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

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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 (Rhyian 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 (Rhyian and Spraker, 2010). All of these changes work to create new interfaces between livestock and wildlife (Gortázar et al., 2007;
Decker et al., 2010; Rhyan 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

![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.](image-url)
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)                                         | 15    | 10                | 91%      | 3        |
| Cattle                     | 4 (2')                                        | 14    | 6                 | 75%      | 3        |
| Equine                     | 4                                             | 11    | 3                 | 43%      | 1        |
| Lagomorphs                 | 1 (1)                                         | 2     | 2                 | 100%     |           |
| Multiple                   | 10                                            | 26    | 16                | 100%     | 13       |
| Sheep and goat             | 4 (1)                                         | 11    | 3                 | 43%      |          |
| Swine                      | 2                                             | 7     | 2                 | 100%     |          |
| Total OIE diseases          | 29 (4)                                        | 86    | 42                | 79%      | 21       |

* 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 bidirectional 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 threefold: 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 (Sterner et al., 2009). Avian influenza, which has a well-documented wild waterfowl reservoir, continues to plague the domestic poultry
| Disease                        | Affected livestock | Wildlife host                                                                 | Citation                                      | Transmission mode |
|-------------------------------|--------------------|-------------------------------------------------------------------------------|-----------------------------------------------|-------------------|
| Anthrax                       | Ruminants, horses, swine | All mammals susceptible, environmental reservoirs                           | (Hugh-Jones and De Vos, 2002)                | Direct            |
| Aujeszky’s disease            | Domestic swine, cattle, sheep, goats, horses | Feral Swine, wild mammals                                                   | (Hahn et al., 1997; Corn et al., 2004; Kirkpatrick et al., 1980; Spickler et al., 2010) | Direct, indirect  |
| Avian chlamydiosis            | Ducks, turkeys, chickens | Gulls, ducks, herons, egrets, pigeons, blackbirds, grackles, house sparrows, kildeer, raptors, shorebirds, migratory birds | (Vanrompay et al., 1995; Thomas et al., 2007; Spickler et al., 2010) | Direct, indirect  |
| Avian infectious bronchitis   | Chickens           | Wild birds                                                                   | (Jonassen et al., 2005; Muradrasoli et al., 2010) | Direct, indirect  |
| Avian influenza               | Chickens, turkeys, ducks, geese, game birds | Numerous wild birds, many mammals susceptible                              | (Cook, 2005; Olsen et al., 2006)             | Direct, indirect  |
| Avian mycoplasmosis (Mycoplasma gallisepticum, Mycoplasma synoviae) | Chickens, turkeys, game birds, ducks, geese | House finches, American goldfinches, purple finches, eastern tufted titmice, pine grosbeaks, evening grosbeaks, others | (Thomas et al., 2007; Luttrell et al., 2001; Ley et al., 1996; Spickler et al., 2010) | Direct, indirect  |
| Bluetongue                    | Sheep, goats, cattle | Wild ovine species, cervids, water buffalo, pronghorn                          | 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             | Cervids                                                                       | (Woldehiwet, 2010; Kuttler, 1984)             | Arthropod-borne   |
| Bovine babesiosis             | Cattle             | White-tailed deer, water buffalo, African buffalo, reindeer                   | (Spickler et al., 2010; Schoelkopf et al., 2005; Cantu-C et al., 2009) | Direct, indirect  |
| Bovine genital campylobacteriosis | Cattle           | Numerous                                                                      | Williams and Barker, 2001                     | Direct, indirect  |
| Bovine tuberculosis          | Primarily cattle   | White-tailed deer, feral swine, 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, camélids, bison | White-tailed deer, mule deer, caribou, pronghorn, elk, moose, bison          | (Passler et al., 2007; Zarnke, 1983; Williams and Barker, 2001; Duncan et al., 2008) | Direct, indirect  |
| Brucellosis (Brucella abortus) | Cattle, sheep, horses | Bison, water buffalo, elk, feral swine, numerous spillover hosts             | (Olsen, 2010b; Zarnke, 1983; Williams and Barker, 2001; Spickler et al., 2010) | Direct, indirect  |
| Brucellosis (Brucella ovis)   | Sheep              | Red deer                                                                      | (Ridler and West, 2002; Spickler et al., 2010) | Direct, indirect  |
| Brucellosis (Brucella suis)   | Domestic swine, horses | Feral swine, European hare, caribou, reindeer, rodents, 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, goats, cattle, camélids | Spanish ibex, roe deer, red deer, white-tailed deer, mule deer, pronghorn, other wild ruminant species | (Verbisck-Bucker et al., 2008); (Spickler et al., 2010); (Leiby et al., 1970; Storandt et al., 2002; Storandt and Kazacos, 1993; Thompson et al., 2006; Spickler et al., 2010) | Direct, indirect  |
| Echinococcosis/hydatidosis   | Sheep, cattle      | Carnivore sp. including canids, rodents, lagomorphs, muskrats              | (Anonymous, 2006)                             | Indirect          |
| Epizootic hemorrhagic disease | Cattle, sheep | White-tailed deer, mule deer, pronghorn, other wild ruminant species         | (Anonymous, 2006)                             | Arthropod-borne   |
| Disease                                      | Affected livestock     | Wildlife host                                                                 | Citation                                                                                           | Transmission mode       |
|---------------------------------------------|------------------------|-------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-------------------------|
| Equine encephalomyelitis (Eastern and Western) | Equids¹, occasional     | Birds², rodents², jackrabbits¹, white-tailed deer¹, numerous species¹     | (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                            | Equids¹                 | Wild birds¹, numerous other species¹                                         | (Munster, 2007)                                                                                   | Direct, indirect        |
| Equine piroplasmosis                        | Equids¹                 | Uncertain                                                                     | (Kellogg et al., 1971; Spickler et al., 2010)                                                  | Arthropod-borne         |
| Equine rhinopneumonitis                     | Equids¹, Poultry²       | Numerous species¹                                                            | (Kinyili and Thorsen, 1979)                                                                      | Direct, indirect        |
| Fowl cholera                                | Poultry²               | Wild birds¹                                                                  | (Thomas et al., 2007; Petersen et al., 2001; Botzler, 1991; Blanchong et al., 2006) (Zarnke, 1983; Kinyili and Thorsen, 1979) | Direct, indirect        |
| Infectious bovine rhinotracheitis/infectious | Cattle²                | Several implicated¹                                                          | (Valas et al., 1997; Spickler et al., 2010)                                                     | Direct, indirect is rare |
| Infectious bursal disease                   | Chickens², turkeys⁴,⁵, | Game birds¹, Waterfowl¹                                                       | (Thomas et al., 2007; Candelora et al., 2010; Anonymous, 2008)                                  | Direct, indirect        |
| Leptospirosis                               | Cattle², sheep²,⁵,⁶,    | Rodents¹, raccoons¹, skunks¹, opossum¹, nutria¹, others¹                     | (Zarnke, 1985; Williams and Barker, 2001)                                                        | Direct, indirect        |
| Maedi-visna                                 | Sheep⁷, goats⁸          | Wild ruminants⁸                                                              | (Valas et al., 1997; Spickler et al., 2010)                                                     | Direct, indirect        |
| Marek’s disease                             | Chickens², Turkeys⁴,   | Galliformes¹                                                                  | (Cho and Kenzy, 1975)                                                                            | Direct, indirect        |
| Myxomatosis                                 | Lagomorpha               | Lagomorphs¹                                                                  | (Williams and Barker, 2001; Dwyer et al., 1990)                                                  | Arthropod-borne         |
| Newcastle disease                           | Chickens², turkeys⁴,⁵, | Wild birds¹, exotic birds¹                                                   | (Thomas et al., 2007; Brugh and Beard, 1984; Seal et al., 2000; Clubb and Hinsch, 1982; Spickler et al., 2010) | Direct, indirect        |
| Paratuberculosis                            | Cattle¹, sheep¹, goats¹ | Wild ruminants¹, rabbits¹, numerous wild mammals¹                           | (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| Swine⁹                  | Feral swine⁹                                                                 | (Williams and Barker, 2001; Corn et al., 2009)                                                   | Direct, indirect        |
| Pullorum disease                            | Chickens², turkeys³,    | Waterfowl¹, numerous wild bird species⁴                                       | (Thomas et al., 2007; Shivaprasad, 2000)                                                         | Direct, indirect        |
| Q fever                                     | Cattle¹, sheep¹,⁵,⁶,    | Numerous species including mammals¹, birds¹, and reptiles¹                   | (Zarnke, 1983; Spickler et al., 2010)                                                             | Direct, indirect, arthropod borne |
| Rabbit hemorrhagic disease                  | Domestic                 | Wild                                                                          | (Williams and Barker, 2001; Spickler et al., 2010)                                              | Direct, indirect        |
| Rabies                                      | Oryctolagus cuniculus¹   | Oryctolagus cuniculus¹ Raccoons¹, coyotes¹, fox¹, bats¹, skunks¹, mongooses¹, bobcats¹, others¹ | (Sterner and Smith, 2006; Krebs et al., 2003; Spickler et al., 2010)                              | Direct, indirect        |
| Transmissible gastroenteritis               | Swine⁶                  | Feral swine⁹                                                                 | (Williams and Barker, 2001)                                                                      | Direct, indirect        |
| Trichinellosis                              | Swine⁶,⁷                | Carnivores³, feral swine³, rodents³, bears³, others³                         | (Murrell et al., 1987)                                                                          | Direct, indirect        |
| Tularemia                                   | Sheep⁴, horses⁷, pigs⁸  | Lagomorphs³, muskrats³, rodents³, mink¹, prairie dogs³, others³               | (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                        | Cattle¹, swine¹, equids¹, camels¹,⁵,⁶,⁷, sheep¹,⁵,⁶, goats¹⁵,⁶,    | 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                                   | Equids¹, domestic       | Wild birds¹, other species⁴                                                  | (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. | Domestic cervids<sup>c</sup>     | Wild cervids<sup>i</sup>                          | (Williams and Barker, 2001; Williams et al., 2002; Baeten et al., 2007; Williams, 2005; Hamir et al., 2001) | Direct, indirect      |
| Chronic Wasting Disease          | Cattle<sup>e</sup>, bison<sup>e</sup>, swine<sup>e</sup>, sheep<sup>e</sup>, goats<sup>es</sup> | Wildebeest<sup>i</sup>, oryx<sup>i</sup>, ibex<sup>i</sup>, cervids<sup>i</sup>, wild ovine and caprinespecies<sup>i</sup>, ground squirrels<sup>i</sup>, other rodents<sup>i</sup>, carnivores<sup>i</sup>, numerous other species<sup>i</sup> | (Williams and Barker, 2001; Spickler et al., 2010) | Direct               |
| Malignant Catarrrhal Fever       | Domestic mammals<sup>c</sup>     | Prairie dogs<sup>i</sup>, chipmunks<sup>i</sup>, ground squirrels<sup>i</sup>, oryx<sup>i</sup>, ground squirrels<sup>i</sup>, other rodents<sup>i</sup>, carnivores<sup>i</sup>, numerous other species<sup>i</sup> | (Salkeld and Stapp, 2006) | Direct, indirect, arthropod-borne |
| Plague                           | Poultry<sup>c</sup>, doves<sup>c</sup>, pigeons<sup>c</sup> | Pigeons<sup>c</sup>, doves<sup>c</sup>, falcons<sup>c</sup>, hawks<sup>c</sup>, others<sup>c</sup> | (Thomas et al., 2007) | Direct, indirect |
| Trichomoniasis                   |                                   |                                                   |                                                                          |                       |
| (Trichomonasagallinae)           |                                   |                                                   |                                                                          |                       |
|                                  |                                   |                                                   |                                                                          |                       |

<sup>c</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>es</sup> <i>B. ovis</i> 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>c</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>es</sup> = clinical

<sup>es</sup> = subclinical

<sup>es</sup> = may be clinical or subclinical

<sup>es</sup> = occasional reports

<sup>es</sup> = reservoir

<sup>es</sup> = spillover

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

<sup>es</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 (Arthropod-borne)  |
| Bluetongue                       |                           | Multiple                  | Yes (Arthropod-borne)  |
| Bovine spongiform encephalopathy |                           |                          |                        |
| Bovine Tuberculosis              |                           | Multiple                  | Yes                    |
| Brucellosis (Brucella abortus)   | Eradication                | Multiple                  | Yes                    |
| Brucellosis (Brucella suis)      | 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               | Eradication                | Equine                   |                        |
| Equine infectious anemia         |                           | Equine                   |                        |
| Equine piroplasmosis             | Eradication                | 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                    |
| Scapie                           | Eradication                | Sheep, Goats             | Yes (Arthropod-borne)  |
| 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.
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 tuberculous, 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 hemoprotezoan parasites 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 Hourigan, 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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