



Evaluating wildlife-cattle contact rates to improve the understanding of dynamics of bovine tuberculosis transmission in Michigan, USA



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ABSTRACT

Direct and indirect contacts among individuals drive transmission of infectious disease. When multiple interacting species are susceptible to the same pathogen, risk assessment must include all potential host species. Bovine tuberculosis (bTB) is an example of a disease that can be transmitted among several wildlife species and to cattle, although the potential role of several wildlife species in spillback to cattle remains unclear. To better understand the complex network of contacts and factors driving disease transmission, we fitted proximity logger collars to beef and dairy cattle ($n = 37$), white-tailed deer (*Odocoileus virginianus*; $n = 29$), raccoon (*Procyon lotor*; $n = 53$), and Virginia opossum (*Didelphis virginiana*; $n = 79$) for 16 months in Michigan's Lower Peninsula, USA. We determined inter- and intra-species direct and indirect contact rates. Data on indirect contact was calculated when collared animals visited stationary proximity loggers placed at cattle feed and water resources. Most contact between wildlife species and cattle was indirect, with the highest contact rates occurring between raccoons and cattle during summer and fall. Nearly all visits (>99%) to cattle feed and water sources were by cattle, whereas visitation to stored cattle feed was dominated by deer and raccoon (46% and 38%, respectively). Our results suggest that indirect contact resulting from wildlife species visiting cattle-related resources could pose a risk of disease transmission to cattle and deserves continued attention with active mitigation.

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1. Introduction

The cattle industry in the USA has been plagued by reoccurrences of bovine tuberculosis (bTB) caused by the *Mycobacterium bovis* (*M. bovis*) bacterium (Cosgrove et al., 2012; Miller and Sweeney, 2013; Palmer, 2013; Barasona et al., 2014). Historically, bTB occurred in 9 distinct locations in North America and persists in 3 of these areas (Miller and Sweeney, 2013). In northern Michigan's (MI) Lower Peninsula, USA, bTB is maintained in free-ranging white-tailed deer (*Odocoileus virginianus*) providing a source for reinfection in cattle and perpetuation of the problem (O'Brien et al., 2006; Fitzgerald and Kaneene, 2013; Palmer 2013). Free-ranging white-tailed deer represent a challenging reservoir in MI, which has

motivated landscape-scale efforts to minimize potential for direct and indirect inter-species contact to reduce transmission of *M. bovis* from deer to cattle.

In the endemic zone of bTB in MI, raccoons (*Procyon lotor*) and opossums (*Didelphis virginiana*) are currently considered to be spillover hosts, testing positive for bTB at similar to higher rates than deer (Walter et al., 2013; Berentsen et al., 2010). Researchers from Michigan State University, USA reported it unlikely that bTB-infected opossums pose risk of pathogen transmission to large ruminants, although they can transmit pathogens via aerosol to other opossums in close contact (Fitzgerald et al., 2003). Such close contact within tightly knit family groups is a common characteristic of wildlife hosts of bTB (Fitzgerald et al., 2003). Both raccoons and opossums are found to share communal dens resulting in increased interaction when resources are abundant such as around feed stockpiled for livestock (Palmer et al., 2002; Atwood et al., 2009). Further, raccoons and opossums utilize the same stored feed, water sources, and feed being consumed by cattle and frequent

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farm buildings which house cattle and/or stored feed (Bruning-Fann et al., 2001; Atwood et al., 2009; Witmer et al., 2010; Walter et al., 2013). In other areas of the world where bTB is endemic, similar mesopredators including European badger (*Meles meles*) in Europe (Garnett et al., 2002; Bohm et al., 2009; Woodroffe et al., 2016) and brush-tailed opossum in New Zealand (Yockney et al., 2013) function as primary reservoirs of reinfection for cattle.

Transmission of *M. bovis* from animal to animal is possible through direct physical contact or exchange of air-borne pathogens, although transmission via contaminated feed or water is the most likely mode of transmission to cattle in the USA (Palmer et al., 2004a,b; Palmer and Whipple, 2006; Knust, 2008; Ribeiro-Lima et al., 2016). Human-manipulated environments, such as livestock production facilities, influence wildlife behavior and often provide unnatural foci for interaction such as at cattle-related resources including feed and water (Wobeser, 2006; Atwood et al., 2009; Gortazar et al., 2011; Barasona et al., 2014; Nunn et al., 2014).

Multi-host-species pathogens that are capable of being transmitted directly and indirectly, such as *M. bovis*, pose unique challenges to understanding risk and targeting mitigation to curb transmission (Cowie et al., 2015). Further, cryptic behavior of wildlife makes quantification of direct inter-species contact rates non-trivial and the ability to determine where, when, and how indirect interactions lead to transmission requires high-resolution contact data (Blyton et al., 2014). Fortunately, tools such as proximity loggers are now available and lend well to estimating previously unknown variables such as contact rates within and among species to provide a more accurate portrayal of the most relevant types and rates of interactions explaining disease dynamics (Cross et al., 2012; Lavelle et al., 2014). Our objectives were to, (1) quantify the extent of interaction occurring between wildlife and cattle in a landscape with bTB and, (2) evaluate the contributing role of cattle-related resources in exacerbating indirect contacts.

2. Materials and methods

2.1. Study area

We conducted our study on 6 privately owned cattle farms including 3 cow-calf and 3 dairy farms in Michigan's Lower Peninsula within Montmorency, Presque Isle, and Alpena Counties. This area lies within the core endemic area of bTB in MI (Walter et al., 2012; Berentsen et al., 2014) and provides highly suitable habitat for white-tailed deer (Felix et al., 2007). High-use, cattle-related areas and feed storage sites were present on each farm. Land cover types adjacent to study farms were dominated by woody wetlands, alfalfa fields, deciduous forest, corn fields, and other non-alfalfa hay fields. Although cattle production occurs in this area, densities are low averaging one beef-cattle farm per 21.5 km² and one dairy-cattle farm per 130.0 km² (Berentsen et al., 2014). Elevations ranged from 150 to 390 m above sea level with average annual snowfall of 175 cm and 72.5 cm of rain (Eichenlaub et al., 1990). Winter snow depths typically peak at 25–50 cm which is typically melted off by mid-April (Beyer et al., 2010). Weather in this region is notably more variable than elsewhere in the state with average summer temperatures of 24.8C and average winter temperatures of – 10.8C (Beyer et al., 2010). Regional deer density is estimated at 10 deer/km² (O'Brien et al., 2011), though concentrations of deer around food sources during winter can result in densities exceeding 19 deer/km² (Beyer et al., 2010) to as high as 35 deer/km² (Sitar, 1996). Apparent bTB prevalence rates in deer, opossum, and raccoon in the region fluctuate around 2% (O'Brien et al., 2011), 6%, and 4% respectively (Walter et al., 2013).

2.2. Wildlife capture and monitoring

We captured free-ranging wildlife primarily in January; though also as needed throughout the study to maintain ≥ 3 monitored adult animals of each species per site, using numerous live trapping techniques. Trap sites were dispersed across each farm within suitable habitat thus all available animals were potential study animals. Pairs of animals making contact were the experimental unit. All procedures were approved by the Institutional Animal Care and Use Committee of the U.S. Department of Agriculture-Animal and Plant Health Inspection Service-Wildlife Services-National Wildlife Research Center (USDA-APHIS-WS-NWRC, QA-1940). All livestock producers providing access to their property provided informed consent and were present during the handling of their livestock.

We monitored wildlife interaction and movement on and around farms relative to cattle-related resources with proximity loggers. Proximity loggers ("loggers" from this point forward; E2C 181C, Sirtrack®, Havelock North, New Zealand) use ultra-high frequency (UHF) transceivers and receivers to transmit and receive unique identification codes and record time, date, and duration of events logged. We programmed loggers with a separation time of 60 s (duration loggers needed to separate before beginning to log a new "event") and range coefficient of 45, which translated to a mean distance of 0.88 m (SD = 0.95) ("contact").

To quantify indirect contacts resulting from visitation to cattle-related resources, we also installed stationary loggers (3 or 4 per farm) of the same model at stored feed sites, water sources, and cattle feeders to record visitation by logger-equipped individuals. The routine shift of stored feed from "stored feed" status to "fed feed" status was not tracked or quantified; thus indirect contacts resulting from contamination by wildlife being concentrated overnight and then delivered to cattle the very next day were underestimated. Stored feed sites including hay, potatoes, beets, high-moisture corn, silage, and haylage were typically accessed ≥ 1 time daily to provide feed to cattle. Where feed quantities changed frequently, loggers were relocated routinely to monitor access points (i.e., open end of agbag). Stationary loggers were maintained every 1–2 weeks by connecting to a laptop computer and downloading data. Over the duration of the study, we monitored 28 (mean = 5/farm; sd = 2.1) cattle-related resources including 8 feeders, 8 water sources, 7 enclosed feed storage facilities, and 5 elongated crop storage bags (agbags).

2.3. Contact data processing

2.3.1. Direct contacts

A direct contact was defined as when at least one of a pair of interacting animals' collars established a connection in any 15-s time window. To account for variability in transmission probability due to contact events of different duration, multiple contacts were counted if the duration of the contact was greater than 15 s. For example, if loggers indicated two animals were in contact for one minute, then we counted that as four contacts whereas if two animals were in contact for three seconds, it was counted as one contact. For each unique pair of individuals that made contact at least once during the study, we calculated daily contact rate per season. This involved taking the count of contacts between a unique pair of individuals (including pairs from 6 different farms) and dividing by the number of days the unique pair was co-monitored (denominator for pairwise contact rates) during the season. Each value of daily contact rate for a unique pair had the following factor data associated with it: species interaction, season, farm, unique ID. These data were analyzed in a statistical model described below. Also, we showed descriptive results in Table 1 by averaging over unique pairs of individuals within a season or within a species

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