

ORIGINAL ARTICLE

**Pathogens co-transported with invasive non-native aquatic species:  
implications for risk analysis and legislation**

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33 invasions.

34

## 35 Abstract

36 Invasive Non-Native Species (INNS) can co-transport externally and internally other  
37 organisms including viruses, bacteria and other eukaryotes (including metazoan parasites),  
38 collectively referred to as the symbiome. These symbiotic organisms include pathogens, a  
39 small minority of which are subject to surveillance and regulatory control, but most of which  
40 are currently unscrutinised and/or unknown. The (putatively) pathogenic symbionts co-  
41 transported by an INNS host may be latent or associated with asymptomatic infection and  
42 unable to cause disease in the INNS, but may be opportunistic pathogens of other hosts,  
43 causing impact to one or more hosts in their new range. These pathogens potentially pose  
44 diverse risks to other species, with implications for increased epidemiological risk to  
45 agriculture and aquaculture, wildlife/ecosystems, and human health (zoonotic diseases).  
46 Aquatic INNS and their symbionts have many introduction pathways, including commodity  
47 and trade (releases, escapes, contaminant), transport (stowaway), and dispersal (corridor,  
48 unaided). The risks and impacts arising from co-transported pathogens, including other  
49 symbionts of unknown pathogenic virulence, remain largely unexplored, unlegislated, and  
50 difficult to identify and quantify. Here, we propose a workflow to determine any known and  
51 potential pathogens of aquatic INNS. This workflow acts as a prerequisite for assessing the  
52 nature and risk posed by co-transported symbionts of INNS. A better understanding of co-  
53 transported organisms, the risks they pose and their impact, is necessary to inform policy and  
54 INNS risk assessments. This leap in evidence will be instrumental to devise an appropriate  
55 set of statutory responsibilities with respect to these symbionts, and to underpin new and  
56 more effective legislative processes relating to the disease screening and risk assessment of  
57 INNS.

58

## 59 KEYWORDS

60

61 INNS, Alien Species, Invasive Pathogen, Parasite, Symbiont, Opportunistic pathogen

62

## 63 1 | INTRODUCTION

64 Invasive Non-Native Species (INNS) are “species whose introduction by human activity  
65 outside their natural past or present distribution threatens biodiversity” as defined by the  
66 Convention on Biological Diversity (CBD, 2010), and are one of the greatest threats to  
67 biodiversity (IPBES global assessment, 2019). New introductions of INNS are increasing

globally each year, with no indication that introduction events are decreasing in frequency (Seebens et al., 2020). It is increasingly recognised that invasions are not the product of single species introduction but are present as holobionts (Skillings, 2016): i.e., units of biological organisation including the host and all its symbionts (external and internal), including pathogenic species. Therefore, organisms such as viruses, bacteria, fungi, protists and other (micro-)eukaryotic parasites and pathogens are introduced to new regions along with their invasive non-native host and can be important factors in the invasion process (Peeler et al., 2011; Roy et al., 2017). A broad basis for referring to these organisms as ‘pathogens’ is required: they may not be recognized as pathogens, or cause disease in the INNS host transporting them, but may impact on or more related (or unrelated) hosts in their new range. Further, pathogenesis can be very context dependent, as described by the symbiotic continuum concept (Bass & del Campo, 2020). Therefore a biologically informed approach to horizon scanning for such ‘pathogens’ is necessary, to enable effective horizon scanning for potentially new and emerging diseases. For the purposes of this paper, to avoid repetition of “parasites/pathogens” to refer to symbionts that take nutritional advantage of their hosts potentially causing disease, we henceforth use “parasite” as a catch-all term.

In the field of invasion biology, invasions by pathogens (emerging infectious diseases in public and wildlife health) are increasingly being researched as important driving factors (Ogden et al., 2019; Thakur et al., 2019); however, this is not currently reflected in national and international policy and legislation. For example, co-introduced pathogens are explicitly excluded from the EU Invasive Alien Species Regulation 1143/2014. Instead, potentially invasive co-introduced pathogens are considered as potential impacts of INNS establishment. Understanding and predicting the impacts of INNS is essential to inform risk analysis, for example, via horizon scanning, risk assessments and impact assessments, which underpin many components of INNS policy and management. However, pathogens associated with most (potential) INNS are very poorly known (Roy et al., 2017; Pagenkopp et al., 2020), except in the few cases where they are recognised under animal disease or human health legislation and are monitored and reported accordingly. In general, INNS risk analyses focus on the environmental and/or cumulative impacts of INNS, without (specific) reference to co-transported pathogens and symbionts (e.g., Dick et al., 2017).

Knowledge and policy gaps result in inadequate scrutiny and assessment of the risks associated with co-introduced symbionts (including parasites/pathogens) into new regions

and countries (Hulme, 2014; Dunn and Hatcher, 2015). Earlier and more comprehensive risk assessments for horizon INNS, with a focus on pathogenic impacts is urgently needed (Roy et al., 2017); supported by the prioritisation of empirical research required to cover knowledge gaps about transmitted pathogens (Chinchio et al., 2020). Therefore, a framework for quantifying and documenting our existing knowledge of invasive animals and plant symbionts (including pathogens) is vital. This involves conducting literature-based and pathogen screening tools to fill knowledge gaps, where such information is lacking. These data will then lead to the development of invader pathogen profiles, outlining what is known about the invader's pathogens/symbionts and those of related taxa.

In this paper we present a framework to meet these imperatives. This can be applied to INNS already present in a region, those with the potential to arrive, and those already present but yet to establish. For the purposes of this paper, we focus on (potentially) pathogenic/parasitic symbionts of aquatic INNS of concern to the UK, which may be permanently or transiently associated with one or multiple water bodies. We include all symbiont types: viral, microscopic, and macroscopic parasites (including Metazoa). The underlying premise can also be applied equally to all habitat types, and all symbionts including pathogens/parasites that manipulate behaviours of one or more of their hosts, and symbionts that have no discernible effect on their hosts.

## 2. | BIOLOGY AND ECOLOGY OF PARASITES CO-TRANSPORTED BY INNS

Movement of INNS beyond their native range can result in changes to established host-pathogen/parasite relationships, including INNS losing or gaining parasites (Peeler et al., 2011; Dunn & Hatcher, 2015; Vilcinskis, 2015). The multitude of potential outcomes resulting from relationship changes are summarized the schematic shown in Figure 1. The **enemy release hypothesis** (see glossary) states that INNS can lose their parasites as they move into a new range, which may be due to ecological factors, or for heteroecious parasites, the absence of a secondary host (Colautti et al., 2004). Co-introduced parasites can potentially infect native species (Keane & Crawley, 2002). In some cases, parasite loss can also increase invasion success by reducing parasite burden and associated health costs as well as reducing/eliminating competing susceptible native species (Prenter et al., 2014). Furthermore, lack of co-evolution potentially results in the increased susceptibility of native hosts to the invading parasite (Taraschewski, 2006). For example, a study comparing invasive

135 parasite pathogenicity in co-introduced and native hosts suggests that in 85% of cases,  
136 pathogenicity is higher in native hosts compared to non-native hosts (Lymbery et al., 2014).

137  
138 INNS can also affect native host-parasite relationships, altering population dynamics and  
139 disease transmission. Theiltges et al. (2008) demonstrated that the presence of invasive  
140 *Crepidula fornicata* and *Crassostrea gigas* significantly reduced the trematode parasite  
141 burden of native *Mytilus edulis*, by interfering with the transmission of free-living infective  
142 trematode larval stages and therefore reducing infection of *M. edulis*. Host-parasite  
143 ecosystem interactions prove complex, creating challenges for the prediction of invasion  
144 success at different locations. The invasive amphipod *Echinogammarus ischnus* has  
145 outcompeted the native *Gammarus fasciatus* at many locations in the Great Lakes and St.  
146 Lawrence River in North America through predation and competition (Dermott et al., 1998).  
147 A native oomycete infects *E. ischnus* and causes greater mortality to the invasive host than to  
148 the native *G. fasciatus*, which facilitates the coexistence of the two species in areas of disease  
149 prevalence (Kestrup et al., 2011). This relationship is further nuanced in that *E. ischnus* can  
150 also act as a reservoir of the oomycete and facilitate **parasite spillback** to native amphipods.

151  
152 Many diseases initially thought to be caused by one primary agent are now known to be the  
153 result of interactions between multiple symbionts, the host, and their environment; resulting  
154 in the pathobiome concept (Bass et al., 2019). Each INNS individually co-transport its own  
155 symbiome, making it difficult to predict its effect on the invaded ecosystem. A survey of  
156 symbionts of the invasive green crab *Carcinus maenas* in its native and invaded range  
157 showed many co-transported parasites persisted within the host at its invasion territory  
158 (Bojko et al., 2018). The latest approximation suggests this species is associated with ~82  
159 known symbionts, many of which are pathogenic and pose risks to native ecosystems and the  
160 bioeconomy (Bojko et al., 2020).

161  
162 The combination of hosts and their symbionts is of more immediate concern than considering  
163 the simple transposition of a pathogenic agent, such as a single virus or bacterium. Co-  
164 introduction of symbionts with an INN host is more likely to result in pathogen establishment  
165 because the co-evolved biological system is already in place to facilitate transmission (Peeler  
166 et al., 2011). Generalist pathogens are the main cause for concern since they can utilize native  
167 hosts more readily (Peeler et al., 2011). Symbiotic co-invaders may also present parasitic  
168 traits in new locations. For example, *Aphanomyces astaci*, the oomycete agent of crayfish

plague, is a symbiont of many invasive North American crayfish species (Tilmans et al., 2014); however, the introduction of *A. astaci* into Europe has resulted in large-scale mortalities in native crayfish populations, including: *Austropotamobius pallipes*, *Astacus astacus* and *Astacus leptodactylus*. In some cases, their local extinction is possible and has been noted in many regions (Mrugula et al., 2014). Box 1 details examples of known co-transported pathogens and their effects, co-transported symbionts and how symbiome research can help to assess invasion risks.

## **BOX 1**

### **1) Co-transportation of Pathogens**

The invasive Asian eel (*Anguilla japonica*) brought with it the parasitic swim-bladder nematode *Anguillicoloides crassus*, which has caused high mortalities in native European eels (*Anguilla anguilla*) and significantly affected the sustainability of future populations (Peeler et al., 2011). The OIE listed pathogen, *Bonamia ostreae* has caused decimation of native oysters (*Ostrea edulis*) in Europe, when it arrived with cultivated American populations of *O. edulis* for aquaculture in the late 1970s (Peeler et al., 2011).

The ornamental trade has been implicated in the introduction of the chytrid *Batrachochytrium dendrobatidis*; a pathogenic agent partly responsible for the global decline of amphibians and species extinctions (Fisher & Garner, 2007). Trade of freshwater molluscs has long caused concern about the potential for snail-mediated zoonotic diseases as they can act as intermediate hosts for parasites of significance to humans and livestock (Ng et al., 2016), e.g., angiostrongyliasis in humans caused by the parasitic nematode *Angiostrongylus cantonensis* co-introduced with the snails *Pomacea canaliculata* and *Pomacea maculata*.

Symbionts co-transported with INNS may be known pathogens which impact on wildlife in an expanded range (e.g., white spot syndrome virus; Diggles et al., 2020), or their pathogenic potential may only be revealed when presented with new and susceptible hosts (e.g., the impact of *Aphanomyces astaci* on white-claw crayfish; Tilmans et al., 2014).

### **2) Co-transportation of commensal organisms**

The killer shrimp *Dikerogammarus villosus*, invaded the UK in 2010, carrying the gregarine protists *Uradiophora longissima* and *Cephaloidophora mucronata* characterised from Polish freshwaters (Ovcharenko et al., 2009; Bojko et al., 2013). Gregarines are common commensal organisms of invertebrates that cover a wide symbiotic to parasitic spectrum (Rueckert et al., 2019) and undergo sexual reproduction in the animal gut, releasing spores into the environment that are consumed by other organisms. *U. longissima* and *C. mucronata* appear to be commensal organisms that have co-invaded with their host and do not exhibit any controlling effect upon the killer shrimp population (Bojko et al., 2013). Further molecular and histological studies will better identify commensal species by screening native and invasive populations of high-risk groups, such as the Amphipoda.

### 3) Invasion of the symbiome

Assessing the symbiome of an organism requires the use of multiple tools, including both visualisation (microscopy) and diagnostic (molecular detection) techniques. By understanding the symbiome, we can explore co-infection and approach the invasion from a pathobiome perspective (Bass et al., 2019). The symbiome of the demon shrimp *Dikerogammarus haemobaphes*, a European invader originating from the Ponto Caspian region, has been shown to include viruses, bacteria, protists (including microsporidia) and metazoans (Bojko et al., 2019; Bojko & Ovcharenko, 2019), identifying risks coupled with the invasion process (Bojko et al., 2015; Allain et al., 2020; Subramaniam et al., 2020). For example, the microsporidian parasite, *Cucumispora ornata*, has been shown to reduce the activity of the demon shrimp and increase its rate of mortality, initiating population control at invasion sites and lowering its host direct impact on local biodiversity and the environment. In tandem, this parasite is also capable of infecting native *Gammarus pulex*, constituting a wildlife risk (Bojko et al., 2019).

Metabarcoding and metagenomic techniques provide us with a capacity to easily pre-screen native species before they may become translocated. Metabarcoding of the *Homarus americanus* cuticle revealed 170 associated bacterial taxa, suggesting that these microbial symbionts may have the capacity to invade with their host (Meres et al., 2012). Without technologies like these being used to advance invasion science, we remain in the dark about the complete symbiome and its associated risks.

## 3 | INNS IN AQUATIC SYSTEMS

Aquatic ecosystems are considered especially vulnerable to the effects of INNS introduction and spread, when compared to terrestrial ecosystems (Thomaz et al., 2015). Aquatic ecosystems are highly connected, and freshwater catchments link terrestrial, estuarine, and marine habitats longitudinally as water moves downstream, providing corridors along which organisms can move easily (Ormerod et al., 2011). Sites at high-risk of INNS introduction occur where vector activity associated with key introduction pathways is high, such as ports, marinas, and aquaculture sites (Keller et al., 2011; Tidbury et al., 2016). Many aquatic organisms have larval stages, which facilitate their dispersal across large distances (Wood et al., 2005). Detection of aquatic INNS often occurs after populations have already established, due to their patchy distribution and low abundance in the early stages of invasion, and difficulty in detecting and identifying early life stages using standard sampling strategies (Robinson et al., 2018).

### 3.1 | Routes of Introduction of Aquatic INNS



The CBD categorizes the pathways of introduction of an invasive species into 3 main categories; movement of commodities (releases, escapes, contaminants), via transport (stowaway), or by dispersal (corridor, unaided) (Hulme et al., 2008; Pergl et al., 2020). The human-mediated spread of INNS in marine systems is predominantly through global shipping networks via transfer in ballast water or hull fouling on vessels (Tidbury et al., 2016; Bailey et al., 2020). A review by Keller et al. (2011) suggests that, in Europe, this has been the pathway of introduction for 47% of established non-native marine species and 25% of established non-native freshwater species.

Releases and escapes via ornamental trade and aquaculture are also responsible for INNS introductions within Europe (Nunes et al., 2015). The aquatic ornamental animal trade is worth \$25 billion per annum worldwide and represents a significant invasion pathway (Padilla & Williams, 2004). INNS are also introduced through the illegal trade of ornamental aquatic animals. Laws regulating the aquatic pet trade are often poorly communicated and enforced, and in some cases can increase unwanted introductions of banned species (Patoka et al., 2018).

Aquaculture production has expanded rapidly in recent years and global demands are expected to increase to meet the needs of the growing worldwide human population (Stentiford et al., 2017). The movement of non-native animals between countries for aquaculture can spread INNS, and the open nature of many aquaculture sites to their surrounding environment can mean that INNS and their symbionts can be released into those environments (Atalah & Sanchez-Jerez, 2020). The biggest risk to aquaculture production and growth has been identified as disease (Jennings et al., 2016), which highlights the importance of potential invasive aquatic pathogens and the need to control emerging disease threats. The increasing pressures on aquaculture to support global food security makes minimising pathogen spill-over to the environment and wildlife, and vice versa, a critical priority to improve both the efficiency of production and ensure environmental sustainability (Stentiford et al., 2020).

Bait used in recreational fishing is a potential pathway for pathogen introduction and dispersal if anglers dispose of bait or storage water/sediment into aquatic systems (Mahon et al., 2018). Discharge of effluent water from aquaria has also been identified as a high risk for incidental INNS release (Duggan, 2010). Transport of live aquatic animals also means that

the water in which they are transported becomes a potential source of non-native microbes (Amaral-Zettler et al., 2018). Furthermore, the transit of live animals can produce stressful conditions that can change the microbial communities that they harbour, often leading to disease (Smith et al., 2012). Analysis of imported fish and their carriage water through the supply chain showed increased levels of opportunistic pathogens such as *Vibrio* spp. (Amaral-Zettler et al., 2018).

Climate change can also facilitate natural range expansion of holobionts (Cottier-Cook et al., 2017). Increased water temperatures, altered hydrodynamics and more frequent extreme weather events are all predicted to increase the rate of aquatic species invasions (Rahel & Olden, 2008). Rising water temperatures may mean that more ornamental species, and their symbiome, are able to survive and establish in the UK. Warmer temperatures also allow pathogenic microbes to complete their life cycle more rapidly and attain higher population densities, increasing their virulence (Dutta & Dutta, 2016).

## 4 | ADDRESSING THE KNOWLEDGE GAP BETWEEN INNS AND THEIR SYMBIONTS

### 4.1 | Literature Search Methodology

Data on the impacts of aquatic INNS is scarce (Ojaveer et al., 2015; Bojko et al., 2020) and although there are some well-known cases of pathogens being introduced along with INNS, in many cases the nature and subsequent effects of symbionts are unknown. This information is essential for assessing the risks posed by co-transportation, or any INNS introduction to a new area. Such risks fall into three main categories: 1) pathogenic threats to native hosts or to species cultured or harvested for consumption or trade, 2) trade and legislative implications; for example, listed pathogens being introduced to regions previously considered free of them, and 3) effects of, or changes, to the invading species' symbiome in a new range, conferring novel ecological/behavioural characteristics on the invader.

Here we propose a literature-based workflow for compiling existing knowledge on a host's symbiome, members of which could be co-transported with INNS. To perform the literature search, both PubMed and Google Scholar were used to develop the best methodology (Figure 2). Figure 2 illustrates the workflow options and key considerations for choosing which database to search. Each has different characteristics that may preferentially suit different

investigations. Both are subscription-free. The search terms used in this paper are given below; these can be adapted as required. This process can be used/adapted for non-aquatic species and with respect to any geographic region.

PubMed

**(*Species or genus name*<sup>#</sup> [All Fields]) AND (microbiome[Title/Abstract] OR symbio\*[Title/Abstract] OR pathogen\*[Title/Abstract] OR parasit\*[Title/Abstract] OR protist[Title/Abstract] OR protozoa[Title/Abstract] OR bacteria\*[Title/Abstract] OR virus[Title/Abstract] OR host[Title/Abstract] OR reservoir[Title/Abstract] OR vector[Title/Abstract] OR infection [Title/Abstract])**

Google Scholar

***"Species name"*<sup>#</sup> AND pathogen OR parasite OR commensal OR symbiont OR protist OR bacteria OR virus**

<sup>#</sup>In cases where INNS taxa have recently been subject to taxonomic changes or are taxonomically ambiguous, multiple searches using alternative but equivalent names may be required.

PubMed search tools enabled a more accurate search as highly structured search criteria could be applied to just the title and abstract of papers allowing a more focused search. However, the library of literature available in PubMed is smaller than on Google Scholar, and data from some figures and tables is not screened, sometimes leading to the omission of useful information. Google Scholar returned a significantly higher number of publications; the library of literature is much larger and it also scans grey literature and academic thesis repositories. However, Google Scholar also returns a much higher rate of irrelevant results which require significant manual sifting, in part because it scans the references of articles, and because the search cannot be narrowed by abstract. It is also important to scrutinise the source of literature from Google Scholar as it includes non-peer reviewed literature which may not always be suitable depending on the remit of the literature search. Haddaway et al. (2015) provides evidence to show that Google Scholar can be a powerful resource when used alongside other search methods; but is best used as a complementary tool.

## 4.2 | Symbiome literature search results

A list of incoming aquatic INNS of concern to the UK was compiled from the lists of Roy et al. (2014) and a GBNNSS horizon scanning exercise (GBNNSS, 2019). Seventy-seven aquatic INNS were identified from these lists (see Table 1). The literature searches were completed between August-October 2020. Using PubMed; 34 of the 77 aquatic INNS were found to have no relevant literature relating to any known symbiotic species or pathogens. At genus level this number falls to 23; however, the relevance of symbionts and potential pathogens associated with the genus-level compared to the target species is uncertain but aids prediction. Symbiont and pathogen information extracted from the literature search for each species is listed in Supplementary Information Table 1.

There were nine taxa for which species-level symbiont/pathogen data were published in 20+ papers; *Neogobius melanostomus*, *Homarus americanus*, *Oncorhynchus gorboscha*, *Carassius gibelio*, *Micropterus salmoides*, *Castor canadensis*, *Marsupenaeus japonicus*, *Myocaster coypus*, and *Ondatra zibethicus*. The importance of these species in aquaculture, fisheries and human health is likely to explain their dominance within the literature. *Homarus americanus*, *Marsupenaeus japonicus* and *Oncorhynchus gorboscha* are all highly valuable aquaculture species. *Carassius gibelio* and *Micropterus salmoides* are associated with the ornamental trade and recreational angling respectively. *Castor canadensis*, *Myocaster coypus* and *Ondatra zibethicus* carry multiple pathogens of human importance (see Supplementary Information Table 1).

The results from PubMed and Google Scholar show some similarity. For taxa with little relevant literature, Google Scholar was more likely to return relevant data. As shown in Table 1, only 26 of the 77 aquatic INNS returned no relevant literature through Google Scholar in comparison to 34 from PubMed. For taxa with more literature; PubMed returned a larger proportion of useful papers in fewer results, and although these were usually also identified in Google Scholar, significantly more manual sifting of results in order to find these papers was required. For example, *Marsupenaeus japonicus* had 65 relevant papers selected from PubMed, but only 28 were identified from the first 100 Google scholar results despite a vastly larger overall return. This is likely to be because PubMed allowed for a more targeted search. We found using both PubMed and Google Scholar in parallel gives the most comprehensive picture.

Where there is a knowledge gap regarding the symbionts and pathogens of the target species, expert advice may be highly beneficial. This is likely to be the case for many known and potential INNS in most countries. Collaborative expert-elicitation is also a highly valuable tool within the field of biological invasion policy and has been implemented in numerous successful studies (Booy et al., 2017; Hughes et al., 2020; Peyton et al., 2019; Roy et al., 2014, 2017, 2018). These methods have been refined to ten guiding principles to consider within expert-elicitation to increase the effectiveness of this tool (see Roy et al., 2020).

## 5. | CURRENT AND FUTURE POLICY AND LEGISLATION

### 5.1 | GB Legislation

Recognition of the negative impacts of INNS is evidenced by the increase in international to national legislation and policy that aim to mitigate or reduce INNS impacts. Aichi Target 9 of the Convention on Biological Diversity commits signatories, including the UK, to minimise new introductions of INNS, and control and eradicate priority species (UNEP, 2011). This commitment is reflected in European legislation, including Regulation (EU) No 1143/2014 on the prevention and management of the introduction and spread of invasive species (EU, 2014), now transposed into national law. There are additional legislative drivers within the EU to reduce the introduction and spread of INNS as a driver of environmental degradation (Water Framework Directive 2000/60/EC) and as an indication of human pressures (Marine Strategy Framework Directive 2008/56/EC). Given increasing numbers of INNS, risk assessment to include consideration of symbionts and pathogens of key INNS, is required to support the prioritisation of species for management. Whilst the role of pathogens in biological invasions has been recognised, much work is still needed to gather the empirical evidence required for robust assessment of risk, as demonstrated in this paper.

The World Organisation for Animal Health (OIE) has the mandate to prevent the spread of important animal pathogens, including those of aquatic animals (defined as amphibians, crustaceans, fish, and molluscs). OIE standards are recognised by the World Trade Organisation (WTO) and applied within its Sanitary and Phytosanitary (SPS) agreement. The 182 members of the OIE include all major economies. National and supra-national (e.g., EU laws) need to be consistent with OIE standards. The EU Regulation 2016/429 (Animal Health Law) provides the legal basis to prevent the spread of important listed infectious pathogens. The criteria necessary for listing a pathogen include a significant negative impact on farmed

animal production or biodiversity (through biosecurity, contingency planning, surveillance, and eradication) and will be applicable from 21 April 2021 (Council of Europe, 2019).

## 5.2 | International and supranational legislation

The Convention on Biological Diversity places an obligation on contracting parties to ‘*as far as possible and as appropriate, prevent the introduction of, control or eradicate those alien species which threaten ecosystems, habitats or species*’.

At an international level, countries under the SPS agreement must provide a risk assessment to support measures to prevent disease spread that go beyond international (OIE) standards. Co-transported pathogens however, cannot be regulated and controlled if they are unknown and unquantified. Therefore, we propose the following methods:

- 1) More intensive study of INNS and their associated symbionts (including known and potential pathogens), using both experimental and diagnostic evidence.
- 2) Identification of high-risk potential INNS and recent invaders and targeted investigation.
- 3) Investigation of which INNS taxa might co-transport high risk pathogens, based on what we know of the pathogens/symbionts of those groups more generally.

As suggested by Roy et al. (2017), the inclusion of information on pathogens within alien species databases, including the communication of such information, is critical to the success of monitoring and managing emerging co-invasive diseases. Future priorities should be to collect baseline information on the distribution and population dynamics of pathogens, hosts and vectors, to determine the relative importance of invasion pathways, and to develop methods for predicting host shifts, pathogen–host dynamics and the evolution of alien pathogens (Roy, 2016). Many aspects of the study and management of emerging infectious diseases and biological invasions work in parallel. Collaboration across disciplines is important to effectively tackle these issues, such as adopting the One Health framework (Ogden et al., 2019; Bojko et al., 2020).

## 6. | CONCLUSION

Invasion biology needs more robust methods for reliably evaluating the risks associated with INNS introductions (Kumschick et al., 2015). One of the important factors to consider as part of risk assessments is evaluating the symbiome of INNS. Therefore, there is a need to better understand symbionts associated with INNS in order to evaluate the potential threat of

emerging co-invasive disease as part of the INNS risk assessment processes (including horizon scanning). The framework proposed here contributes a simple yet elegant methodology for the robust and standardised assessment of symbionts associated with INNS. As such it provides a crucial step towards addressing the knowledge gaps regarding co-transportation of symbionts, facilitating integration of such knowledge into INNS risk assessment.

While limitations exist with respect to INNS data, the increasing use of histological, eDNA, and molecular diagnostics also offer new opportunities for monitoring INNS, potentially enabling the capture of pathological data more easily. Innovative modelling approaches, such as those using evolutionary trait-based frameworks (Barwell et al., 2020), can also inform horizon scanning and risk assessment to identify potentially impactful pathogens.

The introduction of INNS is widely recognised as important in both introducing known pathogens and a driver for the emergence of new pathogens (Peeler et al., 2011). There is a need at both international and national level for a collaborative approach to the assessment of INNS, efficient resource use and the formulation of guidance and risk assessment tools to both prevent and control the introduction of INNS and their symbionts. INNS do not recognise political boundaries so their effective management, particularly the marine environment, requires transboundary co-ordination and collaboration.

This issue is now more pressing than ever; climate change could act synergistically with other stressors, to increase the impacts of invading microbes. Rising water temperatures may mean more INNS and their pathogens are able to survive and establish in the UK. Furthermore, the increasing global demands on aquaculture production, mean that risks arising from emerging aquatic diseases are increasing in frequency, and have increasingly diverse and serious economic implications.

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## CONFLICT OF INTEREST

The authors declare no conflict of interest

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<b>Glossary</b>	
<b>Symbiont</b>	Host-associated organisms and viruses, including long-term or transitory associations, epibionts and endobionts.
<b>Pathogen</b>	A symbiont that causes disease in certain hosts under certain conditions. Its presence need not result in disease. Often used interchangeably with ‘parasite’.
<b>Parasite</b>	A symbiont that derives nutrition/material resource from its host in one of several ways, not necessarily resulting in disease. Includes indirect feeding types including host stomach contents or metabolic products. Often used interchangeably with ‘pathogen’.
<b>Enemy Release Hypothesis</b>	INNS can lose their parasites as they move into a new range, thus increasing host biological fitness as the resources used to fight the infection are no longer required (Keane and Crawley, 2002).
<b>Parasite Spillback</b>	INNS can acquire parasites from the new range, resulting in parasite spillback to native species by increasing the population of infected individuals (Sheath et al., 2015), thus changing disease dynamics of infected native species at individual and population scale levels (Kelly et al., 2009).
<b>Parasite Spillover</b>	When parasites from INNS are transmitted to susceptible native host species (Power and Mitchell, 2004)
<b>Disease Facilitation Hypothesis</b>	INNS may act as ‘disease facilitators’ by aiding the physical transfer of parasites through acting as vectors or a reservoir, or via their role in habitat alteration which may improve parasite environmental conditions (Chalkowski et al., 2018).
<b>Co-transport</b>	Organisms which are transported with an alien host to a new location outside of their native range (Lymbery et al., 2014)
<b>Heteroecious parasites</b>	A parasite that requires at least two hosts.

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## Figure Legends

FIGURE 1. Potential fates of symbionts (including pathogens) co-transported with INN host species. The left-hand panel represents a hypothetical INNS with a symbiome comprising pathogens A, B, and uncharacterised symbionts 1, 2, 3. Potential symbionts already in the native system are pathogens C, D, E, F, and uncharacterised symbionts 4, 5, 6. Symbionts can be gained and/or lost by INNS hosts. The main panel on the right presents, with examples, scenarios of gains, losses, and transfers between non-native and native hosts of different species, and outcomes associated with such interactions. Boxes with grey fill indicate theoretical outcomes for which no empirical evidence was found.

FIGURE 2. Workflow for investigating existing data relating to symbionts (including pathogens) of current and potential INNS. The bullet points in each box indicate key considerations for each step of this customisable process. The list of factors in grey text influence whether PubMed or Google Scholar (or both) would be more appropriate for the particular species being researched.

**Table 1.** Non-native species at risk of arriving in the UK, as defined by Roy et al. (2014) and GB-NNSS (2019), and the results of literature searches as described in the main text. [x] is the number of publications informative about co-transported pathogens/symbionts, from which information was extracted and the publication cited in Supplementary Table 1. When x<4 in PubMed searches; informative publications were also searched for at INNS genus level (filtering to this degree was not possible or practical with Google Scholar). Only the first 100 Google Scholar hits were searched for informative publications. References for all of the informative publications selected are in Supplementary Tables 2 and 3.

Taxonomic abbreviations: AL = Algae; AN = Annelida; ANG = Angiosperms; BR = Bryozoa; CH = Chordata (CH-U = Urochordata, CH-P = Pisces, CH-A = Amphibia, CH-R = Reptilia, CH-A = Aves, CH-M = Mammalia); CR = Crustacea; CT = Ctenophora; EC = Echinodermata; MO = Mollusca; NE = Nemertea; PL = Platyhelminthes; PO = Porifera

Species name	Common name	Taxon	PubMed Genus search [X]	PubMed Species search [X]	Google Scholar Species search [X]
<i>Aglaothamnion halliae</i>	Brazilian red alga	AL	1 [1]	0	34 [0]
<i>Antithamnion pectinatum</i>	Australasian red alga	AL	2 [0]	0	40 [0]
<i>Caulerpa taxifolia</i>	killer alga	AL	43	43 [8]	2660 [4]
<i>Gracilaria vermiculophylla</i>	rough gar weed	AL	90	6 [4]	1140 [4]
<i>Rugulopteryx okamurae</i>	Asian fan weed	AL	0	0	12 [0]
<i>Eudistylia polymorpha</i> / <i>Bispira polyomma</i>	giant feather duster worm	AN	1 [1]	0	6 [0]
<i>Marenzelleria wireni</i>	red gilled worm	AN	1 [1]	0	17 [0]
<i>Limnobium spongia</i>	American frog's-bit	ANG	68	0	128 [1]
<i>Saururus cernuus</i>	swamp lily	ANG	58 [0]	2 [0]	474 [0]
<i>Trapa natans</i>	water chestnut	ANG	17 [1]	7 [1]	1820 [0]
<i>Zostera japonica</i>	Japanese seagrass	ANG	98 [71]	1 [1]	563 [4]
<i>Schizoporella errata</i>	branching bryozoan	BR	0	0	209 [0]
<i>Ommatotriton ophryticus</i>	northern banded newt	CH-A	0	0	21 [0]
<i>Tadorna ferruginea</i>	ruddy shelduck	CH-A	21	10 [10]	562 [15]
<i>Threskiornis aethiopicus</i>	African sacred ibis	CH-A	7 [5]	4 [2]	435 [2]
<i>Aonyx cinerea</i>	short clawed otter	CH-M	232	2 [2]	166 [5]
<i>Castor canadensis</i>	American beaver	CH-M	486	27 [25]	3580 [12]
<i>Myocaster coypus</i>	coypu	CH-M	52	51 [43]	2270 [27]
<i>Ondatra zibethicus</i>	muskrat	CH-M	58	42 [42]	2650 [27]

<i>Babka gymnotrachelus</i>	racer goby	<b>CH-P</b>	2 [2]	2 [2]	80 [8]
<i>Carassius gibelio</i>	Prussian carp	<b>CH-P</b>	516	30 [20]	1670 [30]
<i>Gambusia holbrooki</i>	eastern mosquito fish	<b>CH-P</b>	445	15 [5]	2660 [7]
<i>Micropterus salmoides</i>	largemouth bass	<b>CH-P</b>	1,939	131 [74]	9200 [39]
<i>Neogobius fluviatilis</i>	monkey goby	<b>CH-P</b>	44	6 [6]	400 [15]
<i>Neogobius melanostomus</i>	round goby	<b>CH-P</b>	44	35 [27]	2050 [33]
<i>Oncorhynchus gorbuscha</i>	pink salmon	<b>CH-P</b>	1,776	30 [25]	3560 [32]
<i>Proterorhinus marmoratus</i>	Black Sea tubenose goby	<b>CH-P</b>	9 [6]	2 [2]	383 [12]
<i>Proterorhinus semilunaris</i>	western tubenose goby	<b>CH-P</b>	9	7 [4]	209 [11]
<i>Pterois volitans</i>	red lionfish	<b>CH-P</b>	13 [6]	8 [3]	1140 [12]
<i>Umbra pygmaea</i>	eastern mud minnow	<b>CH-P</b>	5 [4]	0	215 [1]
<i>Chelydra serpentina</i>	snapping turtle	<b>CH-R</b>	22	21 [11]	2180 [14]
<i>Chrysemys picta</i>	painted turtle	<b>CH-R</b>	21	20 [12]	2860 [14]
<i>Ciona savignyi</i>	sea squirt	<b>CH-U</b>	123	123 [12]	1120 [4]
<i>Styela plicata</i>	pleated tunicate	<b>CH-U</b>	35 [6]	15 [2]	1350 [7]
<i>Cercopagis pengoi</i>	fishhook water flea	<b>CR</b>	1 [0]	1 [0]	624 [0]
<i>Chelicorophium robustum</i>	A Ponto-Caspian amphipod	<b>CR</b>	0	0	24 [0]
<i>Chelicorophium sowinskyi</i>	A Ponto-Caspian amphipod	<b>CR</b>	0	0	13 [0]
<i>Cherax destructor</i>	common yabby	<b>CR</b>	81	10 [6]	1420 [7]
<i>Dikerogammarus bispinosus</i>	A Ponto-Caspian amphipod	<b>CR</b>	22 [5]	0	27 [0]
<i>Dyspanopeus sayi</i>	Say's mud crab	<b>CR</b>	2 [1]	2 [1]	172 [0]
<i>Echinogammarus ischnus</i>	bald urchin shrimp	<b>CR</b>	29 [21]	0	322 [2]
<i>Echinogammarus trichiatus</i>	curly haired urchin shrimp	<b>CR</b>	29 [21]	3 [3]	59 [3]
<i>Echinogammarus warpachowskyi</i>	A Ponto-Caspian amphipod	<b>CR</b>	29 [21]	0	16 [0]
<i>Hemigrapsus sanguineus</i>	Asian shore crab	<b>CR</b>	24	6 [5]	251 [4]
<i>Hemigrapsus takanoi</i>	brush-clawed shore crab	<b>CR</b>	24	0	138 [3]

<i>Homarus americanus</i>	American lobster	<b>CR</b>	119	63 [38]	8230 [42]
<i>Jaera istri</i>	A Ponto-Caspian isopod	<b>CR</b>	3 [2]	1 [1]	72 [1]
<i>Limnomysis benedeni</i>	A Ponto-Caspian mysid	<b>CR</b>	1 [0]	1 [0]	169 [0]
<i>Marsupenaeus japonicus</i>	kuruma prawn	<b>CR</b>	2,088	173 [65]	4930[28]
<i>Megabalanus coccopoma</i>	titan acorn barnacle	<b>CR</b>	4 [0]	0	108 [0]
<i>Megabalanus tintinnabulum</i>	sea tulip	<b>CR</b>	4 [0]	0	130 [1]
<i>Mytilicola orientalis</i>	red oyster worm	<b>CR</b>	15 [0]	4 [0]	349 [0]
<i>Neocaridina davidi</i> / <i>Neocaridina heteropoda</i>	cherry shrimp	<b>CR</b>	8 [4]	1 [0]	93 [1]
<i>Obesogammarus crassus</i>	A Ponto-Caspian amphipod	<b>CR</b>	0	0	78 [2]
<i>Obesogammarus obesus</i>	A Ponto-Caspian amphipod	<b>CR</b>	0	0	45 [1]
<i>Orconectes rusticus</i>	rusty crayfish	<b>CR</b>	21 [15]	3 [2]	1280 [5]
<i>Paramysis lacustris</i>	A Ponto-Caspian mysid	<b>CR</b>	0	0	88 [0]
<i>Pontogammarus robustoides</i>	A Ponto-Caspian amphipod	<b>CR</b>	2	1 [1]	250 [3]
<i>Procambarus fallax</i>	marbled crayfish	<b>CR</b>	484	1 [1]	323 [8]
<i>Rhithropanopeus harrisi</i>	Harris' mud crab	<b>CR</b>	2 [1]	1 [1]	1220 [11]
<i>Mnemiopsis leidyi</i>	American comb jelly sea walnut?	<b>CT</b>	36	12 [6]	2860 [15]
<i>Asterias amurensis</i>	Northern Pacific seastar	<b>EC</b>	38	8 [4]	1890 [6]
<i>Bellamya chinensis</i>	Chinese mystery snail	<b>MO</b>	27 [17]	1 [0]	90 [3]
<i>Corbicula fluminalis</i>	Asian clam	<b>MO</b>	37[18]	0	222 [0]
<i>Dreissena rostriformis bugensis</i>	quagga mussel	<b>MO</b>	79	10 [2]	683 [2]
<i>Geukensia demissa</i>	Atlantic ribbed mussel	<b>MO</b>	10	9 [4]	1750 [4]
<i>Lithoglyphus naticoides</i>	gravel snail	<b>MO</b>	4 [4]	3 [3]	373 [4]
<i>Mulinia lateralis</i>	dwarf surf clam	<b>MO</b>	4 [3]	3 [2]	906 [2]
<i>Ocenebrellus inornatus</i>	Japanese sting winkle	<b>MO</b>	0	0	146 [0]
<i>Potamocorbula amurensis</i>	Amur river clam	<b>MO</b>	0	0	887 [0]
<i>Rapana venosa</i>	veined rapa whelk	<b>MO</b>	12	7 [3]	965 [4]



<i>Sinanodonta woodiana</i>	Chinese giant mussel	<b>MO</b>	56	16 [3]	671 [4]
<i>Theora lubrica</i>	Asian semele	<b>MO</b>	0	0	162 [0]
<i>Xenostrobus securis</i>	pygmy mussel	<b>MO</b>	1 [0]	1 [0]	177 [2]
<i>Cephalothrix simula</i>	A NW Pacific Ocean nemertean worm	<b>NE</b>	2 [2]	2 [2]	89 [7]
<i>Gyrodactylus salaris</i>	salmon fluke	<b>PL</b>	422	104 [0]	2710 [0]
<i>Celtodoryx ciocalyptoides</i>	cauliflower sponge	<b>PO</b>	1 [0]	0	21 [0]

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