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Research Strategies of the National Wildlife Research Center to Control Bovine Tuberculosis in Wildlife in Michigan, Usa

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Introduction

Bovine tuberculosis (bTB) is a zoonotic disease caused by *Mycobaterium bovis* and is transmissible to humans, wildlife, and domestic livestock. In the United Kingdom, the suspected wildlife reservoir of bTB is the badger (*Meles meles*) (HUTCHINGS and HARRIS, 1997), and in New Zealand, the culprit is the brush-tailed possum (*Trichosurus vulpecula*) (MORRIS et al., 1994). In northern Michigan, USA, bovine tuberculosis is endemic in white-tailed deer (*Odocoileus virginianus*). In 1975 a hunter-killed white-tailed deer in Alpena County, Michigan, USA, was tested positive for bTB. Subsequent surveillance by the Michigan Department of Natural Resources (MDNR) of hunter-killed deer revealed no additional cases, and the situation was ruled an anomaly. However, in 1994, an additional hunter-killed white-tailed deer tested positive for bTB in Alcona County, only 13 km from the 1975 case. Between 1995 and 2005, a total of 509 deer tested positive for the disease (MDNR, 2005) and evidence suggested that deer transmitted the disease to domestic cattle (PALMER et al., 2004a). From 1997 to 2004, 33 cattle herds and 1 captive cervid farm tested positive for bTB (MDNR, 2005), most of them within a 5-county area. In addition, in 2006, 6 cattle farms and 1 captive cervid farm tested positive for the disease (MDNR, personal communication). In response to this outbreak, in the past several years MDNR has implemented management strategies to reduce the prevalence of bTB in deer in the outbreak area. These include reduction of deer densities through liberal hunting and restriction of baiting and supplemental feeding of white-tailed deer to reduce deer densities. In addition, Michigan Department of Agriculture and USDA/APHIS/Veterinary Services actively test cattle and captive deer herds with subsequent depopulation of infected herds. And while these actions have reduced the apparent prevalence of bTB in deer from 4.7 % to 1.7 %, a 64 % reduction (MDNR, 2005), other wildlife species may act as reservoirs for the disease. Bovine tuberculosis has been documented in many species of wildlife, including raccoons (*Procyon lotor*), coyotes (*Canis latrans*), red fox (*Vulpes vulpes*) and black bear (*Ursus americanus*) (BRUNING-FANN et al., 2001). In the outbreak area, bTB prevalence estimates in coyotes and raccoons are as high as 24% (VERCAUTEREN et al., unpublished data) and 2.5 % (WITMER et al., unpublished data), respectively. This raises the question of whether infected raccoons and coyotes actively shed *M. bovis* through either faeces or oral/nasal secretions, thus increasing risks of infection to cattle and other wildlife.

Material and methods

The research strategy at USDA/APHIS/WS/National Wildlife Research Center (NWRC) is to develop methods to reduce transmission of bTB from wildlife to cattle and possibly eliminate the disease in wildlife. To this end, we are conducting field and laboratory studies to determine whether raccoons and coyotes actively shed *M. bovis* in faeces and oral/nasal secretions. Free-ranging coyotes and raccoons are being sampled in and around the bTB outbreak area in northern Michigan's Lower

Peninsula. Tissue samples (lymph nodes, oral/nasal swabs, and tissues containing lesions) and faecal samples are being collected from each study subject and submitted for laboratory analysis. Tissue samples testing positive for *M. bovis* will have their corresponding faecal samples and oral/nasal swabs cultured for *M. bovis* using modified culture techniques to deal with contaminants. Scientists at Colorado State University, Ft. Collins, have developed a Polymerase Chain Reaction (PCR) method to isolate *M. bovis* from deer faeces, which will be modified at NWRC to accommodate coyote and raccoon faeces. This modified method will be used to determine whether raccoons and coyotes actively shed *M. bovis*. In the laboratory we will be experimentally infecting captive coyotes with cultured *M. bovis* and collecting faeces and oral/nasal secretions for analysis. Faecal samples will be placed in experimental cages with guinea pigs (*Cavia porcellus*) to determine whether they will contract bTB from contact with infected faeces. These studies are part of an overall study to evaluate whether coyotes can be considered sentinel species for early detection of bTB in previously uninfected areas.

In addition to small mammals, the presence of potentially infected deer on and around farms poses a threat to livestock. We are conducting a study to evaluate risk factors associated with the transmission of bTB to cattle from white-tailed deer as a refinement of work done by KANEENE et al. (2002). We captured white-tailed deer on several cattle farms in the bTB outbreak area of Michigan, and fitted them with radio transmitters equipped with a Global Positioning System (GPS). Over the next year, the GPS collars will record locations every two hours. Maps using Geographic Information System (GIS) technology are being generated of each study site (farm) including feeding locations, fences, outbuildings, feed storage areas, etc. Upon retrieval of the locations in early 2008 we will evaluate deer movements in relation to areas frequented by cattle, and recommend appropriate mitigation techniques to minimize space use overlap. The primary method of bTB infection is through inhalation of aerosolized bacilli. However, sharing of feed between infected and non-infected animals (PALMER et al., 2004a, 2004b) and direct fence line contact (VERCAUTEREN et al., in press) have also been implicated in transmission of the disease. Hill (2005) found no direct contact between deer and cattle suggesting this may not be a strong factor in transmission of the disease.

Results and discussion

Our research will continue through September 2008, and although some data is beginning to arrive, it is far too early to speculate on results. The raccoon study will provide important information on the potential transmission of bTB to cattle, as one would be hard pressed to find a farm in which there is not at least one family of raccoons living in a barn or other outbuilding. Deposition of potentially infected faeces in and around food storage areas could serve as reservoirs for the disease and increase the potential for transmission. If we are successful in determining that raccoons shed *M. bovis* in their faeces, we would be better able to recommend exclusionary techniques to reduce the number of raccoons living in barns, food storage areas and other outbuildings, thus decreasing the risk of disease.

USDA/APHIS/Wildlife Services (WS) assists MDNR in controlling coyotes. However, hunters trap and kill coyotes in Michigan, and studies suggest bTB prevalence in coyotes of 24 % in the outbreak area (VERCAUTEREN et al., unpublished data). This high apparent prevalence may allow for easier detection than sampling hunter-killed deer, with the prevalence in deer now down to 1.7 % (MDNR, 2005). This suggests that coyotes may serve as a sentinel species for early detection of the disease. A portion of this work has already been completed with studies in infected counties (ATWOOD et al., in press), but we are expanding the project to include currently uninfected counties. Detection of bTB in coyotes in previously uninfected counties may alert officials to the presence of bTB and allow them to implement

early testing of cattle and captive deer herds as well as be more vigilant in testing of hunter-killed deer. This tool could be a great asset in the early detection of bTB.

As a result of past research at NWRC, we have developed methods and strategies to reduce contact between deer and cattle, including the use of "guard dogs", various types of fencing (VERCAUTEREN et al., 2006, in press), and scare techniques (SEWARD et al., in press) to reduce the contact of deer with cattle feed. We will soon be conducting research to implement an oral baiting program that incorporates a BCG vaccine found to be efficacious in deer when administered through the oral route.

Our objective behind studying deer movements is to ascertain whether certain areas within farms (feeding areas, for example) are more attractive to deer, resulting in more time spent by deer in these locations. This could result in higher deer concentrations which, in turn, can increase the potential of finding tuberculous deer on the property. Understanding where deer move in relation to farms can help us introduce additional mitigation practices (barriers, etc.) to reduce the potential spread of bTB between deer and livestock. Bovine tuberculosis can be spread through sharing feed (PALMER et al., 2004b) or sharing a common fence-line (VERCAUTEREN et al., in press). And although Hill (2005) did not find any direct contact between deer and cattle, it still remains a potential mode of transmission. The sharing of space and feed between deer and domestic cattle remains a significant issue in the spread of bTB. Our goals are to develop methods to reduce these interactions and curtail the spread of bTB from deer to cattle.

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