
A systematic review on wild animal infectious disease outbreaks following conservation translocation

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Running head: Diseases in conservation translocations

Declaration: I, Paulo Colchao-Claux confirm that the work presented in this scientific paper is my own. The information derived from other sources have been indicated in the paper. The research question was proposed by the supervisors and co-developed with the author. The study design, systematic literature review, and write up of this paper have been conducted by the author, with guidance from the supervisors.

This MSc project differs from the Grant Application in the systematic review protocol, doing the search only in digital databases and including only literature in infectious diseases. The analysis was done in one geographical region of the world and the determination of the severity of the disease outbreak was not analyzed. These changes helped to focus on answer the research question in a limited time.

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Abstract

During the last century, human population growth has impoverished biodiversity and wild animal populations are declining. This has pushed conservationist to translocate wild animals as a mitigation strategy and this trend will increase in the future. Translocations carry several risks that could affect ecosystems, animal welfare, and socioeconomic interests. One of these risks is the outbreak of diseases both in translocated animals and animals in the destination site, which compromises the translocation objectives. To maximize the health of organisms and to minimize the risk of disease outbreaks, the management and surveillance of diseases during translocations are important. Wild animal disease risk analysis tools had been proposed, however, they are a slow and uncertain process. Thus, this study aimed to better understand the origin of wild animal disease outbreaks following conservation translocations to focus efforts during the disease risk analysis and mitigation strategies. A systematic review was carried on covering primary research papers on infectious disease in wild tetrapods during or after conservation translocation. The literature reviewed suggested North America as the geographical region with more publications on this subject. The literature search also revealed that mammals received more attention than other taxa, therefore, the bigger number of disease outbreaks were also in this taxonomic class. The disease outbreaks across taxa were caused mainly by viral agents and multi-host parasites. Furthermore, more than half of the disease outbreaks found in this review were caused by a population hazard. Hence, the efforts during the disease risk analysis should be focused on parasites with these characteristics, nevertheless, it is necessary to analyze each translocation due to the heterogeneity of our findings. Information from future translocations should be standardized and uploaded into a common database to better understand the success and failures.

Keywords: conservation; disease risk analysis; epidemiology; hazard; disease outbreak; reintroduction; translocation; wildlife.

Article impact statement: The population hazard is the most common cause of wild animal disease outbreaks following conservation translocation in North America.

Revisión sistemática de brotes de enfermedad en animales silvestres después de translocaciones para la conservación

Resumen

Durante el siglo pasado el crecimiento de la población humana ha empobrecido la biodiversidad y las poblaciones de animales silvestres están en declive. Esto ha llevado a conservacionistas a trasladar animales como estrategia de mitigación, y esta tendencia continuará en el futuro. Las translocaciones traen consigo diversos riesgos que pueden afectar ecosistemas, el bienestar animal, e intereses socioeconómicos. Uno de estos riesgos son los brotes de enfermedad que pueden afectar a los

animales translocados, como a aquellos en el sitio de destino, lo que compromete los objetivos de translocación. Por esta razón, la vigilancia y el manejo de las enfermedades durante las translocaciones son importantes para maximizar la salud de los individuos y minimizar el riesgo de brotes de enfermedades. Se han propuesto herramientas para el análisis de riesgo de enfermedad en animales silvestres, sin embargo, es un proceso lento e incierto. El objetivo de este estudio fue comprender el origen de los brotes de enfermedades en animales silvestres después de las translocaciones para la conservación, para dirigir los esfuerzos durante el análisis de riesgo de enfermedad y durante las estrategias de mitigación. Se realizó una revisión sistemática que abarcó artículos científicos de investigación primaria sobre brotes de enfermedad en tetrápodos silvestres durante o después de la translocación. La literatura revisada sugiere que Norteamérica es la región geográfica con más publicaciones sobre el tema. La revisión también reveló que los mamíferos recibieron más atención que otros taxones, por consecuencia, el mayor número de brotes de enfermedades se dio en esta clase taxonómica. Los brotes de enfermedad fueron causados principalmente por agentes virales y parásitos de hospedadores múltiples. Además, más de la mitad de los brotes fueron causados por un peligro poblacional. Durante el análisis de riesgo de enfermedad se deben enfocar en parásitos con estas características, sin embargo, es necesario analizar cada translocación debido a la heterogeneidad de nuestros hallazgos. La información de futuras translocaciones se debería estandarizar y registrar en una base de datos común para comprender mejor el éxito y los fracasos de estas.

Palabras clave: conservación; análisis de riesgo de enfermedad; epidemiología; peligro; brote de enfermedad; reintroducción; translocación; fauna silvestre.

Declaración de impacto del artículo: La principal causa de brote de enfermedad en fauna después de la translocación para conservación en Norteamérica es el peligro poblacional.

Introduction

During the last century, the human population has triplicated (Cohen 2003) and consequently increased the exploitation of natural resources, changing ecosystems and impoverished biodiversity on a global scale (Ehrlich 1988). Biodiversity loss has not slowed down in the past years despite global agreements (Butchart et al. 2010) and the pressures on biodiversity will continue due to incessant human population growth and climate change (McKee et al. 2004; Kock et al. 2010). However, the loss of biodiversity has urged conservationists to translocate wild animals to mitigate the threat of extinction or to bring back species into their natural distribution (Woodford & Rossiter 1993). The translocations are intentional movement of individuals and the conservation translocations have the objective of restore animal populations within their indigenous range, relocate animals to avoid extinction or introduce animals to perform a specific ecological function in a foreign habitat (Griffith et al. 1989; IUCN/SSC 2013).

Conservation translocations are intended to be beneficial, however, they carry many risks that could affect ecosystems, animal welfare, and socioeconomic interests (Griffith et al. 1989; Kock et al. 2010). Therefore, to ensure that the benefits are greater than the risks, it is necessary to plan, design, and assess the risks and feasibility of any conservation translocation (IUCN/SSC 2013). Several factors influence the outcome of the operation: genetically attributes, habitat quality, competition, inter and intra-specific interaction, recognition of predators, individual traits, diseases, laws, and the management of natural areas (Reinert 1999; Cabezas et al. 2011; McIntosh et al. 2014; Cain 2018). Furthermore, the translocation of wild animals can have negative consequences like an increase in human-wildlife conflicts or the spread of diseases (Chipman et al. 2008).

Diseases in wild animals caused by parasites are an important component of healthy ecosystems, shaping the host population dynamics, altering interspecific competition, influencing the energy flow and acting as an evolution driver (Hudson et al. 2006). These parasites interact in complex communities, where they relate with their landscape, co-specifics, and hosts in multiple scales (Johnson et al. 2015). However, endemic and emerging diseases in a changing ecosystem can cause wild animal population declines (Rachowicz et al. 2005). Outbreaks of infectious diseases in wildlife can be predisposed by anthropogenic or natural alteration of the ecosystems, caused by the spillover of a disease from domestic animals or other host, by natural or assisted movement of parasites, by improvement of pathogens detection and epidemiological techniques, or by unknown implications (Daszak et al. 2000; Williams et al. 2002; Tompkins et al. 2015).

The translocation of wild animals constitutes the movement of a “biological package” (Davidson & Nettles 1992), where the translocated animal transport microparasites (virus, bacteria, fungi, protozoan) and macroparasites (helminths and ectoparasites). This package represents a serious risk of disease: translocated animals can introduce alien parasites to immunological naïve populations and stressors can promote infectious disease in the animal itself. Also, parasites or non-infectious agents in the destination site can cause disease in the translocated animals, and the disease ecology can be altered (Davidson & Nettles 1992; Daszak et al. 2000; Kock et al. 2010). There is evidence that novel infectious agents or those where stressors affect the parasite pathogenicity are of greatest risk (Cunningham 1996; Dobson & Foufopoulos 2001; Dalziel et al. 2017). Furthermore, microparasites, multi-host parasites, parasites with reservoir host or transmitted by vectors, parasites with long incubation or infection period, and parasites with a higher reproductive number (R_0), represent a bigger risk during translocations (Ewen et al. 2012; Tompkins et al. 2015; Rideout et al. 2017).

Parasites translocated with their hosts have the potential to infect naïve animal populations in the destination site. The introduction of rinderpest into Africa after the movement of cattle from Europe caused declines of naïve wildebeest (*Connochaetes* spp.) populations. This decline had a cascade effect decreasing predator populations and consequently affecting the ecosystem (Plowright 1982). The movement of wild animals can also promote the encounter of the translocated animals to novel parasites. Meningeal worm (*Parelaphostrongylus tenuis*) has been implicated in the failure of naïve

elk (*Cervus canadensis*) survival after translocations, where whitetail deer is reservoir at the destination sites (Chitwood et al. 2018). Also, augmenting the number of host animals in the release site can increase the contact rate between individuals and change host-parasite interactions; therefore, the probability of disease spread increases. Mange (*Sarcoptes scabiei*) cases have increased in the population of Yellowstone wolves (*Canis lupus*) in areas with high quality of resources and consequently a high density of wolves (Almberg et al. 2012).

Translocations are stressful interventions for wild animals and this physiological reaction can also influence animal health and welfare (Teixeira et al. 2007). Stimuli or stressor activates the hypothalamic-pituitary-adrenal (HPA) axis in the animal and consequently a neuroendocrine response to maintain homeostasis. The capacity to maintain homeostasis fails when the stress is chronic and it results in a prolonged increase of glucocorticoids (McEwen 2005). This effect can compromise the immune function and exacerbate the impact of disease (Hing et al. 2016). Fecal cortisol metabolite concentration was negatively correlated with strongyle egg count in the woylie (*Bettongia penicillata*) after translocation, reflecting the influence of glucocorticoids on the immune response and consequently affecting the parasite burden (Hing et al. 2017). These physiological changes can also affect the host and parasite interactions. During a trial translocation of ciril buntings (*Emberiza cirilus*), there was a disease outbreak caused by *Isospora* sp., an endemic commensal protozoan of the microbial flora of this species. Ciril buntings are prone to stress, hence, the outbreak was attributed to overcrowding, poor hygiene and other stressors (McGill et al. 2010).

The management and surveillance of diseases during wildlife translocations are important to maximize the health of organisms and to minimize the risk of disease (Mathews et al. 2006). Several authors have adapted a basic risk analysis framework (Covello & Merkhofer 1993) into a disease risk analysis (DRA) during wild animals translocations (Davidson & Nettles 1992; Leighton 2002; Armstrong et al. 2003; Miller 2007; McInnes 2011; Sainsbury & Vaughan-Higgins 2012; Jakob-Hoff et al. 2014). These tools determinate the potential effects of infectious and non-infectious diseases in wildlife, domestic animals, people, and ecosystems during the course of translocations, and help managers to make informed decisions (Hartley & Sainsbury 2017).

Sainsbury and Vaughan-Higgins (2012) proposed a DRA in wildlife that flows in different stages. First, hazards are identified evaluating what parasites can be transmitted during the translocation based on the species involved and the translocation pathway. Hazards are categorized by the source of the animals, the novelty of the parasite to the animals and the stress resulting from the translocation (Table 1). Then, the disease risk is assessed to estimate the likelihood of the hazard to enter, establish and spread in animals and people, and the biological and socioeconomic consequences of it. After assessing the risk of disease, decisions are made to manage the risk and sanitary measures are put in place. A continuous, open, interactive, and iterative communication with stakeholders should be kept during the whole process to do it transparently.

Table 1. Hazard categories definitions (Sainsbury & Vaughan-Higgins 2012).

Hazard	Definition
Source	A novel parasite to the destination site transported with the translocated animal across a barrier.
Destination	A non-existent parasite in the source site but present in the destination site and it is novel to the translocated animal across a barrier.
Carrier	A commensal parasite in the translocated animals that affects the host because of stressors, both in destination site or during transit.
Transport	A parasite in the route of transit and novel in the destination site.
Immunodeficiency	A commensal parasite that infects the host because of stressors only in the destination site.
Population	A parasite in the destination and source site that is predicted to impact population size.

Disease risk analysis in wild animals can be a slow cumbersome process and sometimes uncertain (Sainsbury & Vaughan-Higgins 2012). There is uncertainty in the probability of disease introduction, lack of information about the magnitude of negative consequences, and the analysis could be difficult to translate into management decisions (Sainsbury et al. 2012). Furthermore, the lack of good quality information on wild animal diseases and relying on expert judgment can bias the DRA process. Providing evidence from which experts can make an informed judgment and consequently a justified decision, is an important step forward into the practice of evidence-based conservation (Dalziel et al. 2017). A systematic review contributes to conservation interventions like DRA. It gathers the evidence from all the studies available in a subject, analyzes the outcomes from past experiences, and gives an evidence-based framework to engage scientists, practitioners, and decision-makers (Pullin & Stewart 2006; Cook et al. 2013).

Understand which hazard is more often associated with disease outbreaks following conservation translocation can help to focus efforts in the riskiest hazards during the DRA and target the mitigation efforts. The objectives of this research are: to identify and to characterize the published studies in wild animal disease outbreaks following conservation translocation, to identify the type of parasites most commonly involved in the outbreaks, and to identify which hazard is most common to cause disease. The study hypothesis is that the source and destination hazards will be significantly more likely to be associated with wild animal disease outbreaks following conservation translocation than other hazards.

Methods

Definitions

For this review, several terms require definitions. The term wild animal is defined as “any animal living in an undomesticated state, under human care or free-living”; in this article, it referred to any wild amphibians, reptiles, birds, and mammals (OIE 2019). The disease was defined as “the physiological

dysfunction, abnormality, impairment, or an unhealthy state of an animal (Sergeant & Perkins 2015) caused by a parasite (virus, bacteria, fungus, protozoan, helminths, or ectoparasites)". The term disease outbreak was defined as "a case or cases of disease events within an epidemiological unit" (Sergeant & Perkins 2015). The hazard was defined as "an infectious agent that poses the potential to cause an adverse health effect or disease in an individual" (OIE 2019). The definitions for the hazard categories were those explained in Sainsbury and Vaughan-Higgins (2012) (Table 1). To define the hazard category we delineated the translocation pathway and determine if a geographical or ecological barrier (Riley 1952) was crossed. If there was a contact route for transmission of the parasite among sympatric host individuals between the source and the destination area, the translocation was considered as it did not cross a barrier (Bobadilla et al. 2017).

Systematic review

A systematic literature review was carried out to answer the research question and it followed published guidelines (Pullin & Stewart 2006; Moher et al. 2009). The eligibility criteria were set to answer the research question: Which hazard category has been associated with disease outbreaks in wild animals following conservation translocation? The inclusion criteria covered all papers that reported specific primary research on naturally occurring infectious disease in wild tetrapods during or after their translocation for conservation purposes. This systematic review protocol has not been registered and it is explained below.

Literature search

The literature search was done in 3 search digital interfaces, CAB Direct, Web of Knowledge, and PubMed. They were chosen by their relevance and coverage to maximize the number of databases that covers veterinary science and wildlife conservation research. Databases searched through CAB Direct were CAB Abstracts (1973-2019), VetMed Resource (1973-2019), Global Health (1973-2019), Animal Health and Production Compendium (AHPC), CABI Full Text, CAB Abstracts Archive. Databases searched through Web of Knowledge were Web of Science Core Collection (1900-2019), BIOSIS Citation Index (1969-2019), Current Contents Connect (1998-2019), Data Citation Index (1995-2019), Derwent Innovations Index (1995-2019), KCI-Korean Journals Database (1980-2019), MEDLINE® (1950-2019), Russian Science Citation Index (2005-2019), SciELO Citation Index (2002-2019), Zoological Record (1995-2019). The search was also performed through PubMed database which covers citations and abstracts in biomedicine and health. The last literature search included in this study was carried out on July 16th of 2019.

The search strategy included only those papers published in English since 1900. The search involved 3 strings of keywords based on the research question and they were set to include the maximum of relevant published articles. The search had to include at least one word of each string in the title, abstract or the keywords. The first keyword string referred to the subject: wildlife, wild animal, wild population, and free-ranging. The second keyword string referred to the intervention or movement of

the animals: translocation, reintroduce, and re-introduce. Finally, the third keyword string referred to the outcome of the intervention or disease outbreak: disease, parasite, infected, and pathogen. For example, the strings used to search all databases on Web of Science was: (TS= (Wildlife OR (wild animal) OR (wild population) OR (free-ranging))) AND (TS= (translocate OR reintroduce OR (re-introduce))) AND (TS= (disease OR parasite OR infected OR pathogen)). The articles obtained from the different databases were merged and managed with the reference software EndNote X9 (Clarivate-Analytics 2018). Duplicated articles were removed using the software and by hand. Then, the literature was screened and selected for further analysis.

Literature selection

Titles and abstracts of the literature found were screened for relevance; the articles with evidence of wild animal disease during or after conservation translocation were retained. The inclusion criteria covered non-experimental studies on infectious diseases caused by parasites affecting translocated populations of amphibians, reptiles, birds, and mammals. The exclusion criteria rejected any review, book or book section, any paper that did not refer to disease in wild animals after translocation, and any paper that mentioned infection or seroprevalence without relation to disease, death or population decline. The list of selected articles was exported to a Microsoft Excel (Microsoft-Corporation 2016) spreadsheet. These articles were categorized by the geographical region where the translocation was carried out; the articles from the continent with the biggest number of selected papers were selected for full-text review. The literature was retained for data extraction by relevance in the subject and by the inclusion and exclusion criteria.

Data collection and analysis

The data extracted from retained articles were the information about the article, the species involved in the disease outbreaks, the translocation event, and the disease outbreak. Each disease was treated as an individual disease outbreak in those articles describing multiple disease outbreaks affecting a population. If the article did not mention a specific year of the outbreak, the period mentioned was taken as an outbreak. The outbreaks without a definitive diagnostic were implied by the articles authors' suggestion and research implications. Each outbreak was granted to a hazard category depending on the translocation pathway and the definitions of each category (Table 1). The articles were categorized by the geographical region of the translocation, the taxonomy of the affected animals, the parasite type, and the hazard category. Descriptive statistics were carried out in each of the categories. One-sample Chi-square test was used to compare the frequency of disease outbreaks between the 6 hazard categories. The main hazard involved in wild animal disease outbreaks from the published literature in a geographical area was determined.

Results

The database literature search yield 2945 results. After the exclusion of the duplicate records, 2458 articles were screened for relevance. During the screening of titles and abstracts, 2279 articles were excluded due to the lack of evidence of disease outbreak in wild animals after conservation translocation (Fig. 1). There were 179 articles suitable for full-text review, which were categorized by continent. North America was the continent with the greatest number of articles (n=71), followed by Europe (n=39), Oceania (n=29), Asia (n=20), Africa (n=16), South America (n=4), and one article referred to translocations in Europe and Oceania. The articles from North America were chosen for full-text review; after all exclusion, 28 articles were considered for this review and further analysis.

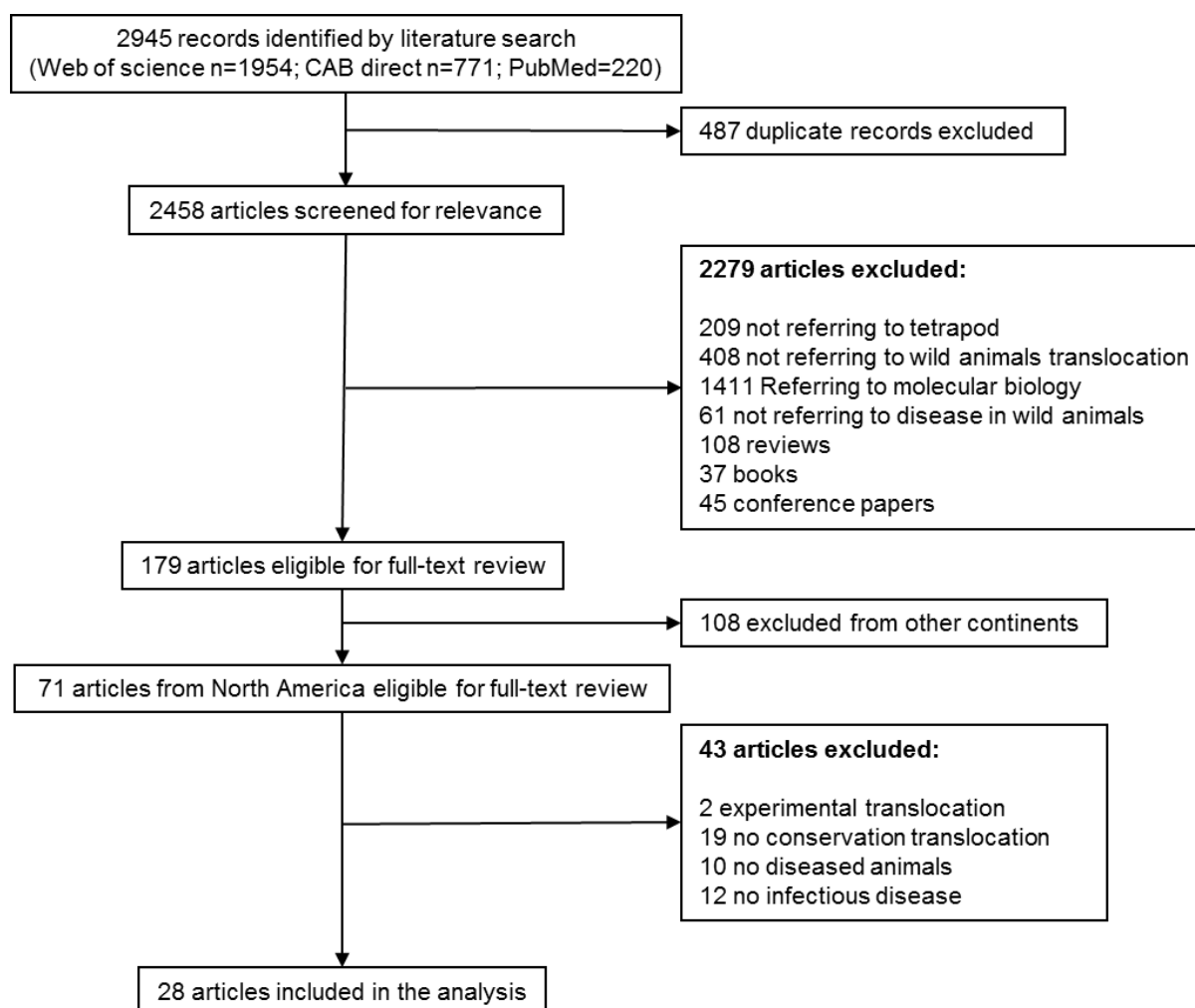


Figure 1. Systematic review flow diagram showing the number of identified, screened, selected, and included articles, following the PRISMA Statement (Moher et al. 2009).

The articles included were identified for each taxon (Table 2). The Mammalia class received greater literature coverage (n=22) than Aves (n=3), Amphibia (n=2), and Reptilia (n=1). The literature was dominated by articles referred to species within the order Carnivora (n=10) and Certartiodactyla (n=9). The absolute number of disease outbreaks within the articles accounted for 54 (Table 2). Mammalia had the greatest number of disease outbreak with 42 outbreaks, followed by Aves (n=8), Amphibia

(n=3), and Reptilia (n=1). The number of outbreaks in the Canidae family (n=13) was greater than the other families, followed by Mustelidae (n=9), Bovidae (n=7), and Cervidae (n=6).

Table 2. Amount of articles and disease outbreaks afforded by taxonomy.

Class	Order	Family	n of articles	n of disease outbreaks	Author & publication year
<u>Amphibia</u>			2	3	
	Anura		1	2	
		Ranidae	1	2	Joseph & Knapp 2018
	Caudata		1	1	
		Cryptobranchidae	1	1	Bodinof et al. 2012
<u>Reptilia</u>			1	1	
	Testudines		1	1	
		Testudinidae	1	1	Hernandez et al. 2010
<u>Aves</u>			3	8	
	Galliformes		1	3	
		Phasianidae	1	3	MacDonald et al. 2019
	Cathartiformes		1	4	
		Cathartidae	1	4	Rideout et al. 2012
	Passeriformes		1	1	
		Corvidae	1	1	Work et al. 2000
<u>Mammalia</u>			22	42	
	Carnivora		10	26	
		Canidae	4	13	Hedrick et al. 2003; Almberg et al. 2009; Almberg et al. 2012; Justice-Allen & Clement 2019
		Felidae	2	4	Wild et al. 2006; Wolfe & Spraker 2007
		Mustelidae	4	9	Hoover et al. 1984; Larkin et al. 2010; Larkin et al. 2011; Spriggs et al. 2018
	Certartiodactyla		9	13	
		Bovidae	4	7	Boyce et al. 2011; Plowright et al. 2013; Smith et al. 2015; Bleich et al. 2018
		Cervidae	5	6	Larkin et al., 2003; Bender et al. 2005; McIntosh et al. 2014; Cain et al. 2018; Chitwood et al. 2018
	Lagomorpha		1	1	
		Leporidae	1	1	Harrenstein et al. 2006
	Rodentia		2	2	
		Cricetidae	2	2	Logiudice 2003; Smyser et al. 2013
Total			28	54	

Within the study results, the majority of disease outbreaks were caused by virus (n=20), followed by those disease outbreaks caused by helminths (n=9), bacteria (n=9), unknown parasites (n=6), fungus (n=5), protozoans (n=4), and ectoparasites (n=1; Fig. 2). The 3 disease outbreaks in Amphibia were caused only by fungal parasites, and a bacterial parasite (n=1) caused the disease outbreak in Reptilia. Disease outbreaks in Aves were attributed to viral (n=5), protozoan (n=1), and fungal (n=2) parasites. In Mammalia the outbreaks were caused by viruses (n=15), protozoan (n=3), bacteria (n=8), helminths (n=9), ectoparasites (n=1), and unknown parasites (n=6), however, fungal parasites

were not reported for this class. Most of the disease outbreaks were caused by multi-host agents (n=48).

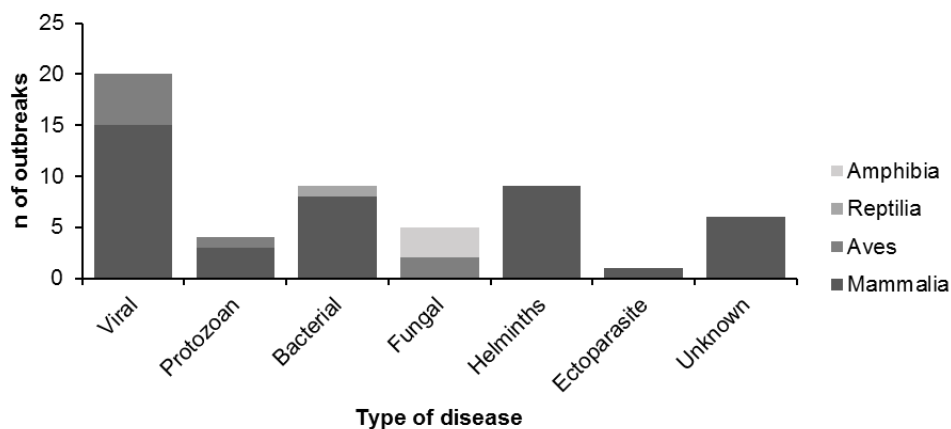


Figure 2. Amount of disease outbreaks afforded by parasite type and animal class

The identified disease outbreaks were categorized by hazard category: source (n=8), destination (n=11), carrier (n=2), immunodeficiency (n=4), and population (n=29; Fig. 3). There were no outbreaks categorized as transport hazards. There were more disease outbreaks due to population hazards than other categories ($P < 0.0001$). The disease outbreaks in Amphibia were categorized as destination (n=1) and population hazard (n=2). In Reptilia, the only outbreak reported was categorized as a population hazard. Those outbreaks in Aves were categorized as source (n=2), destination (n=2), immunodeficiency (n=2), and population hazard (n=2). The 42 disease outbreaks in Mammalia were categorized within all the hazard categories: 6 as source, 8 as destination, 2 as carrier, 2 as immunodeficiency, and 24 as population hazard.

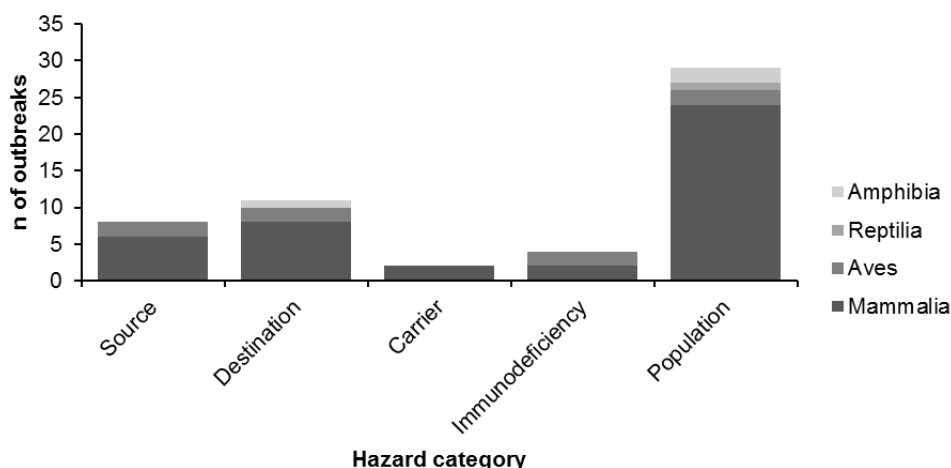


Figure 3. Amount of disease outbreaks afforded by hazard category and animal class

The disease outbreaks categorized as source hazard affected 4 species (Table 3). Five of these outbreaks were caused by a viral parasite in Wild turkeys (*Meleagris gallopavo*, n=1), Mexican wolf (*Canis lupus baileyi*, n=3) and Canada lynx (*Lynx canadensis*, n=1). Furthermore, the 2 outbreaks in

North American river otter (*Lontra canadensis*) were inferred as a bacterial parasite and one was caused by an unknown parasite.

Table 3. Summary of the 8 disease outbreaks found in the literature caused by a source hazard.

Authors & year	Family	Species	Translocation year	Agent	Year of disease
MacDonald et al. 2019	Phasianidae	Wild turkey (<i>Meleagris gallopavo</i>)	1980s	Alpharetrovirus	2011-2017
Hedrick et al. 2003	Canidae	Mexican wolf (<i>Canis lupus baileyi</i>)	1999	Gamaretrovirus	2011-2017
				Canine distemper virus	2000
Wolfe & Spraker 2007	Felidae	Canada lynx (<i>Lynx canadensis</i>)	2003-2006	Canine parvovirus	1999a, 1999b
				Papillomavirus	2003-2006
Hoover et al. 1984	Mustelidae	North American river otter (<i>Lontra canadensis</i>)	1983-1984	<i>Proteus mirabilis</i> & β -hemolytic <i>Streptococcus</i>	1984
				Bronchitis*	1984

*Suspected disease

The disease outbreaks categorized as a destination hazard occurred in 7 different species (Table 4). Five of these outbreaks were caused by viral parasites in California condor (*Gymnogyps californianus*, n=2), gray wolf (*Canis lupus*, n=1), Mexican wolf (n=1), and mule deer (*Odocoileus hemionus*, n=1). Disease outbreaks in Canada lynx (n=3) and bighorn sheep (*Ovis Canadensis*, n=2) were caused by a bacterial parasite. Ozark hellbender (*Cryptobranchus alleganiensis bishop*) had a disease outbreak caused by a fungal parasite at the destination site.

Table 4. Summary of the 11 disease outbreaks found in the literature caused by a destination hazard.

Authors & year	Family	Species	Translocation year	Agent	Year of disease
Bodinof et al. 2012	Cryptobranchidae	Ozark hellbender (<i>Cryptobranchus alleganiensis bishopi</i>)	2008	<i>Batrachochytrium dendrobatidis</i>	2008-2009
Rideout et al. 2012	Cathartidae	California condor (<i>Gymnogyps californianus</i>)	1992, 1997, 1996, 2003	West Nile virus	2005, 2008
Almberg et al. 2009	Canidae	Gray wolf (<i>Canis lupus</i>)	1995-1996	Canine herpesvirus	1997-2007
Justice-Allen & Clement 2019	Canidae	Mexican wolf (<i>Canis lupus baileyi</i>)	Unknown	Canine distemper virus	2017
Wild et al. 2006	Felidae	Canada lynx (<i>Lynx canadensis</i>)	1999, 2000, 2003	<i>Yersinia pestis</i>	2000, 2001, 2003
Bleich et al. 2018	Bovidae	Bighorn sheep (<i>Ovis canadensis</i>)	1956-2014	<i>Mycoplasma ovipneumoniae</i> , <i>Manheimia</i> spp., & <i>Bibersteinia</i> spp.*	1997, 2014
Cain et al. 2018	Cervidae	Mule deer (<i>Odocoileus hemionus</i>)	2013-2014	Bluetongue virus or Orbivirus*	2013

*Suspected disease

The 2 disease outbreaks categorized as carrier hazards were caused by helminths in North American river otter (Table 5). The outbreaks categorized as immunodeficiency hazard occurred in 3 species (Table 6). Two of these were caused by bacterial parasites in elk (*Cervus Canadensis*, n=1) and pygmy rabbit (*Brachylagus idahoensis*, n=1), and 2 by a fungal parasite in California condor.

Table 5. Summary of the 2 disease outbreaks found in the literature caused by a carrier hazard.

Authors & year	Family	Species	Translocation year	Pathogen agent	Year of disease
Hoover et al. 1984	Mustelidae	North American river otter (<i>Lontra canadensis</i>)	1983-1984	<i>Dirofilaria lutrae</i>	1984
				<i>Strongyloides lutrae</i>	1984

The disease outbreaks categorized as population hazard occurred in 10 species from the 4 classes included in this study (Table 7). Nine of these outbreaks were caused by viral parasites in Wild turkey (n=1), gray wolf (n=6), American marten (*Martes Americana*, n=1) and fisher (*Martes pennant*, n=1). Bacterial parasites caused 2 outbreaks, one in gopher tortoise (*Gopherus polyphemus*) and one in bighorn sheep. Four outbreaks were caused by protozoan parasites in Alala (*Corvus hawaiiensis*, n=1), gray wolf (n=1) and fisher (n=2). There were 2 disease outbreaks caused by fungal parasites in Sierra Nevada yellow-legged frog (*Rana sierrae*). Seven outbreaks were caused by helminths in American marten (n=1), elk (n=4), and Allegheny woodrat (*Neotoma magister*, n=2). There was only one disease outbreak caused by an ectoparasite in a gray wolf (n=1). Four of the outbreaks categorized as population hazards were caused by an unknown parasite in bighorn sheep; the category was granted to these outbreaks because the suspected disease happens in source and destination site.

Table 6. Summary of the 4 disease outbreaks found in the literature caused by an immunodeficiency hazard.

Authors & year	Family	Species	Translocation year	Agent	Year of disease
Rideout et al. 2012	Cathartidae	California condor (<i>Gymnogyps californianus</i>)	1992, 1996, 1997, 2003	<i>Aspergillus fumigatus</i>	2005, 2008
Bender et al. 2005	Cervidae	Elk (<i>Cervus canadensis</i>)	1918	Enteritis*	1981-1994
Harrestien et al. 2006	Leporidae	Pygmy rabbit (<i>Brachylagus idahoensis</i>)	2001-2002	<i>Mycobacterium avium</i>	2002-2004

*Suspected disease

Table 7. Summary of the 29 disease outbreaks found in the literature caused by a population hazard.

Authors & year	Family	Species	Translocation year	Agent	Year of disease
Maxwell & Knapp 2018	Cryptobranchidae	Sierra Nevada yellow-legged frog (<i>Rana sierrae</i>)	2006, 2008, 2013, 2015, 2017	<i>Batrachochytrium dendrobatidis</i>	2006-2017, 2008-2017
Hernandez et al. 2010	Testudinidae	Gopher tortoise (<i>Gopherus polyphemus</i>)	2001	<i>Mycoplasma agassizii</i> *	2004
MacDonald et al. 2019	Phasianidae	Wild turkey (<i>Meleagris gallopavo</i>)	1980s	Avipoxvirus	2011-2017
Work et al. 2000	Corvidae	Alala (<i>Corvus hawaiiensis</i>)	1993-1999	<i>Toxoplasma gondii</i>	1998-1999
Almberg et al. 2009	Canidae	Gray wolf (<i>Canis lupus</i>)	1995-1997	Canine adenovirus type-1	1997-2007
				Canine distemper virus	1999, 2002, 2005
				Canine parvovirus	1997-2007
				<i>Neospora caninum</i>	1997-2007
Almberg et al. 2012	Canidae	Gray wolf (<i>Canis lupus</i>)	1995-1996	Canine distemper virus	2008
				<i>Sarcoptes scabiei</i>	2006
Spriggs et al. 2018	Mustelidae	American marten (<i>Martes americana</i>)	mid-20th century	Canine parvovirus	2001-2015
				<i>Diocotophyme renale</i>	2011-2015
Larkin et al. 2010	Mustelidae	Fisher (<i>Martes pennanti</i>)	1994-1998	Lyssavirus	2006
Larkin et al. 2011	Mustelidae	Fisher (<i>Martes pennanti</i>)	1994-1998	<i>Sarcocystis</i> spp.	2002-2008
				<i>Toxoplasma gondii</i>	2002-2008
Boyce et al. 2011	Bovidae	Bighorn sheep (<i>Ovis canadensis</i>)	2002, 2005	Pasteurella, <i>Manheimia</i> spp., Bovine respiratory syncytial virus (BRSV), parainfluenza-3 virus (PI3)*	2002-2007
Plowright et al. 2013	Bovidae	Bighorn sheep (<i>Ovis canadensis</i>)	1997-2010	* <i>Mycoplasma ovipneumoniae</i>	1997-2010
Smith et al. 2015	Bovidae	Bighorn sheep (<i>Ovis canadensis</i>)	1965	*Pneumonia	2010, 2011, 2012
Bender et al. 2005	Cervidae	Elk (<i>Cervus canadensis</i>)	1918	<i>Parelaphostrongylus tenuis</i>	1981-1994
Chitwood et al. 2018	Cervidae	Elk (<i>Cervus canadensis</i>)	2011-2013	<i>Parelaphostrongylus tenuis</i>	2011-2015
Larkin et al. 2003	Cervidae	Elk (<i>Cervus canadensis</i>)	1997-2001	<i>Parelaphostrongylus tenuis</i>	1997-2001
McIntosh et al. 2014	Cervidae	Elk (<i>Cervus canadensis</i>)	1998-2001	<i>Parelaphostrongylus tenuis</i>	1998-2005
Logiudice 2003	Cricetidae	Allegheny woodrat (<i>Neotoma magister</i>)	1996	<i>Baylisascaris procyonis</i>	1996
Smyser et al. 2013	Cricetidae	Allegheny woodrat (<i>Neotoma magister</i>)	2007-2008	<i>Baylisascaris procyonis</i>	2008

*Suspected disease

Discussion

The number of wildlife translocations around the world is increasing, and this trend is most likely to continue due to wild animals' population decline caused by stochastic events, anthropogenic changes in ecosystems and climate change (Kock et al. 2010). Managers and conservationists can benefit from evidence-based practices (Sutherland et al. 2004; Dalziel et al. 2017), hence, evaluation of previous experiences in conservation translocation can help to improve the results in future wild animal movements. Diseases influence the survivorship of translocated animals and animals at the destination, therefore, diseases are an important factor in the success of the translocation (Cunningham 1996). This systematic review compiled the literature in wild animal disease outbreaks following conservation translocations and characterized these events. Some of the characteristics found on the disease outbreaks agree with previous reviews on the riskiest parasites (Rideout et al. 2017). However, we found that population hazard is the most common hazard in the literature causing this disease outbreaks, which disagree with what has been suggested.

Systematic reviews are subject to bias because only a proportion of research projects reach publication in an indexed journal (Higgins et al. 2019). The number of papers found in this literature search can be subject to publication bias, where the research findings are not published due to the nature of the results. The outcome reporting bias can also be seen when the research has negative findings and it is not published. This bias escapes the analysis of this study. Also, the findings in this systematic review are dependent on the search protocol. The method kept a systematic protocol, which could be repeatable and avoids professional judgment. Expert knowledge is valuable, but evidence-based practices try to gather information based on research and publications that have been reviewed by peers (Schmidt 2007), avoiding judgment bias. Some information could be missing because the literature search excluded any publication that was not primary research, previous reviews, books, and gray literature. The collection of literature could be improved expanding the articles search in more databases and literature repositories of institutions specialized in the subject. However, increasing the research effort could be unrelated to the strength of the analysis (Cook et al. 2013). Furthermore, this systematic review was carried out only by the author; this methodology could bring a literature selection bias during the screening and some relevant articles could be omitted. Working in a team is recommended by the Cochrane network, specialist in systematic reviews, to avoid researcher bias (Higgins et al. 2019).

Despite some of the aforementioned limitations, this systematic review was carried out based on the PRISMA Statement recommendations (Moher et al. 2009) with an extensive, comprehensive and reproducible protocol. Strict inclusion and exclusion criteria were followed to reduce the risk of bias. The results provided a much-needed knowledge gap in the disease outbreaks following conservation translocation. The literature reviewed in the present study suggested North America as the geographical region with more studies on disease outbreaks in wild animals following conservation translocation. Researchers working in a non-English speaking country are prone to publish in local journals (Higgins et al. 2019), hence, the higher amount of studies in this region is probably explained

by the use of the English language as inclusion criteria. Furthermore, this probably also reflects the lack of research in wildlife emerging infectious diseases in neglected regions like South America and Africa (Tompkins et al. 2015), which could give a parallel of the research done in these regions.

The literature search also showed that mammals received more attention (78.6%) than other taxa, therefore, the bigger number of disease outbreaks were also in this taxonomic class. There is an evident taxonomic bias in general science and conservation (Cook et al. 2013), and have been recognized in reintroduction projects (Seddon et al. 2005), disease research in wild animal reintroductions (Ewen et al. 2012) and emerging infectious diseases in wildlife (Tompkins et al. 2015). Surprisingly, this finding differs from Griffith et al. (1993), where birds were the group with more translocations in the United States of America and Canada. This difference could be subject to the greater number of game species translocations they reported, with more than half of these on game-bird species. Furthermore, we found that Carnivora and Certartiodactyla were the order with the most number of disease outbreaks. These results can be explained by the number of reintroduction over-represented by species of these orders (Seddon et al. 2005). Also, it has been found that carnivores are the order with more cases of emerging infectious diseases (Tompkins et al. 2015). Additionally, these results could be influenced by wildlife management practices and conservation valorization in the region, directing more resources into research on charismatic animals and species with game value. Furthermore, research resources are put more often in diseases important for farming animals or public health, neglecting other wild animals (Tompkins et al. 2015).

The analysis of the articles revealed that the disease outbreaks were caused mainly by viral agents (37%) followed by helminths (16.6%). Studies of emerging infectious diseases in wild animals also have recorded viral agents as the cause of the majority of disease outbreaks (Dobson & Foufopoulos 2001; Tompkins et al. 2015). Microparasites have the potential to infect different hosts and change from one individual to another due to a faster adaptation and evolution (Rideout et al. 2017). In contrast, macroparasites as helminths have complex life cycles and longer generation times and longer evolution (Cleaveland et al. 2001). Nevertheless, the fact that helminths have been the second most common parasite to cause disease outbreaks could be due to greater reports of these parasites and because they are easier to detect during the necropsies. Furthermore, during this review, I found publications on *Parelaphostrongylus tenuis* as the primary reason for the failure of elk reintroduction in North America (Larkin et al. 2003; Bender et al. 2005; McIntosh et al. 2014; Chitwood et al. 2018).

Most disease outbreaks found in this study were caused by multi-host agents (88.9%). Ewen et al. (2012) reported similar findings, where 90% of the studies were focused on generalist parasites. Multi-host parasites are better invaders because they have a more diverse array of susceptible hosts to infect (Rideout et al. 2017). Thus, most emerging infectious diseases in wildlife have been classified as generalists (Tompkins et al. 2015), explaining their capacity to cause disease in new wild animal populations. Furthermore, research on parasites that affect domestic animals is more advanced with detection and analysis tools more developed. Most of the diseases found in this review

can affect domestic and wild animals, for consequent are easier to detect and are of economic importance.

A valuable finding is that more than half of the disease outbreaks in this review were caused by a population hazard, rejecting the hypothesis of the study. This result challenges what has been suggested by other authors, that novel and non-indigenous parasites are the riskiest hazards during wild animal translocations (Kirkwood & Sainsbury 1995; Cunningham 1996; Kock et al. 2010). However, the second and third causes of disease were destination and source hazard, both hazards caused by novel parasites. Different factors can influence this result. The literature found in this review is influenced by the study design and the systematic review protocol; papers on infectious diseases in wild animals not referring to conservation translocation in the title or abstract were excluded, missing probably some relevant articles. Furthermore, the suggestion that novel parasites are the riskiest hazard was done taking into count the whole variety of wild animal translocations, with handpicked relevant cases and logic reasoning, which can explain the differences. The majority of conservation translocations follow biosecurity protocols to avoid introducing new diseases in the destination site, which could explain the low number of diseases caused by a source hazard. Multi-host parasites are also more prone to be widespread in the region and probably are carry by other animal species, explaining the contact of the parasite and host at source and destination.

Some disease outbreaks found in this review have happened after several years from the translocation (Bender et al. 2005; Almberg et al. 2012; Spriggs et al. 2018; MacDonald et al. 2019). The inclusion criteria on the review allowed including these cases, however, these diseases could not be related directly to the translocation. Parasites interact with their environment within the host, between the host population and host communities, and can spread into a regional or biogeographical scale (Johnson et al. 2015). This shows the link between the parasite and the host, and it could be affected by the environment (Hess et al. 2002). Several changes in the ecosystems and the host population dynamics could occur since the translocation of the animals until the emergence of the disease, predisposing the spread of parasites from animal populations nearby. An example is the emergence of mange in gray wolves detected in Yellowstone after 20 years of the reintroduction of this species (Almberg et al. 2012). This disease could be maintained and spread by sympatric canids in the area, promoting disease emergence. The increase of wildlife populations after translocation and the encroachment of humans and their domestic animals into wild areas can increase the contact rate between animals, increasing the basic reproductive number, and favoring the disease dissemination.

Other factors like the characteristics of the geographical region, biodiversity, human development, parasite pathogenicity, disease surveillance and severity influence the disease outbreaks. However, they have not been addressed in this study because it would be not possible to generalize and it goes beyond the research objectives. North America is a vast continent with a variety of ecosystems with several sympatric animals, geographical barriers, anthropogenic landscapes, big farm industry and developing economies. These characteristics can influence the number of translocations, funding for research, and the spread of diseases. Also, biodiversity limits the spread of diseases by dilution effect

(Civitello et al. 2015), therefore, the increased loss of biodiversity and habitat fragmentation promotes disease outbreaks. On another hand, the parasite pathogenicity varies with host age-class, immune response, and susceptibility (Rideout et al. 2017), thus, it was not possible to analyze in this systematic review which includes all taxa and parasites.

The surveillance of disease in wild animals is reduced, especially after translocation (Kock et al. 2010) what could hide the real magnitude of the diseases and its effect on animal populations. Furthermore, the severity of the disease outbreaks can change between parasites and hazard categories, varying in the number of affected animals and the harm that can cause (Sainsbury et al. 1995). Perhaps, it is necessary to expand the analysis to the other geographical areas to compare results and have a better understanding of the subject on a global scale across taxa and relate the findings to characteristics from each region. However, due to the heterogeneity of the information on papers across taxa, it is also necessary to carry out more specific reviews to answer the effects of the other factors mentioned above on disease outbreaks after translocations in a specific animal group or species.

This study attempts to improve the current knowledge of the characteristics of disease outbreaks after translocation. The most common type of parasite to cause disease outbreaks in wild animals are those viral agents and pathogens capable to infect several host species results, which reaffirm past findings. Furthermore, the analysis of the disease outbreaks showed that the population hazard is most common to cause disease outbreaks; however, other hazards should not be left behind during the disease risk analysis because they are also an important source of disease. The future wild animal disease risk analysis for translocations could focus on those diseases that have the capacity of infect multiple host species in the area to translocate, novel parasites to the destination and source population, and those diseases caused by microparasites. In addition, to improve future translocations is necessary to collect standardized information about the translocation, with dates, locations, motives, number of animals translocated and outcomes in a common database. The information and data recorded could be analyzed and be used to practice evidence-based translocations and disease risk analysis.

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