virus strains is not an essential prerequisite for midge-borne virus transmission and maintenance. This plasticity contributed to the recent emergence and extensive spread of both bluetongue virus 8 (taxonomically very distinct from prior bluetongue virus [BTV] strains already circulating in Europe) and a novel Orthobunyavirus, Schmallenberg virus, across Northern Europe due to transmission by European vectors.
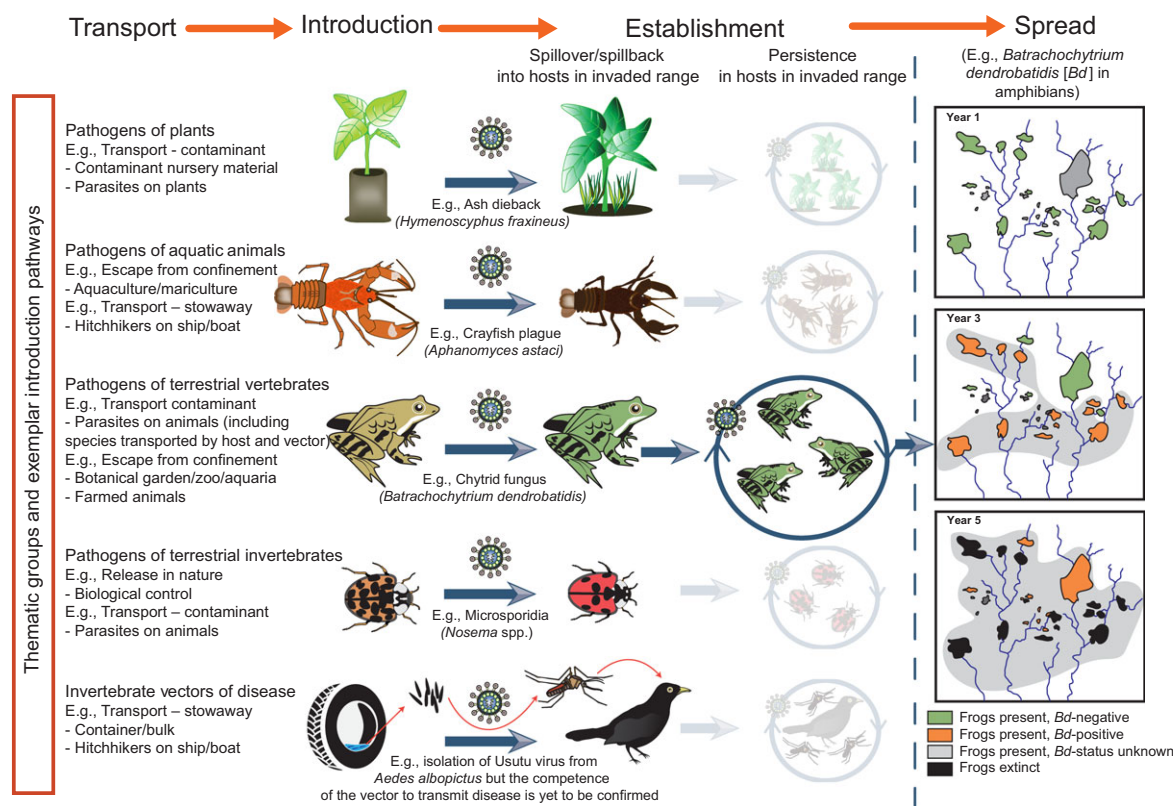
Figure 2 Alien pathogens can be transported and subsequently introduced through a range of pathways; some will successfully establish and persist within hosts present within the introduced range and, furthermore, some will spread with the potential to threaten wildlife, in some cases globally. Here, we provide a schematic representation of examples selected to highlight some of the challenges encountered in understanding the threats posed by alien pathogens. *Hymenoscyphus fraxineus* was not known to be pathogenic in its native range, far East Asia, but led to widespread dieback of the ash species *Fraxinus excelsior* and *Fraxinus angustifolia* within the invaded range (Gross *et al.* 2014). *Aphanomyces astaci*, causal agent of crayfish plague, has devastated crayfish populations in Europe for over 150 years (Filipová *et al.* 2013). The invasive alien *Harmonia axyridis* (harlequin ladybird) is host to microsporidia, which in laboratory experiments infect native ladybirds (Vilcinskas *et al.* 2013), but the ecological relevance is unclear. *Batrachochytrium dendrobatidis* has been described as the "worst wildlife pathogen ever recorded" with nearly half of all amphibian species in decline worldwide owing to this skin-infecting fungus (Fisher *et al.* 2012). *B. dendrobatidis* was discovered in 1997 and subsequently named in 1999; however, analysis of preserved specimens highlights the emergence of *B. dendrobatidis* concurrent with amphibian population declines in southern Mexico in the 1970s and subsequent spread through Central America to Panama in 2007. It is highly pathogenic across a diverse range of amphibians (> 500 species) and has been found on all continents where amphibians occur. The maps illustrate schematically temporal spread and consequences to amphibian populations within a hypothetical invaded region. Some alien insects such as those within the family Culicidae are known vectors of disease but even if a disease is identified within an insect vector, it does not confirm it as a competent host but may highlight the risk. So, for example, Usutu virus has been isolated from the mosquito *Aedes albopictus*, but it is unknown whether the mosquito can transmit the pathogen.

Even if transmission dynamics and virulence are well understood in the native host(s) and ecosystem of origin, the consequences of exposure to novel hosts in the invaded range are difficult to predict. Many of the alien pathogens responsible for severe epidemics of disease in wild plants or animals were not known to be pathogenic before becoming established in the new hosts in the new region; indeed, predictions on the success of alien species are often hampered by postinvasion host shifts (Medley 2010). Similarly, many latent plant pathogens have coevolved with native hosts, in which they behave as endophytes or epiphytes, with low virulence and no evident impact on the host within the native range but with high pathogenicity following introduction into a new region.

The ash fungal pathogen *Hymenoscyphus fraxineus* (≡*Lambertella albida*) was known to be nonpathogenic in its native range, far East Asia (Gross *et al.* 2014), but its introduction into Europe led to widespread dieback of the ash species *Fraxinus excelsior* and *Fraxinus angustifolia,* with which it had not coevolved. These putative pathogens are therefore extremely difficult to detect (Bérubé & Nicolas 2015), although the likelihood of spillover to new hosts is high if the putative pathogen is cointroduced with its original host. However, this is not always the case.

The agent of crayfish plague *A. astaci* was introduced to Europe more than 150 years ago, its spread and spillover occurred only as a result of the introduction of several alien crayfish species (Filipová *et al.* 2013), causing local extinction of several native European crayfish species (Fisher *et al.* 2012).

The sudden discovery of invasive alien pathogens, which were previously completely unknown to science, highlights the potential to predict such threats. The pathogenic amphibian chytrid fungus *B. dendrobatidis*, described as the "worst wildlife pathogen ever recorded" provides a striking example (Fisher *et al.* 2012). The global loss of amphibian biodiversity is driven in part by this emerging pathogen. The origin of *B. dendrobatidis* is unknown (Fisher *et al.* 2012), but evidence is accumulating that it may be endemic to some regions (e.g., Brazil and Japan) and that disease-driven amphibian declines were caused by the emergence of a new hypervirulent lineage in the amphibian trade that enabled the subsequent international spread (Farrer *et al.* 2011). Both *B. dendrobatidis* and Ranavirus, which also cause mass mortality events in amphibians (Cunningham *et al.* 1996), are listed by the World Organization for Animal Health (OIE) and are therefore notifiable by Member Countries of the European Union (EU) (Schloegel *et al.* 2012). However, unlike pathogens affecting crops, livestock, and humans, there is no obligation to screen for pathogens when importing amphibian hosts even though they are commonly infected (Schloegel *et al.* 2012).

Requirement for international policy and partnerships

There are many ways in which alien pathogens differ from other IAS, but there are also parallels including the ways in which they are introduced to a new region. Indeed, managing introduction pathways should be a priority for all IAS. The challenges in determining the identity of, and threat posed by, alien pathogens highlight the need for global and regional initiatives to instigate management measures to target major invasion pathways. There is increasing recognition that management of emerging infectious diseases in wildlife populations requires rapid action through international policy and partnerships (Voyles *et al.* 2014). However, alien pathogens affecting wildlife currently tend to fall into the gaps between regulatory bodies (Dunn & Hatcher 2015). The OIE Terrestrial and Aquatic Animal Health Codes (http://www.oie.int/international-standard-setting/aquatic-code/) both require member countries to report listed or emerging animal diseases, some of which are significant threats to wild populations (e.g., *B. dendrobatidis*, Ranavirus, and *A. astaci*). Similarly, the International Plant Pro-

tection Convention (https://www.ippc.int/en/) aims to manage the introduction and spread of pest organisms including alien plants and plant products. However, the policies that characterize these organizations focus mainly on animals and plants of economic importance and often have little relevance to alien pathogens that affect wildlife. When wildlife diseases are listed within such policies, their emergence does not often trigger action by countries signed up to these agreements (as illustrated by *B. dendrobatidis*), because such member countries are only obliged to report disease and not required to implement management strategies such as preventing spread (e.g., ensuring disease-free status through regulations of trade). Indeed, although alien pathogens negatively affect biodiversity, both directly by disease and indirectly by mediating species invasions, they are specifically excluded under the EU Invasive Alien Species Regulation 1143/2014. This is unfortunate because timely measures to prevent introduction and establishment of alien pathogens (e.g., by implementing action in relation to relevant pathways) would be more cost-effective than reactive measures to halt spread and manage disease epidemics following arrival (Langwig *et al.* 2015). Indeed, measures to control diseases in wildlife are generally highly constrained and eradication is rarely an option.

There is a clear and pressing need to address invasion pathways by, for example, increased controls and health surveillance of wildlife imports (Voyles *et al.* 2014; Langwig *et al.* 2015). The emergence of *B. salamandrivorans*, a relative of *B. dendrobatidis* that is driving local extinctions of European newts and salamanders (Martel *et al.* 2013), highlights the challenges and opportunities of international frameworks to deal with alien pathogens affecting wildlife. This pathogen is at an early stage of emergence (Spitzen-van der Sluijs *et al.* 2016) such that rapid action is critical (Voyles *et al.* 2014; Langwig *et al.* 2015), but the response at the global to local level is lacking. While the United States has enforced a ban for salamanders trade (Gray *et al.* 2015) and the Bern Convention of the Council of Europe recently approved recommendation No. 176 (2015) to "Impose immediate restrictions on salamander and newt trade," the response in Europe is neither rapid nor coordinated. Only Switzerland promptly banned the salamander trade. Within the EU, a trade suspension of all Asiatic species of caudate amphibians is currently under evaluation (https://circabc.europa.eu/sd/a/9b959a1e-bd87-4c3f-a3dc-49cf2a3e1748/75_agenda_srg.pdf) on the basis of their impact on native wildlife (regulated by Article 4(6) of Council Regulation (EC) No. 338/97 for the implementation of CITES = Convention on International Trade in Endangered Species of Wild Fauna and Flora). However,

the actual adoption of this measure may take time; thus, given the rapid spread of *B. salamandrivorans* (Spitzen-van der Sluijs *et al.* 2016), individual EU countries are also considering the implementation of alternative actions, as recommended by the Bern Convention. For instance, in Belgium, a trade ban of salamanders is in preparation.

Unfortunately, these amphibian diseases are not even listed in the EU Regulation 2016/429 (Animal Health Law) on transmissible animal diseases, although this legislation provides a legal basis to tackle diseases that could have a significant negative impact on biodiversity (through biosecurity, contingency planning, surveillance, and eradication). The uncoordinated and extemporary nature of the response, or lack thereof, to this emerging pathogen exemplifies wildlife diseases fall into the gaps between regulatory bodies, and the lack of coordinated response is apparent.

Conclusions

Invasive alien pathogens have the potential to severely affect biodiversity and ecosystem services. Emerging diseases of wildlife are frequently indicative of declining conditions across the wider environment (Dobson & Foufopoulos 2001). Despite the aims of One Health initiatives (e.g., www.onehealthinitiative.com) to bring an interdisciplinary approach to the health of people, domestic animals, and wildlife, a recent analysis highlighted the need for improved integrated approaches that ensure inclusion of the health of wildlife (Jenkins *et al.* 2015). We argue that such a coordinated, interdisciplinary approach to inform research and action is a key to understanding, detecting, and managing the emergence of alien pathogens and their impacts across borders and hosts. The risk is that the goals set by the CBD's Aichi Target 9 will not be achieved unless this is fully recognized by transnational bodies responsible for the implementation of nature conservation legislation. Transnational institutions should identify authorities competent for dealing with wildlife pathogens other than those affecting livestock, plant crops, and human health.

A dedicated, coordinated, and comprehensive set of measures (e.g., inclusion of information on pathogens within alien species databases and sharing of such information) to be implemented from the global to the regional and local level is clearly needed to ensure coordination and interdisciplinary approaches in terms of management policy (e.g., banning trade of potential vectors) and research policy (e.g., funding research projects on wildlife pathogens). We propose the need for a global treaty, recognizing the complexities of invasive alien pathogens while highlighting the need for coordinated action, alongside the mobilization of funding for research including dedicated national and international funding streams for rapid reaction to emerging diseases.

Author contributions

HER conceived and designed the study; AMD, BVP, HH, RS further developed the methods in collaboration with HER. HER, AMD, BVP, HH, RS made a substantial contribution to the conduct of the study and analysis and interpretation of the data. All authors participated in the prioritisation process and provided comments and intellectually critique the output. The final preparation of the manuscript was led by HER, AMD, BVP, HH, RS. KMAT provided administrative and facilitative support throughout.

References

Bass, D., Stentiford, G.D., Littlewood, T. & Hartikainen, H. (2015). Diverse applications of environmental DNA methods in parasitology. *Trends Parasitol.*, **31**, 499-513.

Bérubé, J.A. & Nicolas, G.G. (2015). Alien fungal species on asymptomatic live woody plant material imported into Canada. *Can. J. Plant Pathol.*, **37**, 67-81.

Cunningham, A., Langton, T., Bennett, P. *et al.* (1996). Pathological and microbiological findings from incidents of unusual mortality of the common frog (*Rana temporaria*). *Phil. Trans. R. Soc. Lond. B: Biol. Sci.*, **351**, 1539-1557.

Dobson, A. & Foufopoulos, J. (2001). Emerging infectious pathogens of wildlife. *Phil. Trans. R. Soc. B: Biol. Sci.*, **356**, 1001-1012.

Dunn, A.M. & Hatcher, M.J. (2015). Parasites and biological invasions: parallels, interactions, and control. *Trends Parasitol.*, **35**, 189-199.

EFSA. (2006). Guidance document of the Scientific Panel on Genetically Modified Organisms for the risk assessment of genetically modified plants and derived food and feed. *EFSA J.*, **99**, 1-100.

Essl, F., Bacher, S., Blackburn, T.M. *et al.* (2015). Crossing frontiers in tackling pathways of biological invasions. *BioScience*, biv082.

Farrer, R.A., Weinert, L.A., Bielby, J. *et al.* (2011). Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage. *Proc. Natl. Acad. Sci*, **108**, 18732-18736.

Filipová, L., Petrusek, A., Matasová, K., Delaunay, C. & Grandjean, F. (2013). Prevalence of the Crayfish Plague pathogen *Aphanomyces astaci* in populations of the Signal Crayfish *Pacifastacus leniusculus* in France: evaluating the threat to native crayfish. *PLoS One*, **8**, e70157.

Fisher, M.C., Garner, T.W.J. & Walker, S.F. (2009). Global emergence of *Batrachochytrium dendrobatidis* and amphibian chytridiomycosis in space, time, and host. *Annu. Rev. Microbiol.*, **63**, 291-310.

Fisher, M.C., Henk, D.A., Briggs, C.J. *et al.* (2012). Emerging fungal threats to animal, plant and ecosystem health. *Nature*, **484**, 186-194.

Gray, M.J., Lewis, J.P., Nanjappa, P. *et al.* (2015). *Batrachochytrium salamandrivorans*: the North American response and a call for action. *PLoS Pathog.*, **11**, e1005251.

Gross, A., Holdenrieder, O., Pautasso, M., Queloz, V. & Sieber, T.N. (2014). *Hymenoscyphus pseudoalbidus*, the causal agent of European ash dieback. *Mol. Plant Pathol.*, **15**, 5-21.

Haran, J., Roques, A., Bernard, A., Robinet, C. & Roux, G. (2015). Altitudinal barrier to the spread of an invasive species: could the Pyrenean chain slow the natural spread of the Pinewood Nematode? *PLoS One*, **10**, e0134126.

Hatcher, M.J., Dick, J.T. & Dunn, A.M. (2006). How parasites affect interactions between competitors and predators. *Ecol. Lett.*, **9**, 1253-1271.

Hatcher, M.J., Dick, J.T. & Dunn, A.M. (2012). Diverse effects of parasites in ecosystems: linking interdependent processes. *Front. Ecol. Environ.*, **10**, 186-194.

Jenkins, E.J., Simon, A., Bachand, N. & Stephen, C. (2015). Wildlife parasites in a One Health world. *Trends Parasitol.*, **31**, 174-180.

Kim, K. H., Choi, Y. J., Seo, S. T., & Shin, H. D. (2009). Raffaelea quercus-mongolicae sp. nov. associated with Platypus koryoensis on oak in Korea. *Mycotaxon*, **110**(1), 189-197.

Kikuchi, T., Cotton, J.A., Dalzell, J.J. *et al.* (2011). Genomic insights into the origin of parasitism in the emerging plant pathogen *Bursaphelenchus xylophilus. PLoS Pathog.*, **7**, e1002219.

Langwig, K.E., Voyles, J., Wilber, M.Q. *et al.* (2015). Context-dependent conservation responses to emerging wildlife diseases. *Front. Ecol. Environ.*, **13**, 195-202.

Martel, A., Blooi, M., Adriaensen, C. *et al.* (2014). Recent introduction of a chytrid fungus endangers Western Palearctic salamanders. *Science*, **346**, 630-631.

Martel, A., Spitzen-van der Sluijs, A., Blooi, M. *et al.* (2013). *Batrachochytrium salamandrivorans* sp. nov. causes lethal chytridiomycosis in amphibians. *Proc. Natl. Acad. Sci.*, **110**, 15325-15329.

Medley, K.A. (2010). Niche shifts during the global invasion of the Asian tiger mosquito, *Aedes albopictus* Skuse (Culicidea), revealed by reciprocal distribution models. *Glob. Ecol. Biogeogr.*, **19**, 122-133.

Peeler, E.J., Oidtmann, B.C., Midtlyng, P.J., Miossec, L. & Gozlan, R.E. (2011). Non-native aquatic animals introductions have driven disease emergence in Europe. *Biol. Invasions*, **13**, 1291-1303.

Purse, B.V. & Golding, N. (2015). Tracking the distribution and impacts of diseases with biological records and distribution modelling. *Biol. J. Linnean Soc.*, **115**, 664-677.

Roggero, C., Schaffner, F., Bächli, G., Mathis, A. & Schnyder, M. (2010). Survey of *Phortica* drosophilid flies within and outside of a recently identified transmission area of the eye worm *Thelazia callipaeda* in Switzerland. *Vet. Parasitol.*, **171**, 58-67.

Roy, H.E., Peyton, J., Aldridge, D.C. *et al.* (2014). Horizon scanning for invasive alien species with the potential to threaten biodiversity in Great Britain. *Glob. Chang. Biol.*, **20**, 3859-3871.

Roy, H.E., Scalera, R., Dunn, A.M., & Hesketh, H. (2016). Invasive species: control wildlife pathogens too. *Nature*, **530**, 281.

Schloegel, L.M., Toledo, L.F., Longcore, J.E. *et al.* (2012). Novel, panzootic and hybrid genotypes of amphibian chytridiomycosis associated with the bullfrog trade. *Mol. Ecol.*, **21**, 5162-5177.

Schmidt, B.R., Kéry, M., Ursenbacher, S., Hyman, O.J. & Collins, J.P. (2013). Site occupancy models in the analysis of environmental DNA presence/absence surveys: a case study of an emerging amphibian pathogen. *Methods Ecol. Evol.*, **4**, 646-653.

Spitzen-van der Sluijs, A., Martel, A., Asselberghs, J. *et al.* (2016). Expanding distribution of lethal amphibian Fungus *Batrachochytrium salamandrivorans* in Europe. *Emerg. Infect. Dis.* **22**, 1286–1288.

Tompkins, D.M., Dunn, A.M., Smith, M.J. & Telfer, S. (2011). Wildlife diseases: from individuals to ecosystems. *J. Anim. Ecol.*, **80**, 19-38.

Usher, M. (2012). *Wildlife conservation evaluation*. Springer Science & Business Media, Dordrecht.

Vilcinskas, A., Stoecker, K., Schmidtberg, H., Röhrich, C.R. & Vogel, H. (2013). Invasive harlequin ladybird carries biological weapons against native competitors. *Science*, **340**, 862-863.

Voyles, J., Kilpatrick, A.M., Collins, J.P. *et al.* (2014). Moving beyond too little, too late: managing emerging infectious diseases in wild populations requires international policy and partnerships. *EcoHealth*, 1-4.