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Wildlife health risk analysis for conservation translocation: A scalable approach illustrated for wader population restoration

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Abstract

Conservation translocations are human-mediated movements of wildlife for conservation purposes. They risk compromising the health of wildlife, and potentially domestic animals and humans, in the short and long term, but these risks vary with project context. Wildlife health risk analysis (disease risk analysis) is a process enabling these risks to be characterized and managed; multiple methods have been developed for conservation translocation. It would be beneficial for the depth of health risk analysis to be proportionate to context; however, few methods currently facilitate this flexibility. We aimed to produce a refined methodological framework for health risk analysis that enabled it to be scalable and adaptable to different translocation scenarios. We developed such a framework by adapting and assimilating elements of existing methods. We describe its key features and application to two wader (shorebird) conservation translocations with differing translocation plans and epidemiological circumstances. We then reflect on the framework's utility in light of the observed project outcomes, which exemplified the uncertain and changeable nature of disease risks over time. Our framework has the potential to expedite health risk analysis for repeat translocations of a particular taxon in a region and has application to other taxa and potentially other forms of wildlife translocation.

KEYWORDS

curlew *Numenius* sp. headstarting, godwit *Limosa* sp. conservation, highly pathogenic avian influenza virus, shorebird health and disease, wader health and disease, wildlife conservation translocation, wildlife disease risk analysis, wildlife disease risk assessment, wildlife health risk analysis, wildlife reintroduction

1 | INTRODUCTION

Conservation translocation is defined as, "the deliberate movement of organisms from one site for release in another [for] a measurable conservation benefit at the levels of a population, species or ecosystem" (IUCN/SSC, 2013). Conservation translocations encompass reinforcement or reintroduction for the purpose of population or species restoration, and conservation introduction for the purpose of assisted colonization or ecological replacement (IUCN/SSC, 2013). While conservation translocation has become a widely used tool in biodiversity conservation (Beckmann & Soorae, 2022), around the globe a far greater number of wild animals is likely to be translocated accidentally or intentionally for other purposes (Griffith et al., 1993; Fèvre et al., 2006).

The translocation of wild animals from one ecological context to another poses multiple risks (IUCN/SSC, 2013), including to the health of wildlife and epidemiologically linked populations of domestic animals or humans (Daszak et al., 2000; Kock et al., 2010). The term wildlife health captures an aspiration for individual wild animals and their populations to live in a state of physical and mental wellbeing, such that they fulfill their functional role in an ecosystem and are resilient to change (Deem et al., 2001; Hanisch et al., 2012; Meredith et al., 2022). Disease has been defined as, "any [physical or mental] impairment that interferes with or modifies the performance of [an individual's] normal functions" and may be infectious or non-infectious (Wobeser, 1981). Wildlife diseases of most concern are those with the potential to compromise a wildlife population's ability to adapt to change, that is its population health (Bacon et al., 2023; Stephen, 2014), or to cause population decline, which, in turn may lead to wider ecosystem change (Eads & Biggins, 2015; Ogada et al., 2012). Of further concern are infectious agents of wild animals that cause disease in domestic animals or humans, which can result in economic or public health costs (Daszak et al., 2000; Gortázar et al., 2007). Highly pathogenic avian influenza (HPAI) virus, a notifiable pathogen (OIE 2022), exemplifies this range of impacts: the recent extensive spread of HPAI subtype H5Nx has been associated with marked mortality and population declines in species of conservation concern, profound losses in the livestock sector, and it remains a zoonotic infection with pandemic potential (Ison & Marrazzo, 2025; Lambertucci et al., 2025). Furthermore, in a translocation context, the negative impacts of diseases on animal welfare are important to recognize given our ethical duty to safeguard the welfare of translocated wild animals (Harrington et al., 2013; Sainsbury et al., 1995).

Wildlife translocations risk introducing novel infectious agents and associated disease to other animal and human populations. For example, the international trade in amphibians and their products has driven the global spread of the fungal disease chytridiomycosis in amphibians, causing population declines and species extinctions (Martel et al., 2014; Scheele et al., 2019). While wildlife translocation has undoubtedly been an important driver of emerging infectious disease events in wildlife, domestic animals, and humans, to date such events have rarely been attributed to *conservation* translocation (see Walker et al., 2008; Vadlejch et al., 2017 for rare examples), although "this may simply reflect the challenges associated with undertaking post-release monitoring and disease surveillance" in these projects (Beckmann et al., 2022). More commonly, disease has been reported to affect translocated or released individuals themselves (Warne & Chaber, 2023). Also, non-infectious conditions such as traumatic injury, chronic stress, poisoning and husbandry-related disease have been mentioned as frequently as infectious disease in case reports of conservation translocation (Beckmann et al., 2022).

The nature and magnitude of disease risk in conservation translocations varies greatly across projects and is dependent on the target species, translocation plan and epidemiological circumstances (Beckmann et al., 2022). The risk of novel infectious disease introduction is increased when translocations cross geographical barriers, that is "natural and environmental barriers that prevent natural movement between populations," and ecological barriers, defined as physical, behavioral or reproductive "characteristics... that prevent interaction between populations" (Bobadilla Suarez et al., 2017). Similarly, ex situ environments and ex situ-to-wild translocations present notable disease risks (Bobadilla Suarez et al., 2017; Snyder et al., 1996). Disease concerns are frequently taxon-specific, such as amphibian chytridiomycosis, and the presence of such an infectious disease concern in the source and/or release area presents a clear challenge for translocation (Kock et al., 2010; Muths & McCallum, 2016).

Risk analysis is a well-established, "formal procedure for estimating the likelihood and consequences of adverse effects occurring" in a specified population (Thrusfield et al., 2018). As the potential for disease spread through wildlife translocation was increasingly recognized, methods to characterize and estimate these risks started to be piloted (Ballou, 1993; Davidson & Nettles, 1992). The World Organization for Animal Health (WOAH, formerly OIE) later specified four component steps to import risk analysis for domestic animals and their products: hazard identification; risk assessment, where the likelihood of hazard occurrence is multiplied by the severity of its consequences to produce a risk estimate; risk management; and risk communication

(Brückner et al., 2010). A variety of risk analysis methods suitable for wildlife conservation translocation subsequently evolved from these methods. These included an overarching framework published by the WOAH and the International Union for the Conservation of Nature (IUCN) (Jakob-Hoff et al., 2014b; OIE and IUCN, 2014) (hereafter the "WOAH and IUCN" method), which was developed for any wildlife intervention or risk scenario; and methods developed specifically for conservation translocation by the Zoological Society of London (ZSL), UK (Sainsbury & Vaughan-Higgins, 2012; updated in Bobadilla Suarez et al., 2017; Sainsbury & Carraro, 2023) (hereafter the "ZSL" method), and the Department of Conservation (DOC), New Zealand (McInnes unpublished, as described in Lees et al., 2014) (hereafter the "DOC" method). These and other methods have been termed disease risk analysis (Bobadilla Suarez et al., 2017; OIE and IUCN, 2014) or health risk analysis/assessment (Leighton, 2002; OIE, 2017): here we use the term health risk analysis to reflect our aspiration to foster and safeguard the health of wildlife, domestic animals, humans and their wider ecosystems in a conservation context (Beckmann et al., 2022; Hanisch et al., 2012).

The IUCN recommends that a health risk analysis is undertaken for any conservation translocation, alongside procedures to address other forms of risk, to source population viability, as well as ecological, invasion, genetic, socio-economic and financial risks (IUCN/SSC, 2013). Recently, an increasing number of authors have described the application of, in particular, the WOAH and IUCN and the ZSL health risk analysis methods to conservation translocation. However, they have noted that health risk analysis remains a time-consuming process (Vaughan-Higgins et al., 2021) and that there is no one optimal approach (Dalziel et al., 2016). The IUCN noted that the "depth" of health risk analysis should be "in proportion" to the risks posed (IUCN/SSC, 2013), however, to date such scalability has only been built into the DOC method, where a linear decision tree (the "Disease Risk Assessment Tool") enables in-country translocations meeting certain criteria to bypass the requirement for detailed risk analysis, provided they follow minimum prescribed management measures. This method remains specific to the New Zealand context, however. A concise method of risk analysis is needed for low-risk translocation scenarios in other countries (IUCN/SSC, 2013).

There is also scope for the health risk analysis process to take a more comprehensive and better-defined range of hazards into consideration. Most methods focus on risks of infectious disease spread from the source population, via translocated animals, to the release ecosystem and on risks to the health of translocated individuals post release. The ZSL method also recognizes infectious hazards to translocated animals during their transport and captivity, as well as commensal and zoonotic hazards (Bobadilla Suarez et al., 2017). Further broad potential pathways of infectious agent transmission associated with translocation and monitoring activities also merit explicit inclusion in the health risk analysis process (such as those described by Cook, Grant et al., 2021; Davidson & Nettles, 1992; Sherman et al., 2021; Thorne & Williams, 1988). The non-infectious hazards relevant to health risk analysis also remain poorly defined and methods have focused on these hazards post release, despite stress and husbandry-related disease, for example, being reported commonly in ex situ stages of conservation translocation (Beckmann et al., 2022).

In recent years the Wildfowl & Wetlands Trust (WWT, Slimbridge, Gloucestershire, UK) and partner organizations have employed a technique called "headstarting" to help promote the recovery of a variety of small, threatened waterbird populations. Headstarting aims to mitigate in situ prefledging mortality and involves collection of eggs from the nests of wild breeding pairs, followed by artificial incubation, captive rearing, and release of hatched chicks at fledging age (Donaldson et al., 2024). From 2017 to 2022, the WWT and the Royal Society for the Protection of Birds (RSPB) conducted headstarting for Project Godwit, which aimed to reinforce an important breeding subpopulation of black-tailed godwits (*Limosa limosa limosa*, hereafter "godwits"; Order Charadriiformes, Family Scolopacidae) in eastern England (Donaldson et al., 2024). In 2019, the WWT and Natural England performed a trial translocation and population reinforcement of lowland Eurasian curlews (*Numenius arquata arquata*, Order Charadriiformes, Family Scolopacidae; hereafter "the curlew translocation") in south-west England, which was one of multiple curlew headstarting projects undertaken in England in recent years (Colwell et al., 2020).

We aimed to develop a refined methodological framework for health risk analysis for conservation translocation that enabled the process to be proportionate and adaptable to different translocation contexts. We describe the development of such a framework and illustrate its application to Project Godwit and the curlew translocation, which had differing translocation plans. These health risk analyses aimed to identify hazards and estimate risks to the health of translocated waders and other wild-living, ex situ, and domestic animals and humans; to identify associated uncertainties; and to determine appropriate disease management measures.

2 | METHODS

The translocation projects and management procedures described here were approved by the WWT's Animal Welfare and Ethics Committee.

2.1 | Terminology and development of the methodological framework

Consistent with existing methods, "hazards" were defined as infectious agents or non-infectious conditions that could cause "an adverse health effect" in translocated individuals, or other animals or humans, as a consequence of translocation (Jakob-Hoff et al., 2014b).

The health risk analysis framework incorporated and adapted elements of four principal methods: the WOAH and IUCN method, the ZSL method, the DOC method, and a method developed by the Canadian Wildlife Health Cooperative (CWHC) in partnership with the WOAH (Canadian Wildlife Health Cooperative unpublished; Leighton, 2002; OIE, 2017) (hereafter the "CWHC and WOAH" method). It also drew from IUCN/SSC Conservation Planning (formerly Conservation Breeding) Specialist Group guidelines, which were a precedent to the WOAH and IUCN method (Armstrong et al., 2003; Miller, 2007) (hereafter the "IUCN/SSC CPSG" method).

Our framework comprised eight steps, adapted from the WOAH and IUCN method: (1) Problem description; (2) Taxon-specific reference lists of infectious agents and non-infectious conditions; (3) Hazard characterization and identification; (4) Standard disease management measures; (5) Risk assessment; (6) Management decision making; (7) Disease management protocol; and (8) Implementation, monitoring, and review (Figure 1). Stakeholder consultation and risk communication was an iterative process conducted throughout the analysis (Figure 1).

To enable the scale of risk analysis to be adapted to project context, different approaches to characterizing infectious hazards (Step 3) were developed. For lower-risk translocations, including those that did not cross a geographic or ecological barrier, an "abridged" method was devised. Here, the risk analysis focused on each broad directional pathway of potential infectious agent transmission, with infectious agents considered as a group for each pathway; this differed from the traditional risk analysis approach of conducting a separate risk assessment for each infectious hazard. The broad directional pathways of infectious agent transmission were termed "infectious hazard pathways." To ensure they encompassed a comprehensive range of potential transmission scenarios, the pathways were characterized through detailed consideration of the populations and environments from which an infectious agent could

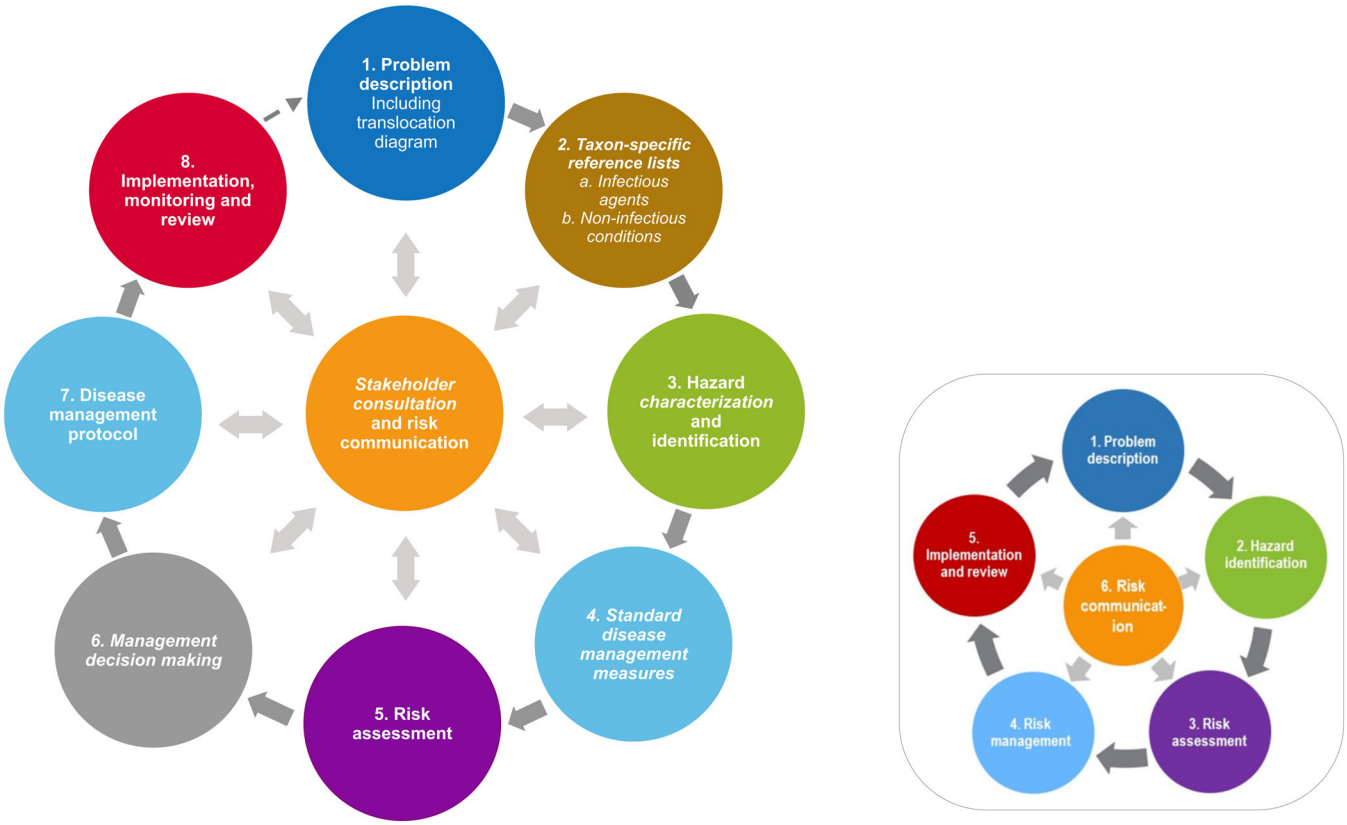

FIGURE 1 Summary methodological framework for the wader health risk analyses, which incorporated steps in the WOAH and IUCN (OIE and IUCN, 2014) risk analysis framework (inset). Italicized text is used to indicate steps or parts of steps that were additional to the WOAH and IUCN framework.

originate, and the populations at risk of harm, at each translocation stage (see Table S1, Supporting Information). Nine infectious hazard pathways were characterized, which incorporated the hazard types described by Bobadilla Suarez et al. (2017) (ZSL method) and some additional broad transmission scenarios. They comprised four pathways of potential hazard transmission *to* the target (source, translocated or released) population, termed "ex situ," "destination," "human-associated," and "carrier" hazards; and five pathways of potential hazard transmission *from* the target population to other populations of animals or humans, termed "source," "zoonotic," "forwarded ex situ," "forwarded human-associated," and "reservoir" hazards (Table 1 and Figure 2).

Briefly, ex situ hazards were those that could be transmitted to translocated individuals during an ex situ stage of translocation (transit, captivity or holding; equivalent to the ZSL method's "transport" hazards); destination hazards were those that could be transmitted to individuals post-release; human-associated hazards were those that could be transmitted from or via humans to individuals at any translocation stage, including to those in the source or released population; and carrier hazards were those that translocated or released individuals could harbor themselves, including commensal and host-adapted agents, and which could cause disease in these individuals under certain conditions. Source hazards were those that wild-sourced individuals could transmit to other animals during handling, an ex situ stage, or post-release; zoonotic hazards were those that could be transmitted to humans from individuals in the target (including source or released) population; forwarded ex situ and forwarded human-associated hazards were ex situ and human-associated hazards (respectively) that could be transmitted onwards in or via individuals of the target population to other populations; and reservoir hazards were infectious agents in the release ecosystem for which released individuals of the target species could serve as a reservoir host and for which releases could potentially intensify the risk of infection for other animals or humans in the release area. More-detailed definitions are provided in Table 1, where additions and differences to the ZSL method's hazard definitions are also described further.

If an abridged risk analysis was justified but a particular infectious agent was considered to pose a notable, specific infectious disease risk, this was considered a discrete infectious hazard in what was termed a "focused" risk analysis (Figure 3), in parallel to the abridged risk analysis for other infectious agents. Translocations posing a comparatively high disease risk were subject to a "comprehensive" risk analysis, which meant a traditional approach in which infectious hazards were each considered separately. A flowchart was adapted from the DOC method's Disease Risk Assessment Tool to guide selection of the risk analysis approach—abridged, focused, or comprehensive (Figure 3).

Non-infectious hazards were categorized as per Beckmann et al. (2022) and considered separately from infectious hazards, focusing on hazards at each translocation stage in turn.

To further expedite health risk analysis, standard (minimum) disease management measures were specified (Step 4) that would be implemented routinely, independent of risk assessment, consistent with the CWHC and WOAH method. They were measures that had already become standard practice in other waterbird translocation projects conducted by the WWT, so they were considered feasible and acceptable, as well as efficacious (Jakob-Hoff et al., 2014a; Stephen & Zimmer, unpublished technical report of the CWHC). This was considered appropriate given that no translocation is risk free (IUCN/SSC, 2013): any translocation scenario is likely to present, for example, ex situ, human-associated, carrier and zoonotic infectious hazards, as well as non-infectious hazards to translocated individuals such as stress-related disorders and traumatic injury (Jakob-Hoff et al., 2014a; Stephen & Zimmer, unpublished technical report of the CWHC).

2.2 | Framework steps and their application to the wader projects

2.2.1 | Step 1: Problem description

First, relevant background information on the wader translocation projects was summarized. Second, the proposed translocation plan was described and a "translocation diagram" was created to illustrate the movement of individuals through different translocation stages, and the animal and human populations that could be epidemiologically linked to the target population at each stage. Any notable infectious disease concerns were also described. Third, the aims of health risk analysis were stated (see above). Fourth, the negative consequences that would be considered as part of the risk assessment were stated (drawing from the CWHC and WOAH and the WOAH and IUCN methods). These included disease in other wild-living, ex situ or domestic animals; a reduction in size of the translocated or released wader population; compromised welfare of translocated or released waders; increased project management costs; and a negative reputational impact for the project, such as could result from a notifiable infection or disease outbreak.

In Project Godwit, the source and release areas were geographically close wet grassland sites, between which

TABLE 1 The broad directional pathways of infection risk associated with conservation translocation, which were termed "infectious hazard pathways" and characterized through detailed consideration of the populations and environments from which an infectious agent could originate and the populations at risk of harm at each translocation stage (Table S1; see Figure 2 for an accompanying illustration).

		Definition	
	Infectious hazard pathway	**Origin of infectious agent (or strain of infectious agent)**	**Populations at risk of harm**
Hazards to translocated individuals			
1	Ex situ hazards[a]	(a) Wild-living, ex situ or domestic animals, or invertebrate vectors, which have direct or indirect[g] contact with individuals in an ex situ environment[h], or (b) the ex situ environment	Translocated individuals in an ex situ environment[h]
2	Destination hazards[b]	(a) Wild-living or domestic animals, or invertebrate vectors, in the release area or (b) the wider release ecosystem	Released individuals
3	*Human-associated hazards*[c]	*Humans, including project personnel, who have direct or indirect[g] contact with individuals in the source, translocated or released population; they may serve as indirect carriers of an infectious agent following contact with an animal or environment remote to the translocation project, or be infected with the agent*[i]	*Individuals in the source, translocated or released population*
4	Carrier hazards	Translocated individuals; these include commensal or host-adapted agents[j] that may have originated from the wild-living source population or from wild-sourced founders (and may have persisted through subsequent captive generations)	Translocated individuals, in which these agents may cause disease under certain conditions such as chronic stress or overcrowding
Hazards to other animals or humans			
5	Source hazards[d]	The wild-living source population from which translocated individuals are captured or collected and continue to harbor these agents, which may be commensal or host-adapted[j] in the species. Includes agents present in wild-sourced founders that may have persisted through subsequent captive generations	Ex situ, domestic or wild-living animals in direct or indirect[g] contact with translocated individuals (a) during an *ex situ* translocation stage[h], or (b) post-release, and for which the agent is novel
6	Zoonotic hazards[e]	Source, translocated or released population	Project personnel and other people in direct or indirect[g] contact with individuals in the source, translocated or released population
7	*Reservoir hazards*[f]	*The release ecosystem, which is a source of infection for released individuals which in turn serve as reservoir hosts of the infectious agent (persistent sources of infection)*	*Other wild-living or domestic animals, or humans, in the release area, for which the addition of reservoir hosts to the area increases the likelihood of infection*
8	*Forwarded ex situ hazards*[f]	*Translocated individuals, which have acquired ex situ hazards as per above*	*Wild-living, ex situ or domestic animals in direct or indirect[g] contact with translocated individuals at (a) a subsequent ex situ stage[h], or (b) in the release area, for which the agent is novel*
9	*Forwarded human-associated hazards*[f]	*Translocated individuals, which have acquired human-associated hazards as per above*	

Note: Pathway names were adapted from the ZSL method (as per Bobadilla Suarez et al., 2017); pathways that were additional to the ZSL method's hazard types are highlighted through italicized text and differences are described further below. Three further infectious hazard pathways were characterized but considered outside the scope of the wader health risk analyses: infectious agents in the source area posing a notable population-level threat to the source population; human-associated hazards from project personnel to other animals (wild-living, ex situ or domestic animals in source, ex situ or release areas); and infectious agents in the source or release area, or other translocation environments, posing a zoonotic risk to project personnel (Table S1). A given infectious agent could be a hazard across multiple pathways.

[a]Here, "ex situ" hazards were similar to the ZSL method's "transport" hazards.

[b]These and other hazard pathways *to* the target (source, translocated or released) population were defined solely according to the broad direction of transmission and not by their novelty to the target population. That is, the infectious agent could either be novel to the target population or might not be novel but have potential to cause disease under certain conditions such as chronic stress or overcrowding. "Destination" hazards therefore encompassed the ZSL method's "population" hazards (Bobadilla Suarez et al., 2017), which those authors had differentiated from destination hazards based on a lack of novelty to the released population (and that population hazards could include non-infectious hazards, which are considered separately in the current method).

[c]A new infectious hazard pathway, "human-associated" hazards, was created to describe the potential for infectious agent transmission to the target population by humans at any stage of the translocation, including to the source or released population.

[d]The ZSL method's definition of a "source" hazard encompasses infectious agents originating from a captive source population; here it referred only to infectious agents originating from a wild-living source population or wild-sourced founders of a captive collection, and explicitly recognized the potential for these agents to be transmitted to other populations during an ex situ translocation stage (defined below).

[e]"Zoonotic" hazards encompassed hazards to project personnel from the target population at any translocation stage, including from the source population.

[f]Reservoir, forwarded ex situ and forwarded human-associated hazards were also newly described pathways.

[g]Includes human-associated transfer via fomites (inanimate objects such as footwear, clothing or project equipment).

[h]Ex situ encompasses any environment in which translocated individuals are transported or housed between their capture/collection and release, that is, transit, captive, or holding environments.

[i]This can be termed zooanthroponotic, anthroponotic, or reverse zoonotic transmission.

[j]Infectious agents adapted to living on or within individuals of the translocated species which do not usually cause them harm.

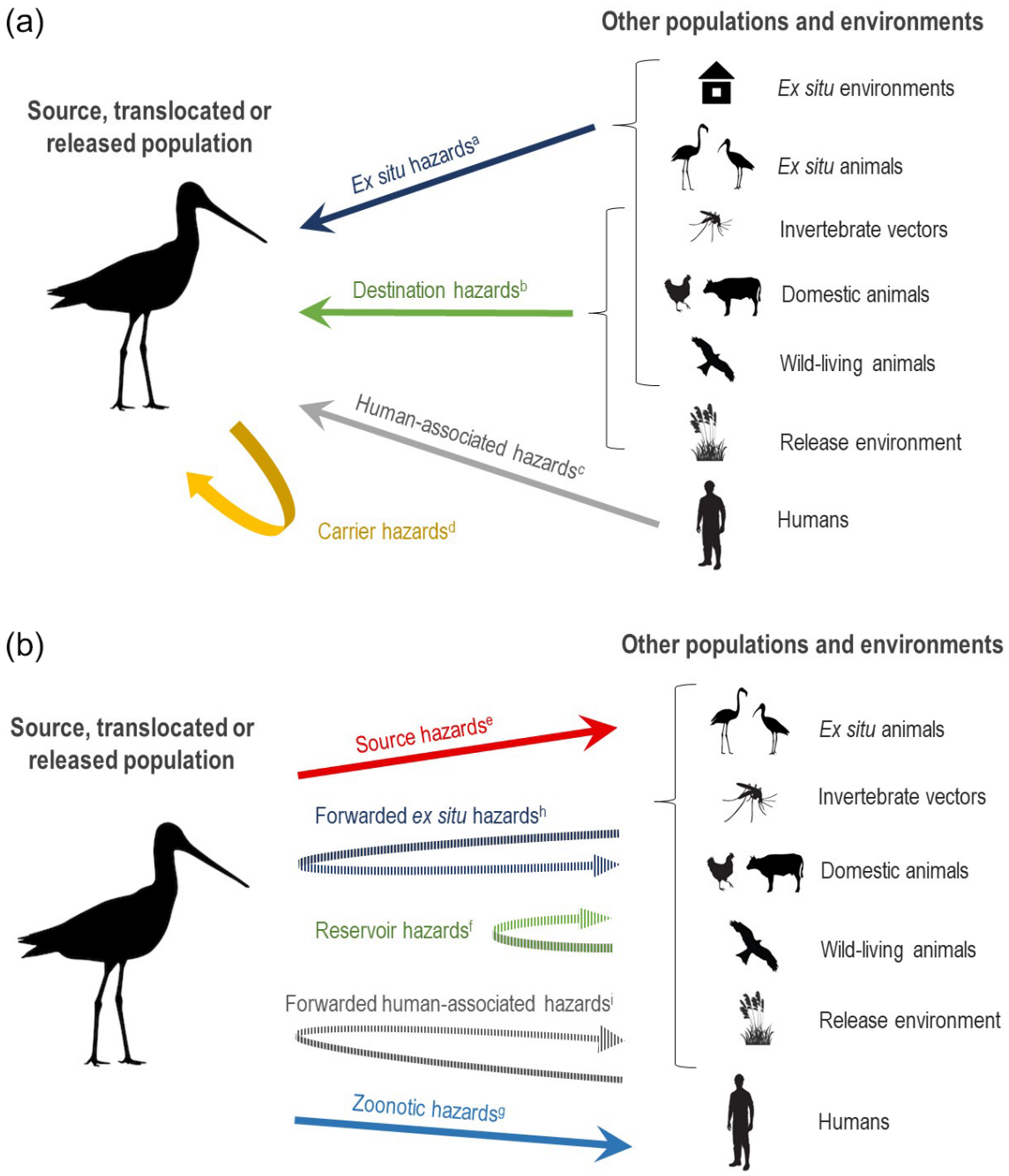

FIGURE 2 Illustration of the "infectious hazard pathways" defined in Table 1, which comprised transmission pathways (a) from other populations or environments *to* the target (source, translocated or released) population, and (b) *from* the target population to other animal populations or humans; dashed lines indicate hazards that could originate from other populations or environments and be transmitted onwards by the target population. A given infectious agent could be transmitted across multiple pathways. Icons were created by the authors or sourced from iStock (iStockphoto LP 2023). Infectious hazards *to* the target population were termed: [a]ex situ hazards, meaning those from animals or invertebrate vectors in proximity to translocated individuals during their transit, captivity, or holding, or from the *ex situ* (transit, captive, or holding) environment; [b]destination hazards, meaning those from animals or invertebrate vectors in the release area, or from the release environment; [c]human-associated hazards, meaning those transmitted from or via humans, at any translocation stage (capture/collection from the source population, transit, captivity, holding, or post release); and [d]carrier hazards, meaning those carried by translocated individuals themselves. Infectious hazards *from* the target population to other populations were termed: [e]source hazards, meaning those originating from the wild-living source population, which could be transmitted to other animals during the translocated individuals' transit, captivity, holding, or post release; [f]reservoir hazards, meaning those acquired by released individuals from the release ecosystem, for which they could serve as reservoir hosts for other animal or human populations; [g]zoonotic hazards, meaning those transmitted to humans, at any translocation stage; [h]forwarded ex situ and [i]forwarded human-associated hazards, meaning ex situ or human-associated hazards that the target population acquired at an earlier translocation stage and could transmit on to other populations.

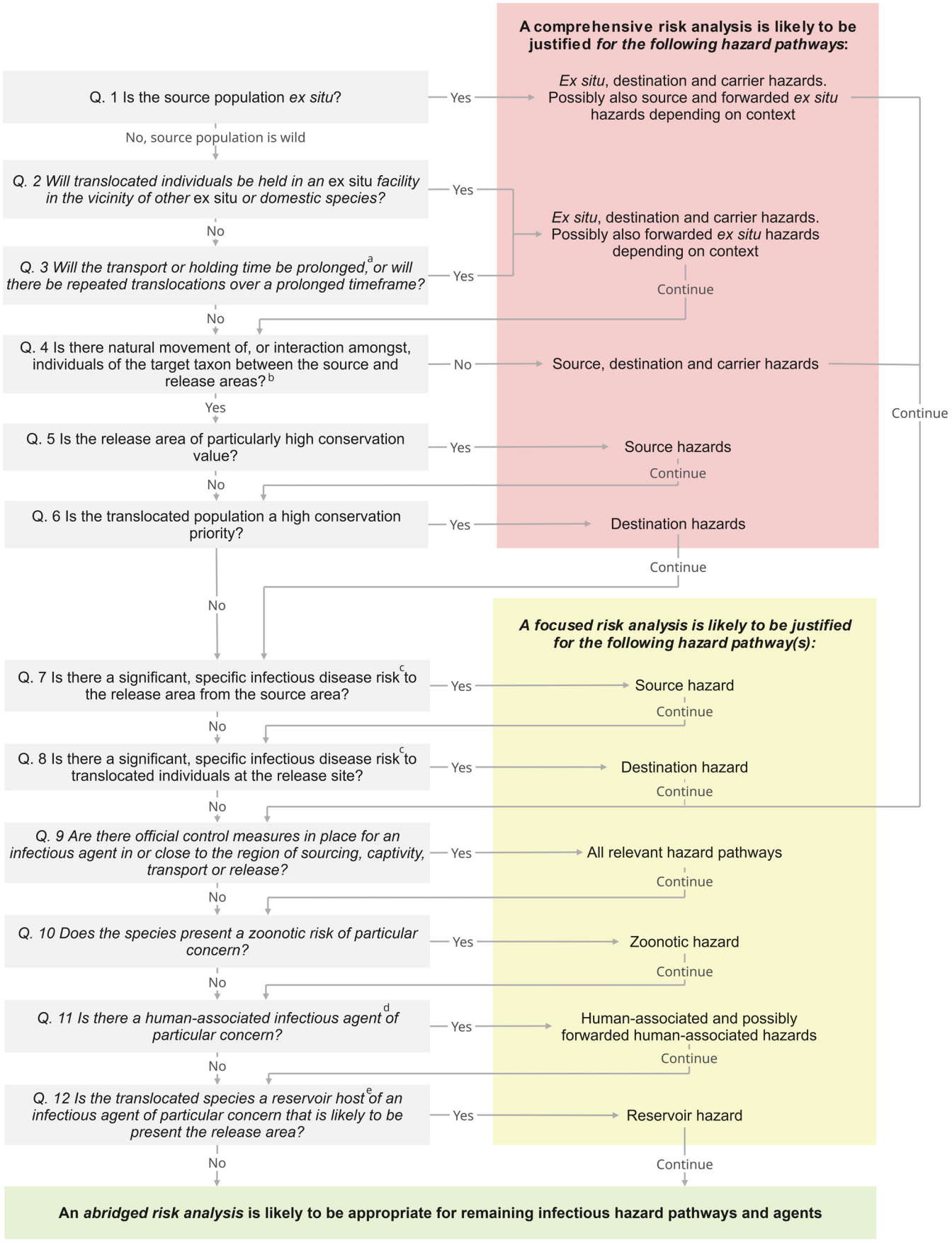

FIGURE 3 Legend on next page.

there was natural movement of godwits and other waterbirds (Donaldson et al., 2024). Godwits were to be collected as eggs from the nests of wild pairs and hatched and reared in dedicated facilities at the release area, from mid-April 2017 onwards, over at least five annual rearing seasons; see Hiscock and Costa (2023) for a detailed description of headstarting techniques, including husbandry methods. A few months prior to the first translocation season, over the winter of 2016–17, highly pathogenic avian influenza (HPAI) H5N8 virus had been circulating in domestic and wild birds in the UK and the virus had been detected in dead wild waterbirds in the release area. National statutory HPAI control measures had been in place and the source and release areas had been within officially designated "Higher Risk Areas" for HPAI until early April 2017.

In the curlew translocation, the source and release areas were approximately 300 km apart; there was thought to be no or minimal movement of wild-living curlews and other waterbirds between these areas. Curlews were to be collected as eggs from the nests of wild pairs and then hatched and reared in dedicated facilities within the boundary of an ex situ waterbird collection, using similar headstarting techniques to Project Godwit. This ex situ facility was adjacent to the release area. As above, the translocation was considered a trial and planned for 2019 only: HPAI virus was a relatively lower concern than in 2017, although HPAI subtype H5N6 virus had been detected in wild birds on the European continent in winter 2018–19.

2.2.2 | Step 2: Taxon-specific reference lists

Reference lists of (a) infectious agents considered to have the potential to infect waders in the UK, and (b) non-infectious conditions to which waders could be susceptible, were compiled through literature review, the authors' personal experience, and communication with other wader experts.

2.2.3 | Step 3: Hazard characterization and identification

Infectious hazards

The risk analysis approach—abridged, focused, or comprehensive—was determined using the flowchart in Figure 3. Then, for all approaches, the infectious hazard pathways were described and visualized by mapping them out on the translocation diagram, as per the IUCN/SSC CPSG method.

In a comprehensive risk analysis, the infectious agent reference list provided the list of potential infectious hazards. Summary information on the infectious agents' geographical distribution, host range, pathogenicity, and zoonotic potential was collated from the wider literature, and they were subjectively identified (selected) as hazards based on their perceived potential to infect the translocated species and to cause disease or notifiable infection (OIE, 2022) in the translocated population, other animals, or humans. "Unknown" infectious agents were also explicitly listed as a hazard. A comprehensive risk analysis was performed for these agents for each infectious hazard pathway of most concern (Figure 3); other infectious hazard pathways were analyzed using an abridged approach.

Non-infectious hazards

Each wader translocation was broken down into the following discrete stages and activities: egg collection, handling and transit; ex situ incubation, rearing and pre-release holding; bird handling (including pre-release

FIGURE 3 Flowchart developed to guide the scale of risk analysis for infectious agents (Step 3 in Figure 1). This was adapted from the DOC method (McInnes, unpublished) and italicized text is used to highlight elements additional or different to the DOC method. These differences included specifying the infectious hazard pathways likely to justify comprehensive risk analysis under different scenarios; infectious hazard pathways are defined in Table 1 and illustrated in Figure 2. A **comprehensive risk analysis** was a traditional approach whereby separate risk assessments were conducted for multiple infectious hazards across relevant infectious hazard pathways; a **focused risk analysis** meant risk assessing a particular infectious hazard of concern across relevant infectious hazard pathways; and an **abridged risk analysis** meant conducting a risk assessment for each relevant infectious hazard pathway as a whole, with infectious agents that could be transmitted via that pathway considered as a group as opposed to individually. The flowchart is intended as a guide, recognizing that any translocation project presents a unique set of considerations and risks. [a]A "prolonged" timeframe was defined on a case-by-case basis using expert judgment. [b]A lack of movement or interaction was equivalent to the presence of geographic or ecological barriers described in the ZSL method (Bobadilla Suarez et al., 2017). [c]A "significant, specific infectious disease risk" was one that might not naturally reach the release area, and if it did, could pose a risk to animal or human populations or to future translocations (Q. 7), or an infectious agent that could be harmful to translocated animals (Q. 8) (McInnes, unpublished). [d]Human-associated infectious agents included those that humans could unwittingly carry on their clothes, footwear, or equipment following contact with an infected animal or contaminated environment remote to the translocation site, or with which they could be infected. [e]Meaning could the species serve as a persistent source of such an infectious agent for other species or humans in the release ecosystem.

catch events) and transit; released population; and monitoring devices and activities. Using the reference list of non-infectious conditions as the list of potential hazards, conditions to which the target population could potentially be susceptible at each translocation stage were specified; non-infectious conditions that could occur in other populations of animals or humans as a consequence of translocation were also considered. Then, conditions were subjectively selected as hazards if (a) they would be managed through disease management measures, and (b) they were considered likely to occur and to cause disease; conditions that would be addressed through other project protocols or risk assessments were not included in the health risk analysis.

2.2.4 | Step 4: Standard disease management measures

As above (section 2.1), standard disease management measures were agreed prior to risk assessment.

2.2.5 | Step 5: Risk assessment

Risk was assessed under the assumption that the standard disease management measures (Step 4) would be implemented, and for the whole project period, expected to be 5 years in Project Godwit (2017–2021) and 1 year in the curlew translocation (2019).

For infectious source hazards, the likelihoods of infectious agent "release" and "exposure" were estimated separately (Sainsbury & Carraro, 2023), and the lowest of these two values was taken to be the likelihood of hazard occurrence (see Supporting Information for further details). Risk was taken to be the product of the likelihood of hazard occurrence and its estimated severity of consequences, as per existing methods (e.g., Jakob-Hoff et al. 2014b; OIE 2017). The overall risk scores combined qualitative and constructed numerical scores, as follows: Negligible (0), Low (1–4), Medium (5–9), High (10–14), and Very High (15–20) risk (Table S2). Ranges in these scores were used to convey uncertainty (as per, e.g., Dufour et al., 2011) and other limitations were clearly articulated.

In an abridged risk analysis, a risk assessment was performed for each infectious hazard pathway as a whole, that is, with relevant infectious agents considered as a group. The infectious agent reference list served as a reference point for the risk assessment, which also drew from the authors' expert knowledge and referenced published literature where appropriate. In a focused risk analysis, a factsheet for the specific infectious hazard of concern was compiled from the literature to inform the risk assessment and to provide additional information for stakeholders; this hazard was risk assessed across each relevant infectious hazard pathway. In a comprehensive risk analysis, the information collated for hazard identification was further augmented through literature review to inform separate risk assessments for each infectious agent. One expert (KMB) conducted the risk assessment for Project Godwit, while two experts (KMB and MFB) contributed to the risk assessment for the curlew translocation.

2.2.6 | Step 6: Management decision making

To guide management decision making, our risk tolerance for the wader translocations was clearly articulated, as follows: Medium risks would require a defined mitigation strategy such as additional disease management measures, providing they were considered feasible, acceptable, and effective; High risks, in addition, would necessitate consideration of a modified translocation plan; and for Very High risks, serious consideration would be given to discontinuing the project (Table S3).

2.2.7 | Step 7: Disease management protocol

The disease management protocol was then finalized and disseminated. It stated the standard (Step 4) and additional (Step 6) agreed disease management measures, with adherence to statutory notifiable disease regulations, and included a health risk communication plan. Further disease surveillance measures, such as sample collection and archiving to facilitate future research studies, were included if they were considered justified, feasible, and acceptable.

2.2.8 | Step 8: Implementation, monitoring, and review

The translocation was conducted in line with the disease management protocol, and detailed health records were kept. After each translocation season, health outcomes were reviewed, further risk mitigation measures were agreed upon as appropriate, and the disease management protocol was updated accordingly.

3 | RESULTS

3.1 | Problem description

Relevant background information on Project Godwit and the curlew translocation is provided in Supporting Information

text. The translocation plans are described above, and the translocation diagrams are illustrated in Figure 4.

3.2 | Taxon-specific reference lists

The taxon-specific reference lists of infectious agents and non-infectious conditions are presented in Tables 2 and 3, respectively.

3.3 | Hazard characterization and identification

In Project Godwit, given the close proximity and population connectivity between source and release areas and that the rearing facilities were at the release area and not close to any other ex situ or domestic animal facility, an abridged risk analysis was conducted (Figure 3). However, it was feasible that HPAI virus could still be present in the source, rearing, or release area and therefore a focused risk analysis for this virus was conducted in parallel to the abridged risk analysis for other infectious agents (Figure 3). The focused and abridged approaches were each conducted for all infectious hazard pathways (Table 1 and Figures 2 and 4) with the exception of reservoir hazards, which were not considered a concern in godwits.

In the curlew translocation, given the apparent lack of population connectivity between source and release areas, and that rearing was to be performed within the boundary of an ex situ collection, a comprehensive risk analysis was performed. This was conducted for ex situ, forwarded ex situ, destination, carrier, and source hazards (Figure 4); an abridged approach was used for zoonotic, human-associated, and forwarded human-associated hazards. The infectious hazards are listed in Table 2: helminths were considered as a group and unknown infectious agents were explicitly included as a hazard.

3.4 | Standard disease management measures

The standard disease management measures are described in Table S4: they included many preventative measures such as implementation of biosecurity barriers, general hygiene, and health monitoring, alongside specified husbandry measures and pest control.

3.5 | Risk assessment

The risk estimates for Project Godwit and the curlew translocation are summarized in Tables S5 and S6, respectively.

In Project Godwit, HPAI virus was estimated to be a Low to Medium risk both as an ex situ hazard to godwits in rearing and release aviaries and as a destination hazard to released godwits. HPAI subtype H5N8 virus was the primary concern in 2017 and HPAI risk was anticipated to vary over the course of the project. Its risk as a source hazard was estimated to be Negligible to Low because individuals were to be collected as eggs from the source population and viable eggs are extremely unlikely to harbor HPAI viruses (Cobb, 2011; Grond et al., 2017) (Table S5). Other infectious agents (aggregated in an abridged risk analysis, including commensal bacteria, helminths, and protozoa such as coccidia) were estimated to pose a Medium risk as carrier hazards and were predicted to become more prevalent in the captive-rearing aviaries year on year. Multiple non-infectious hazards were also estimated to pose a Medium risk to translocated godwits. These included stress-related conditions and incidental traumatic injury during rearing, pre-release holding, handling, transit, and wild-bird monitoring; and husbandry-related disorders such as developmental deformities during rearing (Table S5).

In the curlew translocation, *Aspergillus* sp. was estimated to be a Medium-risk ex situ hazard, and select bacteria and helminths were also considered Low to Medium risks as ex situ hazards; *Mycobacterium avium* complex was estimated to be a Medium-risk destination hazard, and select bacteria, *Aspergillus* sp., coccidia, and helminths were also considered Low to Medium risks as destination hazards (Table S6). Unknown agents were estimated to be a Negligible to Medium risk both as source hazards to other ex situ waterbirds and as carrier hazards. Risk estimates for non-infectious hazards were similar to Project Godwit.

Both risk analyses were limited by a lack of knowledge about the identity and prevalence of infectious agents in wild-living waders in the UK (Tables S5 and S6).

3.6 | Management decision making and disease management protocol

In light of the uncertain (Low to Medium) risks from HPAI (Table S5) in Project Godwit, an HPAI contingency plan was drawn up describing how the project would proceed if the virus was detected in translocated godwits, or if its risk increased or local or national statutory HPAI control measures were enhanced during the project. We decided to conduct pre-release screening for avian influenza viruses, particularly in case the infection status of translocated godwits was ever subject to wider scrutiny such as if HPAI risk

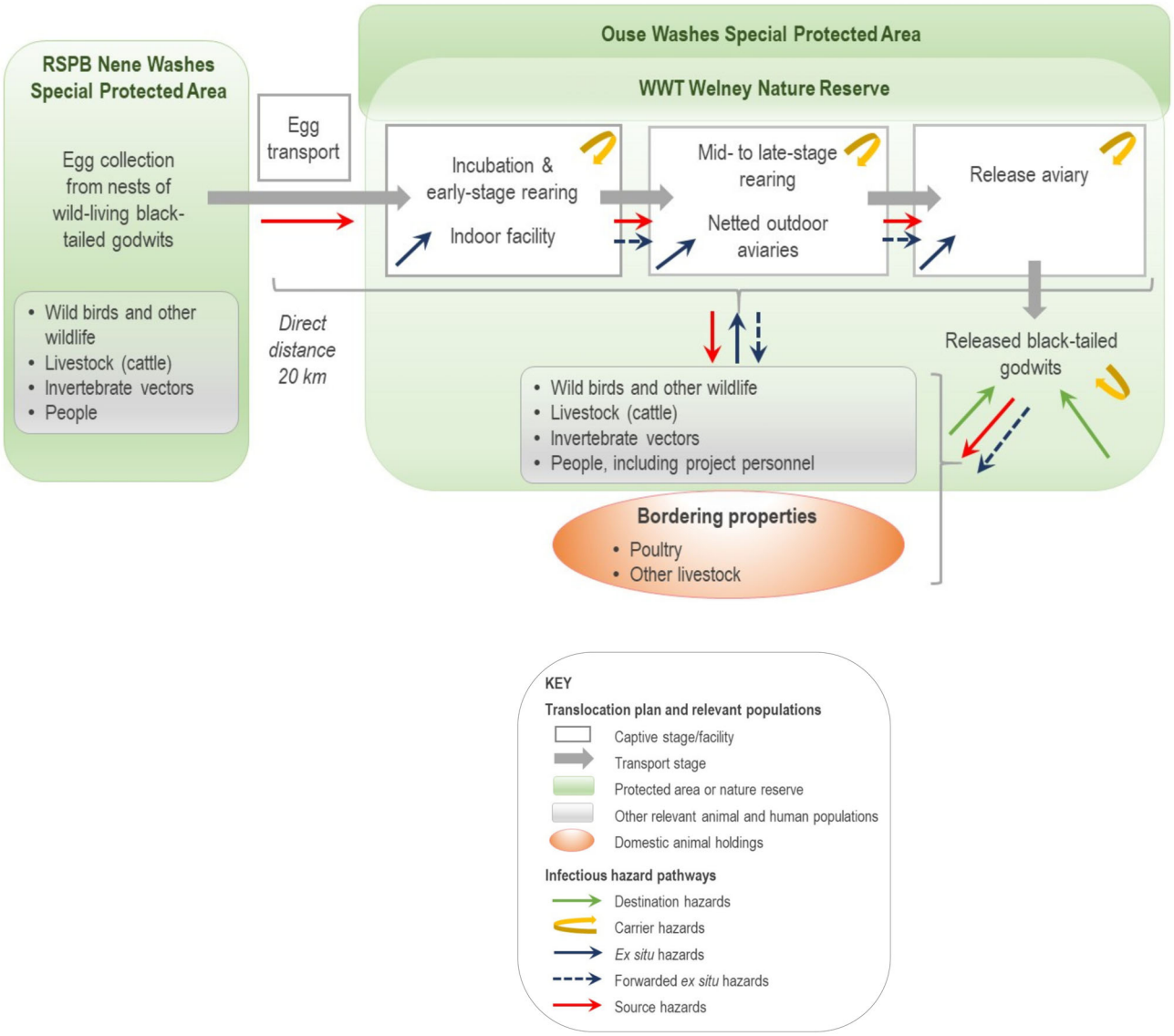

FIGURE 4 Source, ex situ, forwarded ex situ, carrier, and destination infectious hazard pathways, superimposed on the translocation diagrams for (a) Project Godwit and (b) the curlew translocation (see Key). For simplicity, zoonotic, human-associated, and forwarded human-associated pathways are not illustrated; reservoir hazards were not considered a concern in these species. See Table 1 and Figure 2 for infectious hazard pathway definitions. In Project Godwit, a focused risk analysis was performed for highly pathogenic avian influenza (HPAI) viruses, meaning a risk assessment was performed specifically for HPAI viruses, and an abridged risk analysis was performed for other infectious agents, meaning they were risk assessed as a group, across these and other relevant infectious hazard pathways. In the curlew translocation, a comprehensive risk analysis was performed for infectious hazards (Table 2), meaning each infectious hazard was risk assessed separately across these hazard pathways. Both projects were performed in the UK. WWT, Wildfowl & Wetlands Trust; RSPB, Royal Society for the Protection of Birds.

increased or statutory HPAI control measures were introduced during a translocation season. Given the estimated Medium risk from carrier hazards, pooled fecal samples were to be collected at each rearing stage and routinely screened for bacteria, helminths, and protozoa (for further details of screening methods see Supporting Information text). Because of the lack of information about infectious agents in wild-living godwits, fecal and other samples were also to be collected opportunistically from godwits and archived frozen, which would enable retrospective testing and aid decision making in case a previously unknown infectious agent or disease condition was detected in translocated godwits. Mitigation strategies to address non-infectious risks were also implemented as per Tables S4 and S5.

For the curlew translocation, despite its estimated Negligible to Low risk, it was decided to conduct pre-

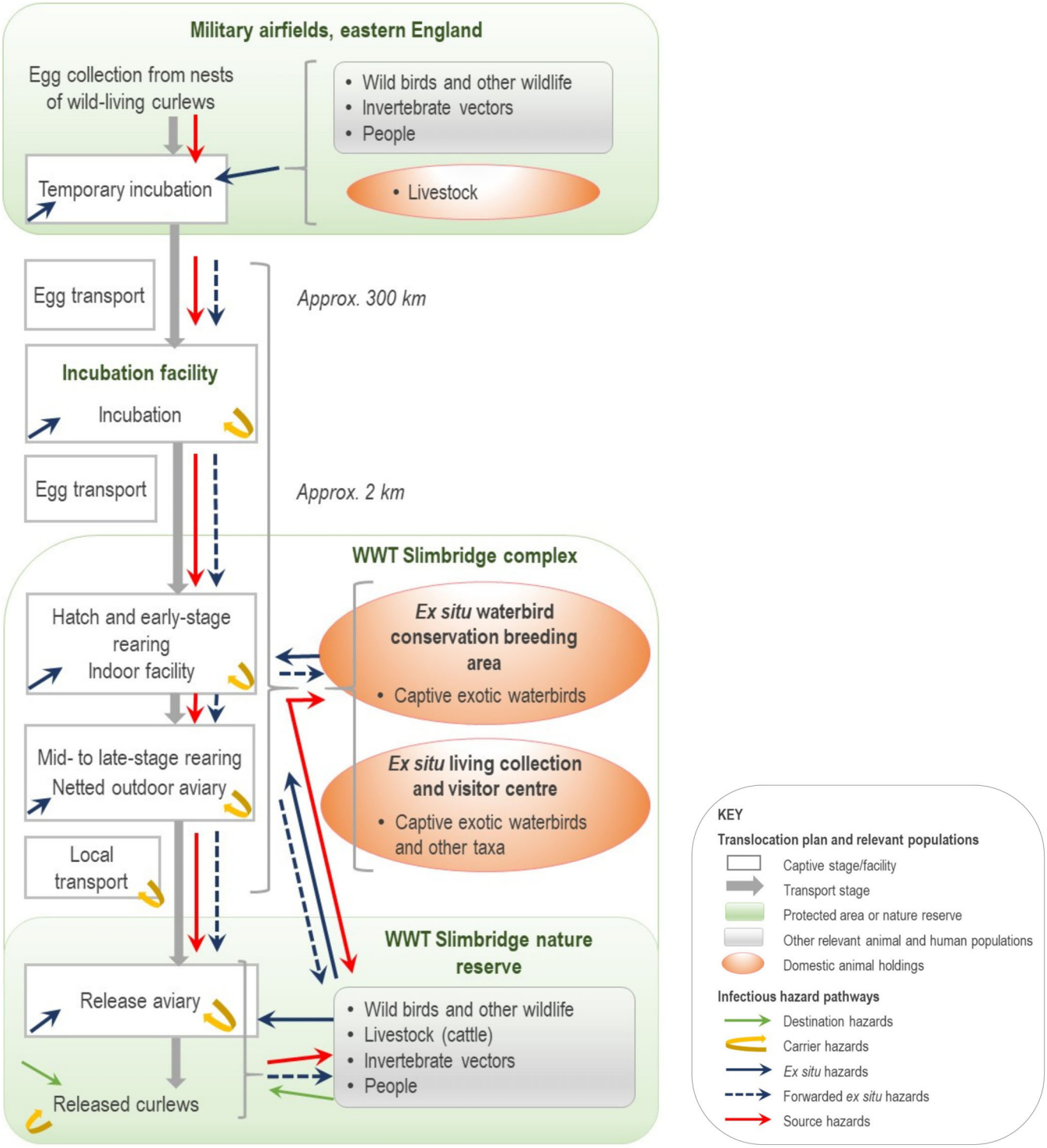

FIGURE 4 (Continued)

release screening for HPAI virus, as for Project Godwit, in case the infection status of translocated curlews was subject to wider scrutiny. Pooled fecal samples were also to be collected during indoor and outdoor rearing and screened for bacteria, helminths, and protozoal parasites (see Supporting Information text), with additional fecal samples archived to facilitate possible future retrospective research.

TABLE 2 Reference list of infectious agents considered to have the potential to infect waders in the UK, compiled through literature review.

Type of infectious agent (and name of related disease or location within the host)	Infectious hazard pathway					
	E	D	H	C	S	Z
Viruses						
For which evidence of infection has been demonstrated in wild-living waders in Europe						
Avian paramyxovirus (APMV) including APMV-1 (Newcastle Disease) and APMV-6 (Gavier-Widén et al., 2012; Hlinak et al., 2006)	•	•	•	•	•	•
Avipoxvirus (avian pox) (Gavier-Widén et al., 2012)	•	•	•	•	•	
Coronavirus (Hughes et al., 2009)	•	•	•	•	•	
Influenza A virus (avian influenza), classified according to its disease-causing potential in poultry as low pathogenic or highly pathogenic avian influenza (LPAI or HPAI) virus (Gavier-Widén et al., 2012; Globig et al., 2017)	•	•	•	•	•	•
Reovirus-like virus (Hlinak et al., 2006)	•	•	•	•	•	
Circovirus (inclusion bodies with an appearance typical of circovirus observed on histology) (Kuiken et al., 2002)						
Flavivirus: West Nile virus, Usutu virus (Michel et al., 2018)						
Togavirus: Sindbis virus (Hubálek, 2004)						
For which evidence of infection has been demonstrated in waders on other continents						
Astrovirus: avian nephritis virus 1-like virus (Honkavuori et al., 2014), avastrovirus (Wille et al., 2018)						
Calicivirus (unclassified) (Wille et al., 2018)						
Picornavirus: avihepatovirus, enterovirus, sapelovirus, tremovirus, megrivirus, unclassified (Wille et al., 2018)						
Reovirus: rotavirus (Wille et al., 2018)						
Rhabdovirus: tupavirus (Wille et al., 2018)						
Togavirus: eastern equine encephalitis virus (Friend & Franson, 1999)						
Bacteria						
Infection demonstrated in waders. Notable disease-causing potential in waders, other animals or humans						
Campylobacter spp. (campylobacteriosis) (Waldenström et al., 2002)	•	•	•	•	•	•
Chlamydia psittaci (avian chlamydiosis) (Astorga et al., 1994)	•	•	•	•	•	•
Mycobacterium avium complex (avian tuberculosis) (Siebert et al., 2012)	•	•	•	•	•	•
Pasteurella multocida (avian cholera) (Thomas et al., 2007)	•	•	•	•	•	•
Salmonella spp. (salmonellosis) (Thomas et al., 2007; Valdebenito et al., 2020)	•	•	•	•	•	•
Sporadic reports from waders. Potential to cause disease in waterbirds, other animals or humans						
Mycoplasma spp. (mycoplasmosis) (Astorga et al., 1994)	•	•	•	•	•	
Borrelia burgdorferi sensu lato (s.l.) (borreliosis) (Lopes de Carvalho et al., 2012)						
Erysipelothrix rhusiopathiae (erysipelas) (Thomas et al., 2007)						
Francisella tularensis (tularaemia) (Lopes de Carvalho et al., 2012)						
Commensal in birds and/or ubiquitous in the environment. An opportunistic or occasional cause of disease in waders or other waterbirds						
Include *Clostridium perfringens* (necrotic enteritis) (Friend & Franson, 1999; Siebert et al., 2012), *Clostridium colinum* (Grond et al., 2017), *Enterobacter* spp., *Enterococcus* spp. (Benskin et al., 2009), *Escherichia coli* (colibacillosis) (Siebert et al., 2012), *Klebsiella* spp. (Benskin et al., 2009), *Listeria monocytogenes* (listeriosis), *Pseudomonas aeruginosa*, *Staphylococcus aureus* (staphylococcosis) (Benskin et al., 2009; Gavier-Widén et al., 2012), *Streptococcus* spp. (streptococcosis) (Siebert et al., 2012), and *Yersinia* spp. (yersiniosis) (Benskin et al., 2009; Gavier-Widén et al., 2012)	•	•	•	•		•

TABLE 2 (Continued)

Type of infectious agent (and name of related disease or location within the host)	Infectious hazard pathway					
	E	D	H	C	S	Z
Fungi						
Aspergillus spp., including *A. fumigatus* (aspergillosis) (Gartrell et al., 2013; Thomas et al., 2007)	•	•		•		
Candida albicans (candidiasis, candidosis) (Friend & Franson, 1999)	•	•		•		
Microsporum gallinae or *Trichophyton gallinae* (ringworm) (Friend & Franson, 1999)						
A range of other environmental fungi could potentially cause opportunistic disease in waders (Gavier-Widén et al., 2012)						
Protozoa						
Occasionally demonstrated to infect wild-living waders in Europe						
Haemosporidia: *Haemoproteus* sp. and *Plasmodium* sp. (avian malaria; vector-transmitted and blood-borne) (Atkinson et al., 2008; Mendes et al., 2013; Pardal et al., 2014)	•	•		•	•	
Coccidia: *Eimeria* spp. and *Isospora* sp. (coccidiosis; intestinal or renal) (Atkinson et al., 2008; Brown et al., 2010; Levine, 1953; Siebert et al., 2012)	•	•	•	•	•	
Rare reports from wild-living or captive waders on other continents						
Haemosporidia: *Leucocyozoon* spp. (leucocytozoonosis) (Atkinson et al., 2008)						
Other protozoa: *Cryptosporidium* spp. (cryptosporidiosis) (Zylan et al., 2008), *Sarcocystis rileyi* (sarcocystosis) (Erickson, 1940), and *Trichomonas* spp. (Morgan, 1944)						
Helminths (parasitic worms) detected in waders in Europe, many of which rarely cause disease	•	•	•	•	•	
Nematodes (roundworms)						
Order Ascaridida Family Anisakidae: *Porrocaecum semiteres* (Cabot, 1969; Sitko & Okulewicz, 2010) and *Anisakidae* gen. sp. (Sitko & Okulewicz, 2010) (gastrointestinal tract or peritoneum) Family Dioctophymatidae: *Eustrongylides tubifex* (eustrongylidosis, verminous peritonitis; gastrointestinal tract or peritoneum) (Atkinson et al., 2008); *Hystrichis tricolor* (Sitko & Okulewicz, 2010) (upper gastrointestinal tract)						
Order Spirurida Family Acuariidae: *Cosmocephalus* spp., *Echinuria* spp. (acuariasis, echinuriasis), *Skrjabinocerca* spp., *Skrjabinoclava horrida* (Cabot, 1969), *Stellocaronema skrjabini* (Sitko & Okulewicz, 2010), *Streptocara crassicauda* (Borgsteede et al., 1988; Sitko & Okulewicz, 2010), *Synhimanthus laticeps* and *Viktorocara* spp. (Sitko & Okulewicz, 2010) (upper gastrointestinal tract) Family Diplotriaenida: *Diplotriaena* spp. (Atkinson et al., 2008) (airsacs or subcutaneous tissues) Family Onchocercidae: *Aproctella* sp., *Cardiofilaria* sp., *Eulimdana* sp. and *Paronchocerca* sp. (Atkinson et al., 2008) (various tissues or tissue spaces) Family Tetrameridae: *Tetrameres* spp. (Cabot, 1969; Sitko & Okulewicz, 2010) (upper gastrointestinal tract)						
Order Strongylida Family Amidostomatidae: *Amidostomum acutum* and *Epomidiostomum orispinum* (Atkinson et al., 2008) ("gizzard worms") Family Strongyloididae: *Strongyloides turkmenica* (Sitko & Okulewicz, 2010) (intestine) Family Syngamidae: *Syngamus* spp. (Atkinson et al., 2008; Cabot, 1969; Sitko & Okulewicz, 2010) (gapeworm, gapes, syngamiasis; trachea or bronchi)						
Order Trichocephalida Family Capillaridae: *Baruscapillaria belopolskaiae* (Atkinson et al., 2008), *Eucoleus* spp. (Atkinson et al., 2008; Sitko & Okulewicz, 2010), *Capillaria* spp. (Borgsteede et al., 1988; Cabot, 1969; Sitko & Okulewicz, 2010) and *Pterothominx totani* (Atkinson et al., 2008) (gastrointestinal tract)						
Trematodes (flukes, flatworms)						
Include *Cardiocephalus longicollis*, *Catatropis verrucosa*, *Cryptocotyle jejuna*, *Cyclocoelum* (*haematotrephus*) *lanceolatum*, *Himasthla leptosoma*, *Levinseniella brachysoma*, *Maritrema subdolum*, *Microphallus* spp. (Cabot, 1969), *Notocotylus* sp. (Borgsteede et al., 1988; Cabot, 1969), *Plagiorchis nanus*,						

(Continues)

TABLE 2 (Continued)

Type of infectious agent (and name of related disease or location within the host)	Infectious hazard pathway					
	E	D	H	C	S	Z
Prosthogonimus ovatus (Cabot, 1969), *Psilostomomum brevicolle* (Borgsteede et al., 1988), and *Sphairiotrema prudhoei* (Cabot, 1969) (trematodiasis)						
Cestodes (tapeworms)						
Include *Anomotaenia* spp., *Aploparaksis* spp., *Choanotaenia tringae*, *Dilepis limosa*, *Gryporhynchus retrirostris*, *Hymenolepis* (*Echinocotyle*) spp., *Hymenolepis* (*Hymenolepis*) spp., *Ophryocotyle proteus*, *Progynotaenia odhneri, Pseudanomotaenia paramicrorhyncha*, *Sacciuterina* spp. and *Trichocephaloides megalocephala* (Cabot, 1969) (cestodiasis)						
Acanthocephalans (hookworms)						
Include *Arhythmorhynchus longicollis* (Cabot, 1969), *Plagiorhynchus* (*Prosthorhynchus*) spp. (Cabot, 1969; Sitko, 2011), *Polymorphus* spp., and *Sphaerirostris lanceoides* (Sitko, 2011) (acanthocephaliasis)						
Ectoparasites (external invertebrate parasites) detected on waders in Europe, many of which rarely cause disease. May harbor and transmit some of the above infectious agents						
Leeches						
Include *Theromyzon tessulatum* (Elliott & Tullett, 1982)						
Lice						
Chewing lice: include *Actornithophilus* spp., *Austromenopon* spp., *Carduiceps* spp., *Lunaceps* spp., *Quadraceps* spp. (Cabot, 1975; Dik et al., 2010) and *Saemundssonia platygaster* (Cabot, 1975)						
Mites						
Nasal mites: include *Rhinonyssus* spp (Radford, 1950)						
Feather mites: numerous species include *Alloptes* spp., *Avenzoaria* spp., *Leptosphyra* spp., *Pterolichus* spp., *Ptiloxenus* spp., *Syringobia* spp. and *Thecarthra* spp. (Radford, 1953)						
Flies						
Blackflies: include *Metacnephia lyra* and *Simulium usovae* (Hellgren et al., 2008)						
Louse flies (hippoboscid flies, keds): *Ornithomyia* spp. (Bartos et al., 2020; Van den Broek & Van Eck, 1969)						
Fleas (Tripet et al., 2002)						
Ticks						
Include *Ixodes* spp. (Martyn, 1988)						
Unknown infectious agents	•	•	•	•	•	

Note: Circles indicate infectious agents prioritized as hazards for the curlew translocation and the hazard pathways for which they were risk assessed: E = ex situ and forwarded ex situ; D = destination; H = human-associated and forwarded human-associated; C = carrier; S = source; and Z = zoonotic hazard pathways, which were defined as per Table 1. Reservoir hazards were not considered a concern in these species. Helminths were considered as a group, and unknown infectious agents were explicitly included as hazards.

3.7 | Implementation, monitoring, and review

Owing to Covid-related restrictions in 2020, headstarting for Project Godwit was ultimately performed in 2017, 2018, 2019, 2021, and 2022. Overall, 248 eggs were collected and 206 godwits were released; see Donaldson et al. (2024) for further details.

In addition to HPAI virus subtype H5N8, HPAI subtypes H5N6, H5N1 and other H5Nx subtypes became new hazards during the course of the project. In 2022, a statutory "Avian Influenza Prevention Zone", which stipulated enhanced biosecurity requirements for domestic poultry and captive birds, was in force close to the source and release sites in the early part of the translocation season. Avian influenza virus was not detected in any of 193 translocated godwits tested. Over multiple release seasons, *Campylobacter* sp. was isolated from 43% of 28 and 100% of 11 pooled fecal samples collected from outdoor rearing and release aviaries respectively (the isolates were not speciated), but not any of 56 pooled fecal samples collected during indoor, early-stage rearing.

Spirurid-type helminth ova were detected in only one pooled fecal sample, from an outdoor rearing aviary (Table S7). No clinical disease was observed in association with these isolates and to the best of our knowledge, no *Campylobacter*-related disease occurred in project personnel or visitors. Developmental wing and leg disorders were observed in 26% and 20% of 217 headstarted godwit chicks respectively, but their prevalence varied markedly across years; the large majority were mild conditions that were addressed prompt through husbandry modifications and/or treatment. The rearing diet and other husbandry practices were modified year on year to try and minimize their prevalence. Though less common, traumatic injuries also occurred, along with yolk sac or navel abnormalities and foot lesions; capture myopathy was not observed (Table S7).

The survival and breeding success of headstarted godwits compared well to wild-hatched godwits, and the project successfully bolstered the local breeding population (Donaldson et al., 2024). Health outcomes in released godwits were largely unknown. In 2021, one released bird was found dead, however heavy predation precluded thorough post-mortem examination, and in 2022 the scant remains of two godwits were found within days of their release and predation was also suspected.

In the curlew translocation, 58 eggs were collected, from which 55 birds hatched and 91% (50) of these 55 birds were released (Table S8). Avian influenza virus was not detected. *Campylobacter* sp. (unspeciated) was detected in a majority of pooled fecal samples from outdoor aviaries but was of no apparent clinical significance (Table S9) and there were no known cases of zoonotic infection. Helminth ova (spirurid- or strongle-type) were detected in 29% (four) of 14 pooled fecal samples from outdoor rearing aviaries but did not appear clinically significant. Foot lesions and developmental wing deformities (45% and 15% of hatched curlews respectively) were the predominant conditions observed during rearing (Table S9).

Recently published age-specific survival estimates for curlews in the UK indicate that approximately 36% of wild-reared fledgling curlews can be expected to survive to recruitment at age 2 years (Cook, Burton et al., 2021). Preliminary data from the curlew translocation indicate survival at that level (WWT unpublished data). Health outcomes in released curlews were largely unknown: one curlew was found dead a few weeks post-release, but decomposition precluded detailed post-mortem examination.

4 | DISCUSSION

Our methodological framework enabled the scale of health risk analysis to be proportionate to the project context. A novel, abridged approach was employed for lower-risk translocation scenarios, which was developed through detailed characterization of the infectious hazard pathways associated with translocation and built on the hazard types described in the ZSL method. The focused risk analysis approach enhanced the flexibility of risk analysis and could have been applied to any novel hazard to emerge over the course of the translocation. The incorporation of standard disease management measures prior to the risk assessment step also helped to expedite the process: these were considered justifiable based on the infectious hazards inherent in any translocation scenario. The consideration of risk management prior to risk assessment diverged from traditional risk analysis approaches (Brückner et al., 2010), although it was consistent with the CWHC and WOAH method and a "precautionary" approach to disease risk reduction as advocated by Travis et al. (2014) and the IUCN/SSC (2013).

The framework also incorporated a comprehensive, defined set of infectious and non-infectious hazards. Additional infectious hazard pathways were recognized and defined, including human-associated hazards, which recognized the risks of human-to-wildlife transmission when sourcing individuals from the wild, during translocation, or post release, such as during monitoring or fieldwork (e.g., Cook, Grant et al., 2021; Sherman et al., 2021). Other newly recognized hazard pathways included reservoir hazards, which were a concern of Davidson and Nettles (1992), and the potential for transmission of source hazards to other animals during an ex situ stage, which was a scenario described by Thorne & Williams (1988) in the context of an early black-footed ferret (*Mustela nigripes*) recovery programme. The process of mapping out infectious hazard pathways on the translocation diagram greatly helped clarify the translocation stages presenting the greatest risk from HPAI, in particular its risk to godwits as an ex situ hazard. The inclusion of "unknown" infectious hazards was appropriate given the ever-increasing diversity of infectious agents being identified in waders (e.g., Wille et al., 2018; Wille et al., 2019). Also, the novel approach of considering non-infectious hazards at sequential translocation stages resulted in, for example, incidental traumatic injury and husbandry-related disorders being recognized as hazards during rearing.

For Project Godwit (the first of these two projects), the focused risk analysis approach for HPAI and abridged approach for other infectious agents still required a significant time investment, typical of other methods (highlighted by, e.g., Vaughan-Higgins et al., 2021). However, the taxon-specific reference lists and disease risk management protocol for Project Godwit were transferable to the curlew health risk analysis, greatly expediting it, illustrating how this methodological framework can

potentially be applied to repeat translocations of a particular taxon. This approach mirrored the DOC method, which directs practitioners to information about infectious "diseases of concern" in New Zealand wildlife and appropriate management measures. The notable lack of data concerning infectious agents in wild-living waders was an important limitation in these risk analyses, however, typical of those conducted for other wild animal species (e.g., Neimanis & Leighton, 2004; Wiemeyer et al., 2025). Clearly, our understanding of the identity, prevalence and pathogenicity of infectious agents and non-infectious conditions in wild-living waders would be improved through further surveillance and research, integrated with other population monitoring activities.

The reference list of potential non-infectious hazards (Table 3) included many health conditions that would typically be considered to result from other types of problems, for example, incidental anthropogenic trauma, predation, or adverse climatic conditions. However, such anthropogenic, ecological, and climatic (as well as socioeconomic) factors have been included in the most expansive conceptual frameworks of wildlife health, reflective of how health has been defined in humans (Wittrock et al., 2019). Here, conditions were only considered hazards if they would be managed through disease management measures (Table 3), since other types of risk were analyzed and managed separately, consistent with a traditional, somewhat compartmentalized approach to conservation translocation planning (IUCN/SSC, 2013). However, the list of conditions presented in Table 3 could potentially inform development of a broader risk analysis framework that encompasses a wider suite of considerations (e. g., Karasov-Olson et al., 2021; National Species Reintroduction Forum, 2014).

In Project Godwit, risks from HPAI virus varied markedly year on year: other HPAI H5Nx virus subtypes became hazards, and there were widespread outbreaks of HPAI in captive and wild birds around the UK in 2021 and 2022, with statutory HPAI regulations being in place close to the source, and rearing and release, areas in 2022. Mass mortalities of waders were observed in association with HPAI viruses in continental Europe over this period (CMS FAO Co-convened Scientific Task Force on Avian Influenza and Wild Birds, 2022). An outbreak of avian influenza or its detection in translocated waders would have jeopardized releases in any given year. Further to the standard management measures, which included biosecurity barriers at aviary entrances and scrupulous hygiene, risks from HPAI were managed through contingency planning and pre-release screening, as well as regular review of statutory HPAI guidance and consultation with the local animal health authority as appropriate. Despite the risks inherent in a positive or false positive (Rideout, 2014) result, HPAI virus screening was considered appropriate given its varied risk level and from a reputational perspective. The negative results also provided the project team with reassurance. The translocation of eggs reduced the likelihood of HPAI virus being translocated from the source population, since eggs are a more sterile "biological package" (Davidson & Nettles, 1992) than birds (Cobb, 2011). Nevertheless, HPAI risks were not eliminated and the use of outdoor, netted rearing and release aviaries, while promoting natural behaviors and environmental adaptation, facilitated possible exposure to HPAI virus. The high prevalence of *Campylobacter* sp. in waders in outdoor aviaries was perhaps unsurprising, given it is common in wild-living waders (Waldenström et al., 2002), but it highlighted the potential for HPAI virus ingress into the aviaries. The lack of detection of *Campylobacter* sp. during indoor, early-stage rearing was consistent with an environmental route of exposure (as per Grond et al., 2017).

Although infectious agents of a commensal nature were detected in both projects, they did not appear to cause disease and non-infectious conditions predominated during rearing, justifying the balanced representation of non-infectious versus infectious hazards in this framework. While the lack of infectious disease was evidence to support our disease management measures, it did not prove their effectiveness. Post-release health outcomes were largely unknown, as it is challenging to conduct health surveillance in these highly mobile species; however, the good survival rates of headstarted godwits and curlews, which were comparable to their wild-reared counterparts, were consistent with them being in a good state of health on release. The primary difference between the curlew and godwit risk estimates was the lower HPAI risk for the curlew translocation, but despite this, avian influenza screening was still undertaken, primarily for the above, reputational reasons.

The utility of the risk analysis framework should be reviewed in time, in other conservation translocation contexts and limited resource settings (Dalziel et al., 2016). While the framework can help to advance health risk analysis methodology for conservation translocation, there is scope for it to be further refined. In the comprehensive risk analysis for the curlew translocation, a more objective approach to the prioritization of infectious hazards and hazard pathways would have provided greater transparency and helped with further "streamlining" of the process (Vaughan-Higgins et al., 2021; Whinfield et al., 2024). In the risk assessment step, our risk scores combined qualitative and constructed numerical scales, similar to Wiemeyer et al. (2025), however, these remained a somewhat crude representation of complex disease transmission scenarios (Dufour et al., 2011). The risk estimates also

TABLE 3 Reference list of non-infectious conditions to which translocated waders were considered susceptible and relevant translocation stages.

	Project stage				
	Egg collection, handling and transit	**Ex situ incubation, rearing and pre-release holding**	**Bird handling, including pre-release catch events, and transit**	**Released population**	**Monitoring activities/ devices**
1. Stress[a] and related conditions[b] (Beckmann et al., 2022; Dickens et al., 2009; Dickens et al., 2010; Gartrell et al., 2013; Reed, 1994; Ward et al., 2011)					
a. Intervention-related stress and capture myopathy			•		•
b. Stress associated with captivity		•			
c. *Stress induced by human or animal disturbance*		•		•	
d. Immediate post-release stress				•	
N.B. Other stress-related conditions can include infectious diseases (Table 2), trauma and other non-infectious conditions (see below)					
2. Traumatic injury					
a. Anthropogenic traumatic injury					
i. *Incidental trauma to eggs*[b]	•				
ii. Intervention-related incidental trauma[b] (Beckmann et al., 2022; Colwell et al., 1988)			•		•
iii. Incidental trauma in the captive environment: collision with or entanglement in aviary structures or furniture[b] (Gartrell et al., 2013; Reed, 1994)		•			
iv. *Incidental trauma in released birds, e.g., collision with road traffic or electricity cables, entanglement in fencing*[b] (Fenton et al., 2018; Siebert et al., 2012)				•	
v. *Nest disturbance*[b]				•	
vi. *Persecution or other offtake*[c] (Beckmann et al., 2022)				•	
b. Ecological or environmental traumatic injury					
i. *Predation*[b,c] (Collins et al., 2016)		•		•	
ii. *Other "natural" trauma including intra-species aggression* (Beckmann et al., 2022; Fenton et al., 2018)		•	•		
3. Toxicity					
a. Chemical toxicants, e.g., lead, pesticide or other contaminant (Bull et al., 1983; Friend & Franson, 1999)		•		•	
b. Biotoxins, including mycotoxins from captive or supplemental diets (Fenton et al., 2018; Friend & Franson, 1999)		•		•	
c. Avian botulism (Friend & Franson, 1999)				•	

(Continues)

TABLE 3 (Continued)

	Project stage				
	Egg collection, handling and transit	**Ex situ incubation, rearing and pre-release holding**	**Bird handling, including pre-release catch events, and transit**	**Released population**	**Monitoring activities/ devices**
4. Undernourishment, nutritional disease or deficiency					
a. Undernourishment in the captive environment[b] (Gartrell et al., 2013)		•	•		
b. *Undernourishment post-release due to, e.g., poor site adaptation or adverse weather such as drought* (Beckmann et al., 2022; Fenton et al., 2018; Friend & Franson, 1999; Siebert et al., 2012)				•	
c. Nutritional disease or deficiency, including nutritional disease from supplemental food (Fenton et al., 2018)		•		•	
d. Obesity, including from supplemental food[b] (Mulcahy, 2014)		•		•	
e. Developmental disorders i. Developmental limb disorders: including angel wing and angular limb deformities[b] (Ball, 2003; Collins et al., 2016; Fenton et al., 2018; Reed, 1994) ii. Other developmental disorders: including metabolic bone disease (Mulcahy, 2014), bill or toe deformities[b] (Ball, 2003), and wry neck[b] Associated with diet (including potential post-release supplementary food provision), inadequate exercise, incubation or hatching conditions, and other husbandry factors		•		•	
5. Physiological responses to climatic extremes					
a. *Incubation or hatching problems from adverse fluctuations in, e.g., temperature or humidity*	•	•			
b. Hyperthermia (or frostbite) in the captive environment or due to catch events[b] (Calle et al., 1982; Collins et al., 2016; Friend & Franson, 1999)		•	•		•
c. *Post release*				•	
6. Other forms of environmental injury[b,c] (Collins et al., 2016; Fenton et al., 2018; Friend & Franson, 1999)					
a. *Saturation of eggs through flooding*	•			•	
b. In captive environment, e.g., electrocution or drowning		•			
c. *Post-release: Electrocution*				•	
7. Behavioral and related disorders					
		•		•	

TABLE 3 (Continued)

	Project stage				
	Egg collection, handling and transit	**Ex situ incubation, rearing and pre-release holding**	**Bird handling, including pre-release catch events, and transit**	**Released population**	**Monitoring activities/ devices**
For example, tameness, poor predator avoidance, or maladaptation (Beckmann et al., 2022)					
8. Other conditions					
a. *Incubation or hatching problems*	•	•			
b. Disorders relating to genetic impoverishment, including congenital abnormalities (Fenton et al., 2018)		•		•	
c. Other side-effects of veterinary intervention ("iatrogenic" disorders) (Beckmann et al., 2022)		•	•		•
d. Foot lesions including cracks or bumblefoot (pododermatitis)[b] (Ball, 2003; Fenton et al., 2018; Gartrell et al., 2013)		•			
e. Foreign-body ingestion[b] (Fenton et al., 2018)		•		•	
f. Other primary disease conditions (which may be related to husbandry or genetic factors), including amyloidosis[b] (Fenton et al., 2018; Reed, 1994)		•		•	

Note: Conditions considered relevant to disease management (alongside other management measures [avicultural, behavioral, and genetic management, as well as overarching translocation and release strategies]) and therefore these wader health risk analysis, are shown in Roman text. Dark circles indicate conditions prioritized as hazards in Project Godwit, while dark circles in gray cells indicate conditions that were not considered hazards in this project. Conditions that were considered outside the scope of health risk analysis are listed in italic text. (Non-infectious conditions that could occur in *other* populations as a consequence of translocation were also included in this category: these included disturbance and stress to other wild-living birds through egg collection, captive rearing and release, or wild-bird monitoring activities; nest trauma through egg collection or wild-bird monitoring activities; and genetic depletion of the source population through egg collection). The categories were adapted from Beckmann et al. (2022) and the list was compiled through literature review, the authors' personal experience and communication with other wader experts.

[a]Stress was considered likely to predispose to other diseases or traumatic injuries.

[b]Conditions familiar to the authors from personal experience or identified through communication with other experts.

[c]These conditions are most likely to cause outright mortality.

represented the opinion of only one or two experts; formal elicitation from a wider group of experts would have provided a more representative range of estimates but would have been more time-consuming to perform (McBride et al., 2012). Importantly, as in other existing methods, there was a lack of clarity about how disease risks, and their management, could actually impact the consequences of concern (here conservation outcomes, wader welfare, disease risk to other animal populations, economic costs, and reputational impact) (Ewen et al., 2015). Furthermore, several of the implemented management actions, such as housing birds in netted aviaries and conducting HPAI screening in the curlew translocation, exemplified how (as above) competing objectives were being taken into account in management decision making; these trade-offs could have been presented more transparently.

In conclusion, we present a scalable and adaptable health risk analysis framework that can be applied to conservation translocations of other wild animal taxa and, potentially, other forms of wildlife translocation. We have illustrated how risk analysis promotes well-considered disease management, which can provide justification for conservation translocation to proceed even in the face of an obvious disease concern. These case studies have also highlighted the potentially changeable and unpredictable nature of disease risks in conservation translocation projects, which necessitate flexibility in risk analysis and management decision-making.

AUTHOR CONTRIBUTIONS

Katie M. Beckmann conceived the study idea and developed the methodological framework through discussion with Rebecca Lee, Ruth L. Cromie, Anthony W. Sainsbury, and Richard A. Kock. The original health risk analyses were authored by Katie M. Beckmann, Nicola C. Dessi, Nigel S. Jarrett, Baz Hughes, Ruth L. Cromie, Jessica-Leigh Penman, Michelle F. O'Brien, and Rebecca Lee. Katie M. Beckmann, Nicola C. Dessi, Rosa Lopez Colom, William H. Costa, Michelle F. O'Brien, and Daniel Calvo Carrasco oversaw disease management and healthcare and collated the health records. They were assisted by Taiana P. Costa, Jessica-Leigh Penman, Tanya Grigg, and other colleagues from the WWT, Royal Society for Prevention of Cruelty to Animals (RSPCA) East Winch Wildlife Centre, and Royal Society for Protection of Birds (RSPB). Katie M. Beckmann collated the data, with assistance from Nicola C. Dessi, Rosa Lopez Colom, and William H. Costa, and prepared the text, tables, and figures. All authors contributed critically to the drafts and approved the final manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

ETHICS STATEMENT

The activities described in this study were approved by the Wildfowl & Wetland Trust's Animal Welfare and Ethics Committee prior to their commencement.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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