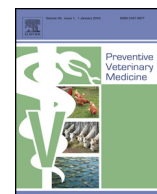




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## Diseases at the livestock–wildlife interface: Status, challenges, and opportunities in the United States

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### ABSTRACT

In the last half century, significant attention has been given to animal diseases; however, our understanding of disease processes and how to manage them at the livestock–wildlife interface remains limited. In this study, we conduct a systematic review of the scientific literature to evaluate the status of diseases at the livestock–wildlife interface in the United States. Specifically, the goals of the literature review were three fold: first to evaluate domestic animal diseases currently found in the United States where wildlife may play a role; second to identify critical issues faced in managing these diseases at the livestock–wildlife interface; and third to identify potential technical and policy strategies for addressing these issues. We found that of the 86 avian, ruminant, swine, poultry, and lagomorph diseases that are reportable to the World Organization for Animal Health (OIE), 53 are present in the United States; 42 (79%) of these have a putative wildlife component associated with the transmission, maintenance, or life cycle of the pathogen; and 21 (40%) are known to be zoonotic. At least six of these reportable diseases—bovine tuberculosis, paratuberculosis, brucellosis, avian influenza, rabies, and cattle fever tick (vector control)—have a wildlife reservoir that is a recognized impediment to eradication in domestic populations. The complex nature of these systems highlights the need to understand the role of wildlife in the epidemiology, transmission, and maintenance of infectious diseases of livestock. Successful management or eradication of these diseases will require the development of cross-discipline and institutional collaborations. Despite social and policy challenges, there remain opportunities to develop new collaborations and new technologies to mitigate the risks posed at the livestock–wildlife interface.

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### 1. Introduction

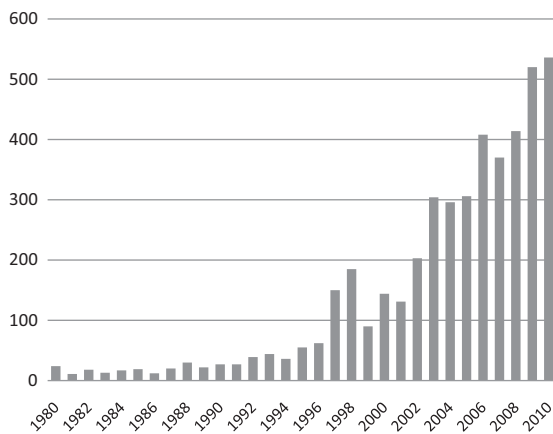
Despite significant attention given to animal diseases in the last half-century, our understanding of disease processes, and how to manage them at the livestock–wildlife interface, remains limited (Rhyan and Spraker, 2010). The increasing role of wildlife in the emergence of livestock

and human diseases is due to multiple changes occurring within wildlife, livestock, and human populations, as well as at the livestock–wildlife interface (Jones et al., 2008). Human driven land use change—which frequently includes encroachment into wildlife habitat—continues to increase along with more intensified livestock production practices (Daszak et al., 2001; Patz et al., 2004). Alteration of wildlife population demographics, such as larger deer populations, increases the potential for contact and pathogen transmission at the livestock–wildlife interface (Rhyan and Spraker, 2010).

All of these changes work to create new interfaces between livestock and wildlife (Gortázar et al., 2007;

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**Fig. 1.** The number of publications in English language journals identified in Scopus database with the words “wildlife” and “parasite” or “disease” in the title, abstract, or key words.

Decker et al., 2010; Rhyhan and Spraker, 2010), potentially exacerbating pathogen transmission processes between them. Globally, the role of wildlife in livestock diseases is expected to increase (Siembieda et al., 2011) in conjunction with human population growth, which is expected to reach 9 billion by 2030. This will create increased demand for animal protein thereby increasing livestock populations (Anonymous, 2004). The demand will further increase potentially infectious contacts between livestock and wildlife leading to an increased potential for new zoonotic diseases to emerge. All of these challenges will require an improved understanding of the ecology of pathogens at the livestock–wildlife interface along with development of tools and mitigations to manage these pathogens.

Historically, managing diseases affecting both livestock and wildlife as a single, linked system in North America, has presented several obstacles. Conflicting agency and institutional missions, program goals, and cultural differences that limit the potential for developing comprehensive mitigation of pathogen transmission contribute to hampering efforts in this area. Nevertheless, research and policy at the livestock–wildlife interface has received increased attention in recent years with the number of scientific publications in English journals addressing this topic rising dramatically (Fig. 1). This is driven, though not exclusively, by a rapid increase in the number of zoonotic disease events associated with wildlife in the latter part of the 20th century (Dobson and Foufopoulos, 2001; Ostfeld and Holt, 2004; Decker et al., 2010). Three-fourths of all emerging infectious diseases (EIDs) of humans are zoonotic with most originating in wildlife (Taylor and Latham, 2001; Jones et al., 2008). A large proportion (77%) of livestock pathogens—and an even higher proportion (91%) of carnivore pathogens—infect multiple hosts including wildlife (Cleaveland et al., 2001). Therefore, diseases that arise from the livestock–wildlife interface are of paramount importance and must be an area of focus for animal health authorities (Siembieda et al., 2011).

One example, Nipah virus—classified as an emerging infectious pathogen—recently moved from its natural host

(fruit bats) to domestic swine, causing disease and mortality in both swine and local agricultural workers and resulting in economic losses (Epstein et al., 2006a). The 1999 Nipah virus outbreak in Malaysia destroyed the Malaysian swine industry while the associated human fatalities simultaneously created massive public panic (Epstein et al., 2006a). This newly recognized virus was carried by fruit bats for decades and emerged as a result of newly occurring habitat destruction, climatic changes, and the encroachment of food–animal production into wildlife domains (Epstein et al., 2006b).

Although little discussed, pathogen transmission at the livestock–wildlife interface is frequently bi-directional (Bengis et al., 2002). In contrast to conventional thinking, livestock have introduced several pathogens, such as bovine brucellosis and tuberculosis bacterium, to naïve wildlife populations in North America. These two pathogens are found in at least five wildlife populations (Tessaro, 1986; Sweeney and Miller, 2010) and create significant challenges for disease control at the livestock–wildlife interface. In some instances, spillover events from livestock into wildlife impact conservation of species of concern (Dobson and Foufopoulos, 2001; Nishi et al., 2002; Joly and Messier, 2005; Cross et al., 2007). An example is the transmission and introduction of bovine brucellosis and tuberculosis from livestock into native wood bison (*Bison bisonathabascae*) populations in Canada, which has created a conservation challenge for the species (Tessaro et al., 1990; Nishi et al., 2002). Another well-publicized example is the introduction of brucellosis into native bison and elk populations of the Yellowstone ecosystem in 1917 (Meagher and Meyer, 1994; Meyer and Meagher, 1995). This resulted in a wildlife management challenge due to conflicts between livestock and bison preservation.

The presence of brucellosis poses continued risk for transmission back into livestock creating biological, social, and policy challenges (Cross et al., 2007, 2010). Obstacles faced by wildlife managers and livestock authorities for mitigating contact between wildlife and livestock has resulted in significant efforts to develop technology that reduces contact and is economically feasible. However, development of effective tools that can be readily deployed has been met with a host of challenges. Many devices prove to be ineffective or only effective for a short duration (VerCauteren et al., 2005, 2006a). The most successful tools have involved fencing technology (e.g. high fence, wire mesh, electrified high-tensile steel wire, or polytape) that reduces contact between wildlife and livestock feed (VerCauteren et al., 2006b, 2007). However, fencing suffers from limitations such as the need for relatively frequent maintenance. More recently, research has focused on the use of historic tools such as livestock protection dogs to prevent contact between livestock and wildlife. In some cases these traditional tools have proven to be the most effective (VerCauteren et al., 2008, 2010). In addition to the challenges faced in developing effective mitigation tools is gaining social acceptance of their use by farmers, which is fundamental in successfully using these tools (Brook and McLachlan, 2006). However, there remains a need for identifying new economically feasible tools that wildlife and

**Table 1**

Number of OIE reportable diseases present in the United States and number with a known potential wildlife component associated with the transmission, maintenance, or life cycle of the causative agent.

	Established free (absent)	Known present (sporadic or limited distribution)	Total	Wildlife component	Zoonotic		
Avian	3 (1)	9 (2)	15	10	91%	3	27%
Cattle	4 (2) <sup>*</sup>	8	14	6	75%	3	38%
Equine	4	6 (1)	11	3	43%	1	14%
Lagomorphs		1 (1)	2	2	100%		
Multiple	10	14 (2)	26	16	100%	13	81%
Sheep and goat	4	6 (1)	11	3	43%	1	14%
Swine	4 (1)	2	7	2	100%		
Total OIE diseases	29 (4)	53	86	42	79%	21	40%

<sup>\*</sup> Bovine spongiform encephalopathy (BSE) is not considered free or present in the United States but rather a controlled risk.

livestock managers can deploy to reduce contact at the livestock–wildlife interface.

Improving our understanding of the biological and anthropogenic processes that promote contact between wildlife and livestock is critical for limiting pathogen transmission at this interface. Given the frequently bi-directional nature of pathogen transmission, cooperation is required between livestock owners, animal health officials, and wildlife managers if control efforts are to be successful. Conflicts will undoubtedly continue to challenge wildlife managers and livestock authorities seeking solutions, which can only be found through the creation of new partnerships and the strengthening of existing ones that bridge the gap between wildlife and livestock agencies at all levels.

Here we conduct a systematic review of the English scientific literature to evaluate the status of diseases and pathogens at the livestock–wildlife interface in the United States. Specifically, the goals of the literature review were three fold: first, to evaluate domestic animal diseases currently found in the United States where wildlife may play a role; second, to identify critical issues faced in managing these diseases at the livestock–wildlife interface; and third, to identify potential technical and policy strategies for addressing these issues. We highlight two examples of emerging diseases at the livestock–wildlife interface in North America, which pose management challenges and offer an opportunity for comprehensive disease management by facilitating cross-agency and state-federal partnering.

## 2. Status of diseases at the livestock–wildlife interface in the United States

In the United States, there are currently 86 avian, ruminant, swine, and lagomorph diseases reportable to the OIE. Of those, 53 are listed as present in the United States (Anonymous, 2011b). Our review of these pathogens identified 42 (79%) which have a potential wildlife component associated with the transmission, maintenance, or life cycle of the pathogen, and 21 (40%) are known to be zoonotic (Tables 1 and 2). Of these 42 pathogens, 12 (29%) have an arthropod vector involved in the transmission while the remaining 71% involve direct or indirect transmission. Sixteen (38%) of the diseases present in the United States affect multiple species of livestock, all of these have a wildlife

component, and 81% are zoonotic. Of the OIE reportable diseases affecting cattle, 6 out of 8 are present in the United States and have a wildlife component; 3 have zoonotic potential. A wildlife component has been identified for 10 out of 11 (91%) OIE reportable avian diseases with 3 of these recognized as zoonotic.

Of the avian, ruminant, and swine diseases, 21 are currently actively managed in the United States with 11 of these having a Federal eradication or control program (Table 3). Thirteen (62%) of these actively managed diseases have a wildlife component and at least 6 (bovine tuberculosis, paratuberculosis, brucellosis, avian influenza, rabies, and cattle fever tick [vector control]) have a wildlife reservoir that is a recognized impediment to eradication due to continued spillover to domestic populations. Of these diseases, 2 (bovine tuberculosis and brucellosis) have foci of infection in wildlife as a result of spillover from livestock—further complicating eradication programs.

Specific estimates of direct and indirect costs to livestock and recreational hunting industries, and to governmental agencies resulting from pathogen transmission at the livestock–wildlife interface, are elusive; however, some estimates are available for specific diseases. Reestablishment of bovine *Babesia* sp. to its historic range in North America via adaptation of *Babesia* sp. vectors to white-tailed deer would cost approximately \$1.2 billion to the cattle industry (Anderson et al., 2010). In Michigan, the loss of bovine tuberculosis accredited-free status is estimated to result in total agriculture and livestock losses of approximately \$12 million per year (Horan and Wolf, 2005). Furthermore, the Michigan Department of Natural Resources spent an estimated \$15 million on defining the extent of the disease in wildlife and initial management steps alone (O'Brien et al., 2006) and to date has spent an estimated \$23 million (O'Brien et al., 2011) on control, surveillance, and management of the disease.

Rabies—an important zoonotic disease with significant public health, agricultural, and ecological impacts—is known to impose a financial burden on countries around the world. The Centers for Disease Control and Prevention estimates that the United States spends in excess of \$300 million annually on rabies prevention, detection, and control (Anonymous, 2011a) with more than \$130 million spent on wildlife vaccination alone (Stern et al., 2009). Avian influenza, which has a well-documented wild waterfowl reservoir, continues to plague the domestic poultry

**Table 2**

OIE reportable livestock diseases present in the United States with a known wildlife component.

Disease	Affected livestock	Wildlife host	Citation	Transmission mode
Anthrax	Ruminants <sup>c</sup> , horses <sup>c-sc</sup> , swine <sup>c-sc</sup>	All mammals susceptible, environmental reservoirs	(Hugh-Jones and De Vos, 2002)	Direct
Aujeszky's disease	Domestic swine <sup>c</sup> , cattle <sup>c</sup> , sheep <sup>c</sup> , goats <sup>c</sup> , horses <sup>o</sup>	Feral Swine <sup>f</sup> , wild mammals <sup>s</sup>	(Hahn et al., 1997; Corn et al., 2004; Kirkpatrick et al., 1980; Spickler et al., 2010)	Direct, indirect
Avian chlamydiosis	Ducks <sup>c</sup> , turkeys <sup>c</sup> , chickens <sup>o</sup>	Gulls <sup>f</sup> , ducks <sup>f</sup> , herons <sup>f</sup> , egrets <sup>f</sup> , pigeons <sup>f</sup> , blackbirds <sup>f</sup> , grackles <sup>f</sup> , house sparrows <sup>f</sup> , killdeer <sup>f</sup> , raptors <sup>s</sup> , shorebirds <sup>s</sup> , migratory birds <sup>s</sup>	(Vanrompay et al., 1995; Thomas et al., 2007; Spickler et al., 2010)	Direct, indirect
Avian infectious bronchitis	Chickens <sup>c</sup>	Wild birds <sup>u</sup>	(Jonassen et al., 2005; Muradrasoli et al., 2010)	Direct, indirect
Avian influenza	Chickens <sup>c</sup> , turkeys <sup>c</sup> , ducks <sup>c</sup> , geese <sup>c</sup> , game birds <sup>c</sup>	Numerous wild birds <sup>f</sup> , many mammals susceptible <sup>a</sup>	(Cook, 2005; Olsen et al., 2006)	Direct, indirect
Avian mycoplasmosis ( <i>Mycoplasma gallisepticum</i> , <i>Mycoplasma synoviae</i> )	Chickens <sup>c</sup> , turkeys <sup>c</sup> , game birds <sup>c</sup> , ducks <sup>c</sup> , geese <sup>c</sup>	House finches <sup>a</sup> , American goldfinches <sup>a</sup> , purple finches <sup>a</sup> , eastern tufted titmice <sup>a</sup> , pine grosbeaks <sup>a</sup> , evening grosbeaks <sup>a</sup> , others <sup>a</sup>	(Thomas et al., 2007; Luttrell et al., 2001; Ley et al., 1996; Spickler et al., 2010)	Direct, indirect
Bluetongue	Sheep <sup>c</sup> , goats <sup>c</sup> , cattle <sup>sc</sup>	Wild ovine species <sup>a</sup> , cervids <sup>a</sup> , water buffalo <sup>a</sup> , pronghorn <sup>a</sup> ,	(Williams and Barker, 2001; Stallknecht et al., 1991; Robinson et al., 1967; Spickler et al., 2010; Hoff and Trainer, 1978)	Arthropod-borne
Bovine anaplasmosis	Cattle <sup>c</sup>	Cervids <sup>f</sup>	(Woldehiwet, 2010; Kuttler, 1984)	Arthropod-borne
Bovine babesiosis <sup>a</sup>	Cattle <sup>c</sup>	White-tailed deer <sup>s</sup> , water buffalo <sup>s</sup> , African buffalo <sup>s</sup> , reindeer <sup>s</sup>	(Spickler et al., 2010; Schoelkopf et al., 2005; Cantu-C et al., 2009)	Arthropod-borne
Bovine genital campylobacteriosis	Cattle <sup>c</sup>	Numerous <sup>f</sup>	(Williams and Barker, 2001)	Direct, indirect
Bovine tuberculosis	Primarily cattle <sup>c</sup>	White-tailed deer <sup>f</sup> , feral swine <sup>f</sup> , numerous spillover hosts	(O'Brien et al., 2006; Buddle et al., 2000; Williams and Barker, 2001; Spickler et al., 2010)	Direct, indirect
Bovine viral diarrhea	Cattle <sup>c</sup> , camelids <sup>c</sup> , bison <sup>o</sup>	White-tailed deer <sup>f</sup> , mule deer <sup>s</sup> , caribou <sup>s</sup> , pronghorn <sup>s</sup> , elk <sup>s</sup> , moose <sup>s</sup> , bison <sup>s</sup>	(Passler et al., 2007; Zarnke, 1983; Williams and Barker, 2001; Duncan et al., 2008)	Direct, indirect
Brucellosis ( <i>Brucella abortus</i> )	Cattle <sup>c</sup> , sheep <sup>c</sup> , horses <sup>o</sup>	Bison <sup>f</sup> , water buffalo <sup>f</sup> , elk <sup>f</sup> , feral swine <sup>u</sup> , numerous spillover hosts	(Olsen, 2010b; Zarnke, 1983; Williams and Barker, 2001; Spickler et al., 2010)	Direct, indirect
Brucellosis ( <i>Brucella ovis</i> ) <sup>**</sup>	Sheep <sup>c</sup>	Red deer <sup>a</sup>	(Ridler and West, 2002; Spickler et al., 2010)	Direct, indirect
Brucellosis ( <i>Brucella suis</i> )	Domestic swine <sup>c</sup> , horses <sup>o</sup>	Feral swine <sup>f</sup> , European hare <sup>f</sup> , caribou <sup>f</sup> , reindeer <sup>f</sup> , rodents <sup>f</sup> , numerous spillover hosts	(Galindo et al., 2010; Olsen, 2010b; Williams and Barker, 2001; Corn et al., 2009; Spickler et al., 2010)	Direct, indirect
Contagious agalactia	Sheep <sup>c</sup> , goats <sup>c</sup> , cattle <sup>o</sup> , camelids <sup>o</sup>	Spanish ibex <sup>u</sup> , roe deer <sup>u</sup> , red deer <sup>u</sup>	(Verbisck-Bucker et al., 2008), (Spickler et al., 2010)	Direct, indirect
Echinococcosis/hydatidosis	Sheep <sup>c</sup> , cattle <sup>c</sup>	Carnivore sp. including canids <sup>f</sup> , and felids <sup>f</sup> , cervids <sup>u</sup> , rodents <sup>u</sup> , lagomorphs <sup>u</sup> , muskrats <sup>u</sup>	(Leiby et al., 1970; Storandt et al., 2002; Storandt and Kazacos, 1993; Thompson et al., 2006; Spickler et al., 2010)	Indirect
Epizootic hemorrhagic disease	Cattle <sup>c-sc</sup> , sheep <sup>sc</sup> , o	White-tailed deer <sup>f</sup> , mule deer <sup>s</sup> , pronghorn <sup>s</sup> , other wild ruminant species <sup>s</sup>	(Anonymous, 2006)	Arthropod-borne

Table 2 (Continued)

Disease	Affected livestock	Wildlife host	Citation	Transmission mode
Equine encephalomyelitis (Eastern and Western)	Equids <sup>c</sup> , occasional reports in cattle, sheep, camelids and pigs	Birds <sup>f</sup> , rodents <sup>f</sup> , jackrabbits <sup>f</sup> , white-tailed deer <sup>s</sup> , numerous species <sup>s</sup>	(Reisen et al., 2000; Emord and Morris, 1984; Komar et al., 1999; Tate et al., 2005; Schmitt et al., 2007; Spickler et al., 2010)	Arthropod-borne
Equine influenza	Equids <sup>c</sup>	Wild birds <sup>f</sup> , numerous other species <sup>s</sup>	(Munster et al., 2007)	Direct, indirect
Equine piroplasmosis	Equids <sup>c</sup>	Uncertain	(Kellogg et al., 1971; Spickler et al., 2010)	Arthropod-borne
Equine rhinopneumonitis	Equids <sup>c</sup>	Numerous species <sup>u</sup>	(Kinyili and Thorsen, 1979)	Direct, indirect
Fowl cholera	Poultry <sup>c</sup>	Wild birds <sup>f</sup>	(Thomas et al., 2007; Petersen et al., 2001; Botzler, 1991; Blanchong et al., 2006)	Direct, indirect
Infectious bovine rhinotracheitis/infectious pustularvulvovaginitis	Cattle <sup>c</sup>	Several implicated <sup>u</sup>	(Zarnke, 1983; Kinyili and Thorsen, 1979)	Direct, indirect
Infectious bursal disease	Chickens <sup>c</sup> , turkeys <sup>sc</sup> , ducks <sup>sc</sup> , guinea fowl <sup>sc</sup> , ostriches <sup>sc</sup>	Game birds <sup>f</sup> , Waterfowl <sup>f</sup>	(Thomas et al., 2007; Candelora et al., 2010; Anonymous, 2008)	Direct, indirect
Leptospirosis	Cattle <sup>c-sc</sup> , sheep <sup>c-sc</sup> , goats <sup>c-sc</sup> , pigs <sup>c-sc</sup> , horses <sup>c-sc</sup> , all mammals <sup>c-sc</sup>	Rodents <sup>f</sup> , raccoons <sup>f</sup> , skunks <sup>f</sup> , opossum <sup>f</sup> , nutria <sup>f</sup> , others <sup>s</sup>	(Zarnke, 1983; Williams and Barker, 2001)	Direct, indirect
Maedi-visna	Sheep <sup>c</sup> , goats <sup>c</sup>	Wild ruminants <sup>u</sup>	(Valas et al., 1997; Spickler et al., 2010)	Direct, indirect is rare
Marek's disease	Chickens <sup>c</sup> , Turkeys <sup>o</sup> , Quail <sup>o</sup>	Galliformes <sup>f</sup>	(Cho and Kenzy, 1975)	Direct, indirect
Myxomatosis	Lagomorphs <sup>c</sup>	Lagomorphs <sup>f</sup>	(Williams and Barker, 2001; Dwyer et al., 1990)	Arthropod-borne
Newcastle disease <sup>***</sup>	Chickens <sup>c</sup> , turkeys <sup>c-sc</sup> , game birds <sup>c-sc</sup> , ducks <sup>sc</sup> , geese <sup>sc</sup> , pigeons <sup>c-sc</sup>	Wild birds <sup>f</sup> , exotic birds <sup>f</sup>	(Thomas et al., 2007; Brugh and Beard, 1984; Seal et al., 2000; Clubb and Hinsch, 1982; Spickler et al., 2010)	Direct, indirect
Paratuberculosis	Cattle <sup>c</sup> , sheep <sup>c</sup> , goats <sup>c</sup>	Wild ruminants <sup>f</sup> , rabbits <sup>f</sup> , numerous wild mammals <sup>u</sup>	(Williams and Barker, 2001; Corn et al., 2005; Greig et al., 1997; Spickler et al., 2010; Ayele et al., 2001)	Direct, indirect
Porcine reproductive and respiratory syndrome	Swine <sup>c</sup>	Feral swine <sup>f</sup>	(Williams and Barker, 2001; Corn et al., 2009)	Direct, indirect
Pullorum disease	Chickens <sup>c</sup> , turkeys <sup>c</sup> , pheasants <sup>c</sup> , other poultry <sup>o</sup>	Waterfowl <sup>f</sup> , numerous wild bird species <sup>u</sup>	(Thomas et al., 2007; Shivaprasad, 2000)	Direct, indirect
Q fever	Cattle <sup>c-sc</sup> , sheep <sup>c-sc</sup> , goats <sup>c-sc</sup>	Numerous species including mammals <sup>f</sup> , birds <sup>f</sup> , and reptiles <sup>f</sup>	(Zarnke, 1983; Spickler et al., 2010)	Direct, indirect, arthropod borne
Rabbit hemorrhagic disease	Domestic <i>Oryctolagusuniculus</i> <sup>c</sup>	Wild <i>Oryctolagusuniculus</i> <sup>c</sup>	(Williams and Barker, 2001; Spickler et al., 2010)	Direct, indirect
Rabies	All mammals susceptible	Raccoons <sup>f</sup> , coyotes <sup>f</sup> , fox <sup>f</sup> , bats <sup>f</sup> , skunks <sup>f</sup> , mongoose <sup>f</sup> , bobcats <sup>u</sup> , others <sup>s</sup>	(Sterner and Smith, 2006; Krebs et al., 2003; Spickler et al., 2010)	Direct
Transmissible gastroenteritis	Swine <sup>c</sup>	Feral swine <sup>f</sup>	(Williams and Barker, 2001)	Direct, indirect
Trichinellosis	Swine <sup>c-sc</sup>	Carnivores <sup>f</sup> , feral swine <sup>a</sup> , rodents <sup>a</sup> , bears <sup>a</sup> , others <sup>a</sup>	(Murrell et al., 1987)	Direct, indirect
Tularemia	Sheep <sup>c</sup> , horses <sup>o</sup> , pigs <sup>o</sup>	Lagomorphs <sup>f</sup> , muskrats <sup>f</sup> , rodents <sup>f</sup> , mink <sup>s</sup> , prairie dogs <sup>s</sup> , others <sup>s</sup>	(Al Dahouk et al., 2005; Williams and Barker, 2001; Spickler et al., 2010; Jellison and Parker, 1945; Morner, 1992)	Direct, indirect, arthropod-borne
Vesicular stomatitis	Cattle <sup>c</sup> , swine <sup>c</sup> , equids <sup>c</sup> , camelids <sup>sc</sup> , sheep <sup>sc</sup> , goats <sup>sc</sup>	Numerous wildlife species susceptible including mammals and birds, reservoir hosts unknown	(Williams and Barker, 2001; Spickler et al., 2010; Webb et al., 1987)	Direct, indirect, arthropod-borne
West Nile	Equids <sup>c</sup> , domestic geese <sup>c</sup>	Wild birds <sup>f</sup> , other species <sup>u</sup>	(Daszak et al., 2001; Thomas et al., 2007; Spickler et al., 2010)	Arthropod-borne

Table 2 (Continued)

Disease	Affected livestock	Wildlife host	Citation	Transmission mode
Diseases of importance that are not OIE listed. Chronic Wasting Disease	Domestic cervids <sup>c</sup>	Wild cervids <sup>f</sup>	(Williams and Barker, 2001; Williams et al., 2002; Baeten et al., 2007; Williams, 2005; Hamir et al., 2001)	Direct, indirect
Malignant Catarrhal Fever	Cattle <sup>c</sup> , bison <sup>c</sup> , swine <sup>c</sup> , sheep <sup>sc</sup> , goats <sup>sc</sup>	Wildebeest <sup>f</sup> , oryx <sup>s</sup> , ibex <sup>s</sup> , cervids <sup>s</sup> , wild ovine and caprinespecies <sup>f</sup>	(Williams and Barker, 2001; Spickler et al., 2010)	Direct
Plague	Domestic mammals <sup>c-sc</sup>	Prairie dogs <sup>f</sup> , chipmunks <sup>f</sup> , ground <sup>f</sup> squirrels <sup>f</sup> , other rodents <sup>f</sup> , carnivores <sup>s</sup> , numerous other species <sup>a</sup>	(Salkeld and Stapp, 2006)	Direct, indirect, arthropod-borne
Trichomoniasis ( <i>Trichomonasgallinae</i> )	Poultry <sup>c</sup> , doves <sup>c</sup> , pigeons <sup>c</sup>	Pigeons <sup>f</sup> , doves <sup>f</sup> , falcons <sup>a</sup> , hawks <sup>a</sup> , others <sup>a</sup>	(Thomas et al., 2007)	Direct, indirect

<sup>\*</sup> Bovine babesiosis is not present in cattle in the United States however the causative agent has been reported in wildlife and a vector eradication program exists.

<sup>\*\*</sup> *B. ovis* has been found to cause poor semen quality in red deer but abortions have not been reported. The role potential role of red deer is still in doubt.

<sup>\*\*\*</sup> The United States is considered free from new castle disease in poultry however new castle disease is present in free ranging species and is included here for completeness.

<sup>c</sup> = clinical

<sup>sc</sup> = subclinical

<sup>c-sc</sup> = may be clinical or subclinical

<sup>o</sup> = occasional reports

<sup>f</sup> = reservoir

<sup>s</sup> = spillover

<sup>a</sup> = affected species (not a true reservoir, nor a spillover host)

<sup>u</sup> = uncertain

Table 3

Diseases actively managed in the United States and corresponding wildlife component.

Disease	National or agency program	Primary domestic species	Wildlife component
Avian influenza	Control	Poultry	Yes
Bluetongue		Multiple	Yes (Arthropod-borne)
Bovine spongiform encephalopathy		Cattle	
Bovine Tuberculosis	Eradication	Multiple	Yes
Brucellosis ( <i>Brucella abortus</i> )	Eradication	Multiple	Yes
Brucellosis ( <i>Brucella suis</i> )	Eradication	Multiple	Yes
Cattle Fever Tick (vector only)	Eradication	Cattle	Yes (Arthropod-borne)
Chronic wasting disease	Eradication	Cervids	Yes
Classical swine fever		Swine	Yes
Contagious equine metritis		Equine	
Equine herpesvirus		Equine	
Equine infectious anemia	Eradication	Equine	
Equine piroplasmiasis		Equine	Uncertain (Arthropod-borne)
Equine viral arteritis		Equine	
Paratuberculosis (Johnes)	Control	Multiple	Yes (Arthropod-borne)
Pseudorabies (Aujeszky's disease)	Eradication	Multiple	Yes
Rabies	Eradication	Multiple	Yes
Scrapie	Eradication	Sheep, Goats	
Vesicular stomatitis		Multiple	Yes (Arthropod-borne)
West Nile		Multiple	Yes (Arthropod-borne)

industry in the United States with estimated outbreak associated losses ranging from \$5 to \$212 million (Capua and Alexander, 2004; Saif and Barnes, 2008). Estimated impacts to the United States in the event of an epizootic avian influenza pandemic are at least \$71 billion (Meltzer et al., 1999; Arnold et al., 2006). Other livestock diseases with wildlife reservoirs including brucellosis, bovine viral diarrhea, and several poultry diseases are associated with significant losses in livestock production.

### 3. Structured approach to livestock–wildlife disease management

Concepts for integrated and adaptive management systems for EIDs at the livestock–wildlife interface are proposed by multiple authors (Thirgood, 2009; Wasserberg et al., 2009). Many countries, have developed passive and active surveillance systems for EID events in wildlife. Some of the earliest systems were developed in Denmark

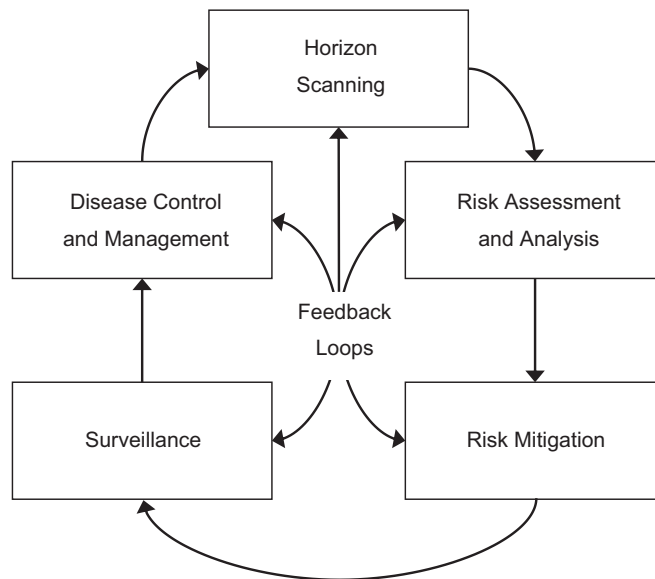


Fig. 2. Conceptual model of adaptive disease management at the livestock–wildlife interface.

(1930s) and Sweden (1940s) however surveillance systems are established in Norway, Finland, France, United Kingdom, Italy, Spain, Switzerland, and the United States (Morner et al., 2002; Pedersen et al., 2012). The United Kingdom (Sainsbury et al., 2001; Lysons et al., 2007; Hartley and Gill, 2010; Hartley and Lysons, 2011) has developed a program to implement integrated risk management and EID monitoring systems for wildlife. These nascent emerging systems have common themes, which may be adaptable to the United States. In the existing literature, five interdependent aspects of disease management are suggested as being necessary for successfully addressing disease issues at the livestock–wildlife interface: (1) horizon scanning (issue identification); (2) risk analysis and assessment; (3) risk mitigation; (4) surveillance and monitoring; and (5) disease control and management. These components, described as integrating sequentially with feedback loops, incorporate learning about the system. As information about the disease agent is improved, management is adapted thereby improving actions performed in the other components (Fig. 2). This process of adaptive management has been well described in the ecological and wildlife management literature (Kendall, 2001; McCarthy and Possingham, 2007), but concepts related to adaptive management have only recently been proposed as a method for managing disease systems (Thirgood, 2009; Wasserberg et al., 2009).

#### 4. Horizon scanning

Rapid identification of new and emerging infectious diseases (horizon scanning) in wildlife is critical to protecting animal agriculture and human health. There is mounting concern over the zoonotic potential, and subsequent wide-ranging socioeconomic impacts, associated with wildlife-borne EIDs (Jones et al., 2008). Recent examples of EIDs emerging from wildlife include Nipah virus in swine

(Chua et al., 2000), severe acute respiratory syndrome (SARS) in humans (Riley et al., 2003), and H5N1 HPAI in domestic poultry, wild birds, and humans (Ferguson et al., 2004). In addition, new issues continue to emerge with well-documented disease systems, such as bovine tuberculosis and brucellosis influencing agricultural systems and wildlife management in North America (Olsen, 2010a; O'Brien et al., 2011). Other EID's of concern to agriculture are certain to emerge in the future, some of which may disperse rapidly across broad geographic scales (Cleaveland et al., 2001; Siembieda et al., 2011). The risks of existing and new EID's to disperse rapidly highlight the need for robust systems for early identification of pathogens, which may have important health, social, economic, or other management consequences.

#### 5. Risk analysis

Risk analysis is an often broadly used term referring to risk characterization, risk communication, and risk management, which provides support for decision making and policy in the face of uncertainty (Suter, 2007). In the case of animal disease, risk analysis is an important tool used to identify and characterize the potential risks posed by implementation of policy or by specific events such as importation of livestock. Risk analyses form the foundation from which animal health policy is established. However, for diseases at the livestock–wildlife interface, quantitative risk assessments are often difficult. Challenges for conducting quantitative risk assessments often result from incomplete information related to the disease status of wildlife or limited understanding of the potential contact between wildlife and livestock leading to pathogen transmission. In addition accurate quantitative data describing the spatial distribution, movement, population structure, and population density are typically unavailable limiting



inference to the population or understanding population level risk factors.

Data quantifying important epidemiologic parameters necessary for describing disease risk such as contact rates, disease status of wildlife, wildlife population size, or biological process of the pathogen in wildlife are often unstudied or poorly understood. Risk assessments often assess the risk of pathogen transmission from wildlife to livestock (Daniels et al., 2003). However, for many diseases of livestock in North America (e.g. bovine tuberculosis, brucellosis) the initial transmission event is from livestock to wildlife, which in some cases results in the establishment of a wildlife reservoir for the pathogen posing continued risks to livestock (Tessaro, 1986; Sweeney and Miller, 2010). For these reasons the most successful and useful risk analyses consider the bi-directional nature of transmission and address questions of risk using statistical methods to explicitly incorporate uncertainty. In addition, studies that estimate contact between livestock and wildlife to understand potential for pathogen transmission are needed.

## 6. Risk mitigation

Mitigating transmission risk between livestock and wildlife has received considerable attention (VerCauteren et al., 2006b, 2010; Wasserberg et al., 2009). The ability to eliminate livestock pathogens from North American wildlife populations has been rare and when successful required extensive culling of wildlife. An example is the eradication of foot-and-mouth disease from the United States in 1925 which required the culling of 22,000 deer from the Stanislaus National Forest in California (Williams and Barker, 2001). Wildlife removal strategies can have unintended consequence, which was exemplified in the United Kingdom where wildlife behavior was changed as a result of culling increasing the risk of bovine tuberculosis transmission to cattle (Woodroffe et al., 2009). In addition protected wildlife can complicate control or eradication efforts to control disease (Meyer and Meagher, 1995). Eradication efforts requiring the culling of large numbers of wildlife are likely untenable in the United States today, thus preventing establishment of livestock diseases in wildlife populations is a central pillar of long-term risk mitigation strategies.

Implementing risk mitigations may offer the greatest potential for reducing economic and social impacts resulting from shared diseases. This often involves modifying animal husbandry practices to reduce contact between livestock and wildlife—including modified livestock housing, which reduces contact with peri-domestic wildlife or altered feeding practices, which reduces available forage for wildlife. Other risk mitigations include tools that prevent direct contact between wildlife such as frightening devices, fencing, or livestock protection dogs (VerCauteren et al., 2005, 2006b, 2010). However, the development and implementation of these tools comes with their own set of challenges. Successful implementation often includes changing social behaviors of livestock producers and developing new tools to manage risk mitigation which are cost effective and efficacious over the long term. Other risk mitigations may include identifying and reducing or

eliminating risky management practices—such as allowing contact between livestock and wildlife which may foster the emergence of new pathogens in the United States. These may include translocation of wildlife or domestic and international wildlife trade.

## 7. Surveillance and monitoring

The need to develop comprehensive surveillance systems that integrate livestock, wildlife, and human components has been suggested (Mörner et al., 2002). Robust surveillance systems in wildlife and at the livestock–wildlife interface to provide early detection of newly emerging EIDs or spillover and spillback of pathogens between livestock and wildlife is essential. Developing a comprehensive national monitoring system for EIDs in wildlife that is logistically and fiscally sustainable could yield economic benefits for livestock health management as a whole by reducing indemnity costs associated with spillover of disease from wildlife to livestock or by helping prevent spillover from livestock to wildlife through early detection. The objectives of such a system could be enhanced by close integration with existing livestock and wildlife health programs to guide “when”, “where”, and “how” surveillance is conducted. In addition, existing programs would benefit from closer working relationships between wildlife biologists, ecologists, epidemiologists, and veterinarians to improve efforts focused on reducing pathogen transmission (Boadella et al., 2011). One obstacle to developing long-term, comprehensive surveillance efforts at the livestock–wildlife interface is inconsistent funding for these activities (Leighton et al., 1997; Stitt et al., 2007). Funding has typically been in response to emergency directives (e.g. HPAI H5N1 surveillance) and focused for a short period until the threat is perceived to no longer exist. This has, predictably, generated problems for developing a comprehensive national infrastructure that can be maintained over the long-term. In addition, there are disease systems that have plagued agriculture for decades, such as bovine tuberculosis, that do not obtain sufficient levels of funding to fully address risks for introduction into new wildlife hosts such as feral swine (Sweeney and Miller, 2010). Another challenge faced by wildlife surveillance systems is that they often rely on hunter observations and reports, which are focused on game species. This increases the difficulty of identifying emergence of disease in non-game species. Finally, due to challenges associated with working across agency departmental boundaries, such as reduced communication, differing priorities, perceived competition in missions, and cultural differences wildlife surveillance efforts often remain less than fully coordinated which reduces their overall benefit.

## 8. Disease control and management

Once a pathogen is identified at the livestock–wildlife interface, active management and control of the disease agent is often the only method for reducing impacts to human health, agriculture, and recreational hunting industries (Boadella et al., 2011). Integrated strategies that bring

wildlife, human, and agricultural agencies together offer the greatest opportunity for success. Management of diseases at the livestock–wildlife interface often requires long-term engagement using a combination of altered livestock husbandry practices, active disease suppression in wildlife, and prevention of transmission using mitigation techniques.

## 9. Inter-agency and cross-sector collaborations and partnership

If surveillance and risk management activities at the livestock–wildlife interface are to be successful, we must recognize the complex nature of current and emerging diseases. These diseases can involve different health jurisdictions, socio-economic dimensions, and a wide range of stakeholders (i.e. livestock industry, conservation organizations, recreational hunters, etc.). We must promote strategic collaboration and partnerships across various disciplines, sectors, departments, ministries, institutions, and organizations at country, regional, and international levels (Binder et al., 1999; FAO et al., 2008). With the recent focus on “One Health”, which recognizes that human, animal (both domestic and wild) and ecosystems are tightly linked, successful management of disease requires an integrated approach where efforts are focused in concert across these domains (King et al., 2008; Welburn, 2011). In response to the One Health focus several countries have developed specific plans to address wildlife health as it relates to human and domestic animal health (Sainsbury et al., 2001; Hartley and Lysons, 2011). However, obstacles still remain in developing robust systems which integrate across the domestic, wild animal, and human domains.

In most countries, sector-specific institutions have clear roles, responsibilities, and budgets—but mechanisms for cross-sector collaboration typically do not exist. Developing collaborations often proves difficult even mandated from the highest levels of government, as exemplified by continued outbreaks of highly pathogenic avian influenza in several countries (FAO et al., 2008). The United States suffers from similar limitations, due in part to the bicameral regulatory and legal authority for oversight of livestock and wildlife. States have clear ownership of wildlife; Federal regulatory authorities do not always extend to control disease in livestock to manage the disease in wildlife. Thus, the effective control of disease incursions from wildlife to livestock requires State and Federal livestock management agencies to foster positive working relationships with wildlife agencies. Unfortunately, such relationships frequently have not been developed resulting in a decision making process on livestock disease management in which wildlife appear as an afterthought, when often they are integral to disease maintenance and spread. Involving all relevant stakeholders (i.e. livestock industry, wildlife conservation groups, wildlife health authorities, livestock health authorities, etc.) in the development of regional or ecosystem-level livestock disease management planning, from the beginning of the process, increases the likelihood of success (Loomis, 2002).

One example of ongoing challenges animal health authorities face is found in the management of brucellosis

in the Yellowstone ecosystem. Controversy has surrounded the management of brucellosis in the bison and elk within the ecosystem. These issues have often pitted Federal, State, agricultural, and wildlife agencies against one another. Several have noted that one of the most important constraints to managing brucellosis in Yellowstone is jurisdictional inertia, or the unwillingness of agencies to relinquish their existing domains of territorial control (Lavigne, 2002; McBeth and Shanahan, 2004). This example underscores the need for wildlife, human, and agricultural agencies to develop strong working relationships prior to emergence of disease. Integrated approaches to prevention before observing outbreaks in both wildlife and livestock may offer an opportunity for agencies to foster working relationships prior to a crisis.

Development of clear mechanisms and agreements will enhance collaboration and interaction at all levels and should include incorporation of the roles and mandates of the various institutions and agencies involved. Often the agreements and working relationships that are established occur only at the highest levels of the organization resulting in little benefit to those working to implement program objectives. Opportunities for professional interactions and working relationships needs to be created and supported at the field level in addition to the administrative level (FAO et al., 2008).

## 10. Opportunities for success

Historically, integrated cross-disciplinary collaboration between livestock and wildlife agencies has been a challenge. However, many programs managing animal health diseases could benefit significantly from increased communication and collaborations that combine program objectives and activities across agency jurisdictions. While challenging from a political and cultural perspective, the outcome could be beneficial and would enhance the ability to quickly identify and respond to new and emerging disease issues. Integrating State and Federal livestock and wildlife agencies into the disease program planning process could reap future rewards.

Below we illustrate the potential for cross-sector collaboration using two disease eradication programs—Cattle fever tick eradication and bovine tuberculosis eradication—facing challenges presented by the livestock–wildlife interface. Other disease eradication and management programs that address issues associated with the diseases and pathogens listed in Table 3 would also likely benefit from increased collaboration across livestock, wildlife, and human agencies at both State and Federal levels.

## 11. Discussion

### 11.1. Cattle fever tick eradication program

Bovine babesiosis, caused by hematoparasite of the genus *Babesia*, is globally among the most significant tick-borne disease of cattle (White et al., 2003; Martinez et al., 2006). In North America, the most important vectors of bovine babesiosis are *Rhipicephalus*

*microplus* and *R. annulatus*—collectively known as cattle fever ticks. Cattle fever ticks were extirpated from the United States in 1960 after a nearly 60-year eradication campaign (Graham and Hourrigan, 1977; Bram et al., 2002). The eradication campaign exploited the perceived narrow host range of cattle fever ticks in combination with highly effective and now banned acaricides, which allowed the program to focus almost exclusively on the treatment of cattle (Bram et al., 2002). Reestablishment of cattle fever ticks and bovine *Babesia* to their historic range in North America is estimated to cost \$1.2 billion in control efforts and cattle production losses (Anderson et al., 2010). As a result, animal health authorities and livestock producers consider mitigating this risk a priority.

In recent years, there have been increasing infestations of cattle fever ticks on cattle along the Texas–Mexico border (de León Adalberto et al., 2010). Historically considered to be highly host specific for cattle, there is increasing evidence that white-tailed deer and other ungulates are suitable hosts for cattle fever ticks (Pound et al., 2010) with infested deer found in locations absent of cattle (Cantu et al., 2007). In Texas, cattle fever ticks have been recovered from free-ranging and captive-exotic ungulates including axis deer, fallow deer, elk, red deer, aoudad sheep, and nilgai antelope (Mertins et al., 1992). Due to the potential ineffectiveness of treating tick infestations in cattle with currently approved methods, such as mandatory removal of cattle from affected pastures for a period of time (i.e. pasture vacation) and treatment of cattle with acaricides the treatment of white-tailed deer and other wildlife has become necessary.

A recent study indicates that cattle fever ticks have a high degree of genetic fluidity, which may allow them to adapt to new host species and therefore provide a potential pathway for reestablishment in the United States via wildlife hosts (De Meeus et al., 2010). White-tailed deer are also increasingly being recognized as a potential reservoir for the *Babesia* species (*B. bigemina*, *B. divergens*, and *B. bovis*) which cause clinical disease in cattle (de León Adalberto et al., 2010). Surveys for *Babesia* in northern Mexico and Texas have identified molecular and serological evidence for the presence of *B. bigemina* and *B. bovis* in white-tailed deer and in nilgai antelope populations (Cantu et al., 2007; Cardenas-Canales et al., 2011). These changes in the host–pathogen system, and gaps in the understanding of cattle fever tick ecology and the host range of *Babesia*, require the formulation of more effective control strategies that include both wildlife and livestock.

To effectively address these challenges, State and Federal Agencies representing both livestock and wildlife authorities need to partner to develop policy that integrates surveillance and risk mitigations across both cattle and wildlife populations. An historic limitation of the program has been the nearly exclusive focus on controlling cattle fever ticks on cattle (León et al., 2010). Recently the program has begun to deploy mitigations to control ticks on wildlife; however, the program is limited by a lack of operational tools to mitigate infestations on wildlife and a regulatory framework that would integrate management of the disease across wildlife and livestock authorities. While challenging, this offers an exciting

opportunity to develop effective strategies and methods to address surveillance at the livestock–wildlife interface and to develop new mitigations that reduce the risk of infestation.

### 11.2. Bovine tuberculosis eradication program

Bovine tuberculosis (bTB), identified in nine geographically distinct wildlife populations in North America and Hawaii, is endemic in at least four populations, including members of the Bovidae, Cervidae, and Suidae families (Sweeney and Miller, 2010). The emergence of bTB in North American wildlife poses a serious and growing risk for livestock and human health and for the recreational hunting industry. Experience in many countries, including the United States and Canada, has shown that while bTB can be controlled when restricted to livestock species, it is almost impossible to eradicate this disease once it has spread into ecosystems with free-ranging maintenance hosts. Recent epidemiological models suggest that once bTB is introduced, the probability of becoming established in a wildlife population once introduced is at least 10% (Ramsey et al., 2011). Spillover into wildlife—and establishment of new foci of infection in wildlife—would be costly to the cattle industry and animal health authorities. In addition, new foci of wildlife infection would complicate eradication efforts. Therefore, preventing spillover of *Mycobacterium bovis* into wildlife may be the most effective way to mitigate economic costs of bTB.

Historically, wildlife control efforts for bTB have focused solely on potential spillover into wild cervid species. However, *M. bovis* has been isolated from free-ranging swine (i.e. wild boar and feral swine) in at least 15 countries (Letts, 1964; Corner et al., 1981; Essey et al., 1981; O'Reilly and Daborn, 1995; Aranaz et al., 1996; Serraino et al., 1999; Palmer, 2007). New evidence from Mediterranean ecosystems supports the role of wild swine as maintenance hosts of bTB—sustaining infection and transmitting the pathogen to other species (Aranaz et al., 1996; Naranjo et al., 2008). Circumstances favoring bTB transmission between wildlife and livestock in the Mediterranean include artificial increases in wild game populations stimulated by a robust hunting industry, feeding and baiting of wildlife, and intensive cattle grazing in proximity to wild swine (Hermoso de Mendoza et al., 2006). All of these characteristics likely apply to conditions in North America. Particularly worrisome is the recent appearance of feral swine in the state of Michigan where the potential exists for interaction with bTB-infected white-tailed deer and cattle. Regions of the southern United States also pose a risk where high densities of feral swine, an established hunting industry, significant baiting and feeding of wildlife, and introductions of bTB infected cattle from Mexico continue to occur (Sweeney and Miller, 2010). Furthermore recent evidence indicates that *M. bovis* may be present in free ranging white-tailed deer in northern Mexico. One study report the presence of *M. tuberculosis* complex identified using amplification of DNA from a tissue by PCR (Barrios-García et al., 2012). The authors also report histopathology consistent with *M. bovis* infection observed in white-tailed deer. Another study reported the

frequent detection of antibodies against mycobacterium antigens in a cross-sectional survey of white-tailed deer in Northern Mexico (Medrano et al., 2012).

While the risks posed by wildlife have been recognized, current investigations and response to potential spillover events from cattle to wildlife (cervid or swine), where disease is exceedingly more difficult to control or eradicate is inconsistently managed. Few standards are in existence which establish best practices for investigating potential spillover into wildlife hosts. Developing national policies and working relationships across agencies responsible for domestic and wildlife health at the State and Federal level would have long-term benefits for preventing the risk of introduction of bTB into new wildlife host populations.

## 12. Conclusions

Nearly 80% of the pathogens present in the United States have a potential wildlife component. To successfully manage and control these pathogens at the livestock–wildlife interface will require the development of cross-discipline collaborations and establishing common goals between agencies and organizations that in some cases have rarely worked together. We believe the principles of adaptive management offer the greatest opportunities to formulate a framework from which collaborations can be developed to manage diseases at the livestock–wildlife interface. EID monitoring systems for wildlife that incorporate and implement integrated risk management in an adaptive management framework offer the best opportunity for success. In addition, new and creative funding mechanisms that bring livestock and wildlife animal health authorities along with livestock industry and wildlife stakeholders together will need to be created. Despite these social and policy challenges, there remain opportunities to develop new collaborations—along with the development of new technologies—to mitigate disease risks at the livestock–wildlife interface. We believe that two diseases eradication programs—bovine tuberculosis and cattle fever tick—offer the best opportunity to apply these principles and demonstrate success.

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