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Michigan Bovine Tuberculosis: Annotated Bibliography

Citation

Acevedo, J., J. Vicente, U. Hofle, J. Cassinello, F. Ruiz-fons, and C. Gortazar. 2007. Estimation of European wild boar relative abundance and aggregation: a novel method in epidemiological risk assessment. Epidemiology and Infection 135:519–527.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wild boars are important disease reservoirs. It is well known that abundance estimates are needed in wildlife epidemiology, but the expense and effort required to obtain them is prohibitive. We evaluated a simple method based on the frequency of faecal droppings found on transects (FBII), and developed a spatial aggregation index, based on the runs test statistic. Estimates were compared with hunting data, and with porcine circovirus and Aujeszky's disease virus seroprevalences and Mycobacterium tuberculosis complex and Metastrongylus spp. prevalence. The FBII and the aggregation index were correlated with the hunting index, but both of the former estimates correlated better than the latter with the disease prevalences. Hence, at least in habitats with high wild boar densities, the FBII combined with the aggregation index constitutes a cheap and reliable alternative for wild boar abundance estimation that can be used for epidemiological risk assessment, even outside the hunting season and in areas with no available data on hunting activities

Key Words European, wild boar, epidemiology

Citation

Acevedo-Whitehouse, K., J. Vicente, C. Gortazar, U. Hofle, I. G. Fernandez-de-Mera, and W. Amos. 2005. Genetic resistance to bovine tuberculosis in the Iberian wild boar. Molecular Ecology 14:3209–3217.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bTB) is an important re-emerging zoonotic disease, causing major economic losses and constraining international trade of animals and their products. Despite eradication programmes, some countries continue to encounter outbreaks, mainly due to wildlife acting as primary hosts or reservoirs. While the genetic component of tuberculosis in humans and cattle is well documented, the role of genetic factors as modulators of bTB resistance remains unclear for natural populations. To address this issue, we investigated the relative contribution of host genetic variability to susceptibility to bTB infection and disease progression in wild boars from southern Spain. We found that genetic heterozygosity is an important predictor of bTB, not only modulating resistance to infection but also influencing containment of disease progression in infected individuals. Our results provide further evidence that host genetic variability plays a central role in natural populations. Testing each marker separately reveals evidence of both general and single-locus associative effects on bTB and several loci reveal high homology to regions of the genome with known immune function. Our results may prove to be crucial for understanding outbreaks of bTB in wildlife that could potentially affect domestic livestock and humans.

Key Words bovine tuberculosis, disease resistance, heterosis, heterozygosity, inbreeding, wild boar

Citation Activities Report and Proceedings of the 2004 Bovine Tuberculosis Conference. Michigan State University, East Lansing, Michigan, USA.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract On June 9 and 10, 2004, the State of Michigan and U.S. Department of Agriculture hosted the eighth annual Bovine Tuberculosis (TB) Conference, with guest speakers from Georgia, Colorado, Iowa, New York and two Canadian provinces. Our guests came together from across North America to receive policy updates and share the latest scientific data and innovative research on bovine TB. Among other things, the speakers shared insight on: the promotion of biosecurity; the $30 million annual costs of TB eradication in New Zealand; the latest research in new and improved blood tests; and the first season results of the Michigan Department of Natural Resources pilot project to target and remove only TB positive deer from the "hot" areas in Northeast Lower Michigan. When the Michigan Bovine TB Eradication Project began in 1996, there was no definitive information on where the disease was, and into what species it had been introduced. Since 1997, the Michigan Department of Community Health has documented 2,284 human TB cases, but only nine were caused by M. bovis, the organism that causes bovine TB. DNR fingerprinting showed that only one of these nine cases had a possible link to exposure to bovine TB infested deer or cattle herd in Lower Northern Michigan. Since testing began, the MDNR has looked at over 123,000 hunter harvested, wild white-tailed deer; and MDA, the USDA and private veterinary practitioners have tested nearly all of the state's 1 million livestock animals on 17,000 farms. We identified the locations of bovine TB positive cattle and deer and feel confident that we know where the disease occurs.

Key Words Bovine tuberculosis, Michigan, Mycobacterium bovis, Odocoileus virginianus, surveillance, white-tailed deer

Citation

Aranaz, A., L. de Juan, N. Montero, C. Sanchez, M. Galka, C. Delso, J. Alvarez, B. Romero, J. Bezos, A. I. Vela, V. Briones, A. Mateos, and L. Domínguez. 2004. Bovine tuberculosis (Mycobacterium bovis) in wildlife in Spain. Journal of Clinical Microbiology 42(6): 2602-2608.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis infection in wildlife and feral species is a potential source of infection for livestock and a threat to protected and endangered species. The aim of this study was to identify Spanish wild animal species infected with M. bovis through bacteriological culture and spacer oligonucleotide typing (spoligotyping) of isolates for epidemiological purposes. This study included samples from red deer (Cervus elaphus), fallow deer (Dama dama), wild boar (Sus scrofa), Iberian lynx (Lynx pardina), hare (Lepus europaeus), and cattle (Bos taurus). They were collected in several geographical areas that were selected for their unique ecological value and/or known relationships between wildlife and livestock. In the areas included in this survey, M. bovis strains with the same spoligotyping pattern were found infecting several wild species and livestock, which indicates an epidemiological link. A locally predominant spoligotype was found in these areas. Better understanding of the transmission and distribution of disease in these populations will permit more precise targeting of control measures.

Key Words wildlife, feral, Spain, Red deer, fallow deer, wild boar, iberian lynx, hare, cattle

Citation Artois, M., R. Delahay, V. Guberti, and C. Cheeseman. 2001. Control of infectious diseases of wildlife in Europe. The Veterinary Journal 162:141–152

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract During the last 30 years, new epidemiological patterns have emerged as free-ranging wildlife have become progressively more involved in the epidemiology of both common and emerging infectious diseases of humans and domestic animals. This has been seen in rabies, bovine tuberculosis and more recently in wildboar classical swine fever. Emerging diseases are of interest to veterinarians as well as public health officials but attempts to control these diseases have not always been successful as in wildlife populations control of either host or pathogen can present particular problems. Lessons should be learnt from previous experiences to help in the management of new emerging diseases in the future.

Key Words Infectious diseases; control; Europe; wildlife

Citation

Atwood, T. C., K. C. VerCauteren, T. J. Deliberto, H. J. Smith, and J. S. Stevenson. 2007. Coyotes as sentinels for monitoring bovine tuberculosis prevalence in white-tailed deer. Journal of Wildlife Management 71(5):1545–1554.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis, the causative agent of bovine tuberculosis (bTB), is endemic in free-ranging white-tailed deer (Odocoileus virginianus) in 5 counties (Alcona, Alpena, Montmorency, Oscoda, and Presque Isle) in the northeastern Lower Peninsula of Michigan, USA. The presence of a wildlife reservoir of tuberculosis in Michigan and the incidence of bTB in cattle (Bos taurus) resulted in Michigan losing its bTB accredited-free status. Subsequent wildlife surveillance programs identified relatively high disease prevalence in coyotes (Canis latrans), generating interest in their potential to serve as a sentinel species to detect bTB prevalence in white-tailed deer. Our goal was to develop an empirical basis for generating hypotheses about the spatial epidemiology of bTB infection in coyotes for future surveillance, management, and modeling efforts. Though variation in coyote home-range size may confound attempts to spatially correlate the incidence of disease in the sentinel and host species at a fine scale, overlap zones (OZs) between adjacent coyote home ranges may be the appropriate sample unit for spatially correlating disease prevalence in coyotes and white-tailed deer. Because overlapping home ranges are generally configured around resource rich (e.g., small mammals and white-tailed deer) timber management patches, the OZ concentrates spatial interaction between adjacent groups in a relatively small area. Furthermore, there is a direct relationship between interaction probabilities and the spatial dispersion of those patches. The latter finding provides a useful metric to incorporate into future efforts to develop spatially explict models of bTB dynamics. Modeling efforts can then be used as a foundation to predict the epidemiological ramifications of alterations in intensively managed forested landscapes.

Key Words bovine tuberculosis, coyote, disease, Mycobacterium bovis, spatial, timber management, white-tailed deer

Citation

Atwood, T. C., T. J. Deliberto, H. J. Smith, J. S. Stevenson, K. C. VerCauteren. 2009. Spatial ecology of raccoons related to cattle and bovine tuberculosis in northeastern Michigan. Journal of Wildlife Management 73(5):647–654.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In 1995, Mycobacterium bovis, the causative bacterium of bovine tuberculosis (bTB), was detected in 5 beef cattle operations in Alcona County, Michigan, USA. In accordance with Federal law, the operations were depopulated to prevent the spread of bTB. Subsequent wildlife surveillance programs identified high prevalence of M. bovis in mesocarnivores, including raccoons (Procyon lotor), which suggested that raccoons may be complicit in vectoring the pathogen among livestock operations. Our goal was to develop an empirical basis for generating hypotheses about the likelihood for raccoons to mediate the transmission of bTB to livestock. We found intersexual differences in scaledependent resource selection and probability of spatial interaction that, under certain circumstances, may form the foundation for a sex-bias in disease transmission. Spatial dispersion of mixed-forest patches facilitated overlap of adjacent males, whereas female overlap zones included pastures. Within overlap zones, probabilities of interaction for male–male and male–female dyads were greater than for female–female dyads, although we documented an elevated likelihood of spatial interaction between raccoons and livestock around cattle-feeding troughs and water sources, regardless of sex. Partial regressions generated by linear models indicated that distance between nearest-neighbor mixed-forest patches explained most of this observed variation. These results supported our prediction that forest patches juxtaposed with anthropogenic features fostered social tolerance between males and, thus, facilitated spatial interaction and exploitation of anthropogenic features. In raccoons, sex and landscape composition influenced pathogen transmission potential. We suggest that livestock producers locate livestock feeding and watering features away from forest patches to mitigate future outbreaks of bTB in endemic areas.

Key Words

bovine tuberculosis, disease, Michigan, Mycobacterium bovis, Procyon lotor, raccoon, resource selection, sexinfluenced, spatial epidemiology

Citation

Ayele, W. Y., S. D. Neill, J. Zinsstag, M. G. Weiss, and I. Pavlik. 2004. Bovine tuberculosis: an old disease but a new threat to Africa. The International Journal of Tuberculosis and Lung Disease 8(8):924–937.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (TB) is a disease characterised by progressive development of specific granulomatous lesions or tubercles in lung tissue, lymph nodes or other organs. Mycobacterium bovis is the causative agent of the disease. Bovine species, including bison and buffaloes, are susceptible to the disease, but nearly all warmblooded animals can be affected. All species are not equally susceptible to the disease; some are spill-over (end) hosts and others maintenance hosts. In Africa, bovine TB primarily affects cattle; however, infection in other farm and domestic animals, such as sheep, goats, pigs, dogs and cats, is not uncommon. Wild ruminants and carnivores are also affected and are the natural reservoirs of the infectious agent in the wild. Man is also susceptible to the disease, the highest risk groups being individuals with concomitant HIV/AIDS infection. In Africa, human TB is widely known to be caused by M. tuberculosis; however, an unknown proportion of cases are due to M. bovis. This infection in humans is underreported as a result of the diagnostic limitations of many laboratories in distinguishing M. bovis from M. tuberculosis. None of the national reports submitted to the OIE and WHO by African member states mention the importance of M. bovis in human TB cases. Consumption of unpasteurised milk and poorly heat-treated meat and close contact with infected animals represent the main sources of infection for humans. This review attempts to examine the impact of bovine TB on the health of animals and humans.

Key Words cattle, bovine tuberculosis, milk, pasteurisation, wild animals, zoonosis

Citation

Ballesteros, C., C. Gortázar, M. Canales, J. Vicente, A. Lasagna, J. A. Gamarra, R. Carrasco-García, J. de la Fuente. 2009. Evaluation of baits for oral vaccination of European wild boar piglets. Research in Veterinary Science 86:388–393.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The objective of this study was to develop and evaluate new baits for the oral delivery of vaccine preparations to 2–4 month-old wild boar piglets. Baits were prepared using a matrix composed of wild boar feed, wheat flour, paraffin, sacarose and cinnamon-truffle powder attractant with polyethylene capsules dipped into the matrix to introduce vaccine formulation. Physical stability studies demonstrated that baits were stable for at least three days at temperatures as high as 42 ┐C. Recombinant Escherichia coli expressing the membrane-displayed BM95-MSP1a fusion protein were usedto test bacterial viability in the baits and the antibody response in orally immunized wild boar. The E. coli viability was not significantly affected after bait incubation at 25 and 37 ┐C for 96 h. Bait acceptance studies using artificial feeders in the field showed that baits were accepted by 2–3 month-old animals, the preferred age for vaccination. Orally immunized wild boar piglets excreted recombinant E. coli in the feces and developed antibody titers to recombinant BM95-MSP1a protein, thus confirming that vaccine composition was released and reached the wild boar gastrointestinal track. The results of these experiments support the use of these baits for oral delivery of vaccine formulations to 2–4 month-old wild boar piglets.

Key Words oral vaccine, wildlife, bait, wild boar, pig, tuberculosis, piglet, Bm95, MSP1a

Citation

Ballesteros, C., J.M. Garrido, J. Vicente, B. Romero, R.C. Galindo, E. Minguijón, M. Villar, M.P. Martín-Hernando, I. Sevilla , R. Juste, A. Aranaz, J. de la Fuente, C. Gortázar. 2009. First data on Eurasian wild boar response to oral immunization with BCG and challenge with a Mycobacterium bovis field strain. Vaccine 27:6662–6668.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The Eurasian wild boar (Sus scrofa) is considered a reservoir for bovine tuberculosis (bTB) caused by Mycobacterium bovis and closely related members of the Mycobacterium tuberculosis complex in southcentral Spain. The vaccination of wildlife with BCG offers an alternative to culling and to movement restriction for the control of bTB among wildlife reservoirs. In this study, we hypothesized that oral BCG immunization of wild boar would affect the expression of immunoregulatory genes and confer protection against M. bovis. Three groups were used to describe the infection, pathological findings and gene expression profiles in wild boar: BCG-vaccinated and M. bovis-challenged (vaccinated challenged group; N= 6), non-vaccinated and M. bovis-challenged (non-vaccinated challenged group; N= 4), and non-vaccinated and mock-infected (control group; N= 2) animals. M. bovis was isolated from 50% (3/6) and 75% (3/4) of vaccinated challenged and non-vaccinated challenged animals, respectively. All four wild boar from the non-vaccinated challenged group developed bTB-compatible lesions 114 days after challenge. In contrast, only 50% of vaccinated challenged wild boar developed lesions. The PBMC mRNA levels of IL4, RANTES, C3, IFN-gamma and methylmalonyl-CoA mutase (MUT) were analyzed at several days post-vaccination (dpi). When vaccinated challenged animals were compared to controls, all five genes were significantly upregulated at the time of M. bovis infection at 186 dpi but IFN-gamma levels were also upregulated at 11 and 46 dpi. The C3 and MUT mRNA levels were higher at 46 dpi, and 11 and 186 dpi, respectively, in vaccinated protected wild boar when compared to non-vaccinated challenged animals. At the end of the experiment (300 dpi), the mRNA levels of selected genes were lower in nonvaccinated challenged animals when compared to control wild boar. Exposing wild boar to a dose of 104 cfu of M. bovis by the oropharyngeal route is an adequate protocol to produce an infection model in this species. Our results suggested that oral BCG immunization of wild boar results in the upregulation of immunoregulatory genes that may be associated with protective response to M. bovis infection in this species. More studies on vaccine efficacy, delivery, and safety will be needed to confirm if oral vaccination with BCG could be used in bTB control programs for reducing M. bovis infection and clinical disease in wild boar.

Key Words gene expression, tuberculosis, Sus scrofa, vaccination and challenge experiment

Citation

Bany, S. A., and J. E. Freier.2000. Use of GIS to evaluate livestock-wildlife interactions relative to tuberculosis spread on Molokai Island, Hawaii. ESRI Online.

Abstract Only ☐

No Abstract ☐

Article Type Other

Abstract

Historically, bovine tuberculosis has occurred and been eradicated several times on the Hawaiian island of Molokai. After the most recent depopulation of cattle, TB was again identified in an adult cow in 1997, thus continuing the investigation into why bovine tuberculosis is reoccurring on the island. The Centers for Epidemiology and Animal Health (CEAH) have implemented spatial analysis using ArcView software that, along with epidemiological investigations, attempts to identify the environmental factors responsible for maintaining this disease in natural foci. To examine the ecological aspects of tuberculosis transmission from wildlife to livestock, and to identify the foci of infection, we have used a combination of classification analysis, 3D modeling, and various spatial analysis techniques.

Key Words

Hawaii, CEAH, spatial analysis, ArcView, environmental, ecological, classification analysis, 3D modeling, livestock, wildlife, interactions, cross-sectional

Citation Barlow, N. D. 2000. Non-linear transmission and simple models for bovine tuberculosis. Journal of Animal Ecology 69:703-713.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. A new model is presented for a possum±tuberculosis (TB) system (Trichosurus vulpecula-Mycobacterium bovis) that is both realistic and parsimonious. The model includes a phenomenological treatment of heterogeneity of risk for susceptible hosts, similar to that used in insect host-parasitoid systems.
2. Parameter values for the model reflect current knowledge and differ significantly from those in other recent models of this system. Associated with these structural and parametric changes are substantially different predictions for the dynamics and control of TB in possums.
3. The model predictions include (i) only limited host suppression due to the disease (< 10%, cf. several earlier simple models for TB in both possums and badgers); (ii) asymptotically stable disease dynamics (cf. homogeneous-mixing models that predict either extremely weak stability such that disease fails to recover when host density is temporarily reduced, or oscillatory behaviour and potential elimination of disease following such a perturbation); (iii) TB that is harder to control than in the homogeneous-mixing model equivalents, in line with practical experience; and (iv) a threshold host density for disease elimination that diers substantially from the host equilibrium density in the presence of disease.
4. Homogeneous-mixing models are unable to reproduce this behaviour, whatever parameter values are chosen. Heterogeneous-mixing models with non-linear transmission may therefore be worth consideration in other endemic wildlife disease systems, as is now commonplace for insect-parasitoid and insect-pathogen ones.

Key Words bovine tuberculosis, epidemiology, mathematical model, population dynamics, possum

Citation

Bengis, R. G., F.A. Leighton, J.R. Fischer, M. Artois, T. Mörner, and C. M. Tate. 2004. The role of wildlife in emerging and re-emerging zoonoses. Revue Scientifique Technical Office International Epizootics 23(2):497-511.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

There are huge numbers of wild animals distributed throughout the world and the diversity of wildlife species is immense. Each landscape and habitat has a kaleidoscope of niches supporting an enormous variety of vertebrate and invertebrate species, and each species or taxon supports an even more impressive array of macro- and micro-parasites. Infectious pathogens that originate in wild animals have become increasingly important throughout the world in recent decades, as they have had substantial impacts on human health, agricultural production, wildlife-based economies and wildlife conservation. The emergence of these pathogens as significant health issues is associated with a range of causal factors, most of them linked to the sharp and exponential rise of global human activity. Among these causal factors are the burgeoning human population, the increased frequency and speed of local and international travel, the increase in human-assisted movement of animals and animal products, changing agricultural practices that favour the transfer of pathogens between wild and domestic animals, and a range of environmental changes that alter the distribution of wild hosts and vectors and thus facilitate the transmission of infectious agents. Two different patterns of transmission of pathogens from wild animals to humans are evident among these emerging zoonotic diseases. In one pattern, actual transmission of the pathogen to humans is a rare event but, once it has occurred, human-to-human transmission maintains the infection for some period of time or permanently. Some examples of pathogens with this pattern of transmission are human immunodeficiency virus/acquired immune deficiency syndrome, influenza A, Ebola virus and severe acute respiratory syndrome. In the second pattern, direct or vector-mediated animal-to-human transmission is the usual source of human infection. Wild animal populations are the principal reservoirs of the pathogen and human-to-human disease transmission is rare. Examples of pathogens with this pattern of transmission include rabies and other lyssaviruses, Nipah virus, West Nile virus, Hantavirus, and the agents of Lyme borreliosis, plague, tularemia, leptospirosis and ehrlichiosis. These zoonotic diseases from wild animal sources all have trends that are rising sharply upwards. In this paper, the authors discuss the causal factors associated with the emergence or re-emergence of these zoonoses, and highlight a selection to provide a composite view of their range, variety and origins. However, most of these diseases are covered in more detail in dedicated papers elsewhere in this Review.

Key Words emerging disease, re-emerging disease, species barrier, wildlife, zoonosis

Citation Bennet,R, and R. Cooke. 2006. Costs to farmers of a tuberculosis breakdown. Veterinary Record 158:429-432.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract An on-farm survey of 151 cattle farmers who had experienced a bovine tuberculosis (Mycobacterium bovis) breakdown on their farms was undertaken in 2003 to assess the costs associated with the breakdown. In 90 per cent of cases the cost was estimated to be less than £18,513 for dairy herds and less than £11,462 for beef herds, but with a range from £229 to £103,817. The main cost was the slaughter of reactor cattle. For the majority of the farmers, the compensation payments seemed to meet most of the costs of their breakdowns, although a majority was still left with net losses.

Key Words bovine tuberculosis, cattle, cost, farmers, Mycobacterium bovis

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Citation Bennett, R. and R. Cooke. 2005. Control of bovine TB: preferences of farmers who have suffered a TB breakdown. Veterinary Record 156: 143-145.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Control, preferences, farmers, strategy, alternative, UK

Citation	Berentsen, A. R., M. R. Dunbar, and R. G. McLean. 2007. Research Strategies of the National Wildlife Research Center to Control Bovine Tuberculosis in Wildlife in Michigan, USA. Wildlife Damage Management, Internet Center for USDA National Wildlife Research Center -Staff Publications. Pp. 174-175.
Abstract Only	☐
No Abstract	☑
Article Type	Report
Abstract	
Key Words	Bovine tuberculosis, Mycobacterium bovis, National Wildlife Research Center, Odocoileus virginianus, research, white-tailed deer

Citation

Berentsen, A. R., M. R. Dunbar, R. Ebersole, and R. G. McLean. 2008. Risks associated with the transmission of bovine tuberculosis from white-tailed deer to cattle in Michigan: current research. Proceedings of the Vertebrate Pest -Conference 23:277-279.

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

Bovine tuberculosis (bTB) is a contagious disease of livestock, wildlife, and humans. Typically, it is transmitted through inhalation of aerosolized bacilli and direct or indirect contact between animals. In northeastern Michigan, bTB is endemic in white-tailed deer, and evidence suggests deer have spread the disease to domestic cattle. Previous research indicates bTB transmission likely occurs through contamination of cattle feeding sources by infected deer and subsequent use by cattle. We are investigating deer movements in relation to farm management practices such as feeding schedules as well as locations of cattle feeding areas, hay storage sites, barns, and water sources. All locations are plotted using ArcMap software. Regular communication with cooperators allows for updates in feeding schedules and locations. We are capturing free-ranging white-tailed deer and fitting them with radio collars equipped with a global positioning system (GPS). As of 15 February 2008, we have retrieved GPS collars from 7 of 16 deer collared in 2007, and 7 new collars have been deployed since 1 January 2008. Each retrieved collar has recorded over 2,500 data points, and preliminary results suggest individual deer are staying within 1.5 km of their capture site. Spatial analysis on deer locations relative to livestock management practices and farm structures will take place when all data is retrieved in late 2008 and early 2009. Once complete, we hope this information will allow us to recommend mitigating measures for livestock producers to reduce the risk of transmission of bTB from free ranging white-tailed deer to domestic cattle.

Key Words

bovine tuberculosis, disease, Michigan, Mycobacterium bovis, Odocoileus virginianus, white-tailed deer

Citation

Berentsen, A. R., M. R. Dunbar, R. G. McLean. 2007. Research strategies to reduce bovine tuberculosis transmission from wildlife to cattle. Proceedings of the Wildlife Damage Management Conference 12:332-339.

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

Bovine tuberculosis (bTB) is a zoonotic disease caused by Mycobaterium bovis, and is transmissible to humans, wildlife and domestic livestock. In the northern Lower Peninsula of Michigan, white-tailed deer (Odocoileus virginianus) serve as a reservoir for the disease and pose a significant threat to domestic cattle and captive cervids. Scientists at USDA, APHIS, Wildlife Services, National Wildlife Research Center have designed a variety of laboratory and field studies aimed at reducing or eliminating bTB infection in cattle by interrupting the transmission of the disease from wildlife reservoirs. These strategies include reducing bTB in deer by delivery of oral vaccines, creating effective barriers to cattle/wildlife interactions, determining the role of other wildlife species in the transmission of M. bovis, and evaluating a sentinel species to monitor prevalence of bTB in the environment. In addition, studies are being conducted to assess transmission risks between deer and cattle on cattle farms and to recommend mitigation measures to reduce these risks. These studies will provide comprehensive information on the role of wildlife-livestock interactions in the maintenance and spread of bTB as well as recommendations of measures to contribute toward its eventual eradication in domestic cattle in cases where wildlife is the source of infection.

Key Words bovine tuberculosis, domestic cattle, Michigan, Mycobacterium bovis, Odocoileus virginianus, white-tailed deer, wildlife diseases

Citation Blanchong, J. A., K. T. Scribner, A. N. Kravchenko, and S. R. Winterstein. 2007. TB-infected deer are more closely related than non-infected deer. Biology Letters 3:104-106.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Identifying mechanisms of pathogen transmission is critical to controlling disease. Social organization should influence contacts among individuals and thus the distribution and spread of disease within a population. Molecular genetic markers can be used to elucidate mechanisms of disease transmission in wildlife populations without undertaking detailed observational studies to determine probable contact rates. Estimates of genealogical relationships within a bovine tuberculosis-infected white-tailed deer (Odocoileus virginianus) population indicated that infected deer were significantly more closely related than non-infected deer suggesting that contact within family groups was a significant mechanism of disease transmission. Results demonstrate that epidemiological models should incorporate aspects of host ecology likely to affect the probability of disease transmission.

Key Words bovine tuberculosis, ecology, microsatellites, wildlife, white-tailed deer, zoonoses

Citation

Blanchong, J., K. T. Scribner, B. K. Epperson, and S. R. Winterstein. 2006. Changes in artificial feeding regulations impact white-tailed deer fine-scale spatial genetic structure. Journal of Wildlife Management 70(4):1037−1043.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Human activities can change the spatial distribution of individuals within wildlife populations that in turn alters population allele frequencies and spatial genetic structure at fine scales. Artificial feeding is one such activity whose impact on wildlife physical condition, population dynamics, and transmission of disease has been well documented. To evaluate the impact of artificial feeding on the spatial distribution and social organization of white-tailed deer (Odocoileus virginianus) we estimated allele frequencies at 3 microsatellite loci for 2 ,177 hunter-harvested deer and characterized microgeographic genetic structure in 2 regions of the northeast lower peninsula of Michigan, USA, during and following cessation of artificial feeding. While artificial feeding was ongoing we observed no evidence of spatial genetic structure across either region. Spatial homogeneity of allele frequencies over such a large area was surprising given numerous studies that have documented spatial genetic structure in other deer populations, and it was likely a function of the aggregation of multiple kin-structured social groups (i.e., matrilines) at artificial feeding sites. Subsequently, when artificial feeding was banned, we found significant genetic differentiation among groups of deer in both regions. Detection of microgeographic genetic structure consistent with a patterns of isolation-by-distance following the ban on artificial feeding was likely the result of increased spatial segregation of social groups of related deer. Our results illustrate how analyses of the degree to which natural populations are spatially genetically structured can be used to infer the effects of human actions on wildlife movement patterns, breeding behaviors, and disease transmission that are difficult to determine using traditional methods.

Key Words artificial feeding, microgeographic genetic structure,microsatellites,Odocoileus virginianus, white-tailed deer, Michigan

Citation

Bohm, M, M. R. Hutchings, P. C. L. White. 2009. Contact networks in a wildlife-livestock host community: identifying high-risk individuals in the transmission of bovine TB among badgers and cattle. PLoS 4(4):1-12.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Background: The management of many pathogens, which are of concern to humans and their livestock, is complicated by the pathogens' ability to cross-infect multiple host species, including wildlife. This has major implications for the management of such diseases, since the dynamics of infection are dependent on the rates of both intra- and inter- specific transmission. However, the difficulty of studying transmission networks in free-living populations means that the relative opportunities for intra- versus inter-specific disease transmission have not previously been demonstrated empirically withinany wildlife-livestock disease system.
Methodology/Principal Findings: Using recently-developed proximity data loggers, we quantify both intra-and interspecific contacts in a wildlife-livestock disease system, using bovine tuberculosis (bTB) in badgers and cattle in the UK as our example. We assess the connectedness of individuals within the networks in order to identify whether there are certain 'high-risk' individuals or groups of individuals for disease transmission within and between species. Our results show that contact patterns in both badger and cattle populations vary widely, both between individuals and over time. We recorded only infrequent interactions between badger social groups, although all badgers fitted with data loggers were involved in these inter-group contacts. Contacts between badgers and cattle occurred more frequently than contacts between different badger groups. Moreover, these inter-specific contacts involved those individual cows, which were highly connected within the cattle herd.
Conclusions/Significance: This work represents the first continuous time record of wildlife-host contacts for any free-living wildlife-livestock disease system. The results highlight the existence of specific individuals with relatively high contact rates in both livestock and wildlife populations, which have the potential to act as hubs in the spread of disease through complex contact networks. Targeting testing or preventive measures at high-contact groups and individuals within livestock populations would enhance the effectiveness and efficiency of disease management strategies.

Key Words badgers, cattle, host, high-risk, livestock, transmission, wildlife

Citation

Bohm, M., K. L. Palphramand, G. Newton-Cross, M. R. Hutchings and P. C. L. White. 2008. The spatial distribution of badgers, setts and latrines: the risk for intra-specific and badger-livestock disease transmission. Ecography 31:525-537.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The spatial distribution of wildlife hosts and the associated environmental distribution of their excretory products are important factors associated with the risk of disease transmission between wildlife and livestock. At a landscape scale, heterogeneous distribution of a wildlife host will create regional hot spots for disease risk, while at the farm level, distributional patterns of wildlife excretory products as well as habitat use are of primary importance to the assessment of disease risk to livestock. In the UK, badgers have been implicated in the transmission of bovine tuberculosis to cattle. In this study, we focus on the spatial and social organization and habitat use of badgers as well as the distributions of their excretions at latrine and sett sites to assess intra- and inter-species (badger-cattle) disease risk. Across the study site, badger latrines and setts were found in prominent clusters, at distances of up to 250 and 200 m respectively. This was partly due to small-scale clustering of latrines around sett sites, so that disease risk may be higher within the vicinity of setts. The clustered distribution suggests that sites of high risk for TB transmission may be localised within farms. Exclusion of cattle from the few sett and latrine sites within their grazing pasture is therefore likely to provide an effective way of reducing the risk of disease transmission. We also found evidence of social sub-division within badger social groups based on differences in the use of main and outlier setts. This may contribute to localised clusters of infection within the badger population, resulting in heterogeneous patterns of environmental disease risk to the wider host community. A greater understanding of variation in host behaviour and its implications for patterns of disease will allow the development of more targeted and effective management strategies for wildlife disease in group-living hosts.

Key Words badgers, intra-specific, latrines, livestock, setts, transmission

Citation

Bohm, M., P. C.L. White, J. Chambers, L. Smith, M.R. Hutchings. 2007. Wild deer as a source of infection for livestock and humans in the UK. The Veterinary Journal. 174:260–276.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wild deer can feature in the epidemiology of a wide range of livestock and human diseases in the United Kingdom by representing a source of disease via various transmission routes. This review highlights current and possible future infections of deer in the UK which may have an impact on livestock and/or human health. Increases in deer abundance as well as range expansion are likely to exacerbate the potential for disease persistence due to the formation of multi-species deer assemblages, which may act as disease reservoirs. Climatic changes are likely to have a direct impact on the presence and abundance of various pathogens and their vectors, so that with a warming climate exotic diseases may play a role in future UK livestock and wildlife disease management. This paper highlights the need for a monitoring strategy for wildlife diseases, in particular infections in wild deer, in the UK.

Key Words climate change, deer; infectious disease, monitoring, transmission, wildlife

Citation

Brook, R. K. and S. M. McLachlan. 2006. Factors influencing farmers' concerns regarding bovine tuberculosis in wildlife and livestock around Riding Mountain National Park. Journal of Environmental Management 80:156-166.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Despite intensive efforts over the last century to eradicate bovine tuberculosis (TB) in North America, several hotspots of infected wildlife and livestock remain, raising concerns that the disease will never be eradicated. The stress and frustration for a farmer caused by having a herd test positive for TB or living in an infected region can be substantial. The goal of this study was to investigate the concerns of farmers around Riding Mountain National Park (RMNP) regarding the presence of TB in wildlife and livestock and conduct an exploratory analysis of causal factors. Data were collected from 786 farmers within 50 km of RMNP using a mail-back questionnaire. Overall, farmers indicated a high level of concern toward diseases in both wildlife and cattle relative to other concerns. The spatial variables that had the greatest influence on TB concern were both the distance of farms to the RMNP boundary and distance of farms to previous cases of TB. The most important aspatial factor associated with high TB concern was the frequency with which farmers observed elk on their land. These results underscore the important differences between 'objective' measures of risk, such as epidemiological estimates of disease prevalence, and subjective measures of disease concern, such as risk perception and acceptability of management actions. Written responses suggest that concerns regarding disease may affect how farmers view wildlife on their land and their relationship with neighbouring protected areas. Management activities that reduce the frequency of elk interactions with farms, but also recognize the complex relationship that farmers have with wildlife and protected areas, will be most effective in mitigating farmer concern regarding this important problem.

Key Words farmer attitudes, bovine tuberculosis, protected areas, logistic regression, Riding Mountain, Canada

Citation

Brook, R. K., and S. M. McLachlan. 2009. Transdisciplinary habitat models for elk and cattle as a proxy for bovine tuberculosis transmission risk. Preventive Veterinary Medicine 91:197–208.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Zoonotic diseases such as bovine tuberculosis (TB) that infect wildlife and livestock are particularly difficult to eradicate where wild animals make extensive use of agricultural landscapes. Transmission of TB between cattle (Bos taurus) and wild elk (Cervus elaphus) in southwestern Manitoba, Canada remains poorly understood but there is a risk when comingling occurs on summer pasture. Elk use of cattle summer pastures was assessed using ecological data (187 VHF and 25 GPS collared elk monitored over four years representing 8% of the elk population). Local knowledge was documented by conducting interviews and participatory mapping exercises with 86 cattle producers (98% of those within the study area). Of the 294 cattle pastures mapped by farmers, 13% were used by radio-collared elk, 38% were reported by farmers as being used by elk, and 42% were identified as used by elk when both when all datasets were combined. Cattle pastures that had been used by elk and those that had no elk were compared using binary logistic regression based on each of the three datasets (i.e. farmer observations, radio-collared elk on pasture, and combined dataset). For all three datasets, distance to protected area and proportion of forest cover on the cattle pasture were identified as the most and second most important predictor variables, respectively. There was strong agreement among the relative probabilities of elk occurrence on each pasture derived from the resource selection function (RSF) models developed using farmer interviews and elk collaring data. The farmer interview and collar datasets were then combined to generate a final integrated RSF map summarizing the probability of elk–cattle comingling and were contrasted over each of four cattle grazing seasons (spring, early summer, late summer, and autumn). These predictive maps indicate that use of cattle pastures by elk is extensive, particularly in spring and early summer. Farmer observations indicate that elk and cattle share water sources and livestock mineral supplements on pasture. Local knowledge and conventional ecological data complement and validate one another and help us better understand the temporospatial aspects of shared space use among wildlife and livestock and more generally the risks of disease transmission in agricultural landscapes.

Key Words bovine TB, disease transmission, farmer knowledge, Mycobacterium bovis, resource selection functions, wildlife disease

Citation

Brook, R.K. 2010. Incorporating farmer observations in efforts to manage bovine tuberculosis using barrier fencing at the wildlife–livestock interface. Preventive Veterinary Medicine. doi:10.1016/j.prevetmed.2010.01.010

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A federal and provincial cost-shared program was initiated in 2001 around Riding Mountain National Park in southwestern Manitoba, Canada to provide free game wire barrier fences for baled hay storage areas to prevent transmission of TB among cattle (Bos taurus), wild elk (Cervus elaphus), and deer (Odocoileus virginianus). Farmer observations of cervids on their farms were evaluated by interviewing 50 farmers that owned a game wire fence for >1 year. Of those interviewed, 82% reported some type of elk or deer damage to hay bales in the field or in their yard prior to fencing. After fencing, 23% of respondents reported some annual damage to stored hay bales that were not inside the fence, but there was a 100% decrease in the estimated annual value of hay losses. Incursions of deer inside the barrier fence were reported by 18% of respondents and most of these were due to leaving gates open. No incursions of elk inside a barrier fence were reported. Despite the important successes achieved, barrier fencing of hay bales alone does not completely protect cattle from bovine tuberculosis.

Key Words

bovine tuberculosis, deer, elk, farmer observations, fencing, exclosure

Citation

Bruning-Fann, C. S., S. M. Schmitt, S. D. Fitzgerald, J. B. Payeur, D. L. Whipple, T. M. Cooley, T. Carlson, and P. Friedrich. 1998. Mycobacterium bovis in coyotes from Michigan. Journal of Wildlife Diseases 34(3):632-636.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

During a survey for tuberculosis in wild carnivores and omnivores, Mycobacteriurn bovis was cultured from pooled lymph nodes of three adult female coyotes (Canis latrans) harvested by hunters in Michigan (USA). No gross or histologic lesions suggestive of tuberculosis were seen in these animals. One coyote was taken from Montmorency county and two coyotes from Alcona county located in the northeastern portion of Michigan's Lower Peninsula where free-ranging white-tailed deer (Odocoileus virginianus) have been found infected with bovine tuberculosis. It is thought that these coyotes became infected with M. boris through the consumption of tuberculous deer. Other species included in the survey were the opossum (Didelphis virginiana), raccoon (Procyon lotor), red fox (Vulpes vulpes), bobcat (Felis rufus), and badger (Taxidea taxus).

Key Words Case report, coyote, Canis latrans, Mycobacterium bovis, survey, tuberculosis

Citation

Bruning-Fann, C. S., S. M. Schmitt,S. D. Fitzgerald, J. S. Fierke, P. D.Friedrich, J. B. Kaneene, K. A. Clarke, K. L. Butler, J. B. Payeur, D. L. Whipple,T. M. Cooley, J. M. Miller, and D. P. Muzo. 2001. Bovine tuberculosis in free-ranging carnivores from Michigan. Journal of Wildlife Diseases 37(1):58-64

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

During a survey of carnivores and omnivores for bovine tuberculosis conducted in Michigan (USA) since 1996, Mycobacterium bovis was cultured from lymph nodes pooled from six coyotes (Canis latrans) (four adult female, two adult male), two adult male raccoons (Procyon lotor), one adult male red fox (Vulpes vulpes), and one 1.5-yr-old male black bear (Ursus americanus). One adult, male bobcat (Felis rufus) with histologic lesions suggestive of tuberculosis was negative on culture but positive for organisms belonging to the Mycobacterium tuberculosis complex when tested by polymerase chain reaction. All the tuberculous animals were taken from three adjoining counties where M. bovis is known to be endemic in the free-ranging white-tailed deer (Odocoileus virginianus) population. There were two coyotes, one raccoon, one red fox, and one bobcat infected in Alpena county. Montmorency County had two coyotes and one raccoon with M. bovis. Two coyotes and a bear were infected from Alcona County. These free-ranging carnivores/omnivores probably became infected with M. bovis through consumption of tuberculous deer. Other species included in the survey were opossum (Didelphis virginiana), gray fox (Urocyon cinereoargenteus), and badger (Taxidea taxus); these were negative for M. bovis.

Key Words

Coyote (Canis latrans), raccoon (Procyon lotor), black bear (Ursus americanus), bobcat (Felis rufus), red fox (Vulpes vulpes), Mycobacterium bovis, survey, tuberculosis

Citation

Buddle, B. M., D. N. Wedlock, M. Denis. 2006. Progress in the development of tuberculosis vaccines for cattle and wildlife. Veterinary Microbiology 112: 191-200.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Vaccination against bovine tuberculosis is likely to become an important disease control strategy in developing countries, which cannot afford a test and slaughter control programme, or in countries which have a wildlife reservoir of Mycobacterium bovis infection. In the past decade, considerable progress has been made in the development and evaluation of tuberculosis vaccines for cattle and for a range of wildlife maintenance hosts including possums, badgers, deer and African buffaloes. Experimental challenge systems have been established for the different target species and the resulting disease process has mimicked that seen in the field. In cattle, neonatal vaccination with BCG appeared to be more effective than vaccination of 6-month-old calves and in most situations no other vaccine has been shown to be better than BCG. However, prime-boost strategies involving combinations of BCG with a protein or DNA vaccine, to improve on BCG vaccination alone, have produced very encouraging results. Differential diagnostic tests have been developed using mycobacterial antigens that are only present in virulent M. bovis to differentiate between BCG-vaccinated and M. bovis-infected cattle. BCG vaccine has been shown to reduce the spread of tuberculous lesions in a range of wildlife species and a prototype oral bait delivery system has been developed. Prospects for the development of improved vaccines against bovine tuberculosis are promising and vaccination approaches could become very valuable in the control and eradication of bovine tuberculosis.

Key Words Tuberculosis; Vaccine; BCG; Cattle; Wildlife; Mycobacterium bovis

Citation

Buddle, B. M., M. A. Skinner, D. N. Wedlock, D. M. Collins, and G. W. de Lisle. 2002. New generation vaccines and delivery systems for control of bovine tuberculosis in cattle and wildlife. Veterinary Immunology and Immunopathology 87: 177-185.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Advances in the understanding of protective immune responses to tuberculosis are providing opportunities for the rational development of improved vaccines for bovine tuberculosis. Protection requires activation of macrophages through stimulation of a Th 1 type immune response. Ideally, a vaccine for cattle should induce protection without causing animals to react in a tuberculin test when exposed to Mycobacterium bovis. A number of new tuberculosis vaccines including attenuated M. bovis strains, killed mycobacteria, protein and DNA vaccines have been developed and many of these are being assessed in cattle. The requirements for a tuberculosis vaccine for wildlife differ from those for cattle. The major goal of a wildlife vaccine is to prevent the transmission of M. bovis to cattle and other wildlife. Although there are a number of technical problems associated with the development of a vaccine delivery system for wildlife, attenuated M. bovis vaccines administered via oral baits or aerosol spray to possums have already been shown to reduce the severity of a subsequent M. bovis infection.

Key Words Mycobacterium bovis, vaccines, delivery systems, cattle, wildlife reservoir

Citation

Buddle, B. M., M.A. Skinner, and M.A. Chambers. 2000. Immunological approaches to the control of tuberculosis in wildlife reservoirs. Veterinary Immunology and Immunopathology. 74:1-16.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Attempts to eradicate tuberculosis from cattle and farmed deer in some countries have been frustrated by the existence of wildlife reservoirs of Mycobacterium bovis infection. Possum control programmes in New Zealand using poisons have shown clearly that the brushtail possum is an important source of infection for cattle and farmed deer, and the sum of evidence strongly suggests that badgers serve as a source of infection for cattle in the UK. Bovine tuberculosis can only be eradicated from these countries by controlling M. bovis infection in both wildlife and domestic animals. The most promising options for control of M. bovis infection in wildlife in the longer term include the development of a tuberculosis vaccine for wildlife and a strategy for biological control of possums. The aim of this review is to address the problems and approaches involved in the control of wildlife tuberculosis from an immunological perspective.

Key Words Mycobacterium bovis; Vaccination; Diagnosis; Wildlife reservoir; Possum; Badger

Citation

Buhr, B., K. McKeever, and K. Adachi. 2009. Economic impact of bovine tuberculosis on Minnesota's cattle and beef sector. University of Minnesota Extension Rapid Agricultural Response Fund.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

This report quantifies the economic impacts of BTB on Minnesota beef cattle producers and related industries. Representative cattle production systems are simulated and the costs of BTB response are incorporated into these systems using a partial budgeting approach. A partial equilibrium market model is then used to simulate the impact of these cost increases on the production of cattle and the prices received by the beef industry in Minnesota. This model also allows for changing assumptions regarding price discounts cattle producers might face given the BTB positive status. Finally, an input-output analysis using IMPLAN is used to evaluate the total economic impacts on related sectors and employment will for the counties affected and Minnesota.

Key Words

bovine tuberculosis, cattle, cost, deer, disease transmission, Michigan, Mycobacterium bovis, Odocoileus virginianus

Citation

Butler, K. L., S. D. Fitzgerald, D. E. Berry, S. V. Church, W. M. Reed, and J. B. Kaneene. 2001. Experimental Inoculation of European Starlings (Sturnus vulgaris) and American Crows (Corvus brachyrhynchos) with Mycobacterium bovis. Avian Diseases 45(3):709-718.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The purpose of this series of pilot studies was to determine whether the passerine species studied are susceptible to infection with Mycobacterium bovis. Separate experiments were conducted on wild-caught starlings (Sturnus vulgaris) and American crows (Corvus brachyrhynchos). In each experiment, four birds were challenged intraperitoneally and four were challenged orally with microorganisms. Challenge dose was 1 x 10^5 colony-forming units of M. bovis cultured from a white-tailed deer (Odocoileus virginianus) case in Michigan. Birds were euthanatized at 1 and 2 mo postinoculation. Histologic lesions suggestive of mycobacteriosis, without the presence of acid-fast bacilli, were noted in all experimental groups. Mycobacterial cultures performed on pooled tissue samples were positive for M. bovis in only some of the intraperitoneal inoculates of each species.

Key Words bovine tuberculosis, starling, crow, mycobacteria, wildlife

Citation

Caley, P. and D. Ramsey. 2001. Estimating disease transmission in wildlife, with emphasis on leptospirosis and bovine tuberculosis in possums, and effects of fertility control. Journal of Applied Ecology 38: 1362-1370.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. We present methods for estimating disease transmission coefficients in wildlife, using Leptospira interrogans infection (a bacterial disease transmitted predominantly during social contacts) in brushtail possums Trichosurus vulpecula as a model system.
2. Using data from a field experiment conducted on a naturally infected possum population, we estimated disease transmission coefficients assuming either 'densitydependent' or 'frequency-dependent' transmission.
3. A model-selection approach determined that density-dependent transmission was the most appropriate form of the transmission of L. interrogans infection in brushtail possums.
4. We used the chosen model of transmission to examine experimentally the effect of tubally ligating female brushtail possums on the epidemiology of L. interrogans. The estimated transmission coefficient was 28% higher (P= 0·16) in populations subject to tubal ligation, raising the possibility that fertility control of this type may increase disease transmission rates.
5. Altering mating behaviour through fertility control may have the potential to control diseases such as bovine tuberculosis in brushtail possums, although the potential of fertility control techniques to change disease transmission coefficients and disease epidemiology requires further investigation. This would require models that examine the combined effects of fertility control on population dynamics, social behaviour and disease transmission coefficients simultaneously.

Key Words epidemiology, Leptospira interrogans, modelling, Mycobacterium bovis, Trichosurus vulpecula

Citation

Caley, P. and J. Hone. 2004. Disease transmission between and within species, and the implications for disease control. Journal of Applied Ecology. 41:94-104.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Disease transmission can occur between and within species for diseases with multiple hosts. If these diseases are undesirable, for economic or health reasons, then the relative importance of each type of transmission should be determined. Bovine tuberculosis (Tb) caused by Mycobacterium bovis is one such undesirable disease.
2. In parts of New Zealand, M. bovis infection is highly prevalent in feral ferret Mustela furo populations, and there is concern they may be acting as a reservoir of infection for domestic livestock, similar to the role played by brushtail possums Trichosurus vulpecula. We undertook a manipulative large-scale field experiment to test for and quantify interspecific transmission of M. bovis from brushtail possums to feral ferrets, and intraspecific transmission of M. bovis within feral ferret populations.
3. Age-specific prevalence data obtained from cross-sectional surveys was modelled to estimate the effect of experimental reductions in possum population density on the force of M. bovis infection in ferrets. A simple analysis estimated the force of M. bovis infection in ferrets to be reduced by 88% at sites previously subjected to a possum population density reduction. A more detailed analysis, incorporating ferret survey data from both before and after possum population density reduction and controlling for the effect of ferret sampling, estimated that possum population density reduction decreased the force of M. bovis infection in ferrets by 29% at sites of high ferret density, and 88% at sites of low ferret density, compared with experimental control sites.
4. There is clearly substantial possum-to-ferret transmission of M. bovis, and controlling possum populations is the logical first step to managing M. bovis infection in ferret populations, especially at sites with low ferret density. Intra-specific transmission is virtually absent in low density ferret populations though evident at higher densities.
5. Synthesis and applications. These results have management implications for other multiple-host diseases around the world, such as bovine tuberculosis and rabies. Control of within-species transmission may not be as effective for disease control as a reduction in between-species transmission. The management decision should be based on empirical estimates of the magnitude of each form of transmission.

Key Words bovine tuberculosis, epidemiology, modelling, Mustela furo, Trichosurus vulpecula

Citation

Caley, P. and J. Hone. 2005. Assessing the host disease status of wildlife and the implications for disease control: Mycobacterium bovis infection in feral ferrets. Journal of Applied Ecology 42:708-719.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Estimating the basic reproductive rate (R0) of disease and/or the related threshold population density (KT) for disease establishment is fundamental to determining the host status of wildlife for disease, and thus the effective management of pathogens in free-ranging wildlife. The strength of inference of host status is largely dependent on the precision with which either R0 or KT is estimated, yet only a small proportion of studies of disease in wildlife have estimated the precision of these parameters.
2. We used a combination of observations, field experiments and modelling to estimate the basic reproductive rate of Mycobacterium bovis infection in ferrets Mustela furo in New Zealand. Estimates of R0 ranged from 0·18 at the lowest standardized annual density (0·5 ferrets km − 2) recorded, to 1·2 at the highest standardized annual density (3·4 ferrets km−2) recorded. The estimates of R0 were moderately imprecise, with a coefficient of variation of 37%.
3. The estimated threshold standardized annual density (KT) for disease establishment was 2·9 ferrets km−2 (95% confidence interval 1·7–10·6 ferrets km −2); however, only in limited geographical areas of New Zealand do ferret population densities exceed this. In these areas, ferrets would be considered maintenance hosts (R0> 1) for the disease, and active management (e.g. density reduction or vaccination) of ferrets would be required to eradicate M. bovis from ferret populations, in addition to the elimination of sources of interspecific transmission, notably brushtail possums Trichosurus vulpecula.
4. Synthesis and applications . The results have considerable implications for the management of M. bovis in ferret populations in New Zealand and elsewhere in the world. In areas of high ferret density, ferrets are probably a maintenance host of bovine tuberculosis, so active management is required to reduce disease incidence. More widely, the results demonstrate clearly how modelling and field observations may be combined to better inform managers of a wildlife disease.

Key Words bovine tuberculosis, epidemiology, maintenance host, modelling, Mustela furo , spill-over host, Trichosurus vulpecula

Citation

Caley, P., and J. Hone. 2002. Estimating the force of infection; Mycobacterium bovis infection in feral ferrets Mustela furo in New Zealand. Journal of Animal Ecology 71:44-54.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Summary
1. The force of Mycobacterium bovis infection (lamba) in feral ferret Mustela furo populations in New Zealand was estimated, by fitting candidate models to age-specific disease-prevalence data. The candidate models were constructed from a set of a priori hypotheses of how M. bovis infection is transmitted to ferrets, and model selection used to assess the degree of support for each hypothesis.
2. The estimated force of M. bovis infection ranged between five sites from 0·14/year to 5·8/year, and was twofold higher in males than in females.
3. The data most strongly supported the hypothesis that transmission of M. bovis to ferrets occurs from the ingestion of
M. bovis-infected material from the age of weaning, as modelled by the force of infection being zero up to the age of weaning, and constant thereafter. Other candidate transmission hypotheses (e.g. mating, suckling, routine social
interaction) and combinations thereof were unsupported in comparison, and hence it was concluded that transmission from these postulated mechanisms must be insignificant compared with dietary-related transmission.
4. The preferred transmission hypothesis was nearly equally supported regardless of whether disease-induced mortality was included or not, although omitting disease-induced mortality resulted in a lower force of infection estimate. The dietary transmission hypothesis (omitting disease-induced mortality) could be easily represented by a generalized
linear model, enabling simple analysis of critical experiments designed to identify the source of M. bovis infection in feral ferrets.

Key Words bovine tuberculosis, ferret, force of infection

Citation

Caley, P., N. J. Spencer, R. A. Cole, and M. G. Efford. 1998. The effect of manipulating population density on the probability of den-sharing among common brushtail possums, and the implications for transmission of bovine tuberculosis. Wildlife Research 25:383–392.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Common brushtail possums (Trichosurus vulpecula) act as a reservoir of bovine tuberculosis (Mycobacterium bovis) in New Zealand and the simultaneous sharing of dens may result in the transmission of Tb between possums. The effect of manipulating population density on the per capita probability of simultaneous den-sharing among possums was investigated at a site near Dunedin, New Zealand. Den characteristics that could affect the probability of simultaneous sharing were also investigated, though none were found to be significant. The daily probability of a possum sharing a den was estimated to be 0.07 for possums denning within uncontrolled areas of the study area. Den-sharing was most common between female pairs, though sharing was also recorded between male–female and male–male pairs. The highest number of possums recorded sharing a single den was four. Reducing population density significantly lowered the probability of possums simultaneously sharing dens within the study area, with greater than 60% reductions estimated to eliminate simultaneous den-sharing altogether. The relationship between the contact rate arising from den-sharing and population density was convex-down, rather than convex-up, as often hypothesised for animal–animal disease contact processes. The implications of simultaneous densharing for the transmission and control of bovine tuberculosis in brushtail possum populations are discussed.

Key Words population, density, brushtail possum, transmission, den-sharing

Citation

Carstensen, M., D. Pauly, M. DonCarlos, and L. Cornicelli. 2007. Managing bovine tuberculosis in white-tailed deer in northwestern Minnesota: A 2007 Progress Report. Minnesota Department of Natural Resources.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

Summary of Findings - Bovine tuberculosis (TB), first discovered in 2005, has now been found in 11 cattle operations in northwestern Minnesota. To date, all of the infected cattle herds have been depopulated and the Board of Animal Health (BAH) has continued an investigation of herds in the area as well as conducted a statewide surveillance effort. The strain has been identified as one that is consistent with bovine TB found in cattle in the southwestern United States and Mexico. In November 2007, the Minnesota Department of Natural Resources (MNDNR) conducted bovine TB surveillance of hunter-harvested white-tailed deer (Odocoileus virginianus) within a 15-mile radius of the infected farms. Results indicated that 5 of the 1,085 deer tested positive for bovine TB; estimated disease prevalence of 0.46% (SE=0.2%). All infected deer were harvested within 5 miles of Skime, Minnesota, which is in close proximity to 7 of the infected livestock operations. In response to additional deer found infected with bovine TB since 2005, the MNDNR also conducted a targeted deer emoval operation during winter 2007, using sharpshooters from the United States Department of Agriculture (USDA) Wildlife Services. An additional 488 deer were removed through this project, yielding 6 more cases of infected deer. Further, a recreational feeding ban, covering 4,000 mi2 in northwestern MN, was instituted in November 2006 to help reduce the risk of deer to deer transmission of the disease and enforcement officers have been working to stop illegal feeding activities. Also, in 2006, the Minnesota State Legislature passed an initiative that allocated $54,000 to deer-proof fencing materials for livestock producers within 5 miles of a previously infected farm; MNDNR erected 15 fences on 11 cattle premises during summer 2007. The findings of additional infection in cattle herds as well as the deer has resulted in the downgrading of Minnesota's bovine TB status to "modified accredited", which has increasing testing requirement for cattle statewide. The MNDNR will continue to conduct hunter-harvested surveillance in fall 2008 to monitor infection in the local deer population, and consider the continuation of aggressive management actions (e.g., sharpshooting deer in key locations) to address concerns of deer becoming a potential disease reservoir.

Key Words Report, Northwestern Minnesota, Department of Natural Resources, MNDR

Citation

Carstensen, M., E. Butler, M. DonCarlos, and L. Cornicelli. 2008. Managing bovine tuberculosis in white-tailed deer in northwestern Minnesota: A 2008 Progress Report. Minnesota Department of Natural Resources.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

Summary of Findings - Bovine tuberculosis (TB), first discovered in 2005, has now been found in 12 cattle operations in northwestern Minnesota. To date, all of the infected cattle herds have been depopulated and the Board of Animal Health (BAH) has continued to test cattle herds in the area. The strain has been identified as one that is consistent with Bovine TB found in cattle in the southwestern United States and Mexico. In response to the disease being detected in cattle, the Minnesota Department of Natural Resources (MNDNR) began surveillance efforts in free-ranging white-tailed deer (Odocoileus virginianus) within a 15-mile radius of the infected farms in fall 2005. To date, 25 deer have been found infected with Bovine TB. All infected deer were sampled within a 164mi2 area, called the Bovine TB Core, which is centered in Skime, Minnesota, and encompasses 8 of the previously infected cattle farms. In fall 2008, Minnesota was granted a Split-State Status for Bovine TB by the United States Department of Agriculture (USDA) that resulted in a lessening of testing requirements for cattle in the majority of the state (status level = "Modified Accredited advanced"), with a small area in northwestern Minnesota remaining more restrictive (status level = "Modified Accredited"). Also in 2008, the Minnesota State Legislature passed an initiative that allocated funds to buy-out cattle herds located in the Bovine TB Management Zone, spending $3 million to remove 6,200 cattle from 46 farms by January 2009; resulting in the discovery of the 12th infected cattle herd. The remaining cattle farms in the Bovine TB Management Zone (n = 27) were required to erect deer-exclusion fencing to protect stored forage and winter feeding areas, costing an additional $690,000 in state funds. In November 2008, the MNDNR conducted Bovine TB surveillance of hunter-harvested white-tailed deer within the newly created Modified Accredited Zone, and results indicated that none of the 1,246 deer tested were positive for the disease. This marked the first large scale surveillance effort that failed to detect the disease in hunter-harvested deer since sampling efforts began in 2005. MNDNR also conducted targeted removal operations in the Bovine TB Core Area, using both aerial and ground sharpshooting, during winters 2007, 2008 and 2009. These intensive winter deer removal operations removed a combined total of 2,163 deer and detected 13 (52%) of the TB-positive deer discovered to date. Further, a recreational feeding ban, covering 4,000mi2 in northwestern MN, was instituted in November 2006 to help reduce the risk of deer to deer transmission of the disease and enforcement officers have been working to stop illegal feeding activities. The MNDNR will continue to conduct hunter-harvested surveillance for the next 5 years to monitor infection in the local deer population, and consider the continuation of aggressive management actions (e.g., sharpshooting deer in key locations) to address concerns of deer becoming a potential disease reservoir.

Key Words Report, Northwestern Minnesota, Department of Natural Resources, MDNR

Citation Chambers, M. A. 2009. Review of the diagnosis and study of tuberculosis in non-bovine wildlife species using immunological methods. Transboundary and Emerging Diseases 56:215–227.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract The infection of a variety of free-ranging wildlife species with Mycobacterium bovis, the causative agent of bovine tuberculosis (TB), can cause problems for biodiversity and species conservation. In some notable cases, particular species act as a reservoir of infection that can spill over into domestic livestock with economic and zoonotic consequences. Immunological methods for the detection of TB infection in wildlife are important for diagnostic and research purposes, especially where post-mortem examination is neither feasible nor desirable. In this review, the approaches taken to the immunological study of TB in wildlife species are summarized, with particular emphasis on their suitability for different applications and their applicability to different species. Different approaches to improving diagnostic sensitivity are discussed together with factors that can confound the use of tests in certain situations. Caution in the interpretation of test results for TB in wildlife is encouraged, especially where it has not been possible to confirm the accuracy of the test.

Key Words Mycobacterium bovis, enzyme-linked immunosorbent assay, serology, cell-mediated immunity, test

Citation

Chambers, M.A., K.P. Lyashchenko, R. Greenwald, J. Esfandiari, E. James, L. Barker, J. Jones, G. Watkins, and S. Rolfe. 2010. Evaluation of a rapid serological test for the determination of Mycobacterium bovis infection in badgers (Meles meles) found dead. Clinical and Vaccine Immunology 17(3):408-411.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Between October 2005 and May 2006, a total of 727 badgers found dead in Wales were reported, and 550 were delivered to the Regional Laboratories of the Veterinary Laboratories Agency (VLA). Of the 459 carcasses suitable for examination, 55 were deemed to be infected with Mycobacterium bovis on the basis of culture, spoligotyping, and variable-number tandem repeat typing. Acid-fast bacteria were observed histologically in a further six badgers, but these bacteria were not confirmed as M. bovis by culture. A rapid serological test (BrockTB Stat-Pak) performed on thoracic blood showed a sensitivity of 35% and a specificity of 99%. Presence of M. bovis infection was 45 times more likely to be confirmed postmortem by culture in BrockTB Stat-Pakreactive animals than in seronegative ones. Using visible carcass lesions as a marker of bovine tuberculosis (bTB) infection had a similar sensitivity (38%) but was significantly less specific (84%) than serology. The overall accuracy of the antibody detection was 93% (346 correct results from 374 tests), whereas the accuracy of regarding visible lesions as a marker for bTB infection was 78% (354 correct from 453 carcasses examined).
Culture remains the gold standard method for detecting M. bovis infection in badgers. However, where resources are limited and/or an instant result is preferred, the BrockTB Stat-Pak could be used in field surveillance efforts to identify animals which should be examined further by only submitting test-negative animals to more detailed postmortem examination and culture.

Key Words badger, bovine tuberculosis, Meles meles, Mycobacterium bovis, serological test

Citation

Clarke K.R., S. D. Fitzgerald, L. S. Zwick, S. V. Church, J. B. Kaneene, A. R. Wismer, C. A. Bolin, J. A. Hattey, and V. Yuzbasiyan-Gurkan. 2007. Experimental Inoculations of meadow voles (Microtus pennsylvanicus), house mice (Mus musculus), and Norway rats (Rattus norvegicus) with Mycobacterium bovis. Journal of Wildlife Diseases 43(3): 353-365.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis has a wide host range that includes several wildlife species, and this can hamper attempts to eradicate bovine tuberculosis from livestock. The purpose of this study was to determine if common rodent species, namely meadow voles (Microtus pennsylvanicus), house mice (Mus musculus), and Norway rats (Rattus norvegicus), that inhabit the bovine tuberculosis endemic area of Michigan, can be experimentally infected with M. bovis. The objectives of the study were: 1) to determine if these rodent species can be infected, and if so, to document attendant pathologic processes/pathogenesis; 2) to detect any fecal shedding of M. bovis; and 3) to evaluate the relative susceptibility of the three species to M. bovis infection. For each species (n536) there were two treatment (n512/group) and one or two control groups depending on species (n56–12/group); the maximum study duration was 60 days. The meadow vole treatments consisted of high dose inocula that were given by oral or intranasal routes, whereas the house mice and Norway rats were given only oral inocula at either a high or low dose. Of the three species, meadow voles were most susceptible to M. bovis infection. Upon intranasal inoculation, all 12 voles were infected as determined by gross and microscopic lesions and culture of M. bovis from tissue and feces. Seven of the 12 meadow voles inoculated orally were infected. House mice also were susceptible; M. bovis was isolated from 14 of 24 animals. Only one Norway rat in the high dose treatment group was positive by culture and this was the only animal from which minimal attendant lesions were observed. Results of this study indicate that meadow voles and house mice can be infected with M. bovis and might serve as spillover hosts. Concerted efforts should, therefore, be made to reduce or eliminate these rodents on premises where M. bovisinfected livestock are present.

Key Words Bovine tuberculosis, Microtus pennsylvanicus, Mus musculus, mycobacteriosis, Mycobacterium bovis, rodents, Rattus norvegicus

Citation

Clifford, D. L., B. A. Schumaker, T. R. Stephenson, V. C. Bleich, M. L. Cahn, B. J. Gonzales, W. M. Boyce, J. A.K. Mazet. 2009. Assessing disease risk at the wildlife–livestock interface: a study of Sierra Nevada bighorn sheep. Biological Conservation 142:2559–2568.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Despite evidence that domestic sheep diseases threaten the persistence of bighorn sheep populations, the economic consequences of restricting domestic sheep grazing has polarized the debate, with some arguing that disease risk posed by domestic sheep has been exaggerated and grazing restrictions should be eased. We constructed a model to assess how different management strategies (grazing allotment closures, grazing time reductions, and reduced probability of stray domestic sheep) affect the risk of respiratory disease transmission from domestic sheep to endangered Sierra Nevada bighorn sheep, and to predict population-level impacts of an outbreak. Even when management strategies reduced risk of interspecies contact to less than 2% per year, our model predicted a 50% probability of a catastrophic respiratory disease outbreak during the next 10 bighorn sheep generations. If an outbreak occurs in the near future, the model predicts that the smallest Sierra Nevada bighorn sheep population would have a 33% probability of quasi-extinction. To eliminate all risk of contact and potential disease transmission, domestic sheep cannot be grazed on allotments that overlap with areas utilized by Sierra Nevada bighorn sheep. Where wildlife and domestic animal populations share limited habitat, and there is documented evidence of a substantial disease threat and extinction risk, stakeholders must recognize that the only way to eliminate contact and risk of disease transmission is to give priority to one species or the other. If conservation is the priority, difficult decisions will need to be made to balance trade-offs between economic livelihoods and species conservation.

Key Words Risk assessment, Modeling, Domestic sheep, Pasteurella, Ovis aries, Ovis canadensis sierrae

Citation

Coleman, J.D. and M. M. Cookes. 2001. Mycobacterium bovis infection in wildlife in New Zealand. Tuberculosis 81(3):191-202.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (Tb) is the most important disease of livestock in New Zealand, and it puts at risk the nation's trade in dairy, beef and venison products. Elimination of the disease from livestock is based on a herd test and slaughter programme and carcass inspection at abbatoirs. However, this programme has not been as successful as expected, because the disease also occurs in wild or feral animals acting as vectors of the disease to livestock. Brushtail possums are the major wildlife vector and self-sustaining maintenance host of Tb, and play a role analogous to that of the badger in Great Britain. In contrast, some deer species and ferrets may act as vectors of the disease, but their role in transmitting Tb to livestock is unclear. Hedgehogs, pigs, cats, sheep and goats are now considered to be amplifier hosts, and spread the disease to other species only when inspected or their carcasses scavenged. In the absence of infected possum populations, these species do not appear to be capable of maintaining the infection in their own populations and are not thought to be involved in the maintenance of Tb in livestock. Tuberculosis has also been recorded from stoats, hares, and a rabbit, but the level of infection recorded in their populations indicates these species are unlikely to spread the disease to other animals and hence are not involved in the transmission of Tb to livestock.

Key Words

wildlife, New Zealand, livestock, amplifier hosts

Citation

Corner, L. A. L. 2001. Bovine tuberculosis in brushtail possums (Trichosurus vulpecula): studies on vaccination, experimental infection, and disease transmission. Thesis. Massey University, New Zealand.

Abstract Only ☐

No Abstract ☐

Article Type Thesis

Abstract

The objectives of the research program were to obtain a better understanding of BCG as a tuberculosis vaccine in possums, and assess its potential as a tool for controlling tuberculosis in wild possum populations. A series of vaccination and challenge experiments were conducted, as well as studies on alternative experimental infection procedures. The program included two field studies, one on the epidemiology of tuberculosis in a population of possums regenerating after localised possum eradication, and the other examined the efficacy of BCG vaccine in a wild population in which tuberculosis was endemic.

The first experiments confirmed the earlier published findings that BCG delivered as an intranasal aerosol induced a protective response. The protective response was found to be present 12 months after vaccination and therefore of sufficient longevity to make vaccination a practical control tool. A second study demonstrated that revaccination of possums enhanced protection and a third showed that conjunctival vaccination was as effective as intranasal aerosol. These findings supported the development of a possum activated self-vaccinator that would deliver vaccine as an aerosol. In delivering the spray to both the external nares and the eyes a simple and cheap device could be designed to efficiently vaccinate wild possums.

The intratracheal experimental infection procedure used in the vaccination and challenge experiments was not entirely suitable for our purposes. Although it provided an assured level of exposure and repeatable results, all infected possums developed fulminant, rapidly progressive disease, irrespective of the vaccination regime used. Two alternative methods of challenge were examined; the conjunctival route of infection, and natural transmission between experimentally infected possums and susceptible in-contact possums. Conjunctival infection was shown to be a reliable procedure for infecting possums, with the disease that resulted from infection having many of the cardinal features of natural tuberculosis in wild possums. Infection following conjunctival inoculation progressed slowly and may be suitable for studying pseudo-vertical transmission and the efficacy of post-infection vaccination.

In studies with captive possums there was little or no transmission of infection between experimentally infected possums and susceptible in-contact possums in the same pen when the experimentally infected animals were selected at random. However, when possums with high levels of social interaction were experimentally infected there was a significant increase in transmission rates. In addition, the possums that became infected by transmission were more socially active than those that remained free of infection.

Two aspects of the pathogenesis of tuberculosis in possums were clarified during the experimental infection and natural transmission studies. The duration of preclinical infection, impossible to determine accurately in longitudinal studies on wild possums, was found to range from 6 - 20 weeks. Secondly, the pre-eminence of the aerosol route in naturally transmitted tuberculosis was confirmed.

After eradication of possums from a 36 ha site, tuberculosis reappeared within four months. Re-emergence of infection on the site was due to immigration of infected possums, not to the survival of M. bovis in the environment. Each of the four restriction endonuclease analysis (REA) types of M. bovis that caused disease in the possum population showed a different temporal and spatial pattern.

BCG vaccine had high efficacy in a wild possum population. Over 2 years, 300 possums were recruited to a study of BCG vaccination. Approximately 50% of the possums were vaccinated, where each possum was vaccinated using both intranasal aerosol and conjunctival instillation. There were significantly more cases of tuberculosis in unvaccinated possums than in vaccinates, with a relative risk of tuberculosis in unvaccinated possums of 3.21. The vaccine efficacy was 69%. The most important question relating to BCG vaccine that remains to be addressed is the ability of vaccination to control tuberculosis in possum populations.

This research has demonstrated that BCG vaccine provided protection against M.bovis infection in both captive and wild possums. Future research should be directed towards developing delivery systems for vaccinating wild possums and strategies for vaccine use in wild tuberculous possum populations.

Key Words brushtail possum, Trichosurus vulpecua, vaccination, transmission, experimental infection, BCG

Citation	Corner, L. A. L. 2006. The role of wild animal populations in the epidemiology of tuberculosis in domestic animals: How to assess the risk. Veterinary Microbiology 112:303–312.
Abstract Only	☐
No Abstract	☐
Article Type	Journal Article
Abstract	Tuberculosis is present in wild animal populations in North America, Europe, Africa and New Zealand. Some wild animal populations are a source of infection for domestic livestock and humans. An understanding of the potential of each wild animal population as a reservoir of infection for domestic animals is reached by determining the nature of the disease in each wild animal species, the routes of infection for domestic species and the risk of domestic animals encountering an infectious dose. The mere presence of infection in a wild animal population does not of itself provide evidence of a significant wildlife reservoir. Although at times counterintuitive, wildlife populations with high disease prevalence may not necessarily have a role in the epidemiology of disease in domestic livestock. The key concepts used in deciding whether an infected wild animal population is involved in the epidemiology of tuberculosis in domestic livestock is illustrated by reference to six well-researched cases: the feral pig (Suis scrofa) and feral Asian water buffalo (Bubalus bubalis) in Australia, white tailed deer (Odocoileus virginianus) in Michigan, and the brushtail possum (Trichosurus vulpecula) and other species, such as the ferret (Mustela furo), in New Zealand. A detailed analysis of Mycobacterium bovis infection in the Eurasian badger (Meles meles) in Ireland and their role as a reservoir of infection for cattle is also presented.
Key Words	tuberculosis, epidemiology, domestic livestock, wild animals, Mycobacterium bovis

Citation

Corner, L. A. L., D. Murphy, E. Costello, and E. Gormley. 2009. Tuberculosis in European badgers (Meles meles) and the control of infection with bacille calmette-gue rin vaccination. Journal of Wildlife Diseases 45(4):1042–1047.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The eradication of tuberculosis (Mycobacterium bovis infection) from cattle herds may be compromised if infected wildlife species, such as European badgers (Meles meles), share the same environment and contribute to transfer of infection. Options for dealing with tuberculosis in this wild reservoir host are limited by conservation and social concerns, despite a clear implication that infected badgers are involved with the initiation of tuberculosis in cattle herds. Vaccination of badgers against M. bovis, if successfully employed, would directly facilitate the completion of bovine tuberculosis eradication in affected areas. Vaccine trials in captive badgers have established that the M. bovis bacille Calmette-Gue´ rin (BCG) vaccine can induce a protective response that limits the distribution and severity of tuberculosis disease following experimental challenge. The protective effect of the vaccine has been demonstrated when the vaccine was delivered by subcutaneous injection, deposited on mucous membranes, and given orally in a lipid formulation. A large-scale field trial of oral BCG vaccine has been designed to measure the protection generated in wild badgers subjected to natural transmission of infection and to estimate vaccine efficacy. These parameters will be estimated by comparing the prevalence of M. bovis infection in vaccinated and nonvaccinated badgers. The results will provide a framework for the development and implementation of a national strategy to eliminate the disease in badger populations and if successful will remove this major impediment to bovine tuberculosis eradication.

Key Words badger, Meles meles, tuberculosis, Mycobacterium bovis, BCG vaccine

Citation

Corner, L. A. L., E. Costello, S. Lesellier, D. O'Meara, D.P. Sleeman, E. Gormley. 2007. Experimental tuberculosis in the European badger (Meles meles) after endobronchial inoculation of Mycobacterium bovis: I. Pathology and bacteriology. Research in Veterinary Science 83:53–62.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The aim was to develop an endobronchial infection procedure for the study of Mycobacterium bovis infection in badgers. The badgers were anaesthetised and a cannula was passed per os to the tracheal bifurcation. When in place 1 ml of M. bovis suspension was inoculated. Three concentrations of M. bovis suspension were used; <10 colony forming units (cfu), ~10^2 cfu and ~3 x 10^3 cfu. The badgers were examined at three weekly intervals for clinical signs of disease and a tracheal aspirate was collected at each examination. The badgers were euthanased 17 weeks post infection (pi) and at the post mortem examination a wide range of tissues were examined for gross and histopathological lesions of tuberculosis and cultured for M. bovis. A sample of bronchial alveolar lavage (BAL) fluid was collected at post mortem for culture. At post mortem examination 17 weeks after infection, gross and histopathological lesions of tuberculosis were observed in all badgers inoculated with the high and medium dose and 1/3 inoculated with the low dose. M. bovis was recovered from all inoculated badgers. Infection in the high dose group was more widely disseminated than in the other groups. The number of sites with gross and histopathological lesions increased with increasing dose of M. bovis. All tracheal aspirates were negative on culture and only one BAL, collected from a badger of the high dose group, was positive on culture. No clinical signs due to the experimental infection were observed. The endobronchial route of inoculation is an effective route for establishing experimental infection, and could be used for studies of tuberculosis pathogenesis, immunology of M. bovis infection in badgers and for challenging badgers in vaccine protection studies. Badgers appeared to be very susceptible to infection by this procedure even with a dose of <10 cfu but appear to control and limit the resulting infection.

Key Words badger, tuberculosis, Mycobacterium bovis, endobronchial infection, experimental infection, pathogenesis

Citation

Courtenay, O., L.A. Reilly, F.P. Sweeney, V. Hibberd, S. Bryan, A. Ul-Hassan, C. Newman, D.W. Macdonald, R.J. Delahay, G.J. Wilson and E.M.H. Wellington. 2006. Is Mycobacterium bovis in the environment important for the persistence of bovine tuberculosis? Biology Letters. 2:460-462.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis is the causative agent of bovine tuberculosis (bTB) in cattle and wildlife. Direct aerosol contact is thought to be the primary route of infection between conspecifics, whereas indirect transmission via an environmental reservoir of M. bovis is generally perceived not to be a significant source for infection. Here, we report on the application of molecular technology (PCR) to quantify the prevalence of M. bovis in the environment and to explore its epidemiological significance. We show that the detectability of viable M. bovis at badger setts and latrines is strongly linked to the frequency of M. bovis excretion by infected badgers, and that putative M. bovis in the environment is prevalent on a large proportion of endemic cattle farms in Britain. These results raise important questions about the role of an environmental reservoir in bTB persistence.

Key Words badger, bovine tuberculosis, environment, Meles meles, Mycobacterium bovis, survival

Citation

Cross, M. L., B.M. Buddle, and F.E. Aldwell. 2007. The potential of oral vaccines for disease control in wildlife species. The Veterinary Journal 174:472–480.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Numerous infectious diseases caused by bacteria or viruses persist in developed and developing countries due to ongoing transmission among wildlife reservoir species. Such diseases become the target of control and management programmes in cases where they represent a threat to public health (for example rabies, sylvatic plague, Lyme disease), or livestock production (for example bovine tuberculosis, brucellosis, pseudorabies), or where they threaten the survival of endangered animal populations. In the majority of cases, lethal control operations are neither economically feasible nor publicly supported as a practical means for disease management. Prophylactic vaccination has emerged over the last 15 years as an alternative control strategy for wildlife diseases, mainly driven by the success of widescale oral rabies vaccination programmes for meso-carnivores in North America and Northern Europe. Different methods have been trialled for the effective delivery of wildlife vaccines in the field, however oral vaccination remains the most widely used approach. Successful implementation of an oral wildlife vaccine is dependent on a combination of three components: an efficacious immunogen, a suitable delivery vehicle, and a species-specific bait. This review outlines the major wildlife disease problems for which oral vaccination is currently under consideration as a disease management tool, and also focuses on the technological challenges that face wildlife vaccine development. The major conclusion is that attenuated or recombinant live microbes represent the most widely-used vaccines that can be delivered by the oral route; this in turn places major emphasis on effective delivery systems (to maintain vaccine viability), and on selective baiting systems, as the keys to wildlife vaccine success. Oral vaccination is a valuable adjunct or alternative strategy to culling for the control of diseases which persist in wildlife reservoirs.

Key Words oral vaccine, wildlife, rabies, tuberculosis

Citation

Cross, P. C., D. M. Heisey, J. A. Bowers, C. T. Hay, J. Wolhuter, P. Buss, M. Hofmeyr, A. L. Michel, R. G. Bengis, T. L. F. Bird, J. T. Du Toit, and W. M. Getz. 2008. Disease, predation and demography: assessing the impacts of bovine tuberculosis on African buffalo by monitoring at individual and population levels. Journal of Applied Ecology 46:467–475.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Understanding the effects of disease is critical to determining appropriate management responses, but estimating those effects in wildlife species is challenging. We used bovine tuberculosis (BTB) in the African buffalo Syncerus caffer population of Kruger National Park, South Africa, as a case study to highlight the issues associated with estimating chronic disease effects in a long-lived host.
2. We used known and radiocollared buffalo, aerial census data, and a natural gradient in pathogen prevalence to investigate if: (i) at the individual level, BTB infection reduces reproduction; (ii) BTB infection increases vulnerability to predation; and (iii) at the population level, increased BTB prevalence causes reduced population growth.
3. There was only a marginal reduction in calving success associated with BTB infection, as indexed by the probability of sighting a known adult female with or without a calf (P= 0·065).
4. Since 1991, BTB prevalence increased from 27 to 45% in the southern region and from 4 to 28% in the central region of Kruger National Park. The prevalence in the northern regions was only 1·5% in 1998. Buffalo population growth rates, however, were neither statistically different among regions nor declining over time.
5. Lions Panthera leo did not appear to preferentially kill test-positive buffalo. The best (Akaike'sInformation Criterion corrected for small sample size) AICc model with BTB as a covariate [exp(β) = 0·49; 95% CI = (0·24–1·02)] suggested that the mortality hazard for positive individuals was no greater than for test-negative individuals.
6. Synthesis and applications. Test accuracy, time-varying disease status, and movement among populations are some of the issues that make the detection of chronic disease impacts challenging. For these reasons, the demographic impacts of bovine tuberculosis in the Kruger National Park remain undetectable despite 6 years of study on known individuals and 40 years of population counts. However, the rainfall and forage conditions during this study were relatively good and the impacts of many chronic diseases may be a non-linear function of environmental conditions such that they are only detectable in stressful periods.

Key Words bovine tuberculosis, Syncerus caffer, detection, predator, disease, population growth

Citation

Daly, M., K. L. Diegel, S. D. Fitzgerald, A. Schooley, D. E. Berry, J. B. Kaneene. 2006. Patterns of antimicrobial susceptibility in Michigan wildlife and bovine isolates of Mycobacterium bovis. Journal of Veterinary Diagnostic Investigations 18:401–404.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The state of Michigan has recognized the presence of Mycobacterium bovis in its free-ranging white-tailed deer population since 1994. This endemic infection is primarily located in a 12-county area in the northeastern lower peninsula of Michigan. A statewide surveillance and eradication program of the disease has been in effect since 1994. Worldwide, Mycobacterium tuberculosis complex organisms have a known predilection toward development of antimicrobial resistance. The objective of this study was to investigate the antimicrobial susceptibility of M. bovis isolates from white-tailed deer in Michigan and detect any changes in susceptibility over time. M. bovis isolates from 2 fall hunting seasons (1999 and 2004) were used in this study. The fall season of 2004 marked the first documented case of direct transmission of M. bovis from a wild deer to a human in Michigan. Since M. bovis is a zoonotic disease, knowledge of susceptibility can expedite treatment options in humans. M. bovis isolates were obtained from 58 deer, 4 coyotes, 3 cattle, 2 raccoons, and 1 human case from the 2 years combined. Methods of susceptibility testing included 1% proportion agar plates and Bactec radiometric broth testing. M. bovis was found to be uniformly resistant to the antibiotic pyrazinamide; this resistance is common to all M. bovis isolates. No other antimicrobial resistance was found in any of the tested M. bovis isolates, which may be, in part, attributed to the lack of any significant treatment pressure in wildlife.

Key Words antimicrobial susceptibility, deer, Mycobacterium bovis, wildlife

Citation Daniels, M. J., M. R. Hutchings, and A. Greig. 2003. The risk of disease transmission to livestock posed by contamination of farm stored feed by wildlife excreta. Epidemiology and Infection 130:561–568.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Livestock feed is susceptible to contamination from wildlife excreta during on farm storage. Pathogens associated with diseases such as paratuberculosis, salmonella and cryptosporidiosis are present in wild rodent and bird excreta. Feed stores on four farms in the east of Scotland were monitored monthly over the winter of 1998/9 to quantify the levels of wildlife faecal contamination. A mean of 79.9 rodent (95% confidence interval: 37.5–165.9) and 24.9 (14.3–41.7) bird faeces were deposited per m2 of stored feed per month. It was estimated that individual cattle and sheep could encounter 1626 and 814 wildlife faeces over the winter. A model based on the numbers of infected faeces consumed per annum was used to estimate 'infectious probabilities ' (Pinf) required to account for the reported prevalence of paratuberculosis, salmonella and cryptosporidiosis in sheep and cattle in the east of Scotland in 1998. Based on empirical data for input variables [the number of faeces encountered (Fe), the number ingested (Fi) and the prevalence of infection in wildlife species (Ip)], Pinf estimates ranged from 1.6x10^-8 for cryptosporidiosis in sheep to 8.2x10^-6 for paratuberculosis in cattle. The model suggested that ingestion of feed contaminated by wildlife faeces could account for the prevalence of all three diseases. Wildlife faecal contamination of stored feed should be given serious consideration as a potential source of infection to livestock.

Key Words livestock, contamination, stored feed, excreta, wildlife

Citation de Kantor, I. N. and V. Ritacco. 1994. Bovine tuberculosis in Latin America and the Caribbean: current status, control and eradication programs. Veterinary Microbiology 40:5-14.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Out of the approximately 300 million head which constitute the bovine population in Latin America and the Caribbean, 80 million are found in countries where rates of Mycobacterium bovis infection are very low or nil. The remaining 220 million are found in countries with either a moderate to high prevalence or where no recent information is available. Argentina and Brazil, both have huge cattle populations with estimated prevalences higher than 1%, and together may harbour 3.5 million infected cattle. Information on the impact of M. bovis on human health in the Region is scarce and does not include data on infection of children. In Argentina, human tuberculosis of bovine origin was found to be mainly an occupational disease, transmitted by aerosol. Control or eradication has been achieved in several countries in the Region by use of the tuberculin test followed by sacrifice of reactors. In countries such as Cuba, where the prevalence is already very low, area tuberculin testing is being replaced by slaughter surveillance and epidemiological trace-back. Other countries, where the prevalence is high (e.g. Chile, Paraguay, Peru and Argentina), promote regional campaigns based on the decision and active participation of cattle farmers. Recent diagnostic developments based on the in vitro measurement of humoral and cellular immune responses could be an aid in control and eradication campaigns, provided their usefulness is demonstrated in field trials. In heavily infected areas complementary or alternative strategies should also be proposed, aiming at lowering the prevalence rates prior to the application of the test and slaughter method.

Key Words Mycobacterium bovis, cattle, tuberculosis, bovine, epidemiology, eradication

Citation

de la Lastra, J. M. P., R. C. Galindo, C. Gortazar, F. Ruiz-Fons, A. Aranaz, and J. de la Fuente. 2009. Expression of immunoregulatory genes in peripheral blood mononuclear cells of European wild boar immunized with BCG. Veterinary Microbiology 134:334–339.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The objective of this study was to analyze the expression of immunoregulatory genes in European wild boar (Sus scrofa) immunized with BCG. Eighteen immunoregulatory genes were selected for expression analysis based on their role in host immune response during tuberculosis and/or for their association with resistance to bovine tuberculosis in European wild boar populations. Initially, mRNA levels were analyzed by quantitative real-time reverse transcription PCR (qRT-PCR) in spleen samples from Mycobacterium bovis-infected (N = 18) and uninfected (N = 22) European wild boar. Statistical analysis of qRT-PCR data revealed that four genes, complement component C3, IFN-gamma, IL-4 and RANTES were downregulated in infected animals ($P < 0.05$). These genes were selected for analysis of mRNA levels in peripheral blood mononuclear cells (PBMCs) from seven wild boar experimentally immunized with BCG and seven non-immunized controls. Blood was collected at 0, 5, 13 and 25 weeks post-immunization (wpi). The mRNA levels of IFN-gamma and C3 showed a peak (>15-fold increase) at 5 wpi, whereas transcripts for RANTES and IL-4 showed a peak (>2-fold increase) at 13 wpi in BCG-immunized animals when compared to non-immunized controls. The pattern of expression of these genes over the time provides the first description of BCG specific immune response in European wild boar. These results provide new insights into the molecular basis of wild boar response to M. bovis infection and BCG vaccination and may be used to monitor BCG vaccination in this species.

Key Words wild boar, porcine, BCG, immunization, tuberculosis, signature, genomics, real-time RT-PCR

Citation

de Lisle, G. W., R. G. Bengis, S. M. Schmitt, and D. J. O'Brien. 2002. Tuberculosis in free-ranging wildlife: detection, diagnosis and management. Rev. sci. tech. Off. Int. Epiz. 21(2):317-334.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis is emerging as an important pathogen of free-ranging wildlife in which it is a potential source of infection for domestic animals and a threat to valuable wildlife species. This review examines the procedures for the detection, diagnosis and management of M. bovis in wildlife populations. The ante-mortem detection of M. bovis infection in wildlife is difficult, due to the common occurrence of subclinical infections and the deficiencies of the currently available diagnostic tests. Serological tests are insensitive, while tests measuring cell-mediated immune responses show promise, but have not been sufficiently developed for routine use in most species. The diagnosis of M. bovis in free-ranging wildlife relies on post-mortem examination supported by histopathology and microbiology. A feature of M. bovis infections is the variation in the appearance and distribution of lesions in the different host species. Bacterial culture remains the gold standard for diagnosis of tuberculosis, while histopathology iss limited by the frequent inability to distinguish lesions caused by M. bovis from those produced by other mycobacterial species. Deoxyribonucleic acid (DNA) fingerprinting and advanced typing techniques are increasingly being used to unravel the epidemiology of mycobacterial infections, including tuberculosis in free-ranging wildlife. And understandign of the epidemiology is essential if procedures are to be developed for the management of tuberculosis in wildlife. Few management options are currently available, especially for protected wildlife. Vaccination is the subject of much research, but further developments are required before it can be used to control tuberculosis in any animals, let alone in free-ranging wildlife.

Key Words Bovine Tuberculosis, diagnosis, Mycobacterium bovis, vaccination, wildlife

Citation

Delahay, R. J., A. N. S. De Leeuw, A. M. Barlow, R. S. Clifton-Hadley, and C. L. Cheeseman. 2002. The status of Mycobacterium bovis Infection in UK wild mammals: a review. The Veterinary Journal 164:90-105.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis caused by Mycobacterium bovis is a zoonotic infection with a wide range of mammalian hosts. In parts of the UK M. bovis infection in cattle is a persistent problem. The European badger (Meles meles) is implicated in the transmission of M. bovis to cattle, and is widely believed to constitute the most important reservoir of infection in UK wildlife. However, few studies have been carried out on the status of M. bovis infection in other UK mammals. In this review we present information on the incidence and pathology of M. bovis infection in UK wild mammals from both published and previously unpublished sources. Although the evidence does not support the existence of a significant self-maintaining reservoir of infection in any wild mammal other than the badger, there is a clear lack of sufficient data to rule out the involvement of other species. In the light of this and the dynamic nature of epidemiological patterns, further surveillance for M. bovis infection in UK wild mammals, using modern methods of diagnosis, is essential.

Key Words M. bovis, wildlife, bovine tuberculosis, United Kingdom, mammals

Citation

Delahay, R. J., C. L. Cheeseman, R. S. Clifton-Hadley. 2001. Wildlife disease reservoirs: the epidemiology of Mycobacterium bovis infection in the European badger (Meles meles) and other British mammals. Tuberculosis 81(1/2):43-49.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis infection has been confirmed in a wide range of mammals hosts throughout the world. The European badger (Meles meles) and the brushtail possum (Trichosurus vulpecula) are implicated as significant sources of infection for domestic cattle in the UK and New Zealand respectively. The risk of transmission of infection between a wildlife population and domestic animals will be determined by both the epidemiology of the disease and the ecology of the host. In the UK, surveys by the UK Ministry of Agriculture, Fisheries and Food (MAFF) have identified M. bovis infection in deer (Cervus sp., Capreolus sp., Dama sp.), red fox (Vulpes vulpes), mink (Mustela vison), feral ferret (Mustela furo), mole (Talpa europaea), brown rat (Rattus norvegicus) and feral cat (Felis catus). However, the potential contribution to cattle herd breakdowns, of reservoirs of M. bovis infection in mammals other than the badger is poorly understood and is the subject of current research. In contrast,M. bovis infection in the badger has been the subject of a long term ecological and epidemiological study at Woodchester Park in South-West England, where the prevalence and distribution of infection in a wild population has been intensively monitored. The pattern of infection in the population and potential risks to cattle, are profoundly influenced by badger social organization and behaviour. The pattern of land use and cattle farming practices in the UK brings badgers into close contact with domestic animals and provides conditions that may enhance the likelihood of disease transfer.

Key Words disease reservoir, epidemiology, European badger, Meles meles, brushtail possum, Trichosurus vulpecula, New Zealand

Citation

Delahay, R. J., G.J. Wilson, G.C. Smith, and C.L. Cheeseman. 2003. Vaccinating badgers (Meles meles) against Mycobacterium bovis: the ecological considerations. The Veterinary Journal 166:43–51.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (TB) is a serious zoonotic disease, which despite a largely successful test and slaughter programme has persisted in cattle herds in parts of the UK. The badger (Meles meles) is widely considered to represent a significant wildlife reservoir for the transmission of Mycobacterium bovis to cattle, and has been the subject of a variety of culling strategies since the mid 1970s. Nevertheless, the incidence of herd breakdowns has continued to rise, and the efficacy of culling is currently the subject of a largescale field trial. One potential alternative tool for the management of disease in wildlife populations is vaccination. However, the successful development of an effective vaccine and a strategy for its delivery will require careful consideration of the practical constraints imposed by ecological factors. In the current paper, we discuss relevant ecological and epidemiological characteristics of badger populations and practical aspects of vaccine delivery in the field.

Key Words badger, Bovine tuberculosis, vaccination, ecology, epidemiology, vaccine delivery

Citation

Delahay, R.J., G.C. Smith, A.M. Barlow, N. Walker, A. Harris, R.S. Clifton-Hadley, C.L. Cheeseman. 2007. Bovine tuberculosis infection in wild mammals in the south-west region of England: a survey of prevalence and a semi-quantitative assessment of the relative risks to cattle. The Veterinary Journal 173:287-301.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In the United Kingdom, badgers are implicated in the transmission of Mycobacterium bovis to cattle, but little information is available on the potential role of other wild mammals. This paper presents the results of the largest systematic UK survey of M. bovis infection in other wild mammals. Mammal carcasses (4715) from throughout the South-West region of England were subjected to a systematic post mortem examination, microbiological culture of tissues and spoligotyping of isolates. Infection was confirmed in fox, stoat, polecat, common shrew, yellow-necked mouse, wood mouse, field vole, grey squirrel, roe deer, red deer, fallow deer and muntjac. Prevalence in deer may have been underestimated because the majority were incomplete carcasses, which reduced the likelihood of detecting infection. Infected cases were found in Wiltshire, Somerset, Devon and Cornwall, Gloucestershire and Herefordshire. Lesions were found in a high proportion of spoligotype-positive fallow, red and roe deer, and a single fox, stoat and muntjac. M. bovis spoligotypes occurred in a similar frequency of occurrence to that in cattle and badgers. Data on prevalence, pathology, abundance and ecology of wild mammals was integrated in a semi-quantitative risk assessment of the likelihood of transmission to cattle relative to badgers. Although most species presented a relatively low risk, higher values and uncertainty associated with muntjac, roe, red and in particular fallow deer, suggest they require further investigation. The results suggest that deer should be considered as potential, although probably localised, sources of infection for cattle.

Key Words bovine tuberculosis, England, mammals, prevalence

Citation

Denny, G.O.and J. W. Wilesmith. 1999. Bovine tuberculosis in northern Ireland: case-control study of risk factors. Veterinary Record 144: 305-310.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

This paper presents the results of the first formal epidemiological study in Northern Ireland of risk factors for bovine tuberculosis (TB) associated with farm boundaries, neighbours and wildlife. The study was designed as a case-control study and 427 dairy herds were investigated between December 1993 and January 1995. The case herds had more than 30 cattle, and herds in which the source of infection had been ascribed to purchased cattle were avoided. Data on the Department of Agriculture Animal Health Computer were used in conjunction with data collected through a questionnaire to examine a range of possible risk factors, including the number and nature of the farm boundaries, the number of neighbours and their TB history, the number of hedgerows, the presence of badger setts, whether badger carcases had been found on the land, and the possible presence of deer. A follow-up telephone survey was conducted to minimise bias. The results highlighted two main associations with TB breakdowns, the presence of badgers, and contiguous neighbours who had had confirmed TB breakdowns. The estimated aetiological fraction for both associations was approximately 40 per cent, suggesting that although infected cattle may have a significant role in the transmission of TB their importance relative to the badger may have been over-estimated in the Northern Ireland TB scheme. The contribution of the badger is possibly one of several main reasons for the lack of significant progress in TB eradication despite strenuous efforts associated with all aspects of the scheme.

Key Words

Ireland, risk factors, farm boundaries, dairy herd, cattle, wildlife, badger, deer, survey, transmission

Citation

Diegel, K. L., S. D. Fitzgerald, D. E. Berry, S. V. Church, W. M. Reed, J. G. Sikarskie, and J. B. Kaneene. 2002. Experimental inoculation of North American opossums (Didelphis virginiana) with Mycobacterium bovis. Journal of Wildlife Diseases 38(2):275–281.

Abstract Only ☑

No Abstract ☐

Article Type Journal Article

Abstract

Eight North American opossums (Didelphis virginiana) were inoculated with 1x10^5 colony forming units of Mycobacterium bovis to investigate their potential as reservoir hosts for bovine tuberculosis in Michigan. Four animals received this dose orally and four were inoculated intramuscularly (IM). In each group, two animals were euthanized 1 mo postinoculation (PI) and two at 2 mo PI. Four control animals were housed separately and sacrificed in the same manner as those inoculated. One of four orally inoculated opossums and three of four Iminoculated opossums were positive for M. bovis by culture of tissues obtained at necropsy. The oral recipient had positive cultures from intestine and pooled lymphoid samples. Pooled lymphoid samples were positive in three IM-inoculated animals and two of these also had positive liver and lung cultures. One animal with gross and histologic lesions compatible with tuberculosis had negative tissue cultures. The findings suggest that opossums are susceptible to M. bovis infection by multiple routes, although their relative susceptibility compared to true reservoir hosts appears to be low.

Key Words Didelphis virginiana, opossum, Mycobacterium bovis, tuberculosis

Citation

Donnelly, C.A., R. Woodroffe, D.R. Cox, J. Bourne, G. Gettinby, A.M. Le Fevre, J. P. McInerney, and W.I. Morrison. 2003. Impact of localized badger culling on tuberculosis incidence in British cattle. Nature 426:834-837.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Pathogens that are transmitted between wildlife, livestock and humans present major challenges for the protection of human and animal health, the economic sustainability of agriculture, and the conservation of wildlife. Mycobacterium bovis, the aetiological agent of bovine tuberculosis (TB), is one such pathogen. The incidence of TB in cattle has increased substantially in parts of Great Britain in the past two decades, adversely affecting the livelihoods of cattle farmers and potentially increasing the risks of human exposure. The control of bovine TB in Great Britain is complicated by the involvement of wildlife, particularly badgers (Meles meles), which appear to sustain endemic infection and can transmit TB to cattle1. Between 1975 and 1997 over 20,000 badgers were culled as part of British TB control policy, generating conflict between conservation and farming interest groups. Here we present results from a large-scale field trial that indicate that localized badger culling not only fails to control but also seems to increase TB incidence in cattle.

Key Words badger, bovine tuberculosis, culling disease

Citation

Dorn, M. L. and Angela G. Mertig. 2005. Bovine tuberculosis in Michigan:stakeholder attitudes and implications for eradication efforts. Wildlife Society Bulletin 33(2):539–552.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (TB) has been discovered in unprecedented levels in Michigan's white-tailed deer (Odocoileus virginianus) herd. Human practices have facilitated the spread of bovine TB in white-tailed deer, and public cooperation is necessary to reduce the spread of the disease. Social data can determine public support for eradication strategies, as well as identify targets and messages for ongoing communication efforts. We conducted a survey of 5 bovine TB-issue stakeholder groups to assess and compare attitudes toward bovine TB-related topics and support for eradication and eradication policies. We also identified knowledge levels and interest in future bovine TB issue communications and preferences for communication sources. Results indicated that stakeholders supported the bovine TB eradication goal, but were less supportive of specific eradication policies. Stakeholders held different beliefs about threats posed by bovine TB, and about the means through which the disease is transmitted; stakeholder groups also had different levels of bovine TB-related knowledge. A strong majority of respondents (89%) were interested in being informed about new bovine TB issue-related information.

Key Words

attitudes, bovine tuberculosis, human dimensions, Michigan, Odocoileus virginianus, stakeholders, white-tailed deer

Citation

Dorn, M.L. 2003. Bovine tuberculosis in Michigan: understanding stakeholder attitudes toward the disease and eradication efforts. Thesis, Michigan State University, East Lansing, MI.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

Bovine tuberculosis has been discovered at unprecented levels in Michigan wildife, especially white-tailed deer (Odocoileus virginianus). Human behaviors, particularly the use of bait and feed, have facilittted the spread of the disease into free-ranging white-tailed deer populations. Policies aimed at eradicating bovine tuberculosis in Michigan require public compliance and cooperation in order to be successful. Because of the human contribution to the spread of bovine tuberculosis in Michigan wildlife, and the social nature of subsequent bovine tuberculosis eradication policies, we conducted a survey of bovine TB issue stakeholder groups in northeast Michigan, including non-resident hunters, resident hunters, livestock producers, business owners/managers, and the general public. Social data can help determine public support for wildlife management policies, such as bovine TB eradication strategies, as well as identify targets and messages for ongoing communication efforts. We also found that different beliefs predict hunter attitudes toward bovine TB eradication in principle versus in practice. We use these results to make recommendations for future communication efforsts aimed at bolstering public support for bovine tuberculosis eradication and eradication policies.

Key Words bovine tuberculosis, Michigan, Odocoileus virginianus, transmission

Citation Duffield, B. J. and D. A. Young. 1984/85. Survival of Mycobacterium bovis in defined environmental conditions. Veterinary Microbiology 10:193-197.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract The survival of Mycobacterium boris was investigated following artificial inoculation in dry and moist soils and bovine faeces held under various environmental conditions. M. bovis survived for 4 weeks in non-sterile dry and moist soils held under 80% shade, in darkness and in the laboratory. It was also isolated from sterile moist soil kept in the shade and in darkness. Re-isolation of M. boris was not made at 4 weeks from any of the substrates exposed to sunlight nor from faeces held under any condition. M. bovis was not re-isolated from any substrate at 8 weeks or up to 32 weeks after inoculation.

Key Words survival, inoculation, environmental conditions, isolation

Citation

Enticott, G. 2008. The spaces of biosecurity: prescribing and negotiating solutions to bovine tuberculosis. Environment and Planning 40:1568-1582.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Using the example of bovine tuberculosis, this paper explores the emergence, understanding, and rejection of new forms of biosecurity. The paper argues that debates over biosecurity can be conceptualized as arguments over the ability to regulate flows of disease and the constructions of space they adopt. Data from parliamentary inquiries and interviews are used to show how attempts to institutionalize forms of biosecurity emerge from a delicate balance of prescribed and negotiated spaces configured by a host of social, natural, and material agents. The interaction between these spaces provides a way of regulating the flows of disease and purifying agricultural space. This balance is resisted by farmers, whose practical knowledge of the constant struggle of managing the contingencies of agriculture lead them to suggest that only uniform versions of space can effectively regulate flows of disease. The author concludes by discussing the importance of recognizing these differences for future biosecurity and animal health policy.

Key Words biosecurity, farmers, regulate, animal health policy

Citation Essey, M. A and M.A. Koller. 1994. Status of bovine tuberculosis in North America. Veterinary Microbiology 40:15-22.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The eradication of bovine tuberculosis from North America is in the advanced stages as Canada and the United States struggle to remove the last vestiges of the disease from the domestic livestock population. Canada realistically anticipates total eradication from the national cattle herd within the next few years. The United States must yet effectively deal with the increased tuberculosis exposure potential from imported steers and from bovine tuberculosis newly discovered in its captive cervid industry. This paper reviews the history and development of tuberculosis eradication programs in North America. The basic evolution is described from area testing to slaughter surveillance with follow-up epidemiological investigations as the program foundation. The current status of both countries is described and recognized deterrents to final eradication are discussed.

Key Words Mycobacterium bovis, cattle, tuberculosis, bovine, epidemiology, eradication

Citation

Fend, R., R. Geddes, S. Lesellier, H.-M. Vordermeier, L. A. L. Corner, E. Gormley, E. Costello, R. G. Hewinson, D. J. Marlin, A. C. Woodman, and M. A. Chambers. 2005. Use of an electronic nose to diagnose Mycobacterium bovis infection in badgers and cattle. Journal of Clinical Microbiology 43(4):1745–1751.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

It is estimated that more than 50 million cattle are infected with Mycobacterium bovis worldwide, resulting in severe economic losses. Current diagnosis of tuberculosis (TB) in cattle relies on tuberculin skin testing, and when combined with the slaughter of test-positive animals, it has significantly reduced the incidence of bovine TB. The failure to eradicate bovine TB in Great Britain has been attributed in part to a reservoir of the infection in badgers (Meles meles). Accurate and reliable diagnosis of infection is the cornerstone of TB control. Bacteriological diagnosis has these characteristics, but only with samples collected postmortem. Unlike significant wild animal reservoirs of M. bovis that are considered pests in other countries, such as the brushtail possum (Trichosurus vulpecula) in New Zealand, the badger and its sett are protected under United Kingdom legislation (The Protection of Badgers Act 1992). Therefore, an accurate in vitro test for badgers is needed urgently to determine the extent of the reservoir of infection cheaply and without destroying badgers. For cattle, a rapid on-farm test to complement the existing tests (the skin test and gamma interferon assay) would be highly desirable. To this end, we have investigated the potential of an electronic nose (EN) to diagnose infection of cattle or badgers with M. bovis, using a serum sample. Samples were obtained from both experimentally infected badgers and cattle, as well as naturally infected badgers. Without exception, the EN was able to discriminate infected animals from controls as early as 3 weeks after infection with M. bovis, the earliest time point examined postchallenge. The EN approach described here is a straightforward alternative to conventional methods of TB diagnosis, and it offers considerable potential as a sensitive, rapid, and cost-effective means of diagnosing M. bovis infection in cattle and badgers.

Key Words diagnosis, badgers, cattle, Electronic Nose

Citation

Fernandez-de-Mera, I. G., J. Vicente, U. Hofle, F. Ruiz Fons, J.A. Ortiz, C. Gortazar. 2009. Factors affecting red deer skin test responsiveness to bovine and avian tuberculin and to phytohaemagglutinin. Preventive Veterinary Medicine 90:119–126.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We studied the effect of management on the responsiveness of red deer (Cervus elaphus) to skin testing with mycobacterial and non-mycobacterial antigens. We hypothesized that individuals from populations of the same species under different management conditions would have a different immune responsiveness. Deer sampled in this study included 1041 adult animals from 6 Spanish farms and 111 adult wild deer. We injected four sites of the neck with 0.1 ml bovine purified protein derivative (PPD), 0.1 ml avian PPD, 0.1 ml negative control PBS and 0.1 ml of Phytohaemagglutinin (PHA, containing 250 mg) as positive control, and measured the skin fold increase at time 72 h. Bovine PPD reactors were identified in 5 of 6 farms and among wild deer. Apparent prevalence among wild deer (18.9%) was not significantly higher than among farmed deer (14.5%). Avian PPD reactors were found among all 7 study populations, but apparent prevalence was lower among wild deer (<1%) than among farmed deer (12.6%; $p < 0.001$). Deermanagement (farmed versus wild) was identified as a key factor affecting deer skin fold thickness increase in response both to mycobacterial (bPPD and aPPD) and non-mycobacterial antigens (PHA). The differences occurred in the same sense, regardless of some interactions; farmed deer showing higher values. The PHA skin fold increase was not affected by the PPD skin test results. We propose that using PHA as a positive control may help in the interpretation of between-population differences in tuberculin responses.

Key Words body condition, cellular immunity, Cervus elaphus, mitogen, paratuberculosis, skin test, tuberculosis

Citation

Fine, A. F. 2006. The role of indirect transmission in the epidemiology of Bovine tuberculosis in cattle and white-tailed deer in Michigan. Dissertation. Michigan State University, East Lansing, MI.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

Understanding the epidemiology of Mycobacterium bovis transmission in Michigan is an essential component of nationwide efforts to control and eradicate bovine tuberculosis (TB). Determining the role of indirect transmission in bovine TB dynamics is key to the application of epidemiologically effective methods of disease control in both livestock and wildlife populations. The objective of this dissertaion was to characterize the persistence of M. bovis in the environment and its potential role in the indirect transmission of disease among and between cattle (Bos taurus) and white-tailed deer (Odocoileus virginianus) in Michigan.

Optimized techniques for isolating M. bovis from environmental substrates were developed. These were applied to the testing of samples collected from cattle farms with a known history of M. bovis infection. Samples collected opportunistically from locations within areas with a high prevalence of M. bovis infection in white-tailed deer were also tested . Though mycobacterial isolation was successful, none of the isolates were identified as M. bovis. The inability to detect M. bovis from sites of known bovine TB transmission suggests that the pathogen is not distributed broadly across the landscape, making identification of a specific site of contaminatation difficult. To address the question of M. bovis persistence in the environment, given the limitation of detecting the bacilli under natural conditions, a 12-month long experiment was designed. Environmental substrates were experimentally inoculated with M. bovis and exposed to natural weather conditions. The effects of environmental conditions on the survival of M. bovis over time were assessed.

Persistence of M. bovis in the Michigan environment under natural weather conditions was recorded for an average of 30 days in the cooler months of the year (November-May), and an average of 7 days in the warmer months (May-August). This recorded persistence strongly suggests an important potential role for indirect transmission in the epidemiology of bovine TB in the region. These data supplement those produced through experimental M. bovis disease transmission studies that have proven the feasibility of indirect transmission of M. bovis among and between cattle and white-tailed deer. They also support the analyses of observational data on M. bovis infection in cattle and white-tailed deer in Michigan that indicated the importance of indirect transmission in the interspecies transmission of M. bovis. Local, state and federal bovine TB control and eradictaion policy needs to consider indirect transmission of M. bovis through contaminated environmental substrates in the creation and implementaion of epidemiologically appropriate disease management plans. In the bovine TB endemic region of Michigan, interspecies transmission of bovine TB should be considered by both wildlife and livestock health agencies. If this component of the epidemiology of M. bovis transmission in the region is ignored, efforts to control and eventually eradicate the disease will fail.

Key Words indirect transmission, epidemiology, cattle, wildlife, environmental persistance, control strategies

Citation

Fischer, E. A. J., H. J. W. van Roermund, L. Hemerik, M. A. P. M. van Asseldonk, M. C. M. de Jong. 2005. Evaluation of surveillance strategies for bovine tuberculosis (Mycobacterium bovis) using an individual based epidemiological model. Preventive Veterinary Medicine 67:283–301.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The Netherlands holds the bovine tuberculosis-free (BTB-free) status according to European Union standards, but in recent years small outbreaks of the infection have occurred. After the last outbreak in 1999 with 10 infected herds the question raised if the current surveillance system, visual inspection of carcasses at the slaughterhouse, is efficient enough to detect infected cattle in time and to maintain the official BTB-free status.

Through epidemiological modelling, the risk of a major outbreak is quantified, using one of six surveillance strategies. These are the currently used visual inspection of carcasses at the slaughterhouse (SL), the ELISA test on blood samples of carcasses at the slaughterhouse (ELISA-B), the ginterferon test on blood samples of carcasses at the slaughterhouse (GAMMA-B), comparative tuberculination of the herd (CT), the combined method of single and comparative tuberculination of the herd (ST + CT) and the ELISA test on samples of bulk milk (ELISA-M). Test frequency of the last three methods was varied as well.

A stochastic individual based model (IBM) was developed to simulate a chain of infected herds, where each individual animal is followed in time. The model mimics the nation-wide situation after the introduction of one infected animal into one herd. BTB-transmission is simulated with an S-E1-E2-I state transition model. Output is time until detection of the infection, prevalence in the detected herd and the number of infected herds at the time of detection. For the assessment 500 simulations were used, representing 500 BTB-introductions. Model robustness to parameter values was analysed with Monte Carlo elasticity analysis, for which 1000 simulations were used.

Results of median time until detection and median number of infected farms at detection for SL (302 weeks and seven farms) were in agreement with estimates from an outbreak in the Netherlands in 1999. ELISA-B and GAMMA-B performed better than SL with a much lower median time until detection (189 and 97 weeks, respectively). The results for the tuberculination methods (ST + Ctand CT) and ELISA-M depended heavily on the frequency in which the tests were performed. The tuberculination methods ST + CT and CT yield comparable results and detect the infection sooner than SL, also at the lowest tested frequency of once in 5 years. ELISA-M is comparable with SL at frequencies of once in 4 or 5 years, and this test works well at frequencies of once a year or higher. Our study results are used for an economical optimisation analysis of the six surveillance strategies.

Key Words

bovine tuberculosis, Mycobacterium bovis, detection method, stochastic simulation, Individual based model

Citation

Fitzgerald S. D., J. B. Kaneene, K. L. Butler, K. R. Clarke, J. S. Fierke, S. M. Schmitt, C. S. Bruning-Fann, R. R. Mitchell, D. E. Berry, and J. B. Payeur. 2000. Comparison of postmortem techniques for the detection of Mycobacterium bovis in white-tailed deer (Odocoileus virginianus). Journal of Veterinary Diagnostic Investigations 12:322-327.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A retrospective study of various diagnostic postmortem techniques used in a 4-year surveillance program for detection of Mycobacterium bovis infection in wild white-tailed deer (Odocoileus virginianus) was conducted. The tests evaluated were routine histopathology, acid-fast staining, detection of acid-fast bacilli in culture, and an M. tuberculosis group-specific genetic probe applied to pure cultures. Each of these techniques were compared with a reference or ‘‘gold standard’’ of mycobacterial culture and identification. Histopathology, the most rapid form of testing for M. bovis infection in white-tailed deer samples, had a sensitivity of 98% and a specificity of 87%, resulting in a positive predictive value of 94%. The detection of acid-fast bacilli by staining was less sensitive than histopathology (90%), but its higher specificity (97%) resulted in a positive predictive value of 99%. The detection of acid-fast bacilli on culture was both highly specific (93%) and sensitive (100%). The group-specific genetic probe had the highest sensitivity and specificity and produced results in complete agreement with those of mycobacterial culture, suggesting that this technique could be used as the new ‘‘gold standard’’ for this particular wildlife tuberculosis surveillance program.

Key Words diagnostic, post-mortem, detection, white-tailed deer, Odocoileus virginianus, histopathology, surveillance

Citation

Fitzgerald S. D., L. S. Zwick, D. E. Berry, S. V. Church, J. B. Kaneene, and W. M. Reed. 2003. Experimental Inoculation of Pigeons (Columba livia) with Mycobacterium bovis. Avian Diseases 47:470-475.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The purpose of this pilot study was to determine if pigeons (Columba livia) are susceptible to infection with Mycobacterium bovis by either oral or intratracheal inoculation and to assess their possible role in the lateral transmission of bovine tuberculosis. Six pigeons were orally inoculated with 1.3 3 105 colony-forming units of M. bovis, six pigeons were intratracheally inoculated with the same dose, and six pigeons served as noninoculated controls. The study continued for 90 days postinoculation (PI), with groups of birds necropsied at 30-day intervals, and fecal samples and tissues were collected for mycobacterial culture. Two pigeons, one intratracheally inoculated and one orally inoculated, shed M. bovis in their feces at 1 day PI, and one intratracheally inoculated bird shed M. bovis in its feces 60 days PI. Whereas no illness or weight loss was present during the course of the study, 2 of 12 inoculated birds exhibited microscopic lesions of mycobacteriosis, and the organism was isolated from tissues of three inoculated birds. Pigeons are susceptible to infection with M. bovis after high dose inoculation and can shed the organism in their feces for up to 60 days PI; intratracheally inoculated birds appear more likely to become active fecal shedders of M. bovis. Although these were high dose inoculations under experimental conditions, pigeons may potentially play a role in the lateral transmission of bovine tuberculosis between infected and uninfected mammalian hosts.

Key Words pigeons, Columba livia, oral, intratracheal, lateral transmission, fecal shedders

Citation

Fitzgerald, S. D., L. S. Zwick, K. L. Diegel, D. E. Berry, S. V. Church, J. G. Sikarskie, J. B. Kaneene, and W. M. Reed. 2003. Experimental aerosol inoculation of Mycobacterium bovis in North American opossums (Didelphis virginiana). Journal of Wildlife Diseases 39(2):418-423.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The goal of this study was to evaluate the susceptibility of North American opossums (Didelphis virginiana) to aerosol inoculation of Mycobacterium bovis at two dose levels in order to gain information on disease pathogenesis, fecal shedding of the organism, and the potential role that opossums play in the spread of this disease in nature. Six opossums received high dose (1x10^7 colony forming units (cfu) by aerosol inoculation, six opossums received low dose (1x10^3 cfu inoculation, and six opossums were sham-inoculated with sterile water and served as controls. Lungs were the most frequently infected tissues, with nine of 12 inoculated opossums positive for M. bovis on culture. Gross lesions consisted of multifocal pneumonia and enlarged lymph nodes. Microscopically, granulomatous pneumonia and granulomatous lymphadenitis associated with acidfast bacilli were present in eight of 12 inoculated opossums. Fecal shedding of M. bovis was uncommon at both inoculation doses. While opossums were highly susceptible to aerosol inoculation of M. bovis, they did not become emaciated or develop widely disseminated lesions. From this study, opossums may transmit tuberculosis by aerosol infection to other opossums in close contact and serve as a source of infection to carnivores that feed upon them, however, transmission of the disease to large herbivores by fecal shedding or direct contact may be less likely.

Key Words aerosol inoculation, Didelphis virginiana, Mycobacterium bovis, opossum, tuberculosis.

Citation

Fitzgerald, S. D., K. G. Boland, K. R. Clarke, A. Wismer, J. B. Kaneene, D. E. Berry, S. V. Church, J. A. Hattey, and C. A. Bolin. 2005. Resistance of mallard ducks (Anas platyrhynchos) to experimental inoculation with Mycobacterium bovis. Avian Diseases 49:1444-146.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The purpose of this study was to investigate whether mallard ducks (Anas platyrhynchos) are susceptible to infection with Mycobacterium bovis by either oral or intratracheal inoculation and to assess their potential role in the spread of bovine tuberculosis. Six ducks were orally inoculated with 1.0 x 10^5 colony-forming units of M. bovis, six ducks were intra-tracheally inoculated with the same dose, and six ducks served as sham-inoculated controls. The study length was 90 days postinoculation, with samples of two birds from each group necropsied at 30-day intervals. Both fecal and tissue samples were collected for mycobacterial culture. None of the inoculated ducks shed M. bovis in their feces at any culture point (days 1, 30, and 60) during the study. No evidence of illness or weight loss was present during the course of the study, and only one duck had M. bovis isolated from any tissue, although there were no associated microscopic lesions. Mallard ducks were highly resistant to infection with M. bovis following high-dose inoculation and did not shed the organism in their feces. This study was conducted using high-dose inoculation; therefore, it appears that ducks are unlikely to play any significant role in the transmission of M. bovis between infected and uninfected mammalian hosts.

Key Words Anas platyrhynchos, mallard duck, Mycobacterium bovis, tuberculosis

Citation

Fulford, G. R. and M. G. Roberts. 2002. The metapopulation dynamics of an infectious disease: tuberculosis in possums. Theoretical Population Biology 61:15–29.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

An SEI metapopulation model is developed for the spread of an infectious agent by migration. The model portrays two age classes on a number of patches connected by migration routes which are used as host animals mature. A feature of this model is that the basic reproduction ratio may be computed directly, using a scheme that separates topography, demography, and epidemiology. We also provide formulas for individual patch basic reproduction numbers and discuss their connection with the basic reproduction ratio for the system. The model is applied to the problem of spatial spread of bovine tuberculosis in a possum population. The temporal dynamics of infection are investigated for some generic networks of migration links, and the basic reproduction ratio is computed—its value is not greatly different from that for a homogeneous model. Three scenarios are considered for the control of bovine tuberculosis in possums where the spatial aspect is shown to be crucial for the design of disease management operations.

Key Words

possums, migration, model, temporal dynamics

Citation

Galindo, R. C., P. Ayoubi, V. Naranjo, C. Gortazar, K. M. Kocan, J. de la Fuente. 2009. Gene expression profiles of European wild boar naturally infected with Mycobacterium bovis. Veterinary Immunology and Immunopathology 129:119–125.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Global gene expression profiles were analyzed in European wild boar naturally infected with Mycobacterium bovis. Spleen RNA was extracted from 23 M. bovis-infected and 17 uninfected animals and analyzed using a Pigoligoarray representing 20,400 genes. Differentially expressed sequences (N = 161) were identified affecting cellular processes such as apoptosis, cell communication and signal transduction, cell growth and/or maintenance, cytoskeleton organization and biogenesis, DNA repair, immune response, metabolism and energy pathways, protein metabolism, regulation of cell proliferation, regulation of gene expression, regulation of nucleic acid metabolism, regulation of physiological processes, and transport. Real-time RT-PCR analysis of mRNA levels was used to corroborate microarray results of selected genes. Immune response genes were among the most represented differentially expressed sequences and were selected for further discussion. Beta-defensin 129, T-cell surface glycoprotein CD8 and B-cell receptorassociated protein 29 were overexpressed in infected animals. Lower expression levels of the immune response genes galectin-1, complement component C1qB and certain HLA class I and class II histocompatibility antigens and immunoglobulin chains were found in infected animals. This study identified new mechanisms by which naturally infected European wild boar respond to M. bovis infection and how the pathogen circumvents host immune responses to establish infection. Gene expression studies in naturally infected wildlife reservoirs of bovine tuberculosis are important for functional genomics and vaccine studies to aid in disease control in wildlife.

Key Words wildlife, microarray, Sus scrofa, tuberculosis, genomics, immune response

Citation Gallagher, J. and R. S. Clifton-Hadley. 2000. Tuberculosis in badgers; a review of the disease and its significance for other animals. Research in Veterinary Science 69:203–217.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract This review examines the current state of knowledge of aspects of tuberculosis in the badger. The gross pathology and pathogenesis are elaborated as well as the immune mechanism, diagnosis of infection and excretion and viability of infected products. The epidemiology in badgers is considered, as is the significance of infection in this species for other wildlife species as well as domestic animals sharing the same habitat. Trials of the effects of the removal of badgers on the occurrence of tuberculosis in cattle are summarised. It is concluded that badgers are well adapted as the primary host of bovine tuberculosis in parts of Britain and much of Ireland.

Key Words Ireland, review, badgers, epidemiology, host

Citation Garcia-Sanchez, A., L. Gomez, P. Fernandez-Llario, A. Parra, and J. Hermoso de Mendoza. 2007. Tuberculous meningoencephalitis in a wild boar. Journal of Wildlife Diseases 43(4):780–783.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Bovine tuberculosis, caused by Mycobacterium bovis, is a zoonotic disease that affects cattle and wildlife worldwide. These animal hosts can serve as reservoirs of infection, thus increasing the risk of human exposure and infection. Tuberculous meningoencephalitis complicating disseminated tuberculosis is described in a 7-mo-old wild boar (Sus scrofa).

Key Words Mycobacterium bovis, spoligotype, Sus scrofa, tuberculous meningoencephalitis, wild boar

Citation	Garner, M.S. 2001. Movement patterns and behavior at winter feeding and fall baiting stations in a population of white-tailed deer infected with bovine tuberculosis in the northeastern lower peninsula of Michigan. Dissertation, Michigan State University, East Lansing, MI.
Abstract Only	☐
No Abstract	☑
Article Type	Thesis/Dissertation
Abstract	
Key Words	baiting stations, bovine tuberculosis, Odocoileus virginianus, white-tailed deer, wildlife damage management, winter feeding

Citation

Garnett, B. T., R. J. Delahay, and T. J. Roper. 2002. Use of cattle farm resources by badgers (Meles meles) and risk of bovine tuberculosis (Mycobacterium bovis) transmission to cattle. Proceedings of the Royal Society B 269:1487–1491.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Nocturnal observations, radio telemetry and time-lapse camera surveillance were used to investigate visits by badgers (Meles meles L.) to two cattle farms. During 59 half-nights (ca. 295 h) of observation and 17 nights (ca. 154 h) of camera surveillance, 139 separate visits to farm buildings, by at least 26 individually identifiable badgers from two social groups, were recorded. The badgers, which included three individuals infected with bovine tuberculosis (Mycobacterium bovis), used cowsheds, feedsheds, barns, haystacks, slurry pits, cattle troughs and farmyards to exploit a range of food resources, including cattle feed and silage. Cattle feed was contaminated with badger faeces and badgers also came into close contact with cattle. The minimum number of badgers visiting farm buildings per night was negatively correlated with local 24 h rainfall. We conclude that exploitation by badgers of resources provided by cattle farms constitutes a potentially important mechanism for tuberculosis transmission from badgers to cattle.

Key Words badgers, cattle, bovine tuberculosis, foraging, farm biosecurity

Citation

Garnett, B. T., T.J. Roper, R.J. Delahay. 2003. Use of cattle troughs by badgers (Meles meles) A potential route for the transmission of bovine tuberculosis (Mycobacterium bovis) to cattle. Applied Animal Behaviour Science 80:1–8.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Cattle feedtroughs that are contaminated with badger excreta constitute a potential transmission route for the spread of bovine tuberculosis (Mycobacterium bovis) from badgers (Meles meles) to cattle. In order to investigate the maximum height to which a trough would have to be raised to make it secure against badgers, we presented wild badgers with an experimental trough that could be set to a range of heights. In two separate experiments, a total of at least 12 badgers from two social groups at Woodchester Park, Gloucestershire, South-West England managed to climb into the trough when it was set at heights above 80 cm (i.e. higher than the current recommended safety guidelines for farmers). The maximum height to which badgers could climb was 115 cm, which would place the trough beyond the reach of calves, young heifers and bullocks. We conclude that there is no safe height at which troughs can be set to feed young cattle while excluding badgers. Exclusion of badgers from cattle troughs therefore requires the development of new trough designs.

Key Words badgers,cattle, cattle troughs, bovine tuberculosis, foraging

Citation

Gonzalez Fernandez, J., I. Fernandez-de-Mera, L. E. Reyes, M. C. Ferreras, V. Perez, C. Gortazar, M. Fernandez, J. F. Garcia-Marin. 2009. Comparison of three immunological diagnostic tests for the detection of avian tuberculosis in naturally infected red deer (Cervus elaphus). Journal of Veterinary Diagnostic Investigations 21:102–107.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Cases of tuberculosis due to Mycobacterium avium subsp. avium in 52 adult red deer (Cervus elaphus) from a farm were studied using different diagnostic techniques. Immunological probes consisted of the comparative cervical tuberculin (CCT) skin test, the interferon-c (IFN-c) assay, and 2 enzyme-linked immunosorbent assays (ELISAs) employing either avian purified protein derivatives or protoplasmatic antigen (PPA-3) as antigens. Three of the animals were euthanized due to severe weakness, loss of weight, and emaciation. Macroscopically, the 3 animals showed tuberculous lesions located mainly in lymph nodes of the digestive system and small intestine but also in other organs and lymph nodes. Polymerase chain reaction was carried out on samples from the 3 deer using primers to detect IS901, IS900, and IS6110, specific for Mycobacterium avium subsp. avium, Mycobacterium avium subsp. paratuberculosis, and Mycobacterium tuberculosis complex, including Mycobacterium bovis, respectively. The last 2 agents cause pathologies very similar to avian tuberculosis in deer. The 3 deer were strongly positive by both ELISAs, slightly positive by the IFN-c test, and 1 of 2 was positive by the CCT test. As with domestic ruminants, ELISA could detect deer in an advanced stage of infection, with large numbers of mycobacteria.

Key Words Avian tuberculosis, deer, enzyme-linked immunosorbent assay, interferon-gamma, Mycobacterium avium

Citation

Gortazar, C., J. Vicente, S. Samper, J. M. Garrido, I. G. Fernandez-de-Mera, P. Gavin, R. A. Juste, C. Martin, P. Acevedo, M. de la Puente, and U. Hofle. 2005. Molecular characterization of Mycobacterium tuberculosis complex isolates from wild ungulates in south-central Spain. Veterinary Research 36:43–52.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The role of European wild ungulates in the epidemiology of tuberculosis (TB) is still under discussion. This study describes the geographical distribution and molecular typing of 77 Mycobacterium tuberculosis complex isolates belonging either to M. bovis or to M. caprae, cultivated from hunter harvested red deer (Cervus elaphus) and European wild boar (Sus scrofa) in 24 Spanish localities, and compares them with spoligotypes detected previously in humans, livestock or wild animals, as described in the literature. The distribution of the molecular type patterns suggests that the population of M. tuberculosis complex strains isolated from Spanish wild ungulates is spatially structured despite the lack of important geographical barriers and despite the increasingly frequent wildlife translocations. Red deer and the European wild boar can share the same molecular types in localities in which the M. tuberculosis complex was isolated from both species. Strains of bovine and caprine origin do circulate in the same local wildlife populations. Six out of 11 spoligotypes were similar to types described in human cases. The isolation of TB strains in fenced estates from wild animals that have not had contact with domestic livestock for at least the past two decades, strongly suggests that the M. tuberculosis complex is able to survive in these populations. Therefore, wildlife including cervids and the wild boar need to be considered in the epidemiology and control of tuberculosis.

Key Words epidemiology, reservoir, typing, tuberculosis, wildlife

Citation

Gowtage-Sequeira, S., A. Paterson, K. P. Lyashchenko, S. Lesellier, and M. A. Chambers. 2009. Evaluation of the CervidTB STAT-PAK for the detection of Mycobacterium bovis infection in wild deer in Great Britain. Clinical and Vaccine Immunology 16(10):1449–1452.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Deer are acknowledged as hosts of Mycobacterium bovis, the causative agent of bovine tuberculosis (bTB), and determining the prevalence of infection in deer species is one of the key steps in understanding the epidemiological role played by cervids in the transmission and maintenance of bTB in the United Kingdom. This study evaluated a rapid lateral-flow test for the detection of bTB in samples from wild deer species in the United Kingdom. Fallow deer (Dama dama), roe deer (Capreolus capreolus), and red deer (Cervus elaphus) from areas in Wales, the Cotswolds, and southwestern England were necropsied for a bTB survey. Serum samples from individual deer were tested with the CervidTB STAT-PAK, and the results were evaluated against the culture of M. bovis from tissues (n = 432). Sensitivity and specificity were 85.7% (95% confidence interval [CI], 42.1 to 99.6%) and 94.8% (95% CI, 92.3 to 96.7%), respectively, with an odds ratio of 109.9 (95% CI, 12.7 to 953.6%) for a positive STAT-PAK result among culture-positive deer. The low prevalence of infection (3.8%, n = 860) affected the confidence of the sensitivity estimate of the test, but all culture-positive fallow deer (n = 6) were detected by the test. In addition, antibodies to M. bovis could be detected in poor-quality serum samples. The results suggest that the CervidTB STAT-PAK could be deployed as a field test for further evaluation.

Key Words deer, Britain, stat-pak, detection, field test, UK, fallow deer, roe deer, red deer

Citation

Griffin, J. F. T. and C. G. Mackintosh. 2000. Tuberculosis in deer: perceptions, problems and progress. The Veterinary Journal 160:202-219.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Since the emergence of deer farming as an alternative farming enterprise over the past 30 years, there has been an increasing awareness of the potential threat posed by tuberculosis (TB) to domesticated deer. TB, caused by Mycobacterium bovis, has been found in deer in every country involved with deer farming. Different types of TB control policies, which vary from whole-herd depopulation to selective testing and slaughter of reactor animals, have been implemented. Extensive research has been carried out, incorporating modern microbiological and immunological concepts and advanced molecular methodologies, to find new solutions for the eradication of TB from domesticated deer. This work has resulted in valuable new insights into the aetiology, transmission, pathogenesis, diagnosis, prevention and heritability of resistance to M. bovis infection in ruminants. This knowledge has complemented the existing literature database on bovine and human TB and will provide new strategies for improved diagnosis, vaccination and selective breeding to control TB, which should be relevant for human, domestic livestock and wildlife populations.

Key Words tuberculosis, Mycobacterium bovis, diagnosis, vaccination, resistance-heritability, TB

Citation Griffin, J. F. T. and G.S. Buchan. 1994. Aetiology, pathogenesis and diagnosis of Mycobacterium bovis in deer. Veterinary Microbiology 40:193-205.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Tuberculosis, caused by Mycobacterium bovis, is emerging as the most important disease affecting fanned deer. While the disease is usually found at a low incidence involving lesions in single lymph nodes, it may present as a rapidly spreading, fulminating disease, especially in animals exposed to stress. The unique susceptibility of cervidae to mycobacteria in general has meant that diagnosis of tuberculosis in deer using conventional intradermal tuberculin tests may be unsatisfactory. Tuberculin testing in deer is more technically demanding than in cattle, with the cervical region being the most sensitive area. False positive skin reactions occur widely in non-diseased deer while seriously infected animals may be "anergic" and fail to react (false negative). Comparative cervical tests have been used to improve test specificity but they suffer from reduced levels of sensitivity. A new blood test for tuberculosis (BTB) has been developed specifically for deer. This assay uses a combination of laboratory tests which measure lymphocyte transformation, antibody and inflammation. The composite BTB has a sensitivity of > 95% and a specificity of > 98% for diagnosis of M. bovis in cervidae.

Key Words Mycobacterium bovis, deer, tuberculosis, cervine, aetiology, pathogenesis

Citation

Griffin, J. F. T., C.R. Rodgers, S. Liggett, C.G. Mackintosh. 2006. Tuberculosis in ruminants: characteristics of intra-tonsilar Mycobacterium bovis infection models in cattle and deer. Tuberculosis 86:404–418.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis infection produces tubercular lymphadenitis in the head lymphatics of cattle and deer, in addition to pulmonary disease. A low-dose intra-tonsilar infection model that establishes tuberculosis (Tb) lymphadenitis in cattle and deer is characterised in this study. Intra-tonsilar infection of red deer (500 cfus of M. bovis) was monitored longitudinally at 6-week intervals over a period of 23 weeks. Lesion characteristics, bacteriological and immunological parameters were assessed, and compared against those observed in cattle at 20 weeks post-infection, where the latter were infected with 500 or 5000 cfus of M. bovis. Intra-tonsilar inoculation of M. bovis established infection in >90% of deer and cattle, with lesion frequencies at the draining sentinel lymphatic site (left medial retropharyngeal node) of 68–86% and tissue bacterial burdens43.5 logs/g of tissue, the tonsil being a major site of M. bovis persistence in deer only. Mineralisation occurred at lesion sites in both species in the later stages (18–23 weeks) of infection, with extensive coarse mineralisation observed mainly in cattle. The severity of infection or disease in cattle that received the higher or lower dose of M. bovis did not differ markedly. Pathogen-induced cellular immune response (lymphocyte transformation) and humoral responses (IgG and IgG1 anti-mycobacterial antibodies) were recorded in both species, and the magnitude of these was noticeably amplified by skin tuberculin testing. IgG1 antibodies were detectable within 6 weeks post- inoculation in deer and could be associated with early detection of lymphadenitis. Deer and cattle show similar levels of susceptibility to M. bovis infection.

Key Words tuberculosis, Mycobacterium bovis, cattle, deer, intra-tonsilar infection

Citation

Griffin, J. F. T., D.N. Chinn, and C.R. Rodgers. 2004. Diagnostic strategies and outcomes on three New Zealand deer farms with severe outbreaks of bovine tuberculosis. Tuberculosis 84:293–302.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Setting: Three commercial deer herds, each containing more than 500 deer, experienced outbreaks of tuberculosis (TB) ranging from a 6% prevalence to disease levels 450%. Intensive diagnostic testing was carried out over short time intervals after the initial diagnosis of TB.
Objective: To eradicate M. bovis infection from herds of farmed red deer (Cervus elaphus) in New Zealand, which had significant outbreaks of tuberculosis (45%), using complementary diagnostic tests and elective slaughter of all test positive animals.
Design: Whole herd mid cervical skin tests (MCT) were used as the primary test and a comparative cervical test (CCT) as an ancillary test. In an attempt to enhance TB eradication, ancillary blood tests comprising; lymphocyte transformation tests (LT) and enzyme-linked immunosorbent assays (ELISA) were used in parallel with MCT, or as serial tests, to complement skin testing.
Results: One deer herd (N), which had an acute outbreak (6%) of TB in adult stock, responded quickly to testing and the disease was eradicated within 12 months. A second more chronically infected herd (B), with low prevalence (2%) of TB initially in pregnant hinds which were retained over the breeding cycle, developed widespread uncontrollable spread of infection, that could not be contained by exhaustive testing. The final herd (S), which had an acute outbreak of TB at a prevalence 490% in young fawns, responded well to testing and became TB-free within 1 year.
Conclusions: TB can be eradicated from infected farmed deer herds, using currently available TB tests, irrespective of disease prevalence. The caveat is that disease must be diagnosed early in the acute phase of infection. Undiagnosed infection over winter in breeding hinds in one herd produced a refractory infection in adult males and females and uncontrollable spread to newborn fawns. Disease could not be eradicated using comprehensive diagnostic schedules. A widespread but controllable outbreak of acute TB in another herd, appeared to have caused sufficient selective pressure on adult stock that genetically resistant adults were selected within a very short time frame (<1 year).

Key Words diagnosis, M. bovis, bovine tuberculosis, deer

Citation

Griffin, J. M., D.H. Williams, G.E. Kelly, T.A. Clegg, I. O'Boyle, J.D. Collins, S.J. More. 2005. The impact of badger removal on the control of tuberculosis in cattle herds in Ireland. Preventive Veterinary Medicine 67: 237–266.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In Ireland, the herd prevalence of bovine tuberculosis has remained stable for several decades, and in common with several other countries, progress towards eradication has stalled. There is evidence in support of the potential role of infected badgers (Meles meles, a protected species) in bovine tuberculosis in Ireland and Britain. However, this evidence on its own has not been sufficient to prove disease causation. Field trials are likely to offer the best opportunity to define this role. Building on the earlier East Offaly project, our objectives were to assess the impact of badger removal on the control of tuberculosis in cattle herds in Ireland.

The study was conducted from September 1997 to August 2002 in matched removal and reference areas (average area of 245.1 km2) in four counties: Cork, Donegal, Kilkenny and Monaghan. Badger removal was intensive and proactive throughout the study period in the removal areas, but reactive (in response to severe tuberculosis outbreaks in cattle) in the reference areas. Removal intensity in the removal and reference areas during the first 2 years of the study averaged 0.57 and 0.07 badgers/km2/ year, respectively.

The outcome of interest was restriction of cattle herds due to confirmed tuberculosis, where tuberculous lesions were detected in one or more animals. Data were analysed using logistic regression (modelling the probability of a confirmed herd restriction) and survival analysis (modelling time to a confirmed herd restriction). During the study period, there was a significant difference between the removal and reference areas in all four counties in both the probability of and the time to a confirmed herd restriction due to tuberculosis. In the final year of the study, the odds of a confirmed herd restriction in the removal (as compared to the reference areas) were 0.25 in Cork, 0.04 in Donegal, 0.26 in Kilkenny and 0.43 in Monaghan. Further, the hazard ratios (removal over reference) ranged from 0.4 to 0.04 (a 60–96% decrease in the rate at which herds were becoming the subject of a confirmed restriction).

Key Words Mycobacterium bovis, tuberculosis, cattle, badgers, Ireland, logistic regression, cox model

Citation

Harrington, N. P., O P. Surujballi, J. F. Prescott, J. R. Duncan, W. R. Waters, K. Lyashchenko, and R. Greenwald. 2008. Antibody responses of cervids (Cervus elaphus) following experimental Mycobacterium bovis infection and the implications for immunodiagnosis. Clinical and Vaccine Immunology 15(11):1650–1658.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Captive and free-ranging wildlife animals are implicated in the maintenance and transmission of bovine tuberculosis and therefore pose a significant obstacle to eradication of the disease from domestic livestock. The current antemortem diagnostic method, the intradermal tuberculin skin test, is impractical for routine use with many wild animals. Antibody-based assays are particularly attractive because the animals are handled only once and immediate processing of the sample is not required. This report characterizes the antibody responses of red deer-elk hybrids (Cervus elaphus) against Mycobacterium bovis and subsequently evaluates the diagnostic performance of select antigens in a rapid-test format. Sequential serum samples were collected from 10 animals experimentally infected with M. bovis and 5 noninfected animals over a 7-month period postinfection (p.i.). Samples were evaluated by enzyme-linked immunosorbent assays, immunoblot analyses, and multiantigen print immunoassays for seroreactivity to mycobacterial antigens. Although all infected animals produced antibodies to M. bovis protein antigens, there was significant animal-to-animal variation in the kinetics and magnitudes of responses and the antigens recognized. The most frequently recognized antigens included MPB83, ESAT-6, CFP10, and MPB70. Responses to some antigens, such as MPB83, were consistently detected as early as 4 weeks after inoculation, whereas other antigens were detected only much later (>140 days p.i.). Antibody responses were boosted by injection of tuberculin for intradermal tuberculin skin testing. Comparison of single-antigen (fluorescence polarization assay) with multiantigen (CervidTB STAT-PAK) rapid tests demonstrated that a highly sensitive and specific serodiagnostic test for tuberculosis in cervids will require multiple and carefully selected seroreactive antigens covering a broad spectrum of antibody specificities.

Key Words Cervid, immunodiagnosis, TB STAT-PAK, free-ranging wildlife, captive wildlife

Citation

Hermoso de Mendoza,J., A. Parra, A. Tato, J.M. Alonso, J.M. Rey, J. Pena, A. Garcia-Sanchez, J. Larrasa, J. Teixido, G. Manzano, R. Cerrato, G. Pereira, P. Fernandez-Llario, M. Hermoso de Mendoza. 2006. Bovine tuberculosis in wild boar (Sus scrofa), red deer (Cervus elaphus) and cattle (Bos taurus) in a Mediterranean ecosystem (1992–2004). Preventive Veterinary Medicine 74:239-247.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

During the last 12 years, an increasing frequency in condemnation of hunted red deer and wild boar carcasses due to the presence of tubercle-like lesions has been observed in Extremadura (Western Spain). Before 1993, tuberculosis was a very rare finding in hunted animals. The current tuberculosis regional prevalence in cattle approaches 0.4% after years of expensive test and slaughter campaigns. It is imperative to investigate the epidemiology of Mycobacterium bovis infection in red dear and wild boar in order to keep a good health status and to maintain the effectiveness of domestic species TB eradication programs. The present paper evaluates the problem in Sierra de San Pedro, estimating the prevalence of TB in wild boar and red deer, the main wild artiodactyls in the area, and domestic cattle since 1992–2004, by the use of a low-cost surveillance method based on detailed pathological inspection of hunted animal carcasses. Microbiology and molecular epidemiology studies on several M. bovis isolates from domestic and wild animals helped to define the interspecies contacts. These findings, as well as recent history of game estates management and descriptive epidemiology field work, throw light on the rise and maintenance of these epizootics.

Key Words bovine tuberculosis, wild artiodactyls, wild boar, red deer, Mediterranean ecosystem

Citation Hickling, G. J. 2002. Dynamics of bovine tuberculosis in wild white-tailed deer in Michigan. Michigan Department of Natural Resources Wildlife Division, Report No. 3363.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

In mid-2001, the author of this report was invited to undertake an exploratory analysis of Michigan Department of Natural Resources' data on bovine tuberculosis (TB) infection in wild white-tailed (Odocoileus virginianus) in the northeastern Lower Peninsula of the state. The aims of this analysis were:
• to quantify the geographic spread of tuberculous deer in Michigan;
• to investigate key factors influencing the prevalence of disease in the core of the infected area;
• to interpret the results in light of overseas experience with wildlife TB, with a view to recommending how current management of the disease might be enhanced.

Key Words Michigan, DNR, Dynamics, White-tailed deer, management

Citation Hickling, G.J., S.M. Schmitt, and D.J. O'Brien. 2003. Spatial and temporal spread of bovine tuberculosis in wild white-tailed deer in Michigan.

Abstract Only ☑

No Abstract ☐

Article Type Report

Abstract

In 1975, a wild white-tailed deer infected with bovine tuberculosis was shot in the northeastern Lower Peninsula, Michigan. The shooting of a second infected deer in the same area in 1994 triggered ongoing disease surveillance in theregion. By 2002, bovine tuberculosis had been confirmed in 12 Michigan counties: from 449 deer; two elk; 41 non-cervid wildlife; one captive cervid facility and 28 cattle herds. We analyzed geographic spread of disease since thesurveillance began and investigated factors influencing the prevalence of disease within the infected area. These analysesreveal that 78 percent of tuberculous deer came from within a 1560 km2 'core' area, within which the prevalence ofapparent disease averaged 2.5 percent. Prevalence declined dramatically outside of the core and was an order ofmagnitude lower 30km from its boundary. This prevalence gradient was highly significant (P<0.0001) and did not alter over the 6year surveillance period (P= 0.98). Within the core, deer density and supplemental feeding by hunters werepositively and independently correlated with tuberculosis prevalence in deer. Together, these two factors explained 55 percent of the variation in prevalence. We conclude that bovine tuberculosis was already well established in the deer population in 1994, that the infected area has not expanded significantly since that time, and that deer over-abundance and food supplementation have both contributed to ongoing transmission of disease. Managers are currently enforcingprohibitions on deer feeding in the core and are working to lower deer numbers there through increased hunting pressure.

Key Words deer, Michigan, Mycobacterium bovis

Citation

Hill, J.A. 2005. Wildlife-cattle interactions in northern Michigan: implications for the transmission of bovine tuberculosis. Thesis, Utah State University, Logan, UT.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

Bovine tuberculosis (Mycobacterium bovis) was discovered in northern Michigan white-tailed deer (Odocoileus virginianus) in 1994, and has been known to exist in Michigan cattle herds since 1998. Despite efforts to eradicate the disease in cattle, infection and re-infection of farms continues to occur, suggesting transmission among cattle, deer, or other wildlife reservoirs. The goals of this study were to document wildlife activity on farms and evaluate the possible role wildlife play in the ecology of bovine tuberculosis (TB) in Michigan. Visual observations were conducted on farms in a 5-county area of northern Michigan to document direct wildlife-cattle interactions (i.e., <5 m between individuals) and indirect interactions (e.g., wildlife visitations to food stores and areas accessible to cattle). Observations were conducted primarily during evening and early morning hours between January and August, 2002, and on a 24-hour schedule between January and August, 2003. Total observation time accumulated through the duration of the study was 1,780 hours. Results indicated that direct interaction between deer and cattle was a rare event; no direct interactions were observed during the first year, and only one direct interaction was observed during the second year. However, through the duration of the study 21 direct interactions were documented between cattle and turkey, and 11 direct interactions were documented between cattle and mammals other than deer. In total, 273 indirect interactions by deer, 112 indirect interactions by turkeys, and 248 indirect interactions by mammals other than deer were observed during the 2 field seasons combined. These data supported the hypothesis that indirect interactions among wildlife and cattle are a potential mechanism for the transmission of TB in Michigan. If direct interactions were important mechanisms of TB transmission to cattle in northern Michigan, my data suggested that feral cats were the species of most concern, even though there were more observations between turkey and cattle. Unlike cats, which can become infected with and transmit TB, there is no evidence for such pathogenesis in turkey.

Key Words bovine tuberculosis, cattle, Michigan, wildlife

Citation

Himsworth, C. G., B. T. Elkin, J. S. Nishi, T. Epp, K. P. Lyashchenko, O. Surujballi, C. Turcotte, J. Esfandiari, R. Greenwald, and F. A. Leighton. 2010. Comparison of test perfomance and evaluation of novel immunoassays for tuberculosis in a captive herd of wood bison naturally infected with Mycobacterium bovis. Journal of Wildlife Diseases 46(1):78–86.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In 1996, the Hook Lake Wood Bison Recovery Project was initiated to establish a small, disease-free, captive, bison-breeding herd. Founders originated from wild bison herds in the Slave River Lowlands in northern Canada, which, like other bison herds in and around Wood Buffalo National Park, are endemically infected with bovine tuberculosis (caused by Mycobacterium bovis) and brucellosis (caused by Brucella abortus). After 9 yr of apparent disease freedom, tuberculosis was detected within the captive herd, leading to complete depopulation. This study examined the performance of antemortem tuberculosis diagnostic tests used during the project. Performances of the caudal-fold test, fluorescent polarization assay, multiantigen print immunoassay (MAPIA), and the rapid test (RT) were assessed by estimating sensitivity, specificity, positive predictive value, and negative predictive value for each test. Kappa values measuring agreement between tests were calculated. Overall, the tests did not differ with respect to sensitivities and specificities, which ranged from 50% to 92% and from 34% to 100%, respectively. The MAPIA tended to show high sensitivity, and there was significant agreement only between the MAPIA and RT. Serum collected from infected animals at slaughter produced highly variable results on the different assays, and one infected bison was negative on all antemortem tests. The results of this analysis suggest use of multiple antemortem tests in parallel, particularly those incorporating multiple antigens, to optimize sensitivity in detecting bovine tuberculosis in bison. However, as demonstrated in this herd, even a seemingly optimal antemortem testing regimen can fail to detect M. bovis–infected individuals.

Key Words Antemortem, bison, diagnostic, Mycobacterium bovis, testing, tuberculosis

Citation

Hone, J. and C. A. Donnelly. 2008. Evaluating evidence of association of bovine tuberculosis in cattle and badgers. Journal of Applied Ecology 45:1660–1666.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Bovine tuberculosis (TB) occurs in cattle and badgers in the UK and control efforts are undertaken to reduce the spread of the disease.
2. This study evaluates relationships predicted by nine epidemiological two-host models of disease spread generated by various combinations of density-dependent, frequency-dependent and environmental pathogen transmission. The relationships of interest are between measures of TB in cattle and in badgers from 10 sites which were randomly selected to be proactive badger culling sites in the UK Randomized Badger Culling Trial. The data are from the initial badger cull only.
3. There was most support (Akaike weight =0·562, R2=0·869) for models that predicted a positive linear relationship between density of infectious cattle per square kilometre and the density index of infectious badgers. There was less support (Akaike weight = 0·060) for a model that predicted a positive linear relationship between density of infectious cattle per square kilometre and the proportion of badgers infectious with Mycobacterium bovis. A correction to reduce effects of badger carcase storage and an examination of effects of the 2001 foot-and-mouth disease epidemic had little impact on estimated relationships.
4. Synthesis and applications . The results provide support for two-host disease models of TB in cattle and wildlife such as badgers, although the form of disease transmission cannot be identified clearly by these analyses. The implication of the results is that the best-fitting models predict that, in the absence of intervention-related changes in badger behaviour, a reduction in density of infectious badgers should reduce the density of infectious cattle. However, analysis of bait-marking data collected following experimental badger culls indicated that culling badgers profoundly alters their spatial organization as well as their population density, potentially influencing contact rates. Effective vaccination of badgers, were it to become available, would be expected to reduce the density of infectious badgers without directly affecting their behaviour.

Key Words

badger, bovine tuberculosis, cattle, host–disease model, multi-host disease models

Citation

Horan, R. D., C. A. Wolf, E. P. Fenichel, and K. H. Mathews, Jr. 2003. Controlling wildlife and livestock disease with endogenous on-farm biosecurity. Department of Agricultural Economics, Michigan State University. Paper prepared for presentation at the American Agricultural Economics Association Annual Meeting, Denver, Colorado, August 2004.

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

The spread of infectious disease among and between wild and domesticated animals has become a major problem worldwide. We analyze the socially optimal management of wildlife and livestock, including choices involving environmental habitat variables and on-farm biosecurity controls, when wildlife and livestock can spread an infectious disease to each other. The model is applied to the problem of bovine tuberculosis among Michigan white-tailed deer. The
optimum is a cycle in which the disease remains endemic in the wildlife, but in which the cattle herd is depleted when the prevalence rate in deer grows too large.

Key Words wildlife, livestock, biosecurity, disease spread, prevalence rate

Citation Horan, R. D., C. A. Wolf, E. P. Fenichel, and K. H. Mathews, Jr. 2008. Joint management of wildlife and livestock disease. Environmental and Resource Economics. 41:47–70.

Abstract Only ☑

No Abstract ☐

Article Type Journal Article

Abstract We analyze a bioeconomic model of a multiple-host disease problem involving wildlife and livestock. The social planner's choices include targeted (i.e., infectious versus healthy) livestock harvests, non-targeted wildlife harvests, environmental habitat variables, and on-farm biosecurity to prevent cross-species contacts. The model is applied to bovine tuberculosis among Michigan white-tailed deer and cattle. We find optimal controls may target the livestock sector more stringently when the livestock sector exhibits low value relative to the wildlife sector. This is in contrast with the conventional wisdom on the issue that controls should primarily target wildlife species that serve as disease reservoirs.

Key Words Bioeconomics, Infectious disease, Ecosystem management , White-tailed deer, Optimal control

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Citation Horan, R., C.A. Wolf, E.P. Fenichel, and K.H. Mathews, Jr. 2005. Spatial management of wildlife disease. Review of Agricultural Economics 27(3):483-490.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Deer, odocoileus, feeding, case report

Citation

Hughey, B.D. 2003. Are there "hot spots" of bovine tuberculosis in the free-ranging white-tailed deer (Odocoileus virginianus) herd of northeastern Michigan. Thesis, Michigan State University, East Lansing, MI.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

This project looks at whether high case frequency areas or "hot spots" of bovine tuberculosis (tb) exist in free ranging white-tailed deer in northeastern Michigan, and examines the factors associated with them. Michigan Department of Natural Resources researchers have been collecting deer heads annually since 1996 in the five county area of Alcona, Alpena, Montmorency, Oscoda, and Presque Isle as part of an effort to manage an outbreak of bovine tb in the wild white-tailed deer population. From these heads a database containing age, sex, and harvest or collection location information was constructed. The townships within these five counties were categorized as having zero case frequency, medium case frequency, or high case frequency. These categories are based on the number of years at least one tb infected deer was detected in that township. Each case frequency category was then examined individually looking at the yearly sample size distribution, yearly case frequency, and cumulative sample size distribution. Using GIS these areas of varying case fequency were compared to five deer use categories, Summer Use (high quality summer habitat), Summer Other (poor summer habitat), Winter Use (high quality winter habitat, Winter Other (poor winter habitat), and Rare Use (includes areas rarely or never used by deer, such as water, urban and industrial areas).

Key Words bovine tuberculosis, Michigan, Odocoileus virginianus, white-tailed deer

Citation

Hutchings, M. R. and S. Harris. 1997. Effects of farm management practices on cattle grazing behaviour and the potential for transmission of bovine tuberculosis from badgers to cattle. The Veterinary Journal 153:149-162.

Abstract Only ☑

No Abstract ☐

Article Type Journal Article

Abstract

Despite the large body of circumstantial evidence to suggest a link, the means by which bovine tuberculosis is passed from badgers to cattle remains unclear; pasture contamination with the urine, faeces and/or sputum of infectious badgers is believed to be the main route of transmission. Therefore the behaviour of grazing cattle was studied to determine whether they avoided investigating and/or grazing pasture contaminated with badger excreta, and whether different farm management practices enhanced the potential for disease transmission. Active latrines were avoided by most cattle until the sward length in the rest of the field was reduced, after which there was an increasing likelihood that active badger latrines would be grazed. Most of the cattle grazed active badger latrines, but cattle of low rank within the herd grazed latrines more heavily. Farm management practices that reduced the availability of long swards shortened the period of investigative behaviour and greatly enhanced the risk that cattle would graze active badger latrines. Cattle were more likely to graze pasture away from latrines that was contaminated either with badger urine or single faeces. Because bacilli remain viable in the soil for up to 2 years, there is the potential for bacilli to accumulate at active badger latrines, and these could pose a significant risk to cattle, even when the latrine is no longer being used by badgers. Cattle readily grazed the lush sward at disused latrines, during which thev could ingest contaminated soil; the amount of soil ingested increases as sward length decreases.

Key Words

TB transmission; tarm management; cattle behaviour; grazing pressure; badger scent marking, badger excreta

Citation	Hutton,T., T. Deliberto, S. Owen, B. Morrison. 2006. Disease risks associated with increasing feral swine numbers and distribution in the United States. Midwest Association of Fish and Wildlife Agencies, Wildlife and Fish Health Committee.
Abstract Only	☐
No Abstract	☑
Article Type	Report
Abstract	
Key Words	bovine tuberculosis, distribution, feral swine, transmission

Citation

Jackson, R., G.W. de Lisle, and R.S. Morris. 1995. A study of the environmental survival of Mycobacterium bovis on a farm in New Zealand. New Zealand Veterinary Journal 43: 346-352.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis organisms absorbed on cotton ribbons were placed in different natural habitats on a farm in New Zealand. Mycobacterium bovis was not re-isolated from ribbons placed on pasture after 4 days. Survival on ribbons was longest in brushtail possum dens, where the maximum period of survival in dens was less than 7 days in summer and greater than 14 days but less than 28 days in winter and spring. The maximum period of survival on a forest floor was intermediate between pasture and dens - less than 4 days in summer and greater than 14 days but less than 28 days in winter. The overall probability of survival was influenced by season and was shortest in summer and longest in spring and winter. Survival time increased as minimum daily temperatures decreased. These studies showed there was a relatively short period of survival of M. bovis outside hosts and support a conclusion that environmental contamination of pasture. narticularlv in summer months, may be relatively unimportant in the epidemiology of tuberculosis in cattle, deer and possums

Key Words

Mycobacterium bovis, cotton ribbons, brushtail possum, New Zealand, farm, temperatures, environmental contamination.

Citation

Jacques, C. N., J. A. Jenks, A. L. Jenny, and S. L. Griffin. 2003. Prevalence of chronic wasting disease and bovine tuberculosis in free-ranging deer and elk in South Dakota. Journal of Wildlife Diseases 39(1):29–34.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Heads of hunter-harvested deer and elk were collected throughout South Dakota (USA) and within established chronic wasting disease (CWD) surveillance areas from 1997–2002 to determine infection with CWD and bovine tuberculosis (TB). We used immunohistochemistry to detect CWD-infected individuals among 1,672 deer and elk sampled via geographically targeted surveillance. A total of 537 elk (Cervus elaphus nelsoni), 813 white-tailed deer (Odocoileus virginianus), and 322 mule deer (O. hemionus) was sampled for CWD. Estimated overall prevalence and associated confidence intervals (95%) in white-tailed deer was 0.001% (0–0.007%). Similarly, estimated overall prevalence in elk and mule deer was 0.0% (0–0.004%) and 0.0% (0– 0.011%), respectively. A total of 401 elk, 1,638 white-tailed deer, and 207 mule deer was sampled for TB. Estimated overall prevalence of infection with TB in elk harvested in South Dakota was 0.0% (0–0.009%). Similarly, estimated overall prevalence of TB in white-tailed deer and mule deer harvested throughout South Dakota was 0.0% (0–0.002%) and 0.0% (0–0.018%), respectively.

Key Words

Bovine tuberculosis, cervid, chronic wasting disease, elk, mule deer, prion, South Dakota, transmissible spongiform encephalopathy, white-tailed deer

Citation

Jenkins, H.E., R. Woodroffe, and C.A. Donnelly. 2010. The duration of the effects of repeated widespread badger culling on cattle tuberculosis following the cessation of culling. PLOS ONE 5(2): e9090. doi:10.1371/journal.pone.0009090

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Background: In the British Isles, control of cattle tuberculosis (TB) is hindered by persistent infection of wild badger (Meles meles) populations. A large-scale field trial—the Randomised Badger Culling Trial (RBCT)—previously showed that widespread badger culling produced modest reductions in cattle TB incidence during culling, which were offset by elevated TB risks for cattle on adjoining lands. Once culling was halted, beneficial effects inside culling areas increased, while detrimental effects on adjoining lands disappeared. However, a full assessment of the utility of badger culling requires information on the duration of culling effects.

Methodology/Principal Findings: We monitored cattle TB incidence in and around RBCT areas after culling ended. We found that benefits inside culled areas declined over time, and were no longer detectable by three years post-culling. On adjoining lands, a trend suggesting beneficial effects immediately after the end of culling was insignificant, and disappeared after 18 months post-culling. From completion of the first cull to the loss of detectable effects (an average five-year culling period plus 2.5 years post-culling), cattle TB incidence was 28.7% lower (95% confidence interval [CI] 20.7 to 35.8% lower) inside ten 100 km2 culled areas than inside ten matched no-culling areas, and comparable (11.7% higher, 95% CI: 13.0% lower to 43.4% higher, p = 0.39) on lands #2 km outside culled and no-culling areas. The financial costs of culling an idealized 150 km2 area would exceed the savings achieved through reduced cattle TB, by factors of 2 to 3.5.

Conclusions/Significance: Our findings show that the reductions in cattle TB incidence achieved by repeated badger culling were not sustained in the long term after culling ended and did not offset the financial costs of culling. These result, combined with evaluation of alternative culling methods, suggest that badger culling is unlikely to contribute effectively to the control of cattle TB in Britain.

Key Words badgers, bovis tuberculosis, cattle, culling

Citation

Johnson, S. R., M. R. Dunbar, L. Martinez, R. L. Jones, R. Bowen, P. Gordy. 2009. Experimental inoculation of coyotes with Mycobacterium bovis: Susceptibility and shedding. Proceedings of the Annual Meeting of the United States Animal Health Association 112:94-97

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

Several wildlife species have tested positive for bovine tuberculosis in Michigan and may potentially transmit the disease to other animals. Coyotes have the highest known prevalence in the endemic area and thus, our objective was to investigate the shedding of Mycobacterium bovis by coyotes. Four coyotes were orally inoculated with 1 ml of 1 x 105 CFU/ml of M. bovis. Oral and nasal swabs, and feces were collected regularly and tested by culture. Fecal samples were also tested by exposing guinea pigs to the coyotes' feces. All animals were necropsied to determine if infection occurred. All swabs, feces and tissues were negative on culture. The dosage of M. bovis given to these coyotes was considered biologically relevant, but was insufficient for causing infection. Due to the lack of infection, we still do not know the risk coyotes pose for shedding M. bovis.

Key Words coyotes, Michigan, guinea pigs, shedding

Citation

Johnston, W. T., G. Gettinby, D. R. Cox, C. A. Donnelly, J. Bourne, R. Clifton-Hadley, A. M. Le Fevre, J. P. McInerney, A. Mitchell, W. I Morrison, and R. Woodroffe. 2005. Herd-level risk factors associated with tuberculosis breakdowns among cattle herds in England before the 2001 foot-and-mouth disease epidemic. Biology Letters 1:53-56.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A case–control study of the factors associated with the risk of a bovine tuberculosis (TB) breakdown in cattle herds was undertaken within the randomized badger culling trial (RBCT). TB breakdowns occurring prior to the 2001 foot-and-mouth disease epidemic in three RBCT triplets were eligible to be cases; controls were selected from the same RBCT area. Data from 151 case farms and 117 control farms were analysed using logistic regression. The strongest factors associated with an increased TB risk were movement of cattle onto the farm from markets or farm sales, operating a farm over multiple premises and the use of either covered yard or 'other' housing types. Spreading artificial fertilizers or farmyard manure on grazing land were both associated with decreased risk. These first case–control results from the RBCT will be followed by similar analyses as more data become available.

Key Words bovine tuberculosis, case–control study, cattle movement, randomized badger culling trial, TB99

Citation Jolles, A. E., D. V. Cooper, and S. A. Levin. 2005. Hidden effects of chronic tuberculosis in African buffalo. Ecology 86(9):2258–2264.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Infectious diseases can bring about population declines and local host extinctions, contributing significantly to the global biodiversity crisis. Nonetheless, studies measuring population-level effects of pathogens in wild host populations are rare, and taxonomically biased toward avian hosts and macroparasitic infections. We investigated the effects of bovine tuberculosis (bTB), caused by the bacterial pathogen Mycobacterium bovis, on African buffalo (Syncerus caffer) at Hluhluwe-iMfolozi Park, South Africa. We tested 1180 buffalo for bTB infection between May 2000 and November 2001. Most infections were mild, confirming the chronic nature of the disease in buffalo. However, our data indicate that bTB affects both adult survival and fecundity. Using an age-structured population model, we demonstrate that the pathogen can reduce population growth rate drastically; yet its effects appear difficult to detect at the population level: bTB causes no conspicuous mass mortalities or fast population declines, nor does it alter host-population age structure significantly. Our models suggest that this syndrome—low detectability coupled with severe impacts on population growth rate and, therefore, resilience—may be characteristic of chronic diseases in large mammals.

Key Words African buffalo, chronic disease, fecundity, mortality, Mycobacterium bovis, population age structure, population growth rate, population resilience, Syncerus caffer, tuberculosis

Citation Joly, J. O. and F. Messier. 2004. Factors affecting apparent prevalence of tuberculosis and brucellosis in wood bison. Journal of Animal Ecology 73:623–631.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Bison (Bison bison) abundance in Wood Buffalo National Park, Canada, declined from in excess of 10 000 bison in the late 1960s to a low of 2200 bison in the late 1990s.
2. Bovine tuberculosis (Mycobacterium bovis) and brucellosis (Brucella abortus), were introduced to Wood Buffalo National Park in the late 1920s. As each of these pathogens have the potential to reduce survival and reproduction in bison, they are suspected to have played a role in the decline in bison abundance.
3. We live-captured bison for disease testing in February and March of 1997, 1998 and 1999. Forty-nine percent tested positive for tuberculosis (i.e. were positive on the caudal fold test and/or fluorescent polarization assay, n= 342). Further, 30·9% of bison were seropositive for brucellosis (i.e. agglutinated in the buffered-plate antigen test and had a titre of 1 : 5 in the complement fixation test or had a titre of ≥1 : 10 in the complement fixation test, n= 346). Prevalence for both diseases increased with age and males were m ore likely to test positive for tuberculosis. Prevalence of either disease did not appear to be directly related to density of bison, as prevalence rates were not greater in the high density Delta population than the lower density Hay Camp and Nyarling River populations.
4. Comparison of our results to previous brucellosis and tuberculosis surveys in Wood Buffalo National Park indicates that prevalence of neither pathogen is a direct function of bison density. These pathogens are endemic within the bison population of the park.

Key Words Bison bison, Mycobacterium bovis, Brucella abortus, apparent prevalence, wildlife disease

Citation Joly, J. O. and F. Messier. 2005. The effect of bovine tuberculosis and brucellosis on reproduction and survival of wood bison in Wood Buffalo National Park. Journal of Animal Ecology 74:543–551.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Wood bison (Bison bison athabascae L.) abundance in Wood Buffalo National Park, Canada, declined from an excess of 10 000 bison in the late 1960s to a low of 2200 bison in the late 1990s.
2. Bovine tuberculosis (Mycobacterium bovis) and brucellosis (Brucella abortus), were introduced to Wood Buffalo National Park in the late 1920s. As each of these pathogens has the potential to reduce survival and reproduction in bison, they are suspected to have played a role in the decline in bison abundance.
3. We live-captured bison in the winters of 1997–2000, tested for tuberculosis, brucellosis and pregnancy and released animals with radio transmitters to evaluate survival.
4. We found that bison that were positive for both diseases were less likely to be pregnant or to survive the winter than bison positive for one or neither disease. Further, in one population, bison that were tuberculosis-positive had a substantially lower pregnancy probability.
5. Demonstrating a negative effect of diseases on survival and reproduction is a necessary, but not sufficient, test of the role of diseases in bison population decline.

Key Words Bison bison, Brucella abortus, disease, epizootiology, Mycobacterium bovis

Citation

Kaneene J. B., C. S. Bruning-Fann, L. M. Granger, R. Miller, and B. A. Porter-Spalding. 2002. Environmental and farm management factors associated with tuberculosis on cattle farms in northeastern Michigan. Journal of the American Veterinary Medical Association 221:837-842.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Objective—To identify major environmental and farm management factors associated with the occurrence of tuberculosis (TB) on cattle farms in northeastern Michigan.
Design—Case-control study.
Sample Population—17 cattle farms with infected cattle and 51 control farms.
Procedure—Each case farm (laboratory confirmed diagnosis of Mycobacterium bovis infection) was matched with 2 to 4 control farms (negative whole-herd test results within previous 12 months) on the basis of type of farm (dairy or beef) and location. Cattle farm data were collected from in-person interviews and mailed questionnaires. Wildlife TB data were gathered through state wildlife surveillance. Environmental data were gathered from a satellite image-based geographic information system. Multivariable conditional logistic regression for matched analysis was performed.
Results—Major factors associated with increased farm risk of TB were higher TB prevalence among wild deer and cattle farms in the area, herd size, and ponds or creeks in cattle housing areas. Factors associated with reduced farm risk of TB were greater amounts of natural open lands in the surrounding area and reducing deer access to cattle housing areas by housing cattle in barns, barnyards, or feedlots and use of electrified wire or barbed wire for livestock fencing.
Conclusions and Clinical Relevance—Results suggest that certain environmental and management factors may be associated with risk of TB on cattle farms.

Key Words

Michigan, Mycobacterium bovis, cattle farm, cattle housing, farm risk, deer access, livestock fencing, environmental, management.

Citation Kaneene, J.B., and C. O. Thoen. 2004. Tuberculosis. Journal of the American Veterinary Medical Association 224(5): 685-691.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Update, reemergence, etiology, epidemiology, pathogenesis, diagnosis, control, overview

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Citation Kao, R. R. and M. G. Roberts. 1999. A comparison of wildlife control and cattle vaccination as methods for the control of bovine tuberculosis. Epidemiology and Infection 122:505-519.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract The Australian brushtail possum is the major source of infection for new cases of bovine tuberculosis in cattle in New Zealand. Using hypothetical values for the cost of putative cattle and possum Tb vaccines, the relative efforts required to eradicate Tb in cattle using possum culling, possum vaccination or cattle vaccination are compared. For realistic assumed costs for 1080 poison bait, possum culling is found to be a cost-effective strategy compared to cattle vaccination if the required control area is below 13 ha per cattle herd, while possum vaccination is cost-effective for control areas of less than 3 ha per herd. Examination of other considerations such as the possible roles of possum migration and heterogeneities in possum population density suggest that each control strategy may be superior under different field conditions. Finally, the roles of the possum in New Zealand, and the Eurasian badger in Great Britain and Ireland in the transmission of bovine tuberculosis to cattle are compared.

Key Words Brushtail possum, vaccination, wildlife control, New Zealand

Citation	Kavanagh-Patrick, B.,Coordinator. 2006. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report and Conference. Michigan Department of Community Health, Lansing, MI.
Abstract Only	☐
No Abstract	☑
Article Type	Proceedings
Abstract	
Key Words	bovine tuberculosis, Mycobacterium bovis, Odocoileus virginianus, white-tailed deer

Citation

Kean, J. M. and N. D. Barlow, and G. J. Hickling. 1999. Evaluating potential sources of bovine tuberculosis infection in a New Zealand cattle herd. New Zealand Journal of Agricultural Research 42:101-106.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In New Zealand, a major source of bovine tuberculosis (Mycobacterium bovis, Tb) infection in farmed cattle is thought to be transmission from infected wildlife, primarily the brushtail possum {Trichosurus vulpecula). At Hohotaka, central North Island, control work from 1988 to 1994 achieved a sustained mean reduction of 87.5% in the density of Tb-infected possums. As expected, annual Tb incidence in local cattle herds consequently declined by a similar amount (83.4%). This decline was gradual, due to withinherd transmission of residual infection and imperfect detection of infected animals. By fitting models to the observed rate of decline in Hohotaka Tb reactors, we are able to deduce the contributions to reactor rates of possums and cattle-to-cattle Tb transmission. Our results suggest that Tb transmission between cattle within the herd may have contributed around 20% to 32% of infections prior to the wildlife control programme. Nevertheless, our estimate for the rate of within-herd transmission is well below that required to maintain cattle Tb in the absence of infectious wildlife. Our analysis supports the policy of wildlife control as the most effective method for reducing cattle Tb in areas such as Hohotaka.

Key Words Mycobacterium bovis, wildlife, brushtail possum, disease transmission, models

Citation

Kelly, G. E., G. E. McGrath, and S. J. More. 2010. Estimating the extent of spatial association of Mycobacterium bovis infection in badgers in Ireland. Epidemiology and Infection 138:270–279.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis infects the wildlife species badgers Meles meles who are linked with the spread of the associated disease tuberculosis (TB) in cattle. Control of livestock infections depends in part on the spatial and social structure of the wildlife host. Here we describe spatial association of M. bovis infection in a badger population using data from the first year of the Four Area Project in Ireland. Using second-order intensity functions, we show there is strong evidence of clustering of TB cases in each the four areas, i.e. a global tendency for infected cases to occur near other infected cases. Using estimated intensity functions, we identify locations where particular strains of TB cluster. Generalized linear geostatistical models are used to assess the practical range at which spatial correlation occurs and is found to exceed 6 in all areas. The study is of relevance concerning the scale of localized badger culling in the control of the disease in cattle.

Key Words

badger, disease clustering, GLGM, Mycobacterium bovis, spatial ranges

Citation

Knust, B. 2008. Reducing the public health impact of bovine tuberculosis by controlling disease transmission between cattle and white-tailed deer in Northwestern Minnesota. Thesis, University of Minnesota, St. Paul, MN.

Abstract Only ☐

No Abstract ☑

Article Type Thesis/Dissertation

Abstract

Bovine tuberculosis, caused by infection with Mycobacterium bovis, is a re-emerging zoonotic disease. It has staged a comeback by establishing infections in wildlife and cattle, creating the potential for human disease in locations where it was thought to be under control. In northwestern Minnesota, infected cattle and white-tailed deer were first discovered in 2005. A major bovine tuberculosis eradication campaign is underway in the state, with multiple efforts employed to control M. bovis infection in both cattle and deer populations. In order to effectively eradicate bovine tuberculosis in Minnesota, there is a need for better understanding of the factors that increase the risk of deer and cattle interacting in a way that facilitates tuberculosis transmission. By reducing the risk of disease transmission within the animal populations, we will also reduce the risk that bovine tuberculosis will again become a common disease in human populations.

The purpose of this study is to characterize the risk of interactions between cattle and white-tailed deer in northern Minnesota in order to prevent M. bovis transmission. A survey originally developed to assess deer-cattle interactions in Michigan was modified for use in Minnesota, introducing a scoring method to evaluate the areas of highest priority at risk of potential deer-cattle interaction. The resulting semi-quantitative deer-cattle interaction risk assessment was used at 53 cattle herds located in the region adjacent to the bovine tuberculosis "Core Area". Two evaluators each scored the farm separately, and then created a management plan for the farm that prioritized the areas of greatest risk for deer-cattle interactions. Herds located within the "Management Zone" were evaluated by Minnesota Board of Animal Health staff, and results from these surveys were used as a point of comparison.

Half the herds visited by the University of Minnesota group had experienced deer damage to stored feeds within the past year. Only 11% of herds reported that deer were most frequently seen in the winter, while spring, summer, or fall were more common times for 50% of the herds. A strong association was found between increasing percentage of land that would serve as deer cover and the presence of deer damage to stored feeds on the farm. Farms most often had deer damage to stored hay, although the feed with highest proportion of damage by deer was silage. Cattle feeding practices were also found to have increased risk for deer-cattle interactions, with average scores for location of feeding site and the rate at which feed was consumed worth >50% of the maximum possible score.

Comparison of risk scores assigned by U of M observers at the same farms revealed that the two evaluators had a high level of agreement for many of the management areas. However, some risk areas had inconsistencies between evaluators, and the risk assessment's repeatability can be improved with some revisions to simplify the scoring system. In spite of these issues, the total risk score was significantly associated with the probability of a farm having deer damage. The total risk score and % deer cover land around the farm were used to create a logistic regression model that accurately predicted the presence of deer damage to stored feeds.

The recommendations made most often were to fence or otherwise protect hay storage, move the feeding location for cattle, move a feed storage site, reduce the amounts of feed fed at a time, or fence beet pulp storage. As described earlier, the risks of management factors varied, but the process of on-farm risk assessment ensured that all potential risk areas were evaluated in order to determine which risks were of greatest importance for the farm.

Management practices in many herds in northwest Minnesota were such that risk of deer-cattle interactions were present and significant. In order to prevent potential transmission of

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bovine tuberculosis between deer and cattle, continued development of biosecurity practices is needed. The on-farm risk assessment evaluated in this study serves as a valuable tool in prioritizing a farm's specific needs. Continued vigilance is necessary to maintain this zoonotic pathogen as a potential rather than a realized public health threat.

Key Words Thesis, public health, control, transmission, cattle, white-tailed deer, Minnesota

Citation	Lees, V.W., S. Copeland, and P. Rousseau.2003. Bovine tuberculosis in elk (Cervus elaphus manitobensis) near Riding Mountain National Park, Manitoba, from 1992 to 2002. The Canadian Veterinary Journal 44:830-831.
Abstract Only	☐
No Abstract	☑
Article Type	Journal Article
Abstract	
Key Words	Elk, Riding Mountain National Park, Manitoba

Citation

Lesellier, S., L. Corner, E. Costello, K. Lyashchenko, R. Greenwald, J. Esfandiari, M. Singh, R. G. Hewinson, M. Chambers, E. Gormley. 2009. Immunological responses and protective immunity in BCG vaccinated badgers following endobronchial infection with Mycobacterium bovis. Vaccine 27:402–409.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

European badgers (Meles meles) are a reservoir host of Mycobacterium bovis and are implicated in the transmission of tuberculosis to cattle in Ireland and Great Britain. The development of a vaccine for use in badgers is considered a key element of any campaign to eradicate the disease in livestock in both countries. In this study we have vaccinated groups of badgers with ∼5×105 cfu of the BCG vaccine delivered via two alternative routes, subcutaneous and mucosal (intranasal/conjunctival). Following experimental endobronchial infection with ∼104 cfu of M. bovis, all badgerswere euthanised at 12weeks post-infection. At post-mortem examination both vaccinated groups had significantly reduced severity of disease compared with the non-vaccinated controls. The analysis of immune responses throughout the study showed that vaccination with BCG did not generate any detectable immunological responses as measured by IFN-gamma production in antigen-stimulated peripheral blood mononuclear cells (PBMC) and IgG serological responses. However, the levels of the responses increased following M. bovis infection, and the kinetic profiles corresponded to the severity of lesions recorded post-mortem. Significant differenceswere observed in the timing of development of the immune responses between vaccinates and controls. The results suggest that the immunological responses are associated with the levels of protective immunity and could be used as markers to monitor control of disease in badgers following vaccination.

Key Words badgers, BCG, vaccine, Mycobacterium bovis, tuberculosis, immunology

Citation

Lesellier, S., L. Corner, E. Costello, P. Sleeman, K. P. Lyashchenko, R. Greenwald, J. Esfandiari, R. G. Hewinson, M. Chambers, E. Gormley. 2009. Immunological responses following experimental endobronchial infection of badgers (Meles meles) with different doses of Mycobacterium bovis. Veterinary Immunology and Immunopathology 127:174–180.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The Eurasian badger (Meles meles) is a wildlife reservoir for Mycobacterium bovis infection in Ireland and Great Britain and has been implicated in the transmission of tuberculosis to cattle. Vaccination of badgers is an option that could be used as part of a strategy to control the disease. In this study we used an endobronchial infection procedure to inoculate groups of badgers with three different doses (3 x 10^3, 2 x 10^2 and <10 Colony Forming Units (CFUs)) of M. bovis. After 17 weeks the disease status of each animal was determined by post-mortem pathology and culture for M. bovis. Each of the inoculum doses resulted in establishment of infection in the badgers. The cell-mediated immune (CMI) responses were measured by lymphocyte transformation assay (LTA) of peripheral blood mononuclear cells (PBMCs) cultured with bovine tuberculin (PPD-B). In each infected group the CMI responses increased with a kinetic profile corresponding to the delivered dose and the post-mortem pathology. The serological responses were measured by ELISA and a multiantigen print immunoassay (MAPIA) in order to investigate any changes in the antigenic repertoire associated with different infective doses. In contrast to the CMI responses, the ELISA and MAPIA showed that the recognition of antigens by the badgers was intermittent and not strongly influenced by the dose of M. bovis.

Key Words Badgers, Tuberculosis, PPD-B, Brock test, MAPIA

Citation

Livingstone, P. G., T.J. Ryan, N.G. Hancox, K.B. Crews, M.A.J. Bosson, G.J.E. Knowles, and W. McCook. 2006. Regionalisation: A strategy that will assist with bovine tuberculosis control and facilitate trade.Veterinary Microbiology 112: 291-301.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

It is expected that the revised chapter on bovine tuberculosis in the Terrestrial Animal Health Code of the Office Internationale des E ´ pizooties (OIE) will embrace regionalisation as a functional means of assisting countries, states or regions to meet the requirements for freedom from tuberculosis and to facilitate trade. The benefits and applications of regionalisation, which comprises zoning and compartmentalisation, are discussed. Regionalisation requires that a country's veterinary administration is able to implement transparent and auditable biosecurity measures that will ensure that the tuberculosis free status of a subpopulation of cattle is maintained despite the presence of infection in another cattle subpopulation, or in other domestic or wild animal species. Zoning, which requires cattle subpopulations to be separated by geographic boundaries, provides a practical basis whereby countries, states or regions, can progress towards freedom from tuberculosis, regardless of the source of infection for defined cattle subpopulations. Compartmentalisation however, requires that husbandry or management practices will be used to prevent a tuberculosis-free cattle subpopulation from contacting interspecific and intraspecific sources of infection. This will be difficult to achieve except for specialised cases such as artificial breeding centers.

Key Words Mycobacterium bovis, tuberculosis, regionalisation, zoning, compartments, cattle, farmed deer, wild animals, epidemiology

Citation

Lugton I. W., P.R. Wilson , R.S. Morris, and G. Nugent. 1998. Epidemiology and pathogenesis of Mycobacferium bowis infection of red deer (Cervus elaphus) in New Zealand. New Zealand Veterinary Journal 46: 147-156.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Aims. This study was initiated to investigate aspects of the epidemiology, pathogenesis and transmission of tuberculosisin wild red deer, with the aim of determining whether this species may be considered a reservoir host of Mycobacterium bovis in New Zealand.
Method. One hundred and six wild red deer (Cervus eluphus) carcasses from the Castlepoint and Hauhungaroa Range areas, which are endemic for bovine tuberculosis, were examined for the presence of M. bovis infection. Samples were also examined from 46 skin test-positive farmed deer killed at two deer slaughter premises. Where possible, a standard set of tissues and excretion site samples was collected for mycobacteriological examination.
Results. Fifty-eight infected deer were identified, and of these 28% showed no gross lesions. The prevalence of tuberculosis confirmed by culture in the wild deer was 32%. Only one of 18 deer younger than 1 year was infected. Mature deer (> 2 years) were 12 times more likely to be infected than those under 1 year of age. Infected older deer were less likely to show typical gross lesions than younger animals. Mycobacterium bovis was isolated from the oropharyngeal tonsil of 34 of 56 (61%) of the infected deer, and this was the most commonly infected site. Gross lesions were found in 18 of the 34 infected tonsils and only one of these showed a purulent tonsillitis. Mycobacterium bovis was recovered from four of 53 nasopharyngeal tonsils, four of 53 oropharyngeal swabs, one of 53 tracheal and nasal swabs, and one of 46 faecal samples, but not from any urine specimens.
Conclusion. These findings suggest that significant bacillary excretion from infected deer was uncommon, and is more likely to occur in severely affected animals. This study has confirmed the importance of mucosa-associated lymphoid tissues (MALT), particularly the oropharyngeal tonsil, in the pathogenesis of tuberculosis in deer. The findings justify investigation of the hypotheses that the prevalence of tuberculosis in wild deer in New Zealand is high due to transmission of infection from possums, and that in the absence of an infected possum population, the prevalence of tuberculosis in deer is likely to be low, and spatially patchy.
Clinical relevance. The results suggest that about one quarter of infected deer show no detectable gross lesions. This implies that many infected carcasses may enter the food chain unrecognised and that the estimated sensitivity and specificity of diagnostic tests may be erroneous if there is a difference in test performance between those conducted on deer with or without gross lesions. Diagnostic sensitivity following slaughter may be improved by routine culture of oropharyngeal tonsils and careful examination of lungs for adhesions and small subpleural tubercles.

Key Words Deer, tuberculosis, epidemiology, excretion route, pathogenesis, tonsil, MALT

Citation

Luna, J. O., M. A. A. Santos, E. L. Durigon, J. P. Araujo, and J. M. B. Duarte. 2003. Tuberculosis survey of free-ranging marsh deer (Blastocerus dichotomus) in Brazil. Journal of Zoo and Wildlife Medicine 34(4):414–415.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Esophageal–pharyngeal fluids from 53 free-ranging marsh deer (Blastocerus dichotomus) captured for a research program in the state of Mato Grosso do Sul, Brazil, were assayed for tuberculosis. Total DNA was extracted,amplified by polymerase chain reaction using specific primers for Mycobacterium tuberculosis complex (M. tuberculosis,M. bovis, M. microti, and M. africanum), and observed by agarose gel electrophoresis stained with ethidium bromide. All samples were negative. This, along with necropsy and histopathology data, suggests that these animals are not shedding and probably do not have active disease.

Key Words tuberculosis, marsh deer, Blastocerus dichotomus, Mycobacterium bovis, PCR

Citation

Lyashchenko, K. P., R. Greenwald, J. Esfandiari, M.A. Chambers, J. Vicente, C. Gortazar, N. Santos, M. Correia-Neves, B.M. Buddle, R. Jackson, D.J. O'Brien, S. Schmitt, M.V. Palmer, R.J. Delahay, W.R. Waters. 2008. Animal-side serologic assay for rapid detection of Mycobacterium bovis infection in multiple species of free-ranging wildlife. Veterinary Microbiology 132:283–292.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Numerous species of mammals are susceptible to Mycobacterium bovis, the causative agent of bovine tuberculosis (TB). Several wildlife hosts have emerged as reservoirs of M. bovis infection for domestic livestock in different countries. In the present study, blood samples were collected from Eurasian badgers (n = 1532), white-tailed deer (n = 463), brushtail possums (n = 129), and wild boar (n = 177) for evaluation of antibody responses to M. bovis infection by a lateral-flow rapid test (RT) and multiantigen print immunoassay (MAPIA). Magnitude of the antibody responses and antigen recognition patterns varied among the animals as determined by MAPIA; however, MPB83 was the most commonly recognized antigen for each host studied. Other seroreactive antigens included ESAT-6, CFP10, and MPB70. The agreement of the RT with culture results varied from 74% for possums to 81% for badgers to 90% for wild boar to 97% for white-tailed deer. Small numbers of wild boar and deer exposed to M. avium infection or paratuberculosis, respectively, did not cross-react in the RT, supporting the high specificity of the assay. In deer, whole blood samples reacted similarly to corresponding serum specimens (97% concordance), demonstrating the potential for field application. As previously demonstrated for badgers and deer, antibody responses to M. bovis infection in wild boar were positively associated with advanced disease. Together, these findings suggest that a rapid TB assay such as the RT may provide a useful screening tool for certain wildlife species that may be implicated in the maintenance and transmission of M. bovis infection to domestic livestock.

Key Words tuberculosis, Mycobacterium bovis, wildlife, serology

Citation

Macdonald, D. W., P. Riordan, and F. Mathews. 2006. Biological hurdles to the control of TB in cattle: a test of two hypotheses concerning wildlife to explain the failure of control. Biological Conservation 131:268-286.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Since the 1970s the control of bovine tuberculosis (bTB) in cattle, predominantly in the SW of England has proved continually recalcitrant; it is currently increasing at an annual rate of 18%. This deterioration has occurred despite a succession of government schemes involving killing badgers, Meles meles, with the intention of reducing transmission of bTB to cattle. Of various hypotheses proposed to explain this failure of control, some concern agricultural practice, but two concern wildlife. The latter are, first, that wild mammalian species other than badgers are important in the transmission of bTB, and second, that a perturbation effect amongst those badgers surviving a cull countermands the hoped-for reduction of bTB transmission to cattle or even increases it. We review our own studies of these two hypotheses in the context of other findings. We conclude that the other species hypothesis does not provide a general explanation for the failure of bTB control.We also conclude that the perturbation hypothesis is supported by the data and does provide one plausible mechanism to explain why culling badgers has not generally achieved control of bTB in cattle.We have reviewed the relevance of perturbation with respect to three key questions: (a) is there evidence of a perturbation effect on badger behavioural ecology? (b) is there evidence of a perturbation effect on prevalence of bTB in badgers? © are any observed effects of a magnitude relevant to bTB control policy? The results of the Randomised Badger Culling Trial (RBCT) and our own studies indicate that to have any prospect of contributing significantly to controlling bTB in cattle, a badger cull would have to be undertaken over a very large area. Considering the likely very important role of cattle-to-cattle transmission, and the opportunities for solutions in terms of farm management and surveillance, it would be inappropriate (and probably impractical) to undertake such a cull now.

Key Words England, control, badger, Meles meles, culling, cattle

Citation

Mackintosh, C. G., T. Quereshi, K. Waldrup, R. E. Labes, K. G. Dodds, and J. F. T. Griffin. 2000. Genetic resistance to experimental infection with Mycobacterium bovis in red deer (Cervus elaphus). Infection and Immunity 68(3):1620-1625

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis (Tb) caused by Mycobacterium bovis is a worldwide threat to livestock and humans. One control strategy is to breed livestock that are more resistant to Mycobacterium bovis. In a 3-year heritability study 6 farmed red deer stags were selected from 39 on the basis of their differing responses to experimental challenge via the tonsillar sac with approximately 500 CFU of M. bovis. Two stags remained uninfected, two were moderately affected, and two developed serious spreading Tb. Seventy offspring, bred from these six stags by artificial insemination using stored semen, were similarly challenged with M. bovis. The offspring showed patterns of response to M. bovis challenge similar to those of their sires, providing evidence for a strong genetic basis to resistance to Tb, with an estimated heritability of 0.48 (standard error, 0.096; $P < 0.01$). This is the first time the heritability of Tb resistance in domestic livestock has been measured. The breeding of selection lines of resistant and susceptible deer will provide an ideal model to study the mechanisms of Tb resistance in a ruminant and could provide an additional strategy for reducing the number and severity of outbreaks of Tb in farmed deer herds. Laboratory studies to identify genetic and immunological markers for resistance to Tb are under way. Preliminary studies showed no associations between NRAMP or DRB genes and resistance to Tb in deer. Patterns of immune responses seen in resistant animals suggest that both innate and acquired pathways of immunity are necessary to produce the resistant phenotype.

Key Words Red deer, Cervus elaphus, experimental infection, genetic resistance, control strategy

Citation Maddock E. C. G. 1934. Further studies on the survival time of the bovine tubercle Bacillus in soil, soil and dung, in dung and on grass, with experiments on feeding Guinea-pigs and calves on grass artificially infected with bovine tubercle bacilli. The Journal of Hygiene 34(3): 372-379.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Soil, dung, grass, feeding, Guinea pigs, calves, artificial infection

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Citation Maddock, E. C. G.1936. Experiments on the infectivity for healthy calves of bovine tubercle bacilli discharged in dung upon pasture. The Journal of Hygiene 36(4): 594-601

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Infectivity, calves, dung, pasture, persistance

Citation

Martin, S. W., J. A. Eves, L. A. Dolan, R. F. Hammond, J. M. Griffin, J. D. Collins, M. M. Shoukri. 1997. The association between the bovine tuberculosis status of herds in the East Offaly Project Area, and the distance to badger setts, 1988- 1993. Preventive Veterinary Medicine 31:113-125.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The proximity of farms to badger setts was compared between farms that had experienced a tuberculosis breakdown and those that had not, over the 6 year period from 1988 to 1993. The data were derived from a badger removal study conducted in East Offaly County in the Republic of Ireland. Badger removal began in 1989 and continued through 1993; by the end of 1990, approximately 80% of all badgers caught in the 6 year period had been removed. All badgers were examined, grossly, for evidence of tuberculosis. Tuberculosis status of the approximately 900 study herds was based on the results of the single intradermal comparative skin test and/or lesions of bovine tuberculosis. All herds were tested at least once annually. The number of herds experiencing bovine tuberculosis declined over the period, particularly in the years 1992 and 1993. The data on farm and badger sett location were stored and analysed, initially, in a geographical information system. Owing to the badger removal programme, the distance between the barn yard of a typical farm and the nearest occupied badger sett increased, by about 300 m year^(-1), and by about 600 m year^(-1) to the closest infected sett. In bivariate analyses, in the years 1988 and 1989, the risk of tuberculosis declined with increasing distance to a badger sett containing one or more tuberculous badgers. In multivariable logistic regression analyses, year and the average number of cattle tested per farm per year were controlled. A second identical analysis was conducted to control for the repeated observations on the same herds using generalised estimating equations. In both analyses, the risk of a multiple reactor tuberculosis breakdown decreased for herds at least 1000 m away from an infected badger sett, and increased as the number of infected badgers per infected sett increased. Despite the significantly reduced risk of a breakdown with increasing distance to infected badger setts, the relationship was not strong (sensitivity and specificity of the model in the low 70% range) and explained only 9-19% of tuberculosis breakdowns.

Key Words

badger, tuberculosis, epidemiology, bovine, cattle, herd, distance, exposure, etiologic fraction, odds ratio, logistic regression, generalised estimating equations

Citation

Martin-Atance, P., F. Palomares, M. Gonzalez-Candela, E. Revilla, M. J. Cubero, J. Calzada, and L.Leon-Vizcaino. 2005. Bovine tuberculosis in a free ranging red fox (Vulpes vulpes) from Donana National Park (Spain). Journal of Wildlife Diseases 41(2):435–436.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

During 1997 and 1998, a survey of Iberian carnivores was conducted to study the epidemiology of bovine tuberculosis in the Donana National Park and surrounding areas in southwestern Spain. Post-mortem examinations were done on seven red foxes (Vulpes vulpes), two Egyptian mongoose (Herpestes ichneumon), one weasel (Mustela nivalis), two genets (Genetta genetta), one Iberian lynx (Lynx pardinus), one Eurasian badger (Meles meles), and two polecats (Mustela putorius). Lesions suggestive of bovine tuberculosis were not detected but, in culture, Mycobacterium bovis was isolated from the retropharyngeal lymph nodes of one adult male red fox. This is the first report of M. bovis infection in red fox in Spain.

Key Words Bovine tuberculosis, carnivores, epidemiology, Mycobacterium bovis, red fox, Vulpes vulpes

Citation

Martin-Atance, P., L. Leon-Vizcaino, F. Palomares, E. Revilla, M. Gonzalez-Candela, J. Calzada, M. J. Cubero-Pablo, and M. Delibes. 2006. Antibodies to Mycobacterium bovis in wild carnivores from Donana National Park (Spain). Journal of Wildlife Diseases 42(3):704–708.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We conducted a retrospective serologic survey for antibodies against the MPB70 protein of Mycobacterium bovis in wild carnivores from Donana National Park (southwestern Spain). Serum samples from 118 red foxes (Vulpes vulpes), 39 Iberian lynx (Lynx pardinus), 31 Eurasian badgers (Meles meles), five Egyptian mongoose (Herpestes ichneumon), four European genet (Genetta genetta), and one Eurasian otter (Lutra lutra) were analyzed using an indirect competitive enzyme-linked immunoassay. Antibodies against the MPB70 protein of M. bovis were detected in seven badgers, five foxes, and one lynx. The frequency of positive animals was significantly higher in badger (23%) than in lynx (3%) and fox (4%). Antibodies were not detected in other species. Annual antibody frequency peaked at 38% in badgers and 11% for red fox. These species may contribute to persistence of bovine tuberculosis in Donana.

Key Words Badger, Donana, epidemiology, Iberian lynx, MPB70, Mycobacterium bovis, red fox, wild carnivores

Citation

Martin-Hernando, M. P., M. J. Torres, J. Aznar, J. J. Negro, A. Gandia and C. Gortazar. 2010. Distribution of lesions in red and fallow deer naturally infected with Mycobacterium bovis. Journal of Comparative Pathology 142:43-50.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wild deer have an important role in the epidemiology of bovine tuberculosis (bTB). The aims of this study were (1) to compare the pattern of lesions present in wild red (Cervus elaphus) and fallow (Dama dama) deer that were naturally infected with Mycobacterium bovis, and (2) to use this information to develop a sampling strategy for the isolation of M. bovis from the lymphoid tissues of the head of these animals. Culture of head lymphoid tissues demonstrated that 28 of 95 red deer and 22 of 100 fallow deer sampled were infected with M. bovis. Approximately 30% of each deer population had no gross lesions. Fallow deer were significantly more likely to have thoracic lesions than red deer. Lesions were observed in the retropharyngeal lymph nodes of 64% of the culture-positive red deer and 43% of the culture positive fallow deer. One third of the red deer, but none of the fallow deer, had well-encapsulated abscess lesions. There were no microscopical differences in the lesions in the lymph nodes of the red and fallow deer. Bacteriological culture from both the tonsil and retropharyngeal lymph nodes increased the rate of isolation of M. bovis by 22% over culture of the retropharyngeal lymph nodes alone in both species. These findings indicate that investigation of wild deer for bTB-compatible lesions should include examination of the medial retropharyngeal, left tracheobronchial, mediastinal, mesenteric and ileocaecal lymph nodes. Sampling for bacteriological culture from head lymphoid tissues should be from the tonsil and the medial retropharyngeal lymph nodes. These protocols may prove useful in bTB surveillance and control in regions where wild deer contribute to the circulation of M. bovis.

Key Words bovine tuberculosis, lymphoid tissue, Mycobacterium bovis, wild deer

Citation

Martin-Hernando, M. P., U. Hofle, J. Vicente, F. Ruiz-Fons, D. Vidal, M. Barral, J. M. Garrido, J. de la Fuente, C. Gortazara. 2007. Lesions associated with Mycobacterium tuberculosis complex infection in the European wild boar. Tuberculosis 87:360–367.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Information on lesion distribution and characteristics is essential to determine the significance of a species as a reservoir host for tuberculosis (TB). Herein, we describe the extension and distribution of lesions in 127 Mycobacterium tuberculosis Complex culture positive European wild boars (Sus scrofa), and use this information to discuss the role of this wildlife species in TB epidemiology in Mediterranean Spain. Macroscopic TB compatible lesions were detected in 105 of 127 wild boars (82.68%). Only microscopic lesions were found in 11 wild boars (8.66%). Lesions were not evident in 11 wild boars (8.66%). A total of 49 wild boars had lesions confined to one anatomical region (42.2%, localized TB), while 67 animals had lesions in more than one anatomical region (57.8%, generalized TB). Head lymph nodes (LNs), particularly the mandibular LNs, were most frequently affected (107/116, 92.24%), and 43 wild boar had only mandibular LN lesions. Histopathology evidenced TB lesions in 38.1% of the lungs, 23% of the livers and 13% of the spleens examined. Mammary gland lesions were observed in three cases. When TB lesions were localized, granulomas characterized by a mixed inflammatory cell population were more predominant, whereas strongly necrotic-calcified granulomas were more prevalent in generalized cases of TB infection. Large lesions in more than one anatomical region were more frequent among juveniles. The histopathological characteristics of the tuberculous reaction and the associated tissue damage in various organs, together with the gross pathology, indicate that at least those wild boar with large lesions and generalized infections have the potential to excrete mycobacteria by several routes. This finding, in the context of unusually high densities of wild boar and fencing and feeding, reinforces the suggestion that wild boar can act as a true TB reservoir under the particular circumstances of Mediterranean Spain. Further studies on the routes of excretion as well as the effect of altering management methods would be of interest to confirm the role of wild boar in TB epidemiology in Spain.

Key Words European wild boar, pathology, reservoir, Sus scrofa, tuberculosis

Citation

Mathews, F., D. W. Macdonald, G. M. Taylor, M. Gelling, R. A. Norman, P. E. Honess, R. Foster, C. M. Gower, S. Varley, A. Harris, S. Palmer, G. Hewinson, and J. P. Webster. 2006. Bovine tuberculosis (Mycobacterium bovis) in British farmland wildlife: the importance to agriculture. Proceedings of the Royal Society B 273:357–365.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bTB) is an important disease of cattle and an emerging infectious disease of humans. Cow- and badger-based control strategies have failed to eradicate bTB from the British cattle herd, and the incidence is rising by about 18% per year. The annual cost to taxpayers in Britain is currently £74 million. Research has focused on the badger as a potential bTB reservoir, with little attention being paid to other mammals common on farmland. We have conducted a systematic survey of wild mammals (Nz4393 individuals) present on dairy farms to explore the role of species other than badgers in the epidemiology of bTB. Cultures were prepared from 10 397 samples (primarily faeces, urine and tracheal aspirates). One of the 1307 bank voles (Clethrionomys glareolus) live-sampled, and three of the 43 badgers (Meles meles), yielded positive isolates of Mycobacterium bovis. This is the first time the bacterium has been isolated from the bank vole. The strain type was the same as that found in cattle and badgers on the same farm. However, our work indicates that the mean prevalence of infectious individuals among common farmland wildlife is extremely low (the upper 95% confidence interval is %2.0 for all of the abundant species). Mathematical models illustrate that it is highly unlikely the disease could be maintained at such low levels. Our results suggest that these animals are relatively unimportant as reservoirs of bTB, having insufficient withinspecies (or within-group) transmission to sustain the infection, though occasional spill-overs from cattle or badgers may occur.

Key Words

bovine tuberculosis, Mycobacterium bovis, epidemiology, voles, PCR, mycobacterium microti

Citation Mathews, F., L. Lovett, S. Rushton, and D.W Macdonald. 2006. Bovine tuberculosis in cattle: reduced risk on wildlife-friendly farms. Biology Letters 2:271-274.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The associations between habitat and other factors that lead to the risk of bovine tuberculosis (bTB) in diary cattle were examined in an unmatched case–control study. Data from 60 herds with recent history of bTB and 60 controls were analysed using logistic regression. The predictors included farmland habitat, topography, indices of badger density and herd size. Information-theoretic approaches were used to identify those predictor variables explaining the greatest variation in cattle herd bTB breakdowns. Reduced risk of bTB was associated with the management of farmland in ways favourable to wildlife conservation, as encouraged by recent (2005) European Common Agricultural Policy reforms.

Key Words badgers, tuberculosis, Akaike Information Criterion, habitat, landscape

Citation

McCarty, C. W. and M. W. Miller. 1998. A versatile model of disease transmission applied to forecasting bovine tuberculosis dynamics in white-tailed deer populations. Journal of Wildlife Diseases. 34(4): 722-730

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A model was derived for disease transmission in dynamic host populations and its application was demonstrated in forecasting possible outcomes of a bovine tuberculosis (Mycobacterium bovis) epidemic in a white-tailed deer (Odocoileus virginianus) population. The approach was mechanistic, based disease transmission on the probability of each susceptible individual becoming infected per unit time, and afforded the flexibility necessary to model epidemics in dynamic wildlife populations. This approach was applied to a sex- and age-structured deer population model. This model predicted that tuberculosis prevalence in a white-tailed deer population could rise from approximately 3% to about 21% over 25 yr. and that neither lowered deer survival nor lowered transmission would be completely effective in eliminating disease from the population. Maternal transmission appeared unimportant to modeled tuberculosis dynamics; in contrast, disease was not maintained for >15 yr in models lacking lateral transmission.

Key Words

bovine tuberculosis, epidemic modeling, modeling, epidemiology, Mycobacterium bovis, Odocoileus virginianus, white-tailed deer.

Citation McDonald, R. A., R. J. Delahay, S. P. Carter, G. C. Smith, and C. L. Cheeseman. 2007. Perturbing implications of wildlife ecology for disease control. Trends in Ecology and Evolution 23(2):53-56.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Britain's Randomised Badger Culling Trial provides robust evidence of the role badgers have in transmission of Mycobacterium bovis to cattle. Culling badgers perturbed their social structure, and brought positive and negative effects for bovine tuberculosis incidence in cattle, leading to the conclusion that culling could not make a meaningful contribution to disease control. The RBCT highlights the complexities of disease transmission in social animals and the importance of host ecology for controlling wildlife diseases.

Key Words Britain, badger, culling, RBCT, control

Citation

Meng, X. J., D. S. Lindsay, and N. Sriranganathan. 2009. Wild boars as sources for infectious diseases in livestock and humans. Philosophical Transactions of the Royal Society B 364:2697–2707.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wild boars (Sus scrofa) are indigenous in many countries in the world. These free-living swine are known reservoirs for a number of viruses, bacteria and parasites that are transmissible to domestic animals and humans. Changes of human habitation to suburban areas, increased use of lands for agricultural purposes, increased hunting activities and consumption of wild boar meat have increased the chances of exposure of wild boars to domestic animals and humans. Wild boars can act as reservoirs for many important infectious diseases in domestic animals, such as classical swine fever, brucellosis and trichinellosis, and in humans, diseases such as hepatitis E, tuberculosis, leptospirosis and trichinellosis. For examples, wild boars are reservoirs for hepatitis E virus, and cluster cases of hepatitis E have been reported in Japan of humans who consumed wild boar meat. In Canada, an outbreak of trichinellosis was linked to the consumption of wild boar meat. The incidence of tuberculosis owing to Mycobacterium bovis has increased in wild boars, thus posing a potential concern for infections in livestock and humans. It has also been documented that six hunters contracted Brucella suis infections from wild swine in Florida. This article discusses the prevalence and risk of infectious agents in wild boars and their potential transmission to livestock and humans.

Key Words wild boar, swine, zoonosis, hepatitis E virus, trichinellosis, tuberculosis

Citation

Menzies,F.D., and S.D. Neill. 2000. Cattle-to-cattle transmission of bovine tuberculosis. The Veterinary Journal 160:92-106.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In developed countries, Mycobacterium bovis infection in cattle is now mostly confined to the respiratory system, which reflects transmission and establishment of infection mainly by this route. A single bacillus transported within a droplet nucleus is probably sufficient to establish infection within the bovine lung. Infected cattle should always be considered as potential sources of infection, since studies have demonstrated that a significant proportion of tuberculous cattle excrete M. bovis. In general, the dynamics of M. bovis transmission are poorly understood and the conditions under which a tuberculous animal becomes an effective disseminator of infection are currently not defined although environmental contamination appears to be a less effective method of disease transmission. Field studies indicate a wide spectrum of transmission rates but generally the spread of M. bovis infection is still considered to be a relatively slow process. Slaughter of diseased cattle detected by tuberculin testing and at meat plant inspection has been shown to be an effective policy for tuberculosis eradication, provided there are no other reservoirs of infection and all involved in the cattle industry are committed to a policy of eradication. Epidemiological approaches, particularly case-control studies, seem to provide the best method for quantifying the relative importance of the various sources of M. bovis transmission to cattle and modelling techniques can be used to assist in the design of cost-effective control measures that may lead to tuberculosis eradication.

Key Words

bovine tuberculosis, Mycobacterium bovis, transmission

Citation

Michel, A. L, M.L. Coetzee, D.F. Keet, L. Mare´, R. Warren, D. Cooper, R.G. Bengis, K. Kremer, P. van Helden. 2009. Molecular epidemiology of Mycobacterium bovis isolates from free ranging wildlife in South African game reserves. Veterinary Microbiology 133:335–343.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis is endemic in African buffalo and a number of other wildlife species in the Kruger National Park (KNP) and Hluhluwe-iMfolozi Park (HiP) in South Africa. It was thought that the infection had been introduced into the KNP ecosystem through direct contact between cattle and buffalo, a hypothesis which was confirmed in this study by IS6110 and PGRS restriction fragment length polymorphism (RFLP) typing. The molecular characterisation of 189 Mycobacterium bovis isolates from nine wildlife species in the HiP, including three smaller associated parks, and the Kruger National Park with adjacent areas showed that the respective epidemics were each caused by an infiltration of a single M. bovis genotype. The two M. bovis strains had different genetic profiles, as demonstrated by hybridisation with the IS6110 and PGRS RFLP probes, as well as with regard to evidence of evolutionary changes to the IS profile. While the M. bovis type in HiP was transmitted between buffaloes and to at least baboon, bushpig and lion without obvious genetic changes in the RFLP patterns, in the KNP a dominant strain was represented in 73% of the M. bovis isolates, whilst the remaining 27% were variants of this strain. No species-specific variants were observed, except for one IS6110 type which was found only in a group of five epidemiologically related greater kudu. This finding was attributed to species-specific behaviour patterns rather than an advanced host–pathogen interaction.

Key Words

Mycobacterium bovis, African wildlife, Kruger National Park, Molecular epidemiology, Genetic typing, IS6110 RFLP

Citation

Michel, A. L., B. Muller, P. D. van Helden. 2010. Mycobacterium bovis at the animal–human interface: A problem, or not? Veterinary Microbiology 140:371–381.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis is a pathogen of significant importance in livestock and a wide range of wild animal species worldwide. It is also known to cause tuberculosis disease in humans, a fact which has raised renewed concerns regarding the zoonotic risk for humans, especially those living at the animal-human interface. This review consolidates recent reports in the literature mainly on animal and zoonotic tuberculosis with an emphasis on evolution, epidemiology, treatment and diagnosis. The information presented reveals the fundamental differences in the complexity and level at which the disease affects the economy, ecosystem and human population of regions where animal tuberculosis control is achieved and regions where little or no control is implemented. In conclusion the review suggests that bovine tuberculosis has essentially been reduced to a disease of economic importance in the developed world, while low-income countries are facing a multifaceted impact which potentially affects the health of livestock, humans and ecosystems and which is likely to increase in the presence of debilitating diseases such as HIV/AIDS and other factors which negatively affect human livelihoods.

Key Words Zoonotic tuberculosis, Mycobacterium bovis, Livestock/human interface, Wildlife tuberculosis

Citation

Michel, A. L., R.G. Bengis, D.F. Keet, M. Hofmeyr, L.M. de Klerk, P.C. Cross, A.E. Jolles, D. Cooper, I.J. Whyte, P. Buss, J. Godfroid. 2006. Wildlife tuberculosis in South African conservation areas: implications and challenges. Veterinary Microbiology 112:91-100.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis, caused by Mycobacterium bovis, was first diagnosed in African buffalo in South Africa's Kruger National Park in 1990. Over the past 15 years the disease has spread northwards leaving only the most northern buffalo herds unaffected. Evidence suggests that 10 other small and large mammalian species, including large predators, are spillover hosts. Wildlife tuberculosis has also been diagnosed in several adjacent private game reserves and in the Hluhluwe-iMfolozi Park, the third largest game reserve in South Africa. The tuberculosis epidemic has a number of implications, for which the full effect of some might only be seen in the longterm. Potential negative long-term effects on the population dynamics of certain social animal species and the direct threat for the survival of endangered species pose particular problems for wildlife conservationists. On the other hand, the risk of spillover infection to neighboring communal cattle raises concerns about human health at the wildlife–livestock–human interface, not only along the western boundary of Kruger National Park, but also with regards to the joint development of the Greater Limpopo Transfrontier Conservation Area with Zimbabwe and Mozambique. From an economic point of view, wildlife tuberculosis has resulted in national and international trade restrictions for affected species. The lack of diagnostic tools for most species and the absence of an effective vaccine make it currently impossible to contain and control this disease within an infected free-ranging ecosystem. Veterinary researchers and policy-makers have recognized the need to intensify research on this disease and the need to develop tools for control, initially targeting buffalo and lion.

Key Words Mycobacterium bovis, African wildlife, epidemiology, wildlife–livestock–human interface

Citation	Miller, M. W. and E. T. Thorne. 1993. Captive cervids as potential sources of disease for North America's wild cervid population: avenues, implications and preventive management. Transactions of the 58th North American Wildlife and Natural Resources Conferences. Wildlife Management Institute.
Abstract Only	☐
No Abstract	☑
Article Type	Proceedings
Abstract	
Key Words	Captive Cervids, wild cervids, implications, transmission

Citation

Miller, R. and John B. Kaneene. 2006. Evaluation of historical factors influencing the occurrence and distribution of Mycobacterium bovis infection among wildlife in Michigan. American Journal of Veterinary Research 67(4):604-615.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Objectives—To determine historical events leading to establishment of bovine tuberculosis in the whitetailed deer population in the northeastern corner of the lower peninsula (NELP) of Michigan and describe factors relevant to the present outbreak of bovine tuberculosis in Michigan.
Sample Population—Cattle and white-tailed deer in Michigan from 1920 to 1990. Procedures—A search of extant historical documents (eg, scientific journals, books, public reports, and correspondence and internal reports from governmental agencies) was conducted. Factors investigated included the number of cattle and prevalence of tuberculosis, deer population and density levels, and changes in regional environments affecting the population and management of cattle and wild deer.
Results—High deer numbers and severe winter feed shortages resulting from habitat destruction in the NELP in 1930 contributed to the transmission of tuberculosis from cattle to deer. Starvation increased the susceptibility of deer to infection and modified behavior such that exposure to infected cattle was increased. Relocation of deer resulted in spread of infection to other sites, including locations at which spatial clusters of tuberculosis presently exist. Ribotyping of Mycobacterium bovis from a human patient suggests that the strain of M bovis presently infecting white-tailed deer in the region is the same strain that affected cattle farms at that time.
Conclusions and Clinical Relevance—Feeding deer to maintain numbers above the normal carrying capacity of the NELP led to deer depending on consumption of livestock feed for survival during winter and increased contact with domestic cattle. This practice should be avoided.

Key Words Michigan, historical factors, distribution, wildlife, whitetailed deer, cattle, feeding

Citation

Miller, R., J. B. Kaneene, Stephen M. Schmitt, D. P. Lusch, S. D. Fitzgerald. 2007. Spatial analysis of Mycobacterium bovis infection in white-tailed deer (Odocoileus virginianus) in Michigan, USA. Preventive Veterinary Medicine 82:111-122.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The wild white-tailed deer (Odocoileus virginianus) population in Michigan, USA, has endemic Mycobacterium bovis. We determined whether there were spatial clusters of retrospective TB cases in white-tailed deer in northeastern Michigan and identified specific factors associated with the spatial clusters. Data from hunter-harvested deer (age, gender, TB status, and geographic section) were collected by the Michigan Department of Natural Resources (MDNR) during TB surveillance from 1995 to 2002. Land cover (vegetation, land-use) and land type (soil types and drainage characteristics, landforms) described potential deer habitats. Specific locations of large-scale supplemental feeding sites were collected from the MDNR aerial surveillance program from 1997 to 2002. Analyses were conducted using principal components derived from environmental data (and other risk factors) on spatial clusters of disease (identified by the spatial scan statistic). Spatial effects were incorporated into the multivariable analyses by using a neighborhood approach. A total of 420 deer with M. bovis infection were identified from 1995 to 2002, out of 39,451 harvested deer from 3216 TRS units, and spatial clusters of cases were identified. A total of seven principal components of environmental data were generated. Clusters were associated with the presence of large expanses of deciduous forests on moraine ridges separated by low areas of forested wetlands, and the presence of many small lakes. Factors that promoted congregation of deer for extended periods of time (natural cover, access to water, and less human contact) appeared to be associated with increased odds of TB positivity. This suggests that there are specific areas where interventions can be implemented to reduce congregation of animals and disrupt the cycle of infection transmission.

Key Words

tuberculosis, Mycobacterium bovis, epidemiology, white-tailed deer, Odocoileus virginianus, spatial analysis, principal components analysis

Citation

Miller, R., J. B. Kaneene, S. D. Fitzgerald, and S. M. Schmitt. 2003. Evaluation of the influence of supplemental feeding of white-tailed deer (Odocoileus virginianus) on the prevalence of bovine tuberculosis in the Michigan wild deer population. Journal of Wildlife Diseases 39(1):84–95.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A retrospective study was conducted to test the hypothesis that supplemental feeding of white-tailed deer (Odocoileus virginianus) from 1995 to 1997 was associated with the prevalence of bovine tuberculosis (TB) in free-ranging deer in northeastern Michigan. Bovine TB prevalence data were obtained from an ongoing surveillance program, while data relating to supplemental feeding and other risk factors were collected via in-person interviews. A multivariable Poisson regression modeling approach was used to test the stated hypothesis while controlling for other risk factors. Of the 389 potential participants, 59% agreed to participate in the study. Results showed that supplemental feeding of deer was associated with bovine TB in whitetailed deer. Specific risk factors associated with increasing risk for bovine TB were locating feed sites in areas with high levels of hardwood forests (O.R.51.8, 95% C.I.51.3–2.4), other largescale feeding sites in the area (O.R.51.1, 95% C.I.51.0–1.2), the number of deer fed per year (O.R.53.9, 95% C.I.51.4–11.4), the numbers of feed sites spreading grain (O.R.514.7, 95% C.I.52.2–98.9), the quantity of grains provided at the site (O.R.51.4, 95% C. I.51.1–1.7), and the quantity of fruits and vegetables provided (O.R.51.4, 95% C.I.51.2–1.7). Conversely, factors associated with decreasing risk of bovine TB were locating feed sites in areas with high levels of hardwood forests (O.R.50.1, 95% C.I.50.02–0.4), locating feed sites in forests (O.R.50.05, 95% C.I.50.01–0.4), and the level of sites providing grain (O.R.50.1, 95% C.I.50.01–0.3). The results of this study suggest that banning the practice of supplemental feeding is a valid policy for control of bovine tuberculosis in free-ranging white-tailed deer.

Key Words

Bovine tuberculosis, epidemiology, feeding, Mycobacterium bovis, Odocoileus virginianus, prevalence, transmission, white-tailed deer

Citation Morris, R.S., D.U. Pfeiffer, and R. Jackson. 1994. The epidemiology of Mycobacterium bovis infections. Veterinary Microbiology 40:153-177.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Mycobacterium bovis has an exceptionally wide host range, but until recent years there was little concern about infection in species other than cattle and man. Diversification of farming enterprises has led to cognizance of the need for control in other domestic animals, notably deer. There has also been recognition that self-maintaining infection is present in wildlife hosts in some countries- notably the European badger in the United Kingdom and Ireland, the Australian brush-tailed possum in New Zealand, and various species of ungulates in limited areas of a number of countries. Although transmission of M. bovis can occur by a number of different routes, control measures imposed on cattle and to a lesser extent on other species have reduced a number of the routes to insignificance. Hence the vast preponderance of transmission within host species is now by the airborne route, and predominantly between species as well. Transmission of infection from badgers to cattle may be an exception, with evidence remaining equivocal about the relative importance of pasture contamination by excretion in badger urine and airborne transmission. In general, contamination of feed and pasture appears to be unimportant in transmission of the disease, because survival times of infective doses of organisms on fomites are relatively short under realistic conditions and because animals are not commonly exposed to a dose high enough to be infective by the alimentary route. Infection through the oro-pharyngeal mucous membrane may be significant, although the infective dose for this route is not known. While many species of animals can become infected with M. bovis, only a few act as maintenance hosts and the rest are spillover hosts in which infection is not self-maintaining. With the exception of cattle and deer, other species have become maintenance hosts only within part of their ecological range. For both badgers and possums, maintenance of infection within a local population is due to pseudo-vertical transmission from mother to young, and horizontal transmission linked to breeding activity. Transmission from possums to domestic animals appears to occur mainly during atypical behavioural interactions between the species, and this may well be important for badgers as well. Difficulties in controlling the disease adequately in domestic animals generally result from administrative problems since the necessary technical procedures are available and have been shown to be effective. Where there is interplay between infection in wildlife and domestic animals, eradication of the disease becomes impractical. Although herd prevalence will then be inescapably higher and characteristically clustered in patches in both time and space, reduction of the incidence rate to a low level in domestic stock is nevertheless achievable with current methods. Further reduction of incidence in the presence of a wildlife host should be possible through application of ecologically designed management procedures at farm level, but greater gains could be made if new control measures could be developed, especially vaccines.

Key Words Mycobacterium bovis, cattle, tuberculosis, bovine, epidemiology

Citation

Munroe, F.A., I.R. Dohoo, W.B. McNab. 2000. Estimates of within-herd incidence rates of Mycobacterium bovis in Canadian cattle and cervids between 1985 and 1994. Preventive Veterinary Medicine 45:247-256.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We analysed the individual-animal data from six of the nine outbreaks of tuberculosis in Canadian cattle and cervids from 1985 to 1994. A ``positive/reactor'' animal was one which had either a positive culture or a positive or suspicious reaction on a mid-cervical, comparative cervical, or gross or histopathological test for tuberculosis. Individual-animal data were collected only for herds which had one or more positive/reactor animals. Data were collected from the outbreak records in the Regional or District offices of Agriculture and Agri-food Canada's Animal and Plant Health Directorate. The within-herd spread of Mycobacterium bovis was studied by determining the most-likely date at which the herd was first exposed to M. bovis and the number of reactions which had developed by the time the herd was investigated. The animal-time units at risk in the herd were probably overestimated, resulting in conservative estimates of the within-herd incidence rates. Negative-binomial regression was used to investigate factors which might have influenced the within-herd spread of tuberculosis. Increasing age appeared to be a risk factor for being a positive/reactor animal. When compared to animals 0±12 months old, animals 13±24 months old had an incidence rate ratio (IRR) of 7.6, while animals >24 months old had an IRR of 10.4 (p=0.009). Actual and predicted incidence rates for tuberculosis in mature (>24 months old) animals were calculated. Actual and predicted incidence rates were similar for cervids, within an outbreak. There was more variability between actual and predicted rates in the dairy and beef animals. In the one outbreak (Ontario) where there were positive/reactor cervid, dairy and beef herds, the actual incidence rate for cervids (IR9.3 cases per 100 animal-years) was almost twice th of dairy cattle.

Key Words

Cattle-microbiological diseases, tuberculosis, Mycobacterium bovis, cervids, incidence rate ratio, within-herd transmission

Citation

Munroe,F.A., I.R. Dohoo, W.B. McNab, and L. Spangler. 1999. Risk factors for the between-herd spread of Mycobacterium bovis in Canadian cattle and cervids between 1985 and 1994. Preventive Veterinary Medicine 41:119-133.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Microorganisms of the genus Mycobacterium cause tuberculosis in many animal species including humans. Generally, Mycobacterium bovis (M. bovis) infects cattle and cervids, but it has the potential to infect virtually all species of mammals. This study examined and analysed the data from the nine outbreaks of tuberculosis in Canadian cattle and cervids from 1985 to 1994. For the purposes of this study, a positive herd was one with at least one culture-positive animal. A reactor herd had at least one animal which was positive or suspicious on a mid-cervical, comparative cervical, or gross or histopathologic test for tuberculosis. Herd classification was either reactor/positive or negative. Data for the study were collected from the outbreak records in the Regional or District offices of Agriculture and Agri-Food Canada. Logistic regression was used to study spread of tuberculosis between herds. Two risk factors were identified: increasing herd size; and, the reason why a herd was investigated as part of the outbreak. This latter factor was interpreted as a
surrogate measure for the nature of contact between the study herd and other potentially infected herds in the outbreak. Increasing herd size was associated with an increased risk of being positive for tuberculosis with herds of 16±35, 36±80, and >80 animals having odds ratios of 2.9, 5.8, and 9.3, respectively, when compared to a herd size of <16 animals ($p < 0.001$). When compared to perimeter testing (i.e. testing herds within a specified radius of an infected herd), all other reasons for investigation had higher odds ratios ($p < 0.001$). These odds ratios were 57.8 for traceout herds
(i.e. herds which had purchased animal(s) from a reactor/positive herd), 31.8 for herds with pasture or fence-line contact with a reactor/positive herd, and 14.9 for traceback herds (i.e. herds which hadbeen a source of animals for reactor/positive herd(s)).

Key Words cattle, cervids, tuberculosis, Mycobacterium bovis, transmission, control programs

Citation

Munyeme, M., J.B. Muma, E. Skjerve, A.M. Nambota, I.G.K. Phiri, K.L. Samui, P. Dorny, M. Tryland. 2008. Risk factors associated with bovine tuberculosis in traditional cattle of the livestock/wildlife interface areas in the Kafue basin of Zambia. Preventive Veterinary Medicine 85:317-328.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We conducted a cross-sectional study from August 2003 to February 2004 to identify risk factors for bovine tuberculosis (BTB) in the Kafue basin of Zambia. We investigated a total of 106 herds of cattle for presence of BTB using the comparative intradermal tuberculin test (CITT) while an interviewer-administered questionnaire was used to gather epidemiological data on herd structure, management and grazing strategies. BTB prevalence at herd level was estimated and possible risk factors were investigated using the multiple logistic regression model. The true herd level prevalence of BTB was estimated at 49.8% (95% CI: 37.9, 61.7%). The logistic regression model showed that cattle herd BTB status was highly associated with area and husbandry practices. When compared to Kazungula, cattle herds in Blue Lagoon were more likely to test positive for BTB when other factors such as management practices were controlled (OR = 10.5). In terms of grazing strategies, transhumant herds (TH) had higher odds (OR = 3.0) of being positive compared to sedentary herds (OR = 1.0). The results in this study provide preliminary information about potential risk factors that were found to be associated with BTB status in cattle.

Key Words bovine tuberculosis, cattle, livestock/wildlife interface, risk factors, Zambia

Citation

Murphy, D., E. Gormley, E. Costello, D. O'Meara, and L.A.L Corner. 2010. The prevalence and distribution of Mycobacterium bovis infection in European badgers (Meles meles) as determined by enhanced post mortem examination and bacteriological culture. Research in Veterinary Science 88:1-5

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The accurate diagnosis of Mycobacterium bovis infection in badgers is key to understanding the epidemiology of tuberculosis in this species and has significant implications for devising strategies to limit spread of the disease. In this study, badgers (n = 215) in the Republic of Ireland were examined at post mortem and tissues were collected from a range of anatomical locations and pooled into groups for bacterial culture of M. bovis. By assessing confirmed gross visible lesions (VL) alone, infection was detected in 12.1% of badgers. However, by including the results of all culture positive pooled samples, the overall infection prevalence increased significantly to 36.3%. Two-thirds (66.7%) of infected animals had no visible lesions (NVL). While the thoracic cavity (lungs and pulmonary lymph nodes) was found to be the most common site of infection, in a proportion of animals infection was absent from the lungs and draining lymph nodes and was confined to the lymph nodes of the carcase or the head. This may indicate an early extrapulmonary dissemination of infection or alternatively, in the case of the head lymph nodes, a secondary pathogenic pathway involving the lymphoid tissues of the upper respiratory tract (URT).

Key Words European badger, Meles meles, tuberculosis, prevalence, pathogenesis

Citation

Naranjo, V., C. Gortazar, J. Vicente, Jose´ de la Fuente. 2008. Evidence of the role of European wild boar as a reservoir of Mycobacterium tuberculosis complex. Veterinary Microbiology 127:1–9.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bTB) is caused by Mycobacterium bovis and closely related mycobacteria of the Mycobacterium tuberculosis complex. They have an extensive host range and may cause zoonotic TB. A major obstacle to bTB eradication in livestock is the implication of wildlife in the natural cycle of the pathogen. The identification of wildlife reservoir hosts is crucial for the implementation of effective control measures. The European wild boar (Sus scrofa) is frequently considered a spillover or dead end host rather than a true reservoir, and scientific evidence is conflicting outside Mediterranean Spain. The aim of this review is to update current scientific evidence of the wild boar as a TB reservoir and to underline those aspects that need further research. Evidences supporting that wild boar is a TB reservoir host include: (i) presence of common M. tuberculosis complex genotypes in wild boar, domestic and wild animals and humans, (ii) high prevalence of M. bovis among wild boar in estates fenced for decades in complete absence of contact with domestic livestock, and other wild ungulates (iii) TB lesions are frequently seen in thoracic lymph nodes and lungs, suggesting that respiratory infection and excretion may occur, and (iv) extensive tuberculous lesions in more than one anatomical region occur in a high proportion of juvenile wild boar that probably represents the main source of mycobacterial excretion. Hence, epidemiological, pathological and microbiological evidence strongly suggests that, at least in Spanish Mediterranean ecosystems, wild boar are able to maintain TB infection in the wild and are most probably able to transmit the disease to other species, acting as a true wildlife reservoir. These results expand the list of wildlife species that act as natural reservoirs of TB in different parts of the world and suggest the need to control the infection in wild boar populations for the complete eradication of the disease in Spain.

Key Words bovine tuberculosis, Mycobacterium tuberculosis complex, wildlife, reservoir host, European wild boar

Citation

Naranjo, V., P. Ayoubi, J. Vicente, F. Ruiz-Fons, C. Gortazar, K. M. Kocan, J. de la Fuente. 2006. Characterization of selected genes upregulated in non-tuberculous European wild boar as possible correlates of resistance to Mycobacterium bovis infection. Veterinary Microbiology 116:224–231.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bTB), caused by Mycobacterium bovis (Mycobacterium tuberculosis complex), is a zoonotic disease that affects cattle and wildlife worldwide. These animal hosts can serve as reservoirs of infection, thus increasing the risk of human exposure and infection. In this study we quantified by RNA macroarray fluorescent hybridization and real-time RT-PCR the mRNA levels of genes differentially expressed in oropharyngeal tonsils and mandibular lymph nodes of three and seven individual non-tuberculous and tuberculous wild boars naturally exposed to M. bovis, respectively. These results demonstrated upregulation of two genes, complement component 3 (C3) and methylmalonyl-CoA mutase (MUT), in the non-tuberculous wild boars. These upregulated genes may contribute to resistance of wild boars to bTB by modifying the innate immunity, which limits the ability of the mycobacterium to infect and persist within macrophages. The C3 and MUT genes, therefore, are likely to be good candidates to study as markers of bTB resistance using functional genomics in animal model systems. Identification of genes upregulated in wild animals resistant to bTB contributes to our understanding of the mechanisms of protective immunity and resistance to mycobacterial organisms.

Key Words Mycobacterium bovis, Mycobacteria, tuberculosis, resistance, complement component, C3, Methylmalonyl-CoA mutase, MUT

Citation

Nation, P. N., E. A. Fanning, H. B. Hopf, T. L. Church. 1999. Observations on animal and human health during the outbreak of Mycobacterium bovis in game farm wapiti in Alberta. The Canadian Veterinary Journal 40:113-117.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

This report describes and discusses the history, clinical, pathologic, epidemiologic, and human health aspects of an outbreak of Mycobacterium bovis infection in domestic wapiti in Alberta between 1990 and 1993, shortly after legislative changes allowing game farming. The extent and seriousness of the outbreak of M. bovis in wapiti in Alberta was not fully known at its onset. The clinical findings in the first recognized infected wapiti are presented and the postmortem records for the herd in which the animal resided are summarized. Epidemiologic findings from the subsequent field investigation are reviewed, the results of recognition and investigation of human exposure are updated, and recommendations for reduction of human exposure are presented.

Key Words Alberta, Wapiti, human health, game farm

Citation

Nishi, J. S., T. Shury, and B. T. Elkin. 2006. Wildlife reservoirs for bovine tuberculosis (Mycobacterium bovis) in Canada: strategies for management and research. Veterinary Microbiology 112:325–338.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In Canada, there are two known regional foci where wildlife populations are infected with bovine tuberculosis (Mycobacterium bovis) and considered to be disease reservoirs. Free-ranging populations of wood bison (Bison bison athabascae) in and around Wood Buffalo National Park (WBNP) and wapiti (Cervus elaphus manitobensis) in and around Riding Mountain National Park (RMNP) are infected with bovine tuberculosis. In this paper, we provide an overview of these diseased wild ungulate populations and the complexities of attempting to manage issues relating to bovine tuberculosis in and around protected areas. We do not describe the quantitative science and epidemiological data in detail from these case histories, but instead compare and contrast these two cases from a broader perspective. This is achieved by reviewing the context and process by which a diverse group of stakeholders engage and develop strategies to address the controversial problems that diseased wildlife populations often present. We suggest that understanding the factors that drive the strategic-level management processes is equally important for addressing a wildlife disease problem as the tactical-level issues, such as design and implementation of technically sound field research and management programs. Understanding the experiences within the WBNP and RMNP areas, particularly the strategies that have failed or succeeded, may prove useful to understanding and improving management approaches when wildlife are infected with M. bovis. Applying this understanding is consistent with the principles of adaptive management in which we learn from previous experiences to develop better strategies for the future.

Key Words

bovine tuberculosis, Mycobacterium bovis, adaptive co-management, Wood Buffalo National Park, Riding Mountain National Park, bison, wapiti, elk

Citation

Nol, P., K. P. Lyashchenko, R. Greenwald, J. Esfandiari, W. R. Waters, M. V. Palmer, B. J. Nonnecke, T. J. Keefe, T. C. Thacker, J. C. Rhyan, F. E. Aldwell, and M. D. Salman. 2009. Humoral immune responses of white-tailed deer (Odocoileus virginianus) to Mycobacterium bovis BCG vaccination and experimental challenge with M. bovis. Clinical and Vaccine Immunology 16(3):323–329.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Monitoring of the kinetics of production of serum antibodies to multiple mycobacterial antigens can be useful as a diagnostic tool for the detection of Mycobacterium bovis infection as well as for the characterization of disease progression and the efficacy of intervention strategies in several species. The humoral immune responses to multiple M. bovis antigens by white-tailed deer vaccinated with BCG orally via a lipid-formulated bait (n = 5), orally in liquid form (n = 5), and subcutaneously (n = 6) were evaluated over time after vaccination and after experimental challenge with virulent M. bovis and were compared to the responses by unvaccinated deer (n ┌ 6). Antibody responses were evaluated by using a rapid test (RT), a multiantigen print immunoassay (MAPIA), a lipoarabinomannan enzyme-linked immunosorbent assay (LAM-ELISA), and immunoblotting to whole-cell sonicate and recombinant antigen MPB83. MAPIA and RT detected minimal to no antibody responses over those at the baseline to multiple M. bovis antigens in vaccinated white-tailed deer after challenge. This was in contrast to the presence of more readily detectable antibody responses in nonvaccinated deer with more advanced disease. The LAM-ELISA results indicated an overall decrease in the level of production of detectable antibodies against lipoarabinomannan-enriched mycobacterial antigen in vaccinated animals compared to that in nonvaccinated animals after challenge. Immunoblot data were inconsistent but did suggest the occurrence of unique antibody responses by certain vaccinated groups to Ag85 and HSP70. These findings support further research toward the improvement and potential use of antibody-based assays, such as MAPIA, RT, and LAM-ELISA, as tools for the antemortem assessment of disease progression in white-tailed deer in both experimental and field vaccine trials.

Key Words BCG, vaccine, white-tailed deer, experimental challenge

Citation	Nolan, A. and J.W. Wilesmith. 1994. Tuberculosis in badgers (Meles meles). Veterinary Microbiology 40:179-191.
Abstract Only	☐
No Abstract	☑
Article Type	Journal Article
Abstract	This review examines the incidence of tuberculosis in badgers, the pathogenesis and diagnosis of the disease in the badger, and the control prospects related to spread of tuberculosis from badgers to cattle.
Key Words	Mycobacterium bovis, cattle, tuberculosis, bovine, badger; Meles meles

Citation

Nugent, G. 2005. The role of wild deer in the epidemiology and management of bovine tuberculosis in New Zealand. Thesis, University of Nebraska, Lincoln, Nebraska, USA.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

The eco-epidemiology of bovine tuberculosis (Tb) in wild deer (mainly red deer Cervus elaphus) in New Zealand was investigated. Bovine Tb is caused by Mycobacterium bovis. Specific aims were to clarify the likely routes of infection in deer, and to determine the status of deer as hosts of Tb, the likely rates and routes of inter- and intra-specise transmission between deer and other wildlife hosts, the role of deer in spreading Tb, and the likely utility of deer as sentinels of Tb presence in wildlife. As the possum (Trichosurus vulpecula) is the main wildlife hosts of Tb, the research also included some investigation of transmission routes in possums. Patterns of infection were measured in 994 deer killed between 1993 and 2003. Tb prevalence varied between areas (range 8-36%). Few deer had generalised infection, with 21-68% of infected deer having no visible lesions, depending on the area. The retropharyngeal lymph nodes and oropharyngeal tonsils were commonly infected. No dependent fawns<0.75 y were infected, indicating intra-species transmission is rare in wild deer. Where possums were not controlled, the net (cumulative) force of infection in young (1-4 y) deer was 0.10-0.24 y^(-1) in males and 0.09-0.12 y^(-1) in females, but much lower in older deer (<0.05y^(-1)). Possum control reduced the net force of infection quickly, and evetually to zero. However, Tb persisted in possum-controlled areas through immigration of infected deer and, for almost a decade, through the survival of resident deer infected before possum control. Tb was lost from the infected deer at an exponential rate of 0.13 y^(-1), mostly as a result of deer recovering from infection rather than dying from it. Wild deer do die of Tb, but there was no discernible effect on age structure. The occurrence of infection in deer was not linked to the local deer or possum density at their kill sites (i.e. in their home range), but the area-wide prevalence of Tb in deer was closely correlated with Tb levels in possums, which were in turn correlated wth area-wide measures of possum density. For wild deer in New Zealand, Tb is persistent but usualy inconsequential disease of the lymphatic system. It is acquired mainly by young independent deer, usually orally via the tonsils, and probably as a result of licking infected possums. Many species fed on deer carrion, including possums. Most possums encountering carrion did not feed on it, but a few fed for long periods. Other scavengers such as ferrets (Mustela furo), hawks (Circus approximans), and weka (a hen-sized flightless native bird; Gallirallus australis) fed in a way that probably increased the infectivity of carrion to possums; Commercial deer hunting may have facilitated the historical establishment of Tb in possums. Scavenging (including cannibalism) and interations with dead and dying possums are identified for the first time as potentially important routes for transmission of Tb to possums, and I develpoe new hypotheses involving peri- and post-mortem transmission in possums that explain many of the epidemiological patterns that are characteristic of the disease in possum.

Key Words

Epidemiology, bovine tuberculosis, Mycobacterium bovis, wild deer, Cervus elaphus, New Zealand, Tb, pathogenesis, brushtail possum, Trichosurus vulpecula, prevalence, intra-species transmission, inter-species transmission, resolution of infection, scavenging, cannibalism, sentinel

Citation

Nugent, G. and J. Whitford. 2004. Are deer important long-term reservoir hosts of Tb? Landcare Research Contract Report. LC0405/028

Abstract Only ☑

No Abstract ☐

Article Type Report

Abstract

Project and Client: Research to determine whether wild deer are important long-term reservoir hosts of Tb was undertaken by Manaaki Whenua – Landcare Research, Lincoln, for the Animal Health Board (Contract No. R-10537) between June 2000 and September 2004.
Objectives: To confirm that wild deer are predominantly spillover hosts for bovine tuberculosis, and to determine how long the disease persists in wild deer populations in the absence of infected possums, by:
• monitoring Tb prevalence in wild deer in the eastern Hauhungaroa (EHR) and Umukarikari (UR) ranges for the period 6–9 years after initial possum control.
Methods: Between 2000 and 2003, trends in the prevalence of Tb in deer were measured in two areas where possums had been controlled since 1994. Previously, patterns of infection and trends in Tb prevalence in deer were measured in the same two controlled areas and in two other areas where possums were not controlled over the 1993-2000 period.
Results: In total, 145 deer were necropsied as part of this study. Seven infected deer were found: three adult females (all >11yrs) and four subadult or adult males (all <7yrs). No infection was found in fawns. Prevalence of Tb in adults in the sample was higher than in subadults and fawns but there was little difference in overall prevalence between males and females. Prevalence continued to decline from about 30% (n = 85) in 1993 in both areas to just 5% over the three years of this study. Infected deer were found in all three years in EHR and in 2001 in UR.
Conclusions: Tb has largely disappeared from the deer population in the 9 years since possum numbers were first reduced. The lack of infection in fawns and the low rates of infection in deer born after possum control indicate that deer are primarily spillover hosts. Tb has persisted in both controlled areas, largely through survival of already-infected females and the immigration of infected males. Females pose the greatest long-term threat to eradication of Tb from infected areas because they can potentially carry the disease for up to 20 years (whereas males do not, simply because very few survive for more than 10 years). Conversely, males are more likely to contribute to the spread of Tb to new areas, or to areas previously cleared of Tb in possums, because they are the more dispersive sex. In both instances the threat depends mainly on the unknown rate at which scavenging possums contract Tb from infected deer carcasses. That threat may be very low but is unlikely to be
zero.
Recommendations: The AHB should not routinely include deer control as part of ongoing vector control operations, except in areas with both high densities of deer and high prevalences of Tb in other wildlife. As there is some unquantified risk from the medium-to-long term persistence of Tb, deer control should also be considered where Tb is still prevalent in deer and vector managers aim to cease possum control within 10 years. The likelihood of Tb re-establishing in a recovering possum population after cessation of possum control should be quantified by determining how often possums might acquire Tb by coming into contact with or scavenging infected deer (and possum, pig and ferret) carcasses, and by determining or modelling how often those infected possums transmit Tb to other possums.

Key Words deer, reservoir hosts, spillove hosts, wild deer populations

Citation

Nugent, G., J. Whitford, and N. Young. 2002. Use of released pigs as sentinels for Mycobacterium bovis. Journal of Wildlife Diseases 38(4):665–677.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Identifying the presence of bovine tuberculosis (TB; Mycobacterium bovis) in wildlife is crucial in guiding management aimed at eradicating the disease from New Zealand. Unfortunately, surveys of the principal wildlife host, the introduced brushtail possum (Trichosurus vulpecula), require large samples (┌95% of the population) before they can provide reasonable confidence that the disease is absent. In this study, we tested the feasibility of using a more wide-ranging species, feral pig (Sus scrofa), as an alternative sentinel capable of indicating TB presence. In January 2000, 17 pigs in four groups were released into a forested area with a low density of possums in which TB was known to be present. The pigs were radiotracked at 2 wk intervals from February to October 2000, and some of them were killed and necropsied at various intervals after release. Of the 15 pigs successfully recovered and necropsied, one killed 2 mo after release had no gross lesions typical of TB, and the only other pig killed at that time had greatly enlarged mandibular lymph nodes. The remainder were killed at longer intervals after release and all had gross lesions typical of TB. Mycobacterium bovis was isolated from all 15 pigs by mycobacterial culture. Home range sizes of pigs varied widely and increased with the length of time the pigs were in the forest, with minimum convex polygon range-size estimates averaging 10.7 km2 (range 4.7–20.3 km2) for the pigs killed after 6 mo. A 6 km radius around the kill site of each pig would have encompassed 95% of all of their previous locations at which they could have become infected. However, one pig shifted 35 km, highlighting the main limitation of using unmarked feral pigs as sentinels. This trial indicates use of resident and/or released free-ranging pigs is a feasible alternative to direct prevalence surveys of possums for detecting TB presence.

Key Words

Bovine tuberculosis, brushtail possums, epidemiology, feral pigs, Mycobacterium bovis, Trichosurus vulpecula, sentinels, Sus scrofa

Citation

O'Brien, D. J., S. D. Fitzgerald, T. J. Lyon, K. L. Butler, J. S. Fierke, K. R. Clarke, S. M. Schmitt, T. M. Cooley, and D. E. Berry. 2001. Tuberculous lesions in free-ranging white-tailed deer in Michigan. Journal of Wildlife Diseases 37(3): 608-613

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Descriptions of the anatomical distribution of Mycobacterium bovis gross lesions in large samples of white-tailed deer (Odocoileus virginianus) are lacking in the scientific literature. This report describes the distribution of gross lesions in the 58 white-tailed deer that cultured positive for M. bovis among the 19,500 submitted for tuberculosis testing in Michigan (USA) in 1999. For the vast majority (19,348) of those tested, only the head was submitted; for others, only extracranial tissues (33) or both the head and extracranial tissues (119) were available. Among those deer that cultured positive, cranial gross lesions were noted most frequently in the medial retropharyngeal lymph nodes, although solitary, unilateral parotid lymph node lesions also were found. Extracranial lesions occurred most commonly in the thorax. The distribution of lesions largely agreed with the few existing case reports of the M. bovis in white-tailed deer, although gross lesions were also found in sites apparently not previously reported in this species (liver, spleen, rumen, mammary gland). Some practical issues that may assist future surveillance and public education efforts are also discussed.

Key Words

Bovine tuberculosis, Mycobacterium bovis, white-tailed deer, Odocoileus virginianus, disease surveillance

Citation

O'Brien, D. J., S. M. Schmitt, D. E. Berry, S. D. Fitzgerald, J. R. Vanneste, T. J. Lyon, D. Magsig, J. S. Fierke, T. M. Cooley, L. S. Zwick, and B. V. Thomsen. 2004. Estimating the true prevalence of Mycobacterium bovis in hunter-harvested white-tailed deer in Michigan. Journal of Wildlife Diseases 40(1):42-52.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Apparent prevalence, although useful as a consistent index, may underestimate the true prevalence of disease. In Michigan, the ability to estimate the true prevalence of bovine tuberculosis (TB; caused by Mycobacterium bovis) in free-ranging white-tailed deer (Odocoileus virginianus) will become increasingly important to accurately assess progress towards eradication. Our objectives were threefold: to estimate the true prevalence of M. bovis in free-ranging deer in Michigan, to evaluate the effectiveness of existing TB surveillance methods, and to indirectly assess whether TB epidemiologic data from captive cervid herds can be meaningfully extrapolated to free-ranging populations. The study population consisted of all free-ranging deer submitted for TB testing in 2001 from six townships in northeastern Lower Michigan. Tissue samples of tonsil and cranial lymph nodes were collected bilaterally from all deer eligible for the study that did not have gross lesions suggestive of TB (n5701). Samples were subjected to histopathologic, acid-fast (AF) staining, mycobacterial culture, and polymerase chain reaction (PCR) testing. Seven deer cultured positive for M. bovis that would not have been detected by current surveillance, yielding apparent and true prevalence estimates (95% confidence limits) of 2.7% (1.6, 3.8) and 3.6% (2.3, 4.9), respectively. The sensitivity, specificity, and positive and negative predictive values of the current surveillance protocol were 75, 100, 100, and 99%, respectively. Histologic lesions were present only in tonsils, and ranged from simple necrosis to caseation, suppuration, and granuloma formation. Acid-fast staining and PCR detected M. bovis in only one of the seven culture-positive deer. Our study provides the first estimate of the true prevalence of M. bovis in Michigan's free-ranging deer population and suggests modest underestimation of that prevalence by current surveillance. This study also suggests that caution is warranted when extrapolating epidemiologic data on TB in captive cervids to free-ranging populations and confirms the pivotal role of the tonsil in early infections.

Key Words Bovine tuberculosis, diagnostic tests, disease frequency, Mycobacterium bovis, Odocoileus virginianus, white-tailed deer

Citation

O'Brien, D. J., S. M. Schmitt, D. E. Berry, S. D. Fitzgerald, T. J. Lyon, J. R. Vanneste, T. M. Cooley, S. A. Hogle, and J. S. Fierke. 2008. Estimating the true prevalence of M. bovis in free-ranging elk in Michigan. Journal of Wildlife Disease 44(4):802-810.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Although relatively small, Michigan's elk (Cervus elaphus nelsoni) herd is highly valued by both hunters and the general public. Elk and red deer (Cervus elaphus elaphus) are highly susceptible to infection with Mycobacterium bovis, the causative agent of bovine tuberculosis (TB), and outbreaks have been documented worldwide. The Michigan elk range lies entirely within counties where TB is known to be enzootic in white-tailed deer (Odocoileus virginianus). Consequently, a project was undertaken to estimate the true prevalence of TB in Michigan's free-ranging elk herd. All elk harvested by licensed hunters during 2002–2004, and all nonharvest elk mortalities examined by the Michigan Department of Natural Resources Wildlife Disease Laboratory from November 2002–May 2005, were screened for gross lesions of TB with samples of cranial lymph nodes and palatine tonsils collected for histopathology and mycobacterial culture. In all, 334 elk were included in the study. Twenty-three elk with gross lesions were considered TB suspects; all were culture-negative for M. bovis. However, M. bovis was cultured from two elk without gross lesions. The sensitivity, specificity, and negative predictive value of the current TB surveillance protocol were 0%, 100%, and 99.4%, respectively, while the apparent prevalence and true prevalence calculated directly from the sample were 0% and 0.6%, respectively. The positive predictive value and the estimated true prevalence of the population were undefined. The poor sensitivity of current surveillance was likely an artifact of its application to a relatively small sample, in order to detect a disease present at very low prevalence. The low prevalence of TB in Michigan elk, and the early stage of pathogenesis of the few infected animals, does not suggest elk are maintenance hosts at the present time.

Key Words bovine tuberculosis, Cervus elaphus spp., diagnostic tests, elk, Mycobacterium bovis

Citation	O'Brien, D. J., S. M. Schmitt, G. J. Hickling. 2002. Comments offered on Michigan bovine TB study. Journal of the American Veterinary Medical Association 221(10):1380-1382.
Abstract Only	☐
No Abstract	☑
Article Type	Other
Abstract	
Key Words	Letter to the editor, deer, cattle

Citation

O'Brien, D. J., S. M. Schmitt, J. S. Fierke, S. A. Hogle, S. R. Winterstein, T. M. Cooley, W. E. Moritz, K. L. Diegel, S. D. Fitzgerald, D. E. Berry, J. B. Kaneene. 2002. Epidemiology of Mycobacterium bovis in free-ranging white-tailed deer, Michigan, USA, 1995–2000. Preventive Veterinary Medicine 54:47-63

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

An endemic area of bovine tuberculosis (TB) (Mycobacterium bovis) currently affecting wild white-tailed deer (Odocoileus virginianus) in northern lower Michigan, USA, constitutes the first self-sustaining outbreak of the infection in free-ranging North American cervids. Given this precedent, epidemiologic insights gained from the outbreak afford the opportunity to guide not only current surveillance and intervention but also control efforts for future outbreaks involving wildlife reservoirs. Our specific objectives were to evaluate retrospective data from field surveillance conducted from 1995 to 2000 to determine apparent prevalence, trends in apparent prevalence, and the effects of various factors on the odds of being M. bovis positive. Data were gathered from post-mortem examinations of 62,560 wild deer collected from all 83 Michigan counties. Records of survey method, sex, age, geographic area and infection status as determined by mycobacterial culture were subjected to trend analysis and multivariable logistic regression. Apparent prevalence for the period was 0.54% (336/62,560) statewide. Prevalence varied widely with geographic area, but significantly decreased since 1995 in the core area of the outbreak—which coincided with implementation of control strategies. Significant risk factors were geographic area, sex, age, and the sex-by-age interaction. The survey method by which deer were obtained for testing was not a predictor of infection. Our results to date suggest an outbreak characterized by broad areas of very low prevalence surrounding focal areas where prevalence is sometimes orders-of-magnitude higher (e.g., deer originating from the core area were up to 147 times more likely to be TB positive than deer from other areas). Our results also identify older male deer as most likely to be M. bovis positive (OR ¼ 11:3, 95% CI 3.2, 40.3 for bucks >5 years vs. does <1.5 years)—an observation consistent with the biology and behavior of the species. Synthesizing these results with those of other ongoing investigations, we hypothesize a two-stage model of disease transmission where TB is maintained at very low prevalence in matriarchal groups, with primary dissemination of the disease attributable to the dispersal and movements of bucks (as well as to the large aggregations of animals created by human activities).

Key Words tuberculosis, Mycobacterium bovis, white-tailed deer, Odocoileus virginianus, cervids, wildlife reservoirs, disease modeling

Citation

O'Brien, D. J., S. M. Schmitt, K. P. Lyashchenko, W. R. Waters, D. E. Berry, M. V. Palmer, J. McNair, R. Greenwald, J. Esfandiari, and M. K. Cosgrove. 2009. Evaluation of blood assays for detection of Mycobacterium bovis in white-tailed deer (Odocoileus virginianus) in Michigan. Journal of Wildlife Diseases 45(1):153–164.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Surveillance and control activities related to bovine tuberculosis (TB) in free-ranging, Michigan white-tailed deer (Odocoileus virginianus) have been underway for over a decade, with significant progress. However, foci of higher TB prevalence on private lands and limited agency ability to eliminate them using broad control strategies have led to development and trial of new control strategies, such as live trapping, testing, and culling or release. Such strategies require a prompt, accurate live animal test, which has thus far been lacking. We report here the ability of seven candidate blood assays to determine the TB infection status of Michigan deer. Our aims were twofold: to characterize the accuracy of the tests using field-collected samples and to evaluate the feasibility of the tests for use in a test-and-cull strategy. Samples were collected from 760 deer obtained via five different surveys conducted between 2004 and 2007. Blood samples were subjected to one or more of the candidate blood assays and evaluated against the results of mycobacterial culture of the cranial lymph nodes. Sensitivities of the tests ranged from 46% to 68%, whereas specificities and negative predictive values were all .92%. Positive predictive values were highly variable. An exploratory analysis of associations among several host and sampling-related factors and the agreement between blood assay and culture results suggested these assays were minimally affected. This study demonstrated the capabilities and limitations of several available blood tests for Mycobacterium bovis on specimens obtained through a variety of field surveillance methods. Although these blood assays cannot replace mass culling, information on their performance may prove useful as wildlife disease managers develop innovative methods of detecting infected animals where mass culling is publicly unacceptable and cannot be used as a control strategy.

Key Words bovine tuberculosis, diagnostic tests, Mycobacterium bovis, Odocoileus, virginianus, white-tailed deer

Citation

O'Brien, D. J., S. M. Schmitt, S. D. Fitzgerald, D. E. Berry, G. J. Hickling. 2006. Managing the wildlife reservoir of Mycobacterium bovis: The Michigan, USA, experience. Veterinary Microbiology 112: 313-323.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Historical, social and economic factors combined to provide a focus where bovine tuberculosis has become established in free-ranging wildlife in northeastern lower Michigan. White-tailed deer, the primary reservoir and maintenance host of tuberculosis, are highly valued by the public, and particularly hunters, for cultural and economic reasons. Since 1995, significant progress has been made in defining and reducing the reservoir of tuberculosis in deer. As yet, no other wildlife species has been shown to play an epidemiologically important role in the disease cycle. The importance of deer and deer hunting to Michigan has uniquely shaped tuberculosis control policies, and poses ongoing challenges as wildlife managers strive to maintain momentum for broad control strategies, and develop focused strategies that are publicly acceptable. Even if momentum and funding can be maintained, tuberculosis will likely continue to be present for a decade or longer. Thus, cattle producers waiting for tuberculosis to be eradicated from wildlife to eliminate risks to their herds and markets face disappointment for the foreseeable future. Such unrealistic expectations also place Michigan's federal tuberculosis accreditation status at perpetual risk. Accredited free status is unlikely to be regained without accompanying changes in cattle management. In Michigan, management of tuberculosis has clearly demonstrated that social issues and public approval are likely to be the critical limiting factors in control.

Key Words bovine tuberculosis, Mycobacterium bovis, wildlife, white-tailed deer, Odocoileus virginianus

Citation Olea-Popelka, F. J., J.M. Griffin, J.D. Collins, G. McGrath, S.W. Martin. 2003. Bovine tuberculosis in badgers in four areas in Ireland: does tuberculosis cluster? Preventive Veterinary Medicine 59:103–111.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract We described the distribution of badger populations in four different areas in the Republic of Ireland. The data came from periodic targeted badger-removal and subsequent post-mortem examinations conducted between 1989 and September 1997, and from a formal badger-removal project in the same areas from 1997 through 1999. Records were complete for 2292 badgers regarding the date of capture, tuberculosis status, geographical area and specific sett from where the badgers were snared. Of 3187 setts, 2290 had no badgers recorded against them (i.e. were inactive). The badger-level prevalence of tuberculosis differed among areas (range 13–29%). Badger populations were highly clustered by sett, and this result was similar over the four study areas. The median number of badgers per active sett was 2. Tuberculous badgers also clustered within a sett. The third quartile of tuberculous badgers was 1 per active sett. The prevalence of tuberculous badgers within a sett was not related to the total number of badgers. There was little evidence of spatial clustering with only one local cluster of tuberculous setts in each of three areas, and none in the fourth area. After adjusting for the number of badgers per sett, only one area had spatial clusters identified.

Key Words spatial, distribution, bovine tuberculosis, badgers, Ireland, cluster

Citation

Olea-Popelka, F. J., P. Fitzgerald, P. White, G. McGrath, J.D. Collins, J. O'Keeffe, D.F. Kelton, O. Berke, S. More, S.W. Martin. 2009. Targeted badger removal and the subsequent risk of bovine tuberculosis in cattle herds in county Laois, Ireland. Preventive Veterinary Medicine 88:178–184.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We investigated the impact of targeted removal of badgers on the subsequent bovine tuberculosis (BTB) risk in cattle herds in county Laois, Ireland. The study periodwas 1989– 2005. For each of 122 targeted badger-removal licenses (permit to remove badgers in the proximity of cattle herds undergoing a serious BTB episode), the herd number (index herd) for which the license was given was obtained. The herds in the proximity of the index herd were identified from another database. The main ''exposure'' in our study was the geographical location of herds relative to the area in which targeted badger removal was conducted.Wecategorized herds into five different exposure groups: herds were classified as non-exposed and denoted as group 0 (reference group) if they were located 500 m or more from the edge of any parcel of land of the index herd; group 1, was the index herds, group 2 the immediate (contiguous) neighbors of the index herd, group 3 herds were not immediate neighbors but within 150 m and group 4 herds were between 150 m and 500 m distance from the edge of any parcel of land of the index herd, respectively. We conducted a survival analysis (allowing multiple failures per herd) to compare the hazard of having a BTB episode in any of the four groups of exposed herds vs. the hazard in herds in the reference group. We controlled for other known risk factors as well taking into account a temporal component. Our analysis showed that the hazard ratio for the index herds (group 1) were non-significantly increased, indicating that there was no difference in the hazard of failing a BTB test (after the targeted badger removal was conducted) between index herds and reference herds. For the rest of the herds farther away from badger removal activities the hazards were lower than herds in areas not under badger removal. The hazard in the reference group decreased over the study period.

Key Words

bovine tuberculosis, badger removal, Ireland

Citation

O'Reilly, L. M., C. J. Daborn. 1995. The epidemiology of Mycobacterium bovis infections in animals and man: a review. Tubercle and Lung Disease 76(1):1-46

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis is primarily a respiratory disease and transmission of infection within and between species is mainly by the airborne route. Mycobacterium bovis, the cause of bovine-type tuberculosis, has an exceptionally wide host range. Susceptible species include cattle, humans, non-human primates, goats, cats, dogs, pigs, buffalo, badgers, possums, deer and bison. Many susceptible species, including man, are spillover hosts in which infection is not self-maintaining. In countries where there is transmission of infection from endemically infected wildlife populations to cattle or other farmed animals, eradication is not feasible and control measures must be applied indefinitely. Possible methods of limiting spread of infection from wildlife to cattle including the use of vaccines are outlined. The usefulness of DNA fingerprinting of M. bovis strains as an epidemiological tool and of BCG vaccination of humans and cattle as a control measure are reviewed. The factors determining susceptibility to infection and clinical disease, and the infectiousness of infected hosts and transmission of infection, are detailed. Reports of the epidemiology of M. bovis infections in man and a variety of animal species are reviewed. M. bovis infection was recognised as a major public health problem when this organism was transmitted to man via milk from infected cows. The introduction of pasteurization helped eliminate this problem. Those occupational groups working with M. bovis infected cattle or deer, on the farm or in the slaughter house, are more likely to develop pulmonary disease than alimentary disease. In recent years, tuberculosis in farmed cervidae has become a disease of economic as well as public health importance in several countries. Nowadays, the human immunodeficiency virus (HIV) is associated with a greatly increased risk of overt disease in humans infected with Myobacterium tuberculosis. It is believed this increased risk also occurs in the case of M. bovis infections in humans.

Key Words epidemiology, human, susceptibility, cows, milk, public health, farmed deer, HIV

Citation

Palmer, M. V. and D. L. Whipple. 2006. Survival of Mycobacterium bovis on feedstuffs commonly used as supplemental feed for white-tailed deer (Odocoileus virginianus). Journal of Wildlife Diseases 42(4):853-858.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis, the causative agent of bovine tuberculosis, has become established in free-ranging white-tailed deer Odocoileus virginianus in northeastern Michigan. The practice of supplemental feeding of white-tailed deer during the winter is believed to contribute to transmission of M. bovis between deer. The current study was conducted to determine the ability of M. bovis to survive on various feedstuffs commonly used as supplemental feed for deer in northeast Michigan (i.e., apples, corn, carrots, sugar beets, potatoes, and hay) and the effect of maintenance at 220 C, 8 C, and 23 C on survival. Mycobacterium bovis survived on all feedstuffs at all temperatures tested for at least 7 days. At 23 C, M. bovis could still be isolated from samples of apples, corn and potatoes at 112 days. This study suggests that contamination of feedstuffs by M. bovis-infected deer could act as a source of indirect transmission between deer because M. bovis is able to survive in temperatures similar to those recorded during winter months in northeastern Michigan. Current efforts to ban or control supplemental feeding of deer should have a positive effect on decreasing transmission of M. bovis among deer.

Key Words Feedstuffs, Mycobacterium bovis, Odocoileus virginianus, survivability, tuberculosis, white-tailed deer

Citation

Palmer, M. V. and W. Ray Waters. 2006. Advances in bovine tuberculosis diagnosis and pathogenesis: What policy makers need to know. Veterinary Microbiology 112:181–190.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The mainstay of tuberculosis diagnosis in cattle and deer has been the tuberculin skin test. Recent advances have allowed the incorporation of blood based assays to the diagnostic arsenal for both cattle and deer. Use of defined and specific antigens has allowed for improved specificity of cell mediated assays in both cattle and deer and advances in antibody tests for tuberculosis have potential for use in free-ranging and captive cervid populations. Combined use of blood-based assays with skin testing will require further understanding of the effect of skin testing on the accuracy of blood based assays. Models of experimental infection of cattle have allowed for increased understanding of natural disease pathogenesis. Differences likely exist; however, between cattle and deer in both disease distribution and primary route of inoculation in naturally infected animals.

Key Words

cattle, Cervidae, deer, diagnosis, Mycobacteria, Mycobacterium bovis, pathology, tuberculosis

Citation

Palmer, M. V., T.C. Thacker, and W. R. Waters. 2007. Vaccination of white-tailed deer (Odocoileus virginianus) with Mycobacterium bovis bacillus Calmette Guerin. Vaccine 25:6589–6597.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wildlife reservoirs of Mycobacterium bovis represent serious obstacles to the eradication of tuberculosis in domestic livestock. In Michigan, USA tuberculous white-tailed deer transmit M. bovis to cattle. One approach in dealing with this wildlife reservoir is to vaccinate deer in order to interrupt the cycle of deer to deer and deer to cattle transmission. Thirty-one white-tailed deer were assigned to one of three groups; 2 SC doses of 10^7 CFU of M. bovis BCG (n = 11); 1 SC dose of 10^7 CFU of M. bovis BCG (n = 10); or unvaccinated deer (n = 10). After vaccination, deer were inoculated intratonsilarly with 300 CFU of virulent M. bovis. Gross lesion severity scores of the medial retropharyngeal lymph node were significantly reduced in deer receiving 2 doses of BCG compared to unvaccinated deer. Vaccinated deer had fewer lymph node granulomas than unvaccinated deer, and most notably, fewer late stage granulomas characterized by coalescent caseonecrotic granulomas containing numerous acid-fast bacilli. BCG was isolated from 7/21 vaccinated deer as long as 249 days after vaccination. In one case BCG was transmitted from a vaccinated deer to an unvaccinated deer. In white-tailed deer BCG provides measurable protection against challenge with virulent M. bovis. However, persistence of vaccine within tissues as well as shedding of BCG from vaccinates remain areas for further investigation.

Key Words BCG, deer; Mycobacterium bovis, tuberculosis, vaccination

Citation

Palmer, M. V., D. L. Whipple, and W. R. Waters. 2001. Experimental deer-to-deer transmission of Mycobacterium bovis. American Journal of Veterinary Research 62(5): 692-696.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Objective—To determine whether Mycobacterium bovis can be transmitted from experimentally infected deer to uninfected in-contact deer.
Animals—Twenty-three 6-month-old white-tailed deer.
Procedure—On day 0, M bovis (2 X 108 colony-forming units) was administered by intratonsillar instillation to 8 deer; 3 control deer received saline (0.9% NaCl) solution. Eight in-contact deer were comingled with inoculated deer from day 21. On day 120, inoculated deer were euthanatized and necropsied. On day 180, 4 in-contact deer were euthanatized, and 4 new incontact deer were introduced. On day 360, all in-contact deer were euthanatized. Rectal, oral, and nasal
swab specimens and samples of hay, pelleted feed, water, and feces were collected for bacteriologic culture. Tissue specimens were also collected at necropsy for bacteriologic culture and histologic analysis.
Results—On day 90, inoculated and in-contact deer developed delayed-type hypersensitivity (DTH) reactions to purified protein derivative of M bovis. Similarly, new in-contact deer developed DTH reactions by 100 days of contact with original in-contact deer. Tuberculous lesions in in-contact deer were most commonly detected in lungs and tracheobronchial and medial retropharyngeal lymph nodes. Mycobacterium bovis was isolated from nasal secretions and saliva from inoculated and in-contact deer, urine and feces from in-contact deer, and hay and pelleted feed.
Conclusions and Clinical Relevance—Mycobacterium bovis is efficiently transmitted from experimentally infected deer to uninfected in-contact deer through nasal secretions, saliva, or contaminated feed. Wildlife management practices that result in unnatural gatherings of deer may enhance both direct and indirect transmission of M bovis.

Key Words

Transmission, white-tailed deer, deer-to-deer, experimentally infected, inoculated, delayed-type, hypersensitivity, DTH, feed, nasal, saliva

Citation Palmer, M. V., D. L. Whipple, K. L. Butler, S. D. Fitzgerald, C. S. Bruning-Fann, S. M. Schmitt. 2002. Tonsillar lesions in white-tailed deer (Odocoileus virginianus) naturally infected with Mycobacterium bovis. Veterinary Record 151(5):149-50

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words bovine tuberculosis, Mycobacterium bovis, Odocoileus virginianus, tonsillar lesions, white-tailed deer

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Citation Palmer, M. V., D. L. Whipple, W. R. Waters. 2001. Tuberculin skin testing in white-tailed deer (Odocoileus virginianus). Journal of Veterinary Diagnostic Investigations 13:530–533.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract The comparative cervical skin test for antemortem diagnosis of tuberculosis was done 169 times on 116 different white-tailed deer of known Mycobacterium bovis infection status. The sensitivity and specificity were 97 and 81%, respectively. The magnitude of change in skin thickness at test sites was not significantly influenced by dosage of inoculum, dissemination of the disease process, or repeated skin testing. However, the magnitude of change in skin thickness was significantly greater in deer infected for less than 109 days than in deer infected for more than 109 days. As used in the present study, the comparative cervical skin test is a sensitive method of antemortem diagnosis of M. bovis infection in white-tailed deer.

Key Words Cervical skin test, diagnosis, white-tailed deer, Odocoileus virginianus

Citation

Palmer, M. V., T.C. Thacker, and W.R. Waters. 2008. Vaccination with Mycobacterium bovis BCG strains Danish and Pasteur in white-tailed deer (Odocoileus virginianus) experimentally challenged with Mycobacterium bovis. Zoonoses and Public Health 56:243–251.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wildlife reservoirs of Mycobacterium bovis represent serious obstacles to the eradication of tuberculosis in domestic livestock and the cause for many faltering bovine tuberculosis eradication programmes. One approach in dealing with wildlife reservoirs of disease is to interrupt inter-species and intraspecies transmission through vaccination of deer or cattle. To evaluate the efficacy of BCG vaccination in white-tailed deer, 35 deer were assigned to one of three groups; one s.c. dose of 107 CFU of M. bovis BCG Pasteur (n = 12); 1 s.c. dose of 10^7 CFU of M. bovis BCG Danish (n = 11); or unvaccinated deer (n = 12). After vaccination, deer were inoculated intratonsilarly with virulent M. bovis. Lesion severity scores of the medial retropharyngeal lymph node, as well as all lymph nodes combined, were reduced in vaccinated deer compared to unvaccinated deer. BCG Danish vaccinated deer had no late stage granulomas characterized by coalescent caseonecrotic granulomas containing numerous acid-fast bacilli compared to BCG Pasteur vaccinated or unvaccinated deer where such lesions were present. Both BCG strains were isolated as late as 250 days after vaccination from deer that were vaccinated but not challenged. In white-tailed deer, BCG provides protection against challenge with virulent M. bovis. Issues related to vaccine persistence, safety and shedding remain to be further investigated.

Key Words BCG, Danish, deer, Mycobacterium bovis, Pasteur, tuberculosis, vaccination

Citation

Palmer, M. V., W. R. Waters, and D. L. Whipple. 2002. Lesion development in white-tailed deer (Odocoileus virginianus) experimentally infected with Mycobacterium bovis. Veterinary Pathology 39:334–340.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The recent discovery of tuberculosis in free-living white-tailed deer in northeastern Michigan underscores the need for increased understanding of the pathogenesis of tuberculosis in wildlife species. To investigate lesion development in white-tailed deer, 32 deer were experimentally infected by intratonsilar instillation of 300 colony-forming units of Mycobacterium bovis. Three deer each were euthanatized and examined at days 15, 28, 42, and 56 after inoculation, and five deer each were euthanatized and examined at days 89, 180, 262, and 328 after inoculation. Microscopic lesions first were seen in the medial retropharyngeal lymph node and lung 28 and 42 days after inoculation, respectively. Lung lesions were present in 12 (38%) of 32 deer, involving 23 lung lobes. Left caudal and right middle and caudal lobes were involved in 17 (74%) of the 23 affected lung lobes. Lesions in the medial retropharyngeal lymph node first appeared as granulomas composed of aggregates of macrophages and Langhans-type giant cells. Some early granulomas contained centrally located neutrophils. As granulomas developed, neutrophils were replaced with a central zone of caseous necrosis that first showed signs of mineralization 42 days after inoculation. Granulomas increased in size as the zone of caseous necrosis expanded. Peripheral fibrosis, first seen at 56 days after inoculation, progressed to only a thin fibrous capsule by 328 days after inoculation. By the termination of the study, the central necrotic core of the granuloma contained abundant liquefied necrotic material and grossly resembled an abscess. Although tuberculous lesions in white-tailed deer follow a developmental pattern similar to that in cattle, fibrosis is less pronounced and the advanced lesions may liquefy, a change seldom reported in cattle. An understanding of lesion development will aid in the identification of the spectrum of disease that may be seen in this important wildlife reservoir of tuberculosis.

Key Words deer, granuloma, Mycobacterium bovis, Odocoileus virginianus, tuberculosis

Citation

Palmer, M. V., W. R. Waters, and D. L. Whipple. 2002. Milk containing Mycobacterium bovis as a source of infection for white-tailed deer fawns (Odocoileus virginianus). Tuberculosis 82(4/5):161-165.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Setting: White-tailed deer represent the first wildlife reservoir of Mycobacterium bovis in the United States.The behavior of does with nursing fawns provides several potential mechanisms for disease transmission.Little information exists concerning transmission between doe and fawn, specifically transmammary transmission. Objective: Determine if fawns can become infected by ingestion of milk replacer containing M. bovis, thus simulating transmission from doe to fawn through contaminated milk. Design: Seventeen, 21-day-old white-tailed deer fawns were inoculated orally with 2x10^8 CFU (high dose, n=5), 2.5x10^5 to 2.5x10^6 CFU (medium dose, n=5), and 1x10^4 CFU (low dose, n=5) of M. bovis in milk replacer. Dosages were divided equally and fed daily over a 5-day period.Positive control fawns (n=2) received 1x10^5 CFU of M. bovis instilled in the tonsillar crypts.Fawns were euthanized and examined 35--115 days after inoculation and various tissues collected for bacteriologic and microscopic analysis.
Results: All fawns in the tonsillar, high oral and medium oral dose groups developed generalized tuberculosis involving numerous organs and tissues by 35--84 days after inoculation. Three of five fawns in the low-dose oral group had tuberculous lesions in the mandibular lymph node, and one of five had lesions in the medial retropharyngeal lymph node when examined 115 days after inoculation.
Conclusion: White-tailed deer fawns can become infected through oral exposure to M. bovis.Therefore, the potential exists for fawns to acquire M. bovis while nursing tuberculous does.

Key Words milk, wildlife, transmammary, transmission, white-tailed deer, behavior, doe, fawn

Citation

Palmer, M. V., W. R. Waters, and D. L. Whipple. 2003. Aerosol exposure of white-tailed deer (Odocoileus virginianus) to Mycobacterium bovis. Journal of Wildlife Diseases 39(4):817-823.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis due to Mycobacterium bovis affects both captive and free-ranging Cervidae in the United States. Various animal models have been developed to study tuberculosis of both humans and animals. Generally, tuberculosis is transmitted by aerosol and oral routes. Models of aerosol exposure of large animals to M. bovis are uncommon. In order to develop a reliable method of aerosol exposure of white-tailed deer (Odocoileus virginianus) to M. bovis, 12 healthy white-tailed deer, aged 8–10 mo, were infected by aerosol exposure to 23105 to 13106 colony forming units (CFU) (high dose, n54) of M. bovis or 63102 to 1.63103 CFU (low dose, n58) of M. bovis. Tuberculous lesions were more widely disseminated in deer receiving the high dose, while lesions in deer receiving the low dose were more focused on the lungs and associated lymph nodes (tracheobronchial and mediastinal). Aerosol delivery of M. bovis to white-tailed deer results in a reliable manner of experimental infection that may be useful for studies of disease pathogenesis, immune response, mycobacterial shedding, and vaccine efficacy.

Key Words aerosol, Mycobacterium bovis, Odocoileus virginianus, tuberculosis, white-tailed deer

Citation

Palmer, M. V., W. R. Waters, and D. L. Whipple. 2004. Investigation of the transmission of Mycobacterium bovis from deer to cattle through indirect contact. American Journal of Veterinary Research 65(11):1483-1489.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

OBJECTIVE: To investigate the infection of calves with Mycobacterium bovis through oral exposure and transmission of M. bovis from experimentally infected white-tailed deer to uninfected cattle through indirect contact. ANIMALS: 24 11-month-old, white-tailed deer and 28 6-month-old, crossbred calves. PROCEDURE: In the oral exposure experiment, doses of 4.3 x 10(6) CFUs (high dose) or 5 x 10(3) CFUs (low dose) of M. bovis were each administered orally to 4 calves; as positive controls, 2 calves received M. bovis (1.7 x 10(5) CFUs) via tonsillar instillation. Calves were euthanatized and examined 133 days after exposure. Deer-to-cattle transmission was assessed in 2 phases (involving 9 uninfected calves and 12 deer each); deer were inoculated with 4 x 10(5) CFUs (phase I) or 7 x 10(5) CFUs (phase II) of M. Bovis. Calves and deer exchanged pens (phase I; 90 days' duration) or calves received uneaten feed from deer pens (phase II; 140 days' duration) daily. At completion, animals were euthanatized and tissues were collected for bacteriologic culture and histologic examination. RESULTS: In the low- and high-dose groups, 3 of 4 calves and 1 of 4 calves developed tuberculosis, respectively. In phases I and II, 9 of 9 calves and 4 of 9 calves developed tuberculosis, respectively. CONCLUSIONS AND CLINICAL RELEVANCE: Results indicated that experimentally infected deer can transmit M. bovis to cattle through sharing of feed. In areas where tuberculosis is endemic in free-ranging white-tailed deer, management practices to prevent access of wildlife to feed intended for livestock should be implemented.

Key Words white-tailed deer, cattle, calves, indirect contact, feed

Citation

Palmer, M. V., W. R. Waters, and D. L. Whipple. 2004. Shared feed as a means of deer-to-deer transmission of Mycobacterium bovis. Journal of Wildlife Disease 40(1):87-91.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

To determine the ability of experimentally inoculated white-tailed deer (Odocoileus virginianus) to transmit Mycobacterium bovis to naive deer through the sharing of feed, four deer were intratonsillarly inoculated with 43105 colony-forming units of M. bovis. On a daily basis, feed not consumed by inoculated deer after approximately 8 hr was offered to four naïve deer maintained in a separate pen, where direct contact, aerosol transmission, or transmission through personnel were prevented. After 150 days, naive deer were euthanized and examined. All naive deer had lesions consistent with tuberculosis and M. bovis was isolated from various tissues. The most commonly affected tissues were lung, tracheobronchial lymph nodes, and mediastinal lymph nodes. This study demonstrates the potential for indirect transmission of M. bovis through the sharing of feed. Intentional or unintentional feeding of deer by wildlife or agricultural interests in regions where M. bovis infection is endemic should be avoided because both direct and indirect transmission through sharing of feed are enhanced.

Key Words deer, feeding, Mycobacterium bovis, Odocoileus virginianus, transmission, tuberculosis

Citation

Palmer, M. V., W. R. Waters, D. L. Whipple, R. E. Slaughter, S. L. Jones. 2004. Evaluation of an in vitro blood-based assay to detect production of interferon-g by Mycobacterium bovis–infected white-tailed deer (Odocoileus virginianus). Journal of Veterinary Diagnostic Investigations 16:17–21

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis due to Mycobacterium bovis in captive Cervidae was identified as an important disease in the United States in 1990 and prompted the addition of captive Cervidae to the USDA Uniform Methods and Rules for eradication of bovine tuberculosis. As well, M. bovis infection was identified in free ranging white-tailed deer in northeast Michigan in 1995. Tuberculosis in both captive and free-ranging Cervidae represents a serious challenge to the eradication of M. bovis infection from the United States. Currently, the only approved antemortem tests for tuberculosis in Cervidae are the intradermal tuberculin skin test and the blood tuberculosis test (BTB). At present, the BTB is not available in North America. Tuberculin skin testing of Cervidae is time-consuming and involves repeated animal handling and risk of injury to animals and humans. This study evaluated the potential of a new blood-based assay for tuberculosis in Cervidae that would decrease animal handling, stress, and losses due to injury. In addition, a blood-based assay could provide a more rapid diagnosis. Twenty 6–9-month-old white-tailed deer, male and female, were experimentally inoculated by instillation of 300 colony-forming units of M. bovis in the tonsillar crypts. Seven, age-matched uninfected deer served as controls. Blood was collected on days 90, 126, 158, 180, 210, 238, 263, and 307 after inoculation and was analyzed for the production of interferon-g (IFN-g) in response to incubation with M. bovis purified protein derivative (PPDb), M. avium PPDa, pokeweed mitogen (PWM), or media alone. Production of IFN-g in response to PPDb was significantly greater (P , 0.05) at all time points in samples from M. bovis–infected deer as compared with uninfected control deer, whereas IFN-g production to PWM did not differ significantly between infected and control deer. Measurement of IFN-g production to PPDb may serve as a useful assay for the antemortem diagnosis of tuberculosis in Cervidae.

Key Words in vitro, blood-based assays, white-tailed deer, Odocoileus virginianus, antemortem test, cervidae, intradermal

Citation

Palmer, M.V, D. L. Whipple, J. B. Payeur, D. P. Alt, K. J. Esch, C. S. Bruning-Fann, J. B. Kaneene. 2000. Naturally occurring tuberculosis in white-tailed deer. Journal of American Medical Association 216(12):1921-1924.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Objective—To determine the distribution of lesions and extent of tissues infected with Mycobacterium bovis in a captive population of white-tailed
deer.
Design—Cross-sectional study.
Animals—116 captive white-tailed deer.
Procedure—Deer were euthanatized, and postmortem examinations were performed. Tissues with gross lesions suggestive of tuberculosis were collected for microscopic analysis and bacteriologic culture. Tissues from the head, thorax, and abdomen of deer with no gross lesions were pooled for bacteriologic culture. Tonsillar, nasal, oral, and rectal swab specimens, fecal samples, and samples of hay and pelleted feed, soil around feeding sites, and water from 2 natural ponds were collected for bacteriologic culture.
Results—Mycobacterium bovis was isolated from 14 of 116 (12%) deer; however, only 9 of 14 had lesions consistent with tuberculosis. Most commonly affected tissues included the medial retropharyngeal lymph node and lung. Five of 14 tuberculous deer had no gross lesions; however, M bovis was isolated from pooled tissue specimens from the heads of each of these deer. Bacteriologic culture of tonsillar swab specimens from 2 of the infected deer yielded M bovis. Mean (± SEM) age of tuberculous deer was 2.5 ± 0.3 years (range, 0.5 to 6 years). Mycobacterium bovis was not isolated from feed, soil, water, or fecal
samples.
Conclusions and Clinical Relevance—Examination of hunter-killed white-tailed deer for tuberculosis commonly includes only the lymph nodes of the head. Results of such examinations may underestimate disease prevalence by as much as 57%. Such discrepancy should be considered when estimating disease prevalence.

Key Words white-tailed deer, cross-sectional study, disease prevalence

Citation

Palmer, M.V., D. L. Whipple, and S. C. Olsen. 1999. Development of a model of natural infection with Mycobacterium bovis in white-tailed deer. Journal of Wildlife Diseases 35(3): 450-457.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The objective of this study was to develop a suitable experimental model of natural Mycobacterium bovis infection in white-tailed deer (Odocoileus virginianus), describe the distribution and character of tuberculous lesions, and to examine possible routes of disease transmission. In October 1997, 10 mature female white-tailed deer were inoculated by intratonsilar instillation of 2 x 10^3 (low dose) or 2 x 10^5 (high dose) colony forming units (CFU) of M. bovis. In January 1998, deer were euthanatized, examined, and tissues were collected 84 to 87 days post inoculation. Possible routes of disease transmission were evaluated by culture of nasal, oral, tonsilar, and rectal swabs at various times during the study. Gross and microscopic lesions consistent with tuberculosis were most commonly seen in medial retropharyngeal lymph nodes and lung in both dosage groups. Other tissues containing tuberculous lesions included tonsil, trachea, liver, and kidney as well as lateral retropharyngeal, mandibular, parotid, tracheobronchial, mediastinal, hepatic, mesenteric, superficial cervical, and iliac lymph nodes. Mycobacterium bovis was isolated from tonsilar swabs from 8 of 9 deer from both dosage groups at least once 14 to 87 days after inoculation. Mycobacterium bovis was isolated from oral swabs 63 and 80 days after inoculation from one of three deer in the low dose group and none of four deer in the high dose group. Similarly, M. bovis was isolated from nasal swabs 80 and 85 days after inoculation in one of three deer from the low dose group and 63 and 80 days after inoculation from two of four deer in the high dose group. Intratonsilar inoculation with M. bovis results in lesions similar to those seen in naturally infected white-tailed deer; therefore, it represents a suitable model of natural infection. These results also indicate that M. bovis persists in tonsilar crypts for prolonged periods and can be shed in saliva and nasal secretions. These infected fluids represent a likely route of disease transmission to other animals or humans.

Key Words Mycobacterium bovis, Odocoileus virginianus, pathology, transmission, tuberculosis, white-tailed deer

Citation

Parra, A., J. Larrasa, A. Garcia, J.M. Alonso, and J. Hermoso de Mendoza. 2005. Molecular epidemiology of bovine tuberculosis in wild animals in Spain: A first approach to risk factor analysis. Veterinary Microbiology 110:293–300.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In human tuberculosis (Mycobacterium tuberculosis), molecular epidemiology has accurately indicated the risk factors involved in active transmission of the disease, by comparing individuals whose isolates belong to a cluster with patients whose strains are considered unique. Nevertheless, this application has not been used in bovine tuberculosis (Mycobacterium bovis). Our study describes the integration of epidemiological data into molecular classification data on M. bovis isolates. These were isolated from wild ungulates in Extremadura (western Spain) with the objective of detecting the risk factors linked to the association of strains in clades, which are indicators of the active spread of the disease. The molecular markers used were spoligotyping + VNTR typing (loci: VNTR 2165, VNTR 2461, VNTR 0577, VNTR 0580, VNTR 3192 VNTR 2163a and VNTR 2163b) on a population of 59 M. bovis strains isolated from deer (Cervus elaphus), 112 from wild boar (Sus scrofa), six from bovines, 28 from pigs and 2 from goats (n = 207). Epidemiological variables included the animal species from which the strain was isolated, pathological condition of the host (incipient lesion, early and late generalisation), date of sampling (during or after the reproductive period) and hunting season. Bivariant analysis was used to establish the risk factors connected to the association of strains and later, the variables were evaluated by means of logistic regression. Molecular typing grouped a total of 131 strains (64.21%) in 28 clusters and 76 isolates shows unique profiles. The association of strains was connected to the appearance of macroscopic lesions during the reproductive period (O.R. 4.80; 95% CI 1.09–22.99, $P < 0.005$), showing a possible higher transmission during the courting period. This happened mainly during the last hunting season analysed (2002–2003, O.R. 3.69; 95% CI 1.27–11.9, $P < 0.05$), clashing with the time of higher prevalence of the disease in wild ungulates. Active spread was not connected to any species in particular, or to any concrete pathological condition.

Key Words molecular typing, Mycobacterium bovis, risk analysis

Citation

Peyton, R.B. 1997. Recommendations for elimination of bovine tuberculosis in free-ranging white-tailed deer in Michigan. A Report Submitted to the State Committee on Bovine TB in Wild Deer. Michigan State University, East Lansing, MI.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

Executive Summary - A significant infection rate of bovine TB in the deer population of the northeastern lower peninsula poses a potential risk to several important values including public health, United States Department of Agriculture (U.S.D.A.) TB-free accreditation for Michigan cattle, wildlife health, wildlife-related recreation and tourism and economic stability in several sectors. A risk assessment study by the U.S. D.A. Centers for Epidemiology and Animal Health (Fort Collins, CO.) predicted that if no changes were made in the management of the affected free-ranging deer population, the TB prevalence in the core area could reach 6.5% (compared to the current prevalence of 2.3%). Although the current annual risk of TB transfer to cattle in the affected area is 0.1%, the report estimated a 12% cumulative risk that at least one head of cattle would become infected over the next 25 years if no changes are made in deer and/or cattle management.

Representatives of the State Departments of Agriculture, Natural Resources and Community Health responded to the presence of bovine TB in the wild deer by initiating a surveillance and monitoring program. The group also established a statewide committee of scientists and stakeholders to formulate recommendations for management. This committee investigated the complex bovine TB problem and its uncertainties and explored options for eliminating the disease fiom Michigan's deer herd. This report serves as an integration of the perspectives and thoughts of scientists, managers, and citizens regarding those options. It does not constitute a plan, but does identify a range of needs and options that should be addressed in a planning effort. A few of the recommendations have already been implemented as part of an ongoing information gathering process. However, an effective response will require an aggressive application of support and

resources fiom the administrators of each agency. For example, a recommendation to seek legislative authority to halt winter feeding in the af5ected area would require considerable political support. We respecifidly request that you initiate a formal planning process, establish priorities and support the implementation of effective options to eliminate bovine TB from white-tailed deer and to manage the associated problems.

Members of this Statewide Core Committee on Bovine TB in Miclugan Deer were invited fiom both the scientific community (wildlife management, veterinary medicine, public health, communications and research in several disciplines) and public stakeholders (agriculture livestock producers, recreational land owners and hunters). The Committee determined its goal to be development of recommendations toward the elimination rather than control of bovine TB in Michigan deer.

Key Words bovine tuberculosis, livestock, Mycobacterium bovis, surveillance, white-tailed deer

Citation

Pfeiffer, D.U. 1994. The role of a wildlife reservoir in the epidemiology of bovine tuberculosis. Thesis, Massey University, Australia.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

The objective of this project was to study the epidemiology of bovine tuberculosis in the presence of a wildlife reservoir species. Cross-sectional and longitudinal studies of possum populations with endemic bovine tuberculosis infection were analysed. The results were used to develop a computer simulation model of the dynamics of bovine tuberculosis infection in possum populations. A case-control study of breakdowns to tuberculosis infection in cattle herds in the Central North Island of New Zealand was conducted to identify risk factors other than exposure to tuberculosis in local possum populations.

Key Words

bovine tuberculosis, epidemiology, Mycobacterium bovis, reservoir

Citation	Pfeiffer, D.U. 2006. Communicating risk and uncertainty in relation to development and implementation of disease control policies. Veterinary Microbiology 112:259-264
Abstract Only	☐
No Abstract	☐
Article Type	Journal Article
Abstract	Scientific evidence is one of the key factors to be considered in the development of disease control policies. It is generated using investigations into cause–effect relationships, which usually produce results that are associated with a varying degree of uncertainty. Experience has shown that taking account of these uncertainties can become a formidable challenge for policy makers when devising the strategies and when communicating them to stakeholders. The situation has been further complicated by a reduction in public trust in scientific evidence. It is now recognised that this challenge cannot be managed by simply providing more information, but it is also necessary to consider the influence that variation in risk perception amongst stakeholders has on their response to and commitment towards the policies
Key Words	tuberculosis, perception, bias, cause-effect

Citation

Phillips, C. J. C., C.R.W. Foster, P.A. Morris, and R. Teverson. 2003. The transmission of Mycobacterium bovis infection to cattle. Research in Veterinary Science 74: 1-15.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The prevalence of Mycobacterium bovis infection in cattle is increasing rapidly in some countries, including the UK and Ireland. The organism infects a wide range of mammalian hosts, and eradication of the disease is difficult if there is an extensive reservoir in the wildlife population. Existing evidence suggests that wildlife vectors include the European badger in the UK and Ireland, the brush-tailed possum and ferret in New Zealand and ungulates in some other countries. Cattle grazing field boundaries or short swards are at particularly high risk, since the chance of contact with the intermediate host or their excreta is increased. There is evidence that the transmission of the disease between cattle following movement accounts for 10–15% of outbreaks in the British Isles and that transmission can occur across farm boundaries. The prevalence of single reactors in herds suggested that within-herd transmission was not common. In herds with infected cattle, spreading slurry is a risk factor, which can be minimised by prolonged storage of the slurry, by spreading it on fields not used for grazing or by soil injection. M. bovis also survives in water and may enter the respiratory tract during drinking. It is concluded that M. bovis infection in cattle can be transmitted by a number of routes, some of which can be controlled by appropriate husbandry, but that circumstantial evidence suggests that the existence of a widespread intermediate host is the greatest contributor to infection in cattle.

Key Words transmission, prevalence, British Isles, UK, Ireland, cattle

Citation

Pope, L. C., R. K. Butlin, G. J. Wilson, R. Woodroffe, K. Erven, C. M. Conyers, T. Franklin, R. J. Delahay, C. L. Cheeseman, and T. Burke. 2007. Genetic evidence that culling increases badger movement: implications for the spread of bovine tuberculosis. Molecular Ecology 16: 4919–4929.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The Eurasian badger (Meles meles) has been implicated in the transmission of bovine tuberculosis (TB, caused by Mycobacterium bovis) to cattle. However, evidence suggests that attempts to reduce the spread of TB among cattle in Britain by culling badgers have mixed effects. A large-scale field experiment (the randomized badger culling trial, RBCT) showed that widespread proactive badger culling reduced the incidence of TB in cattle within culled areas but that TB incidence increased in adjoining areas. Additionally, localized reactive badger culling increased the incidence of TB in cattle. It has been suggested that culling-induced perturbation of badger social structure may increase individual movements and elevate the risk of disease transmission between badgers and cattle. Field studies support this hypothesis, by demonstrating increases in badger group ranges and the prevalence of TB infection in badgers following culling. However, more evidence on the effect of culling on badger movements is needed in order to predict the epidemiological consequences of this control strategy. Here, analysis of the genetic signatures of badger populations in the RBCT revealed increased dispersal following culling. While standard tests provided evidence for greater dispersal after culling, a novel method indicated that this was due to medium- and long-distance dispersal, in addition to previously reported increases in home-range size. Our results also indicated that, on average, badgers infected with M. bovis moved significantly farther than did uninfected badgers. A disease control strategy that included culling would need to take account of the potentially negative epidemiological consequences of increased badger dispersal.

Key Words dispersal, genetic population structure, Meles meles, microsatellite, sex bias, spatial autocorrelation

Citation

Porphyre, T., M. A. Stevenson, and J. Mckenzie. 2008. Risk factors for bovine tuberculosis in New Zealand cattle farms and their relationship with possum control strategies. Preventive Veterinary Medicine 86:93-106.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

This paper reports the investigation of farm-level risk factors for confirmed bovine tuberculosis (TB), based on a retrospective cohort study of a population of cattle in the lower North Island of New Zealand. Data were obtained from the TB testing surveillance programme operational in this area since the mid-1970s and comprised 190,665 cattle-years at risk from July 1980 to June 2004 (inclusive). A mixed-effects Poisson regression model was used to investigate the influence of farm-level covariates on the number of cattle confirmed with TB throughout the study period. This model was interpreted in context of depopulation strategies for the wildlife reservoir for TB, the brushtail possum Trichosurus vulpecula, that were applied in this area. The model showed that, despite intensification of possum control strategies over time, proximity to forest parks (a principal possum habitat in this area) remained a significant predictor of the number of confirmed cases of TB detected per farm per year. Our analyses showed a significant, three-fold increase in TB risk in dairy cattle relative to beef conditional on the size of local possum habitat, and confirmed the positive influence of cattle population size and the presence of previous infection status as a determinant of the number of confirmed TB cases per farm per year.

Key Words Mycobacterium bovis, cattle farm, brushtail possum, epidemiology

Citation

Raizman, E.A., S.J. Wells, P.A.Jordan, G.D. DelGiudice, and R.R. Bey. 2005. Mycobacterium avium subsp. Paratuberculosis from free-ranging deer and rabbits surrounding Minnesota dairy herds. The Canadian Journal of Veterinary Research 69:32-38.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The objectives of this study were to estimate the prevalence of Mycobacterium avium subsp. paratuberculosis (MAP) among deer and rabbits surrounding infected and noninfected Minnesota dairy farms using fecal culture, and to describe the frequency that farm management practices were used that could potentially lead to transmission of infection between these species. Fecal samples from cows and the cow environment were collected from 108 Minnesota dairy herds, and fecal pellets from free-ranging white-tailed deer and eastern cottontail rabbits were collected from locations surrounding 114 farms; all samples were tested using bacterial culture. In addition, a questionnaire was administered to 114 herd owners. Sixty-two percent of the dairy herds had at least 1 positive fecal pool or environmental sample. A total of 218 rabbit samples were collected from 90% of the herds, and 309 deer samples were collected from 47% of the herds. On 2 (4%) of the farms sampled, 1 deer fecal sample was MAP positive. Both farms had samples from the cow fecal pool and cow environment that were positive by culture. On 2 (2%) other farms, 1 rabbit fecal sample was positive by culture to MAP, with one of these farms having positive cow fecal pools and cow environmental samples. Pasture was used on 79% of the study farms as a grazing area for cattle, mainly for dry cows (75%) and bred or prebred heifers (87%). Of the 114 farms, 88 (77%) provided access to drylot for their cattle, mainly for milking cows (77/88; 88%) and bred heifers (87%). Of all study farms, 90 (79%) used some solid manure broadcasting on their crop fields. Of all 114 farms, the estimated probability of daily physical contact between cattle manure and deer or rabbits was 20% and 25%, respectively. Possible contact between cattle manure and deer or rabbits was estimated to occur primarily from March through December. The frequency of pasture or drylot use and manure spreading on crop fields may be important risk factors for transmission of MAP among dairy cattle, deer, and rabbits. Although the MAP prevalence among rabbits and deer is low, their role as MAP reservoirs should be considered.

Key Words

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of MAP among dairy cattle, deer, and rabbits. Although the MAP prevalence among rabbits and deer is low, their role
as MAP reservoirs should be considered.
Bovine tuberculosis, Mycobacterium bovis, rabbits, white-tailed deer

Citation

Ramsey, D., N. Spencer, P. Caley, M. Efford, K. Hansen, M. Lam, and D. Cooper. 2002. The effects of reducing population density on contact rates between brushtail possums: implications for transmission of bovine tuberculosis. Journal of Applied Ecology 39:806–818.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. Interactions during mating are thought to be an important mechanism for transmission of tuberculosis (Tb) Mycobacterium bovis in the brushtail possum Trichosurus vulpecula. However, little information is available on the frequency of contacts between males and females in oestrus during the breeding season, and the relationship between mating contacts and population density.
2. We used radio-telemetry to record contacts between male and oestrous and nonoestrous female possums, and determined paternity of offspring using DNA analysis. This was repeated following the removal of c. 70% of the resident possums to determine the effect of reducing density on the contact rate.
3. We could not detect any significant differences in the contact rate between oestrous and non-oestrous females and males, either before or after the density reduction, even when paternity was positively identified from DNA analysis. This suggests that actual mating contacts could not be distinguished from other agonistic or affiliative contact behaviours.
4. Despite this, the relationships between male–female and male–male contact rates and population density were non-linear convex-up, implying that the contact rate during the breeding season did not decrease in proportion to reductions in density. This appeared to be driven by the enlargement of male ranges and a corresponding increase in male overlap of female ranges following the density reduction.
5.The form of the contact rate function will influence predictions of disease spread in epidemiological models for Tb in wildlife. This has major implications for the development of tactical approaches to disease management based on such models.

Key Words epidemiology, mating systems, Mycobacterium bovis, population density, Trichosurus vulpecula

Citation

Rhyan, J. C., D. A. Saari, E. S. Williams, M. W. Miller, A. J. Davis, and A. J. Wilson. 1992. Gross and microscopic lesions of naturally occurring tuberculosis in a captive herd of wapiti (Cervus elaphus nelsoni) in Colorado. Journal of Veterinary Diagnostic Investigations 4:428-433.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A Mycobacterium bovis-infected herd of captive wapiti (Cervus elaphus nelsoni) in Colorado was depopulated after lesions of bovine tuberculosis were confirmed in 8 of 10 tuberculin skin test reactors. Of the 43 animals > 1 year of age, 26 had gross lesions suggestive of tuberculosis, 24 had microscopic lesions of tuberculosis, and 23 had acid-fast bacilli associated with the lesions. Lungs and retropharyngeal lymph nodes were the most frequently affected sites. Most lesions grossly and microscopically resembled tuberculosis in cattle; however, some lesions resembled abscesses or ovine caseous lymphadenitis lesions. Special stains and immunohistochemical techniques labeled few to numerous mycobacteria associated with the lesions.

Key Words Elk, wapiti, Colorado, captive, Cervus elaphus nelsonii,

Citation Rhyan, J. C., and T. R. Spraker. 2010. Emergence of diseases from wildlife reservoirs. Veterinary Pathology 47(1):34-39.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Interest in the epidemiology of emerging diseases of humans and livestock as they relate to wildlife has increased greatly over the past several decades. Many factors, most anthropogenic, have facilitated the emergence of diseases from wildlife. Some livestock diseases have ‘‘spilled over’’ to wildlife and then ‘‘spilled back’’ to livestock. When a population is exposed to an infectious agent, depending on an interaction of factors involving the host, agent, and environment, the population may be resistant to infection or may become a dead-end host, a spillover host, or a maintenance host. Each exposure is unique; the same species of host and agent may respond differently in different situations. Management actions that affect the environment and behavior of a potential host animal may allow the emergence of a new or as yet undetected disease. There are many barriers in preventing, detecting, monitoring and managing wildlife diseases. These may include political and legal hurdles, lack of knowledge about many diseases of wildlife, the absence of basic data on wildlife populations, difficulties with surveillance, and logistical constraints. Increasing interaction between wildlife and humans or domestic animals may lead to disease emergence and require innovative methods and strategies for disease surveillance and management in wildlife.

Key Words emerging diseases, wildlife, wildlife reservoirs, zoonotic diseases, surveillance, disease management

Citation

Rhyan, J., K. Aune, B. Hood, R. Clarke, J. Payeur, J. Jamagin, and L. Stackhouse. 1995. Bovine Tuberculosis in a Free-ranging Mule Deer (Odocoileus hemionus) from Montana. Journal of Wildlife Diseases 31(3): 432-435.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A survey of 41 mule deer (Odocoileus hemionus) and three white-tailed deer (0. virginianus) for bovine tuberculosis was conducted on a Montana (USA) cattle ranch from 2 November 1993 through January 1994. Gross and microscopic lesions typical of tuberculosis were present in tonsil and lymph nodes of the head, thorax, and abdomen of one adult female mule deer. Additionally, a single microgranuloma considered morphologically suggestive of tuberculosis was present in one lymph node of the head of a second mule deer. Mycobacterial isolates from lymph nodes of the head and thorax of the first deer were identified as Mycobacterium bovis.

Key Words Mule deer, Odocoileus hemionus, tuberculosis, Mycobacterium bovis, game farm, pathology

Citation

Richomme, C., M.L. Boschiroli, J. Hars, F. Casbianca, and C. Ducrot. 2010. Bovine tuberculosis in livestock and wild boar on the Mediterranean Island, Corsica. Journal of Wildlife Diseases 46(2):627-631.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The zoonotic agent of bovine tuberculosis (bTB), Mycobacterium bovis, can be transmitted between domestic and wild animals, threatening wildlife populations and control programs for bTB in cattle. In Corsica, a French Mediterranean island where domestic and wild species have close interactions, bTB cases have been reported in cattle, pigs, and wild boar. Moreover, genotypes of M. bovis found in wild and domestic animals from the same area were identical. These data strongly suggest that wild and domestic animals are associated in an epidemiologic bTB-transmission cycle. More investigations are needed, not only to understand the role played by each species in order to implement appropriate control measures, but also to assess the risk of transmission to humans.

Key Words Bovine tuberculosis, Corsica, epidemiology, wild boar, zoonosis

Citation

Rodgers, J.D., N.L. Connery, J. McNair, M.D. Welsh, R.A. Skuce, D.G. Bryson, D.N. McMurray, and J.M. Pollock. 2007. Experimental exposure of cattle to a precise aerosolised challenge of Mycobacterium bovis: a novel model to study bovine tuberculosis. Tuberculosis 87:405-414.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Summary
Non-aerosol models of bovine tuberculosis are limited in reproducibility and relevance to natural cases seen in farmed animals. Therefore, there is a need for aerosol models of infection in cattle that can reproduce bovine tuberculosis as seen in natural cases of the disease.
This manuscript describes a cattle tuberculosis model based on the inhalation of a precisely defined dose of Mycobacterium bovis in aerosol form, and defines those sites of M. bovis deposition following aerosol inhalation. The dissemination of bacilli and the resultant pathological change following infection is also described. Cattle aged 4–5 months, were infected with approximately 104 colony forming units (CFU), using a Madison chamber that had been modified to deliver aerosols to calves. In Experiment 1, calves were examined for gross pathology at post mortem (PM) examination at 93 and 132 days postinfection (PI), respectively. In Experiment 2, pairs of calves were examined for gross pathology at PM examination at 1 day PI and 7 days PI, respectively. At PM examination, samples were taken for bacteriology. Retrospective counts showed that the calves inhaled between 3┐104 and 8┐104 CFU of M. bovis. I Experiment 1, pathology indicative of tuberculosis and detection of M. bovis by qualitative bacteriology was found throughout the lower respiratory tract (LRT). In Experiment 2, pathology was only observed in a single site of one calf at day 7 PI. Samples positive for M. bovis by bacteriology were predominantly in the LRT. The numbers of M. bovis CFU recovered and the distributions of positive sites were greater at day 7 PI than day 1 PI.
This study describes an aerosol exposure method that can deliver a defined dose of M. bovis almost exclusively to the LRT. The distribution of M. bovis and lesions indicative oftuberculosis suggests this aerosol method replicates the primary mode of tuberculosis transmission in cattle.

Key Words aerosol, bovine tuberculosis, Mycobacterium bovis, model

Citation

Rohonczy, E. B., A. V. Balachandran, T. W. Dukes, J. B. Payeur, J. C. Rhyan, D. A. Saari, T. L. Whiting, S. H. Wilson, J. L. Jarnagin. 1996. A comparison of gross pathology, histopathology, and mycobacterial culture for the diagnosis of tuberculosis in elk. Canadian Journal of Veterinary Research 60:108-114.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Using the isolation of Mycobacterium bovis as the reference standard, this study evaluated the sensitivity, specificity and kappa statistic of gross pathology (abattoir postmortem inspection), histopathology, and parallel or series combinations of the two for the diagnosis of tuberculosis in 430 elk and red deer. Two histopathology interpretations were evaluated: histopathology I, where the presence of lesions compatible with tuberculosis was considered positive, and histopathology II, where lesions compatible with tuberculosis or a select group of additional possible diagnoses were considered positive. In the 73 animals from which M. bovis was isolated, gross lesions of tuberculosis were most often in the lung (48), the retropharyngeal lymph nodes (36), the mesenteric lymph nodes (35), and the mediastinal lymph nodes (16). Other mycobacterial isolates included: 11 M. paratuberculosis, 11 M. avium, and 28 rapidly growing species or M. terrae complex. The sensitivity estimates of gross pathology and histopathology I were 93% (95% confidence limits [CL] 84,97%) and 88% [CL 77,94%], respectively, and the specificity of both was 89% [CL 85,92%]). The sensitivity and specificity of histopathology II were 89% (CL 79,95%) and 77% (CL 72,81%), respectively. The highest sensitivity estimates (93- 95% [CL 84,98%]) were obtained by interpreting gross pathology and histopathology in parallel (where an animal had to be positive on at least one of the two, to be classified as combination positive). The highest specificity estimates (94-95% [CL 91-97%]) were generated when the two tests were interpreted in series (an animal had to be positive on both tests to be classified as combination positive). The presence of gross or microscopic lesions showed moderate to good agreement with the isolation of M. bovis (Kappa = 65-69%). The results show that post-mortem inspection, histopathology and culture do not necessarily recognize the same infected animals and that the spectra of animals identified by the tests overlaps.

Key Words pathology, histopathology, elk, red deer

Citation

Rudolph, B. A., S. J. Riley, G. J. Hickling, B. J. Frawley, M. S. Garner, S. R. Winterstein. 2006. Regulating hunter baiting for white-tailed deer in Michigan: biological and social considerations. Wildlife Society Bulletin 34(2):314–321.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Eradication of bovine tuberculosis (TB) from free-ranging white-tailed deer (Odocoileus virginianus) requires mortality rates of infected deer exceed the rate of new infection. Efforts to reduce TB transmission in Michigan, USA, are based on 2 assumptions: 1) deer mortality may be increased through recreational hunting, and 2) encounter rates between infected and noninfected deer may be reduced by prohibiting baiting and supplemental feeding. Spatial correlation of TB-infected deer and supplemental feeding sites detected using aerial surveys validated a ban on artificial feeding in Michigan. Similar analysis could not be used to evaluate the effects of a baiting ban because bait distribution was unknown. Furthermore, a ban on deer baiting could confound attempts to increase deer mortality through reduced hunter participation or efficacy. We reviewed the process used to evaluate a strategy for regulating bait use by hunters. This review included an assessment of 5 factors: statewide spatial analysis of apparent TB prevalence, deer intraspecific interactions at bait sites, effects of bait on hunter harvest rates, impacts of disease presence and practice of eradication efforts on hunting participation in the infected area, and input from law enforcement personnel. Our analysis suggested that restricting baiting to a limited, consistent region incurred less biological risk than allowing bait to be used statewide and less political risk than a statewide ban.

Key Words

baiting, bovine tuberculosis, hunter participation, Michigan, Odocoileus virginianus, policy, risk analysis, white-tailed deer

Citation

Ryan, T. J., P.G. Livingstone, D.S.L. Ramsey, G.W. de Lisle, G. Nugent, D.M. Collins, and B.M. Buddle. 2006. Advances in understanding disease epidemiology and implications for control and eradication of tuberculosis in livestock: The experience from New Zealand. Veterninary Microbiology 112: 211-219.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A deteriorating tuberculosis problem in cattle and deer in New Zealand has been halted and then reversed over the last decade. Mycobacterium bovis infection in both wild and domestic animal populations has been controlled. This has been achieved by applying a multi-faceted science-based programme. Key features of this have been a comprehensive understanding of the epidemiology of tuberculosis in animals, confidence in sampling wild animal populations, effective application of diagnostic tests in cattle and deer, and the ability to map M. bovis genotypes.

Key Words Mycobacterium bovis, tuberculosis, cattle, farmed deer, wildlife, epidemiology, immunodiagnostics

Citation

Sangster, C., D. Bergeson, C. Lutze-Wallace, V. Crichton, and G. Wobeser. 2007. Feasibility of using coyotes (Canis latrans) as sentinels for bovine Mycobacteriosis (Mycobacterium bovis) infection in wild cervids in and around Riding Mountain National Park, Manitoba, Canada. Journal of Wildlife Diseases 43(3):432–438.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Elk (Cervus elaphus manitobensis) and white-tailed deer (Odocoileus virginianus) in the Riding Mountain National Park (RMNP) region of southwestern Manitoba have been identified as a likely wildlife reservoir of Mycobacterium bovis, the causative agent of bovine mycobacteriosis in livestock. The feasibility of using coyotes (Canis latrans) collected from trappers as a sentinel species was investigated. Retropharyngeal, mesenteric, and colonic lymph nodes and tonsils collected at necropsy from 82 coyotes were examined by bacterial culture, polymerase chain reaction (PCR), and acid-fast histopathology. Mycobacterium bovis was not identified in any animal by culture or PCR although Mycobacterium avium species were isolated. A single acid-fast organism was identified on histopathologic examination of one animal. Based on the methods used in this study, trapper-caught coyotes do not appear to be a sensitive sentinel species of M. bovis infection in cervids in and around RMNP.

Key Words

Bovine mycobacteriosis, Canis latrans, cervid, coyote, Mycobacterium bovis, Riding Mountain National Park, sentinel

Citation

Scantlebury, M., M. R. Hutchings, D. J. Allcroft, and S. Harris. 2004. Risk of disease from wildlife reservoirs: badgers, cattle, and bovine tuberculosis. Journal of Dairy Science 87:330–339.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Livestock face complex foraging options associated with optimizing nutrient intake while being able to avoid areas posing risk of parasites or disease. Areas of tall nutrient-rich swards around fecal deposits may be attractive for grazing, but might incur fitness costs from parasites. We use the example of dairy cattle and the risks of tuberculosis transmission posed to them by pastures contaminated with badger excreta to examine this trade-off. A risk may be posed either by aerosolized inhalation through investigation or by ingestion via grazing contaminated swards. We quantified the levels of investigation and grazing of 150 dairy cows at badger latrines (accumulations of feces and urine) and crossing points (urination-only sites). Grazing behavior was compared between strip-grazed and rotation-grazed fields. Strip grazing had fields subdivided for grazing periods of <24 h, whereas rotational grazing involved access to whole fields for 1 to 7 d each. A higher proportion of the herd investigated badger latrines than crossing points or controls. Cattle initially avoided swards around badger latrines but not around crossing points. Avoidance periods were shorter in strip- compared with rotation-grazing systems. In rotation-grazing management, latrines were avoided for longer times, but there were more investigative contacts than with strip-grazing management. If investigation is a major route of tuberculosis transmission, the risk to cattle is greatest in extensive rotation-grazing systems. However, if ingestion of fresh urine is the primary method of transmission, strip-grazing management may pose a greater threat. Farming systems affect the level and type of contact between livestock and wildlife excreta and thus the risks of disease.

Key Words bovine tuberculosis, dairy cow, lactation, nutrition

Citation

Schmitt, S. M., S. D. Fitzgerald, T. M. Cooley, C. S. Bruning-Fann, L. Sullivan, D. Berry, T. Carlson, R. B. Minnis, J. B. Payeur, and J. Sikarskie. 1997. Bovine tuberculosis in free-ranging white-tailed deer from Michigan. Journal of Wildlife Diseases 33(4):749-758.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

A 4.5 yr-old male white-tailed deer (Odocoileus virginianus) killed by a hunter during the 1994 firearm hunting season in northeastern Michigan (USA) had lesions suggestive of tuberculosis and was positive on culture for Mycobacterium bovis the causative agent for bovine tuberculosis. Subsequently, a survey of 354 hunter-harvested white-tailed deer for tuberculosis was conducted in this area from 15 November 1995 through 5 January 1996. Heads and/or lungs from deer were examined grossly and microscopically for lesions suggestive of bovine tuberculosis. Gross lesions suggestive of tuberculosis were seen in 15 deer. Tissues from 16 deer had acid-fast bacilli on histological examination and in 12 cases mycobacterial isolates from lymph nodes and/or lungs were identified as M. bovis. In addition, lymph nodes from 12 deer (11 females and 1 male) without gross or microscopic lesions were pooled into 1 sample from which M. bovis was cultured. Although more male (9) than female (3) deer had bovine tuberculosis infections, this difference was not statistically significant. Mycobacterium bovis culture positive deer ranged in age from 1.5 to 5.5 yr with a mean of 2.7 yr (median 2.5 yr) for males and 3.2 yr (median 3.5 yr) for females. This appears to be the first epidemic occurrence of M. bovis in free-ranging cervids in North America. A combination of environmental (high deer density and poor quality habit) and management-related factors (extensive supplemental feeding) may be responsible for this epizootic.

Key Words

Bovine tuberculosis, epidemic, Mycobacterium bovis, Odocoileus virginianus, pathology, white-tailed deer

Citation

Schmitt, S. M., D. J. O'Brien, C. S. Bruning-Fann, and S. D. Fitzgerald. 2002. Bovine tuberculosis in Michigan wildlife and livestock. New York Academy of Sciences 969:262-268.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Since 1994, the state of Michigan has recognized a problem with bovine tuberculosis (TB), caused by Mycobacterium bovis, in wild white-tailed deer from a 12-county area in northeastern Lower Michigan. A total of 65,000 free-ranging deer have been tested, and 340 have been found to be positive for M. bovis. The disease has been found in other wildlife species, and, in 1998, in domestic cattle, where to date 13 beef cattle and 2 dairy cattle herds have been diagnosed with bovine TB. Unfortunately, the situation is unique in that there have never been reports of self-sustaining bovine TB in a wild, free-ranging cervid population in North America. Scientists, biologists, epidemiologists, and veterinarians who have studied this situation have concluded that the most logical theory is that high deer densities and the focal concentration caused by baiting (the practice of hunting deer over feed) and feeding are the factors most likely responsible for the establishment of self-sustaining TB in free-ranging Michigan deer. Baiting and feeding have been banned since 1998 in counties where the disease has been found. In addition, the deer herd has been reduced by 50% in the endemic area with the use of unlimited antlerless permits. The measures of apparent TB prevalence have been decreased by half since 1997, providing hopeful preliminary evidence that eradication strategies are succeeding.

Key Words

bovine tuberculosis, Mycobacterium bovis, white-tailed deer

Citation

Schmitt, S., D. O'Brien, E. Carlson, D. Smith, Z. Cooley, B. Rudolph, G. Hickling, G. Nugent and P. Butchko. 2004. Evaluation of a new strategy for the control of bovine tuberculosis in Michigan white-tailed deer: Year 1 progress report. Report Prepared for: Wildlife Division, Michigan Department of Natural Resources.

Abstract Only ☐

No Abstract ☐

Article Type Report

Abstract

The State of Michigan is striving to eliminate bovine tuberculosis (Tb) infection among free-ranging white-tailed deer in the northeastern Lower Peninsula of the state. Aggressive reduction in the overall deer population abundance may help to further reduce TB prevalence, but this course of action is unacceptable to many hunters and landowners. Targeted culling of sick deer would likely be far more acceptable to these stakeholders, so in the winter of 2003 the Michigan Department of Natural Resources pilot-trialed a new strategy based on live-trapping and Tb-testing of wild deer. The field study was conducted in a township with relatively high TB prevalence within Deer Management Unit 452 in the northeastern Lower Peninsula.

Over a 2-month trapping period, 119 individual deer were live-trapped, blood sampled, fitted with a radio-collar, and released. A total of 31 of these deer were subsequently classified as Tb-suspect by at least one of five blood tests employed (however there was a low level of agreement among tests). A delay in testing meant that only six of these suspect deer were culled by sharpshooters before pre-programmed release of their radio-collars, after which they could no longer be located. Mycobacterium bovis was cultured from one of these six suspect deer; the other five were negative on culture.

All target deer were located to within shooting range with 1 - 2 days of effort, and all the radio-collars on the apparently-healthy deer dropped off after the intended 90-day interval, and were thereafter recovered for re-use.

There was considerable support for this pilot project among hunters, farmers, state and federal agriculture agencies, the media and the general public, and so we recommend that further field trials be undertaken using this technique. The initial focus of these trials should be on improving the efficacy and reliability of the blood testing procedure.

Key Words Michigan, control, white-tailed deer, lower peninsula

Citation

Serraino, A., G. Marchetti, V. Sanguinetti, M. C. Rossi, R. G. Zanoni, L. Catozzi, A. Bandera, W. Dini, W. Mignone, F. Franzetti, and A. Gori. 1999. Monitoring of transmission of tuberculosis between wild boars and cattle: genotypical analysis of strains by molecular epidemiology techniques. Journal of Clinical Microbiology 37(9):2766–2771.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

An epidemiological survey for the monitoring of bovine tuberculosis transmission was carried out in western Liguria, a region in northern Italy. Fifteen Mycobacterium bovis strains were isolated from 63 wild boar samples (62 from mandibular lymph nodes and 1 from a liver specimen). Sixteen mediastinal lymph nodes of 16 head of cattle were collected, and 15 Mycobacterium bovis strains were subsequently cultured. All M. bovis strains isolated from cattle and wild boars were genotyped by spoligotyping and by restriction fragment length polymorphism (RFLP) analysis with the IS6110 and IS1081 probes. All M. bovis strains showed the typical spoligotype characterized by the absence of the 39 to 43 spacers in comparison with the number in M. tuberculosis. A total of nine different clusters were identified by spoligotyping. The largest cluster included 9 strains isolated from wild boars and 11 strains isolated from cattle, thus confirming the possibility of transmission between the two animal species. Fingerprinting by RFLP analysis with the IS6110 probe showed an identical single-band pattern for 29 of 30 strains analyzed, and only 1 strain presented a five-band pattern. The use of IS1081 as a second probe was useful for differentiation of M. bovis from M. bovis BCG but not for differentiation among M. bovis strains, which presented the same undifferentiated genomic profile. In relation to the epidemiological investigation, we hypothesized that the feeding in pastures contaminated by cattle discharges could represent the most probable route of transmission of M. bovis between the two animal species. In conclusion, our results confirmed the higher discriminatory power of spoligotyping in relation to that of RFLP analysis for the differentiation of M. bovis genomic profiles. Our data showed the presence of a common M. bovis genotype in both cattle and wild boars, confirming the possible interspecies transmission of M. bovis.

Key Words transmission, wild boars, cattle, molecular epidemiology, survey, Liguria, Italy

Citation	Shaw, S. 2008. Public Health Implications of Surveillance Programs for Zoonotic Pathogens: A case study of Mycobacterium bovis in the state of Minnesota. MPH Thesis.
Abstract Only	☐
No Abstract	☑
Article Type	Thesis/Dissertation
Abstract	
Key Words	Public health, zoonotic, surveillance, case study, thesis

Citation

Sleeman, D. P., J. Davenport, S. J. More, T. A. Clegg, J. M. Griffin, and I. O'Boyle. 2009. The effectiveness of barriers to badger Meles meles immigration in the Irish Four Area project. European Journal of Wildlife Research 55:267–278.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

This study's objective was to estimate the permeability of barriers to badger immigration during the Irish Four Area project. These barriers were at the boundaries of removal areas, where there was proactive culling of badgers. Data from the last 3 years of the study were used. Each length of barrier was allocated a space within the removal area. These were further sub-divided into spaces of 0–2, 2–5 km and sometimes of more than 5 km from the edge of the removal area. It is assumed that all, or some, of the badgers caught within these spaces came across the barriers. The barriers were one of the following: external buffers, sea, rivers and political boundaries. The total lengths of the barriers in all areas were: external buffer 128.5 km; sea 70.9 km; river 78.6 km; political 32.2 km. We assume three scenarios: (1) all badgers caught in the final 3 years were immigrants, (2) 75% were immigrants or (3) 50% were immigrants. We test these scenarios using chi-square tests, applying internal buffers of 1 km to counter movements of badgers across zones. Using this approach and multivariate analysis, we found that the permeability of barrier types varied, with sea and external buffers being the most effective barriers. The combined capture data are further examined by the sex ratio in each range, and then the sex ratio in total. Equal numbers of males and females were found, but the source populations were probably predominantly female. If badger management options are to achieve maximum benefits, then the field effectiveness of such barriers needs to be understood.

Key Words tuberculosis spillover to cattle, removal study, dispersal movements, permeability-chi-square test

Citation Smith, G. C. 2001. Models of Mycobacterium bovis in wildlife and cattle. Tuberculosis 81(1/2): 51-64.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Following the first model of wildlife tuberculosis (in European badgers) there has been a spate of papers modelling wildlife TB. These have looked at population parameters and disease dynamics in the badger and possum. Recent papers in particular have looked at various methods of controlling the wildlife vector to reduce the incidence of TB in cattle. The author examines the role of modelling to show what insights it has given us, which issues have not been addressed, and where the shortfalls lie. Particular attention will be paid to a comparison between models of badgers and possums, and between simple and more complex models, and possible areas of future research will be revealed.

Key Words model, wildlife, European badgers, population parameters, disease dynamics, possum

Citation Smith, G. C. and C. L. Cheeseman. 2002. A mathematical model for the control of diseases in wildlife populations: culling, vaccination and fertility control. Ecological Modelling 150:45–53.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract Recent advances have permitted the red fox (Vulpes vulpes) to be vaccinated against rabies in order to control the European epidemic. Vaccination is also the preferred long-term strategy for controlling bovine tuberculosis Mycobacterium bovis) (TB) in the European badger (Meles meles) in England. We discuss a model to compare the efficacy of various disease control strategies, including temporary and permanent sterilisation. By using rabies and TB as examples of acute and chronic diseases, the model shows that lethal control can be more effective at disease eradication in an isolated population than vaccination. This is due to the birth of larger numbers of susceptible individuals during a vaccination campaign, which makes it harder to keep the population below the critical threshold density. This difference was very marked for the progressive disease of tuberculosis. The inclusion of an abortifacient increased the chances of disease control to levels close to that of lethal control. If the abortifacient is replaced by a permanent contraceptive then the chances of disease eradication and population extinction were very similar to that of lethal control, since the birth of susceptibles is now much reduced. These results are also of relevance in the control of wildlife diseases in threatened populations or species.

Key Words fox, rabies, badger, bovine TB, disease control, vaccination

Citation

Smith, G.C., C.L. Cheeseman, D. Wilkinson, R.S. Clifton-Hadley. 2001. A model of bovine tuberculosis in the badger Meles meles: the inclusion of cattle and the use of a live test. Journal of Applied Ecology 38(3):520-535.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Summary
1. An individual-based stochastic simulation model was used to investigate the control of bovine tuberculosis (TB) in the European badger Meles meles by using a live test to determine the presence of infection. The model was an extension of earlier models, and nearly all population and epidemiological parameters were derived from one study site.
2. This is the first TB model to examine sex differences in disease epidemiology, and the transmission of TB from badgers to cattle. The latter is an essential step if reactive badger control strategies are to be modelled.
3. Heterogeneity was introduced to the simulation model by the use of a carrying capacity, which defined the maximum number of breeding females per social group.
4. The prevalence of TB, and the number of simulated cattle herd breakdowns, was reduced for all control strategies using a live test, namely localised culling, ring culling and proactive culling. However, only proactive culling resulted in a marked reduction in these values within a few years.
5. If trapping efficacy was increased above its current value (80%), this did not improve the effectiveness of these culling strategies.
6. If the number of individual badgers caught and tested per social group was doubled from two to four animals per group, then the overall level of effectiveness of these strategies could be doubled.
7. The effectiveness could be improved if the sensitivity of the live test was increased, but did not continue to show an improvement above a sensitivity of about 70%.
8. Given the constraints of the current live test sensitivity (41%) and a trapping efficacy of 80%, proactive culling, following the testing of four individuals per group, led to an average of three cattle herd breakdowns per year in the simulation, compared with an average of 31 per year when simulating the live test trial as used between 1994 and 1996.

Key Words control, individual-based model, TB, wildlife disease

Citation

Smith, G.C., C.L. Cheeseman, R.S. Clifton-Hadley, and D. Wilkinson. 2001. A model of bovine tuberculosis in the badger Meles meles: an evaluation of control strategies. Journal of Applied Ecology 38(3):509-519.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Summary
1. An individual-based stochastic simulation model was used to investigate the control of bovine tuberculosis (TB) in the European badger Meles meles. Nearly all population and epidemiological parameters were derived from one study site, and the transmission of TB from badgers to cattle was included. The latter is an essential step if reactive badger control strategies are to be modelled.
2. The model appeared to underestimate slightly the rate of population recovery following widespread culling. This may have been due to simulating an isolated population with no immigration and no compensatory increase in fecundity. This should not affect the relative efficacy of each control strategy, but does require further investigation.
3. Of the historical methods of badger control, gassing and the 'clean ring' strategies were the most effective at reducing disease prevalence in the badger and cattle herd breakdown rates. These results agree with those of earlier models.
4. The proactive badger removal operation as part of the current field trial should cause a dramatic decrease in the number of cattle herd breakdowns, but also has the greatest effect on the badger population size.
5. The proactive use of a live test to detect TB, followed by vaccination, appears to reduce substantially cattle herd breakdowns and disease prevalence in the badger.
6. Three combined control strategies gave the best initial reduction in cattle herd breakdown rate and disease prevalence in the badger: (i) a proactive cull followed by reactive test and cull; (ii) a continued vaccination and proactive test and cull; and (iii) a continuous proactive test and cull.
7. The results of simulation models suggest that badger vaccination is a very good method of TB control. This is at odds with simple models and requires further investigation.

Key Words cattle, individual-based model, TB, wildlife disease

Citation State Commiftee on Bovine TB in Wild Deer. 1997. Recommendations for Elimination of Bovine Tuberculosis in Free-ranging White-tailed Deer in Michigan.Department of Fisheries and Wildife, Michigan State University, East Lansing, Michigan.

Abstract Only ☐

No Abstract ☑

Article Type Report

Abstract

Key Words

Citation State of Michigan. 2000. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report. 42 pp.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract

Key Words Bovine tuberculosis, Michigan, Mycobacterium, surveillance, white-tailed deer

Citation State of Michigan. 2003. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report. 40 pp.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract

Key Words Bovine tuberculosis, Michigan, Mycobacterium bovis, Odocoileus virginianus, surveillance, white-tailed deer

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Citation State of Michigan. 2005. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report. 31 pp.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract

Key Words Bovine tuberculosis, Michigan, Mycobacterium, surveillance, white-tailed deer

Citation State of Michigan. 2007. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report. 31 pp.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract

Key Words Bovine tuberculosis, Michigan, Mycobacterium, surveillance, white-tailed deer

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Citation State of Michigan. 2008. Proceedings of the Michigan Bovine Tuberculosis Eradication Project Activities Report. 36 pp.

Abstract Only ☐

No Abstract ☑

Article Type Proceedings

Abstract

Key Words Bovine tuberculosis, Michigan, Mycobacterium, surveillance, white-tailed deer

Citation

Stronen, A. V., R. K. Brook, P. C. Paquet, S. Mclachlan. 2007. Farmer attitudes toward wolves: implications for the role of predators in managing disease. Biological Conservation 135:1-10.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The potential for disease transmission between wild and domestic animals may interfere with wildlife and habitat conservation on lands surrounding protected areas. Recently, possible transmission of bovine tuberculosis (Mycobacterium bovis) from wild ungulates to domestic livestock has affected the Riding Mountain National Park region in Manitoba, Canada. Wolf (Canis lupus) predation on ungulate populations may help lessen the risk of disease transmission to livestock. We conducted an exploratory analysis of causal factors associated with farmer attitudes toward observing wolves on their farms. A survey to 4220 farms within 50 km of the Park resulted in an adjusted response rate of 25%. We constructed several logistic regression models with factors hypothesized to influence whether farmers agreed with the statement ‘‘I enjoy seeing wolves on my land’’, and three candidate models received reasonable support. Factors most affecting attitudes were, in order of importance, perceived wolf population size, frequency of seeing wolves, perceived seriousness of wolf damage, distance to Park boundary and number of beef cattle (Bos taurus) owned. The factors least influential on attitudes were education and age. Concern over bovine tuberculosis in wild elk also had minimal influence. Of respondents who perceived the wolf population as ‘‘too high’’, 60% were extremely concerned about bovine tuberculosis in wild elk. Although the role of wolf predation as a potential natural regulator of disease in wild ungulates might not be widely recognized in many areas, we believe this provides a unique opportunity to re-examine the significance of maintaining viable wolf populations.

Key Words

bovine tuberculosis, Canis lupus, Cervus elaphus manitobensis, elk, logistic regression, Mycobacterium bovis, transboundary

Citation

Swinton, J., F. Tuyttens, D. Macdonald, D. J. Nokes, C. L. Cheeseman, and R. Clifton-Hadley. 1997. A comparison of fertility control and lethal control of bovine tuberculosis in badgers: the impact of perturbation induced transmission. Philosophical Transactions of the Royal Society B 352: 619-631.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In this paper we use mathematical modelling to consider the broad advantages and disadvantages of fertility control over lethal control for bovine tuberculosis in badger populations. We use a deliberately simple model, attempting to capture only the key transmission processes. The model is parametrized with reference to the long-term Woodchester Park study. Estimates of mortality rate from this study suggest no significant extra mortality risk for animals with evidence of infection as indicated by the presence of anti-Mycobacterium bovis antibodies or M. bovis isolation. We find that large reductions in prevalence are sometimes the consequence of only moderate reductions in population numbers. If we assume that the act of control does not in itself affect transmission rates, then as far as eradication is concerned, both fertility control and mortality control operate through the same epidemiological mechanism, the removal of susceptibles: if one is in principle capable of keeping a population low enough to be infection free then so is the other. It is necessary to continue either form of control at regular intervals to maintain a constant level of infection in the long term. If control were to be stopped, return to precontrol levels of badger population and infection prevalence would be expected within a few years. Fertility control is less effective in reducing population density than lethal control since it can only act, at maximum, to remove one age cohort per year. It is also less effective in reducing transmission as it can only ever remove susceptibles, while lethal control also removes infectious badgers. However, if the social disturbance caused by lethal control does in fact increase contact rates for the remaining infectious badgers, the relative efficacies of the two strategies become a great deal less clear. While we have no quantitative data on the extent to which social perturbation does act to promote transmission, model simulations show that it is possible to develop plausible scenarios in which the lethal control may actually act to increase the absolute numbers of animals infected, while reducing the number of uninfected animals to very low numbers.

Key Words fertility control, lethal control, badgers, induced transmission

Citation Tessaro, S. V. 1986. The existing and potential importance of brucellosis and tuberculosis in Canadian wildlife: a review. The Canadian Veterinary Journal 27: 119-124.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract As the campaign to eradicate bovine brucellosis (Brucella abortus) and tuberculosis (Mycobacterium bovis) in Canadian livestock nears completion, the importance of extraneous sources of these diseases increases. This review summarizes the literature on brucellosis and tuberculosis in Canadian wildlife species to determine existing and potential hosts. Canadian caribou (Rangifer tarandus) are reservoirs of Brucella suis biotype 4 which is pathogenic in caribou, humans and muskoxen but reportedly nonpathogenic in livestock. Bison (Bison bison) and elk (Cervus canadensis) are significant reservoirs of B abortus and M. bovis. The bison in and around Wood Buffalo National Park have both diseases and are the only wildlife reservoir in Canada. Free-ranging elk are important reservoirs of brucellosis in Wyoming, and captive elk initiated the recent outbreak of bovine tuberculosis in 20 American states which has also involved bison and cattle herds. If bison and elk ranching continues to develop in Canada, the industry will have to be monitored to prevent the introduction and spread of infectious diseases like brucellosis and tuberculosis. This requires the evaluation and/or development of effective diagnostic methods for use in these animals.

Key Words wildlife, brucellosis, tuberculosis, Canada, disease control

Citation

Thoen, C. O., P. A. LoBue, D. A. Enarson, J. B. Kaneene, and I. N. de Kantor. 2009. Tuberculosis: a re-emerging disease in animals and humans. Veterinaria Italiana 45(1): 135-181.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Tuberculosis continues to be an important disease both in humans and animals. It causes morbidity, mortality and economic loss worldwide. The occurrence of Mycobacterium bovis disease in humans, domesticated and wild animals confirms the relevance of this zoonosis. M. bovis in humans continues to be reported in industrialised countries and in immigrants from regions of the world where tuberculosis in cattle is endemic. The real incidence of M. bovis in humans in developing countries continues to be roughly underestimated due to the scarcity of appropriate laboratory facilities to isolate and to differentiate M. bovis strains. In Latin America, less than 1% of tuberculosis cases are reported as being due to M. bovis. However, the economic relevance that meat and dairy industries play in these countries stimulates the promotion of bovine tuberculosis eradication programmes. Human-to-human airborne transmission of M. bovis does occcur and it may be important where human immunodeficiency virus (HIV) infection in humans is prevalent, M. bovis infection in cattle is enzootic and pasteurisation of dairy products is not routinely practised. Eradication of M. bovis in cattle and pasteurisation of dairy products are the cornerstones of prevention of human disease. Measures should be developed to identify and control M. bovis infection in wild animals as these may be important reservoirs of infection for domesticated food-producing animals. There is a need for medical and veterinary professionals to cooperate on disease outbreaks. The information presented herin strongly supports the 'One World/ One Health/ One Medicine' concept.

Key Words health, Mycobacterium bovis, Mycobacterium tuberculosis, One health, public health, tuberculosis

Citation Thoen, C. O., W. J. Quinn, L. D. Miller, L. L. Stackhouse, B. F. Newcomb, J. M. Ferrell. 1992. Mycobacterium bovis infection in North American elk (Cervus elaphus) 4:423-427.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract A naturally occurring outbreak of Mycobacterium bovid infection in captive wild elk (wapiti) in Montana was confirmed by mycobacteriologic examination. Twenty-eight of 143 elk responded to M. bovis purified protein derivative (PPD) tuberculin injected intradermally in the cervical region (SCT). The results of comparative cervical tuberculin skin tests conducted within 9 days of SCT revealed greater responses to M. bovis PPD tuberculin than to M. avium PPD tuberculin in 23 of 28 elk responding. At necropsy, several grossly visible tuberculous lesions were observed in the parenchyma of the lung, thoracic lymph nodes, and submandibular lymph nodes. Microscopic examination of appropriately stained tissue sections revealed the presence of granulomatous lesions containing acid-fast bacilli. An enzyme-linked immunosorbent assay (ELISA) was developed using a sarkosyl extract of M. bovis (antigen) and peroxidase-labeled protein G (conjugate); reactions were detected in the sera of 8 of 9 elk responding to M. bovis PPD tuberculin. Lymphocyte blastogenic assay responses were detected using M. bovis antigens in 7 of 9 elk positive on skin tests using M. bovis PPD.

Key Words Elk, Cervus elaphus, naturally occurring, Montana

Citation Thorpe,L.E., T.R. Frieden, K.F. Laserson, C.Wells, G.R. Khatri. 2004. Seasonality of tuberculosis in India: is it real and what does it tell us? The Lancet 364:1613-1614.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract India has a third of the world's tuberculosis cases. Large-scale expansion of a national programme in 1998 has allowed for population-based analyses of data from tuberculosis registries. We assessed seasonal trends using quarterly reports from districts with stable tuberculosis control programmes (population 115 million). In northern India, tuberculosis diagnoses peaked between April and June, and reached a nadir between October and December, whereas no seasonality was reported in the south. Overall, rates of new smear-positive tuberculosis cases were 57 per 100 000 population in peak seasons versus 46 per 100 000 in trough seasons. General health-seeking behaviour artifact was ruled out. Seasonality was highest in paediatric cases, suggesting variation in recent transmission.

Key Words India, tuberculosis, surveillance

Citation

Tolhurst, B. A., R. J. Delahay, N. J. Walker, A. I. Ward, T. J. Roper. 2009. Behaviour of badgers (Meles meles) in farm buildings: opportunities for the transmission of Mycobacterium bovis to cattle? Applied Animal Behaviour Science 117:103–113.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Eurasian badgers (Meles meles) are implicated in the transmission of bovine tuberculosis (Mycobacterium bovis) to cattle. Here we investigate potential spatio-temporal foci of opportunities for contact between badgers and cattle in farm buildings. We discuss the relative occurrence of different badger behaviours and their potential for facilitating disease transmission, and examine correlates of building use by badgers including availability of specific farm-based resources, badger demography, and environmental variables. In addition, we investigate seasonal variation in home range structure with respect to farm building use. Badger activity and ranging behaviour were monitored intensively on six cattle farms throughout the year between July 2003 and June 2005 using remote surveillance, radio-tracking and faecal analysis. Badgers foraged in buildings, exhibited close, investigative 'nose-to-nose' contact with housed cattle and excreted/scent marked on and around feed. A negative correlation was observed between frequency of visits and 24 h rainfall and a positive correlation with minimum temperature. Badgers visited feed stores most intensively and selected cattle 'cake' over other available food types. A peak in visits was detected in spring and summer, and male badgers were more likely to visit buildings than females. Management prescriptions for disease prevention centre on reducing opportunities for direct or indirect contact between badgers and housed cattle. It is thus recommended that effort to exclude badgers from buildings should focus on feed stores and cattle housing during spring and summer in warm, dry weather.

Key Words badger, farm buildings, foraging behaviour, ranging behaviour, bovine tuberculosis, disease transmission

Citation

Tompkins, D. M., D. S. L. Ramsey, M. L. Cross, F. E. Aldwell, G. W. de Lisle and B. M. Buddle. 2009. Oral vaccination reduces the incidence of tuberculosis in free-living Brushtail Possums. Proceedings of the Royal Society B 276:2987-2995.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (Tb) caused by Mycobacterium bovis has proved refractory to eradication from domestic livestock in countries with wildlife disease reservoirs. Vaccination of wild hosts offers a way of controlling Tb in livestock without wildlife culling. This study was conducted in a Tb-endemic region of New Zealand, where the introduced Australian brushtail possum (Trichosurus vulpecula) is the main wildlife reservoir of Tb. Possums were trapped and vaccinated using a prototype oraldelivery system to deliver the Tb vaccine bacille Calmette–Guerin. Vaccinated and control possums were matched according to age, sex and location, re-trapped bimonthly and assessed for Tb status by palpation and lesion aspiration; the site was depopulated after 2 years and post-mortem examinations were conducted to further identify clinical Tb cases and subclinical infection. Significantly fewer culture-confirmed Tb cases were recorded in vaccinated possums (1/51) compared with control animals (12/71); the transition probability from susceptible to infected was significantly reduced in both males and females by vaccination. Vaccine efficacy was estimated at 95 per cent (87–100%) for females and 96 per cent (82–99%) for males. Hence, this trial demonstrates that orally delivered live bacterial vaccines can significantly protect wildlife against natural disease exposure, indicating that wildlife vaccination, along with existing control methods, could be used to eradicate Tb from domestic animals.

Key Words bovine tuberculosis, oral vaccine, possum, wildlife, BCG, badger

Citation

Tuyttens, F. A. M. and D. W. MacDonald. 1998. Sterilization as an alternative strategy to control wildlife diseases: bovine tuberculosis in European badgers as a case study. Biodiversity and Conservation 7:705-723.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Sterilization has rarely been considered as an alternative to culling or vaccination to control wildlife diseases. Disease control by sterilization, as by culling, has most promise when the host's ability for compensatory growth following the removal of density-dependent inhibitions is limited, and when moderate reductions in population density cause disproportionately large reductions in disease prevalence, or even eliminate the disease. For many host/disease examples this will not be the case and vaccination may have overwhelming advantages or may be the only practical option. The impact of sterilization on host density and disease prevalence will develop relatively slowly because sterilization can prevent the recruitment of only one age-cohort at a time. Moreover, unless there is vertical transmission, this age-cohort will consist only of susceptibles. Culling, on the contrary, removes infected as well as susceptible animals. However, for certain disease/host examples, the relative effectiveness of the dierent control strategies may be altered considerably if their variable effects on the probability of disease transmission are taken into account. Social perturbation or stress could render certain culling strategies ineective or even counter-productive. Depending on how disease dynamics are infuenced by the host's age-structure and reproductive investment, fertility control could offer epidemiological advantages that have been ignored by most disease/host models. We illustrate someof these principles by investigating the theoretical and practical feasibility of an hypothetical sterilization campaign to control bovine tuberculosis in badgers (and hence cattle) in Britain.

Key Words Meles meles, Mycobacterium bovis, fertility control, wildlife disease, population control

Citation Tweddle, N. E., and P. Livingstone. 1994. Bovine tuberculosis control and eradication programs in Australia and New Zealand. Veterinary Microbiology 40:23-39.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract This paper reviews the current and future programs for control of bovine tuberculosis in Australia and New Zealand. The paper highlights the similarities between the approach taken in these countries and compares and contrasts the strengths and weaknesses of these campaigns. The successful Australian campaign was based on a sound technical program, with good cattle control and strong industry support. In contrast, the presence of a significant wildlife reservoir (brushtail possum) of Mycobacterium bovis in New Zealand has hindered the eradication of bovine tuberculosis.

Key Words Mycobacterium bovis, Cattle, tuberculosis, bovine, eradication, control

Citation

VerCauteren, K. C., T. C. Atwood, T. J. DeLiberto, H. J. Smith, J. S. Stevenson, B. V. Thomsen, T. Gidlewski, and J. Payeur. 2008. Sentinel-based surveillance of coyotes to detect bovine tuberculosis, Michigan. Emerging Infectious Diseases 14(12):1862-1868.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (TB) is endemic in white-tailed deer (Odocoileus virginianus) in the northeastern portion of Michigan's Lower Peninsula. Bovine TB in deer and cattle has created immense fi nancial consequences for the livestock
industry and hunting public. Surveillance identified coyotes (Canis latrans) as potential bio-accumulators of Mycobacterium bovis, a fi nding that generated interest in their potential to serve as sentinels for monitoring disease risk. We sampled 175 coyotes in the bovine TB–endemic area. Fifty-eight tested positive, and infection prevalence by county ranged from 19% to 52% (statistical mean 33%, SE 0.07). By contrast, prevalence in deer (n = 3,817) was lower (i.e., 1.49%; Mann-Whitney U4,4 = 14, p<0.001). By focusing on coyotes rather than deer, we sampled 97% fewer individuals and increased the likelihood of detecting M. bovis by 40%. As a result of reduced sampling intensity, sentinel coyote surveys have the potential to be practical indicators of M. bovis presence in wildlife and livestock.

Key Words coyotes, surveillance, white-tailed deer, Michigan

Citation Vicente, J., U. Hofle, I. G. Fernandez de Mera, and C. Gortazar. 2007. The importance of parasite life history and host density in predicting the impact of infections in red deer. Oecologia 152:655–664.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract We studied a macroparasite (Elaphostrongylus cervi, Nematoda) and a microparasite infection (tuberculosis, TB) in red deer (Cervus elaphus) across diVerent populations where managers manipulated host condition, density and aggregation by providing supplemental food. We aimed to test whether and, if so, how persistence and transmission of both parasites diVerentially varied as host body condition and population density varied. We took account of sex, as red deer life history greatly concerns sex-related traits. Changes in host factors had diVerent consequences for the spread of each parasite type. Individual presence of tuberculosis was positively associated with host density, whereas E. cervi abundance negatively related to host density and enhanced body condition. There was lack of body condition density dependence; and body condition was mainly dependent on the amount of supplemental food provided, but also on habitat quality descriptors. Overall, our results suggest that body condition was improved at the cost of increased host contact rates, which implied an ecological trade-offbetween acquiring resources to cope with E. cervi, a macroparasite, and concurrent exposure to mycobacteria. By the simultaneous study of both infections, this research suggests that the eVects of changes in host number and population structure on disease spread and persistence need to take into account variation in life histories of the parasites. These Wndings also raise concern about the ecological consequences of diseases and management of wildlife on host life history.

Key Words life history , trade-off, sex-related, differences, tuberculosis, wildlife disease

Citation

Vicente, J., U. Hofle, J. M. Garrido, I. G. Fernandes de Mera, R. Juste, M. Barral, and C. Gortazar. 2006. Wild boar and red deer display high prevalences of tuberculosis-like lesions in Spain. Veterinary Research 37:107–119.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

We describe the distribution of tuberculosis-like lesions (TBL) in wild boar (Sus scrofa) and red deer (Cervus elaphus) in Spain. Animals with TBL were confirmed in 84.21% of mixed populations (n = 57) of red deer and wild boar and in 75% of populations of wild boar alone (n = 8) in central and southern Spain (core area). The prevalence of TBL declined towards the periphery of this region. In the core area, the prevalence ranged up to 100% in local populations of wild boar (mean estate prevalence 42.51%) and up to 50% in red deer (mean estate prevalence 13.70%). We carried out exploratory statistical analyses to describe the epidemiology of TBL in both species throughout the core area. Prevalence of TBL increased with age in both species. Wild boar and red deer mean TBL prevalence at the estate level were positively associated, and lesion scores were consistently higher in wild boars than in red deer. The wild boar prevalence of TBL in wild boar did not differ between populations that were or were not cohabiting with red deer. Amongst the wild boars with TBL, 61.19% presented generalized lesions, and the proportion of generalized cases was similar between sex and age classes. In red deer, 57.14% of TBL-positive individuals presented generalized lesions, and the percentage of generalized cases increased with age class, but did not differ between the sexes. These results highlight the potential importance of wild boar and red deer in the maintenance of tuberculosis in south central Spain.

Key Words Mycobacterium tuberculosis complex, tuberculosis-like lesions, red deer, Spain, wild boar

Citation

Vicente, J., U. Hofle, J. M. Garrido, I. G. Fernandez de Mera, P. Acevedo, R. Juste, M. Barral, C. Gortazar. 2007. Risk factors associated with the prevalence of tuberculosis-like lesions in fenced wild boar and red deer in south central Spain. Veterinary Research 38:451–464.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In recent decades the management of large game mammals has become increasingly intensive in south central Spain (SCS), resulting in complex epidemiological scenarios for disease maintenance, and has probably impeded schemes to eradicate tuberculosis (TB) in domestic livestock. We conducted an analysis of risk factors which investigated associations between the pattern of tuberculosis-like lesions (TBL) in wild boar (Sus scrofa) and red deer (Cervus elaphus) across 19 hunting estates from SCS and an extensive set of variables related to game management, land use and habitat structure. The aggregation of wild boar at artificial watering sites was significantly associated with an increasing risk of detecting TBL in both species, which probably relates to enhanced opportunities for transmission. Aggregation of wild boar at feeding sites was also associated with increased risks of TBL in red deer. Hardwood Quercus spp. forest availability was marginally associated with an increased risk of TB in both species, whereas scrubland cover was associated with a reduced individual risk of TBL in the wild boar. It is concluded that management practices that encourage the aggregation of hosts, and some characteristics of Mediterranean habitats could increase the frequency and probability of both direct and indirect transmission of TB. These findings are of concern for both veterinary and public health authorities, and reveal tuberculosis itself as a potential limiting factor for the development and sustainability of such intensive game management systems in Spanish Mediterranean habitats.

Key Words Mycobacterium tuberculosis complex, red deer, risk factors, tuberculosis, wild boar

Citation

Vidal, D., V. Naranjo, R. Mateo, C. Gortazar, J. de la Fuente. 2006. Analysis of serum biochemical parameters in relation to Mycobacterium bovis infection of European wild boars (Sus scrofa) in Spain. European Journal of Wildlife Research 52: 301–304.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bTB) caused by Mycobacterium bovis (Mycobacterium tuberculosis complex) is a zoonotic disease that affects cattle and wildlife worldwide. European wild boar (Sus scrofa) is a major reservoir host of M. bovis in south-central Spain. The identification of biomarkers to predict bTB in wild boars by dependable methods that do not require killing the host would greatly contribute to the implementation of effective control programs for bTB in this region. In this study, we have characterized serum biochemical values in European wild boars in Spain to determine whether biochemical parameters in the serum varied significantly with the presence of bTB in this species. Although apolipoprotein A1 and IgG levels were higher in uninfected boars, the results did not support good predictive value for serum biochemical parameters studied for European wild boars in relation to bTB in Spain.

Key Words tuberculosis, Mycobacterium tuberculosis complex, Apolipoprotein A1

Citation

Wahlstrom, H. 2004. Bovine tuberculosis in Swedish farmed deer: detection and control of the disease. Dissertation. Swedish University of Agricultural Science, Uppsala, Sweden.

Abstract Only ☐

No Abstract ☐

Article Type Thesis/Dissertation

Abstract

Bovine tuberculosis (BTB) was introduced into Swedish farmed deer herds in 1987. Epidemiological investigations showed that 10 deer herds had become infected (July 1994) and a common source of infection, a consignment of 168 imported farmed fallow deer, was identified (I).
As trace-back of all imported and in-contact deer was not possible, a control program, based on tuberculin testing, was implemented in July 1994. As Sweden has been free from BTB since 1958, few practising veterinarians had experience in tuberculin testing. In this test, result relies on the skill, experience and conscientiousness of the testing veterinarian.
Deficiencies in performing the test may adversely affect the test results and thereby compromise a control program.
Quality indicators may identify possible deficiencies in testing procedures. For that purpose, reference values for measured skin fold thickness (prior to injection of the tuberculin) were established (II) suggested to be used mainly by less experienced veterinarians to identify unexpected measurements. Furthermore, the within-veterinarian variation of the measured skin fold thickness was estimated by fitting general linear models to data (skin fold measurements) (III). The mean square error was used as an estimator of the within-veterinarian variation. Using this method, four (6%) veterinarians were considered to have unexpectedly large variation in measurements.
In certain large extensive deer farms, where mustering of all animals was difficult, meat inspection was suggested as an alternative to tuberculin testing. The efficiency of such a control was estimated in paper IV and V. A Reed Frost model was fitted to data from seven BTB-infected deer herds and the spread of infection was estimated (< 0.6 effective contacts
per deer and year) (IV). These results were used to model the efficiency of meat inspection in an average extensive Swedish deer herd. Given a 20% annual slaughter and meat inspection, the model predicted that BTB would be either detected or eliminated in most herds (90%) 15 years after introduction of one infected deer. In 2003, an alternative control
for BTB in extensive Swedish deer herds, based on the results of paper V, was implemented.

Key Words

cervidae transmission, modelling, intra-observer variability, tuberculin test, reference intervals, meat inspection, Sweden, epidemiological investigation, surveillance

Citation

Wahlstrom, H., L. Englund, T. Carpenter, U. Emanuelson, A. Engvall, I. Vagsholm. 1998. A Reed-Frost model of the spread of tuberculosis within seven Swedish extensive farmed fallow deer herds. Preventive Veterinary Medicine 35:181-193.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The within-herd transmission of tuberculosis, after introduction of infection, was evaluated in seven Swedish herds of farmed fallow deer. The evaluation was based on a subset of data obtained from a previous epidemiological investigation, comprising 13 tuberculosis-infected deer herds, with the purpose of tracing the source of infection. A computer spreadsheet model based on the Reed- Frost method was developed to estimate the number of new infections. For each herd, a k-value (the number of effective contacts made by an individual during a time period) was estimated through fitting the model to the observed incidence in each herd. We concluded that, despite the relatively short observation periods and uncertain tuberculosis incidence estimates for the observed herds, the k's obtained could be used to quantify the estimated spread of tuberculosis in extensive deer herds in Sweden.

Key Words deer, Mycobacterium bovis, tuberculosis, modelling, transmission, zoonoses

Citation

Ward, A. I., G. C. Smith, T. R. Etherington, and R. J. Delahay. 2009. Estimating the risk of cattle exposure to tuberculosis posed by wild deer relative to badgers in England and Wales. Journal of Wildlife Diseases 45(4):1104–1120.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Wild deer populations in Great Britain are expanding in range and probably in numbers, and relatively high prevalence of bovine tuberculosis (bTB, caused by infection with Mycobacterium bovis) in deer occurs locally in parts of southwest England. To evaluate the M. bovis exposure risk posed to cattle by wild deer relative to badgers in England and Wales, we constructed and parameterized a quantitative risk model with the use of information from the literature (on deer densities, activity patterns, bTB epidemiology, and pathology) and contemporary data on deer, cattle, and badger (Meles meles) distribution and abundance. The median relative risk score for each of the four deer species studied—red (Cervus elaphus), fallow (Dama dama), and roe (Capreolus capreolus) deer, and muntjac (Muntiacus reevesi)—was lower than unity (the relative risk set for badgers, the putative main wildlife reservoir of M. bovis in England and Wales). However, the 95th percentiles associated with risk estimates were large, and the upper limits for all four deer species exceeded unity. Although M. bovis exposure risks to cattle from deer at pasture are likely to be lower than those from badgers across most areas of England and Wales where cattle are affected by bTB because these areas coincide with high-density badger populations but not high-density deer populations, we predict the presence of localized areas where relative risks posed by deer may be considerable. Moreover, wherever deer are infected, risks to cattle may be additive to those posed by badgers. There are considerable knowledge gaps associated with bTB in deer, badgers, and cattle, and data available for model parameterization were generally of low quality and high variability, and consequently model output were subject to some uncertainty. Improved estimates of the proportion of time that deer of each species spend at pasture, the likelihood and magnitude of M. bovis excretion, and local badger and deer densities appear most important for improving estimates of relative risk in this system.

Key Words

Bovine tuberculosis, Eurasian badger, fallow deer, Mycobacterium bovis, quantitative risk assessment, red deer, Reeves' muntjac, risk model, roe deer

Citation

Waters, W. R., M. V. Palmer, D. L. Whipple. 2002. Mycobacterium bovis–infected white-tailed deer (Odocoileus virginianus): detection of immunoglobulin specific to crude mycobacterial antigens by ELISA. Journal of Veterinary Diagnostic Investigations 14:470–475.

Abstract Only ☐

No Abstract ☐

Article Type

Abstract

White-tailed deer (Odocoileus virginianus) have recently emerged as a source of Mycobacterium bovis infection for cattle within North America. The objective of this study was to evaluate the antibody response of M. bovis–infected deer to crude mycobacterial antigens. Deer were experimentally inoculated with M. bovis strain 1315 either by intratonsilar instillation or by exposure to M. bovis–infected (i.e., in contact) deer. To determine the time course of the response, including the effects of antigen administration for comparative cervical skin testing, serum was collected periodically and evaluated by enzyme-linked immunosorbent assay (ELISA) for immunoglobulin (i.e., IgG heavy and light chains) reactivity to mycobacterial antigens. The reactivity to M. bovis purified protein derivative (PPDb) exceeded ($P < 0.05$) the reactivity to M. avium PPD (PPDa) only after in vivo administration of PPDa and PPDb for comparative cervical testing of the infected deer. The mean immunoglobulin response, as measured by ELISA, of intratonsilar-inoculated deer to a proteinase K–digested whole-cell sonicate (WCS-PK) of M. bovis strain 1315 exceeded ($P < 0.05$) the mean of the prechallenge responses to this antigen at approximately 1 month after inoculation and throughout the remainder of the study (i.e. ~11 months). This response also exceeded ($P < 0.05$) that of the uninfected deer. Although this is encouraging, further studies are necessary to validate the use of the proteinase K–digested M. bovis antigens in the antibody-based assays of tuberculosis.

Key Words

white-tailed deer, Odocoileus virginianus, immunoglobulin, ELISA

Citation

Waters, W. R., M. V. Palmer, J. P. Bannantine, R. Greenwald, J. Esfandiari, P. Andersen, J. McNair, J. M. Pollock, and K. P. Lyashchenko. 2005. Antibody responses in reindeer (Rangifer tarandus) infected with Mycobacterium bovis. Clinical and Diagnostic Laboratory Immunology 12(6):727–735.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Despite having a very low incidence of disease, reindeer (Rangifer tarandus) are subject to tuberculosis (TB) testing requirements for interstate shipment and herd accreditation in the United States. Improved TB tests are desperately needed, as many reindeer are falsely classified as reactors by current testing procedures. Sera collected sequentially from 11 (experimentally) Mycobacterium bovis-infected reindeer and 4 noninfected reindeer were evaluated by enzyme-linked immunosorbent assay (ELISA), immunoblotting, and multiantigen print immunoassay (MAPIA) for antibody specific to M. bovis antigens. Specific antibody was detected as early as 4 weeks after challenge with M. bovis. By MAPIA, sera were tested with 12 native and recombinant antigens, which were used to coat nitrocellulose. All M. bovis-infected reindeer developed responses to MPB83 and a fusion protein, Acr1/MPB83, and 9/11 had responses to MPB70. Other antigens less commonly recognized included MPB59, ESAT-6, and CFP10. Administration of purified protein derivatives for skin testing boosted serum antibody responses, as detected by each of the assays. Of the noninfected reindeer, 2/4 had responses that were detectable immediately following skin testing, which correlated with pathological findings (i.e., presence of granulomatous lesions yet the absence of acid-fast bacteria). The levels of specific antibody produced by infected reindeer appeared to be associated with disease progression but not with cell-mediated immunity. These findings indicate that M. bovis infection of reindeer elicits an antibody response to multiple antigens that can be boosted by skin testing. Serological tests using carefully selected specific antigens have potential for early detection of infections in reindeer.

Key Words reindeer, Rangifer tarandus, antibody response, improved testing, early detection

Citation

Waters, W. R., M. V. Palmer, R. E. Sacco, and D. L. Whipple. 2002. Nitric oxide prodution as an indication of Mycobacterium bovis infection in white-tailed deer (Odocoileus virginianus). Journal of Wildlife Diseases 38(2):338–343.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

White-tailed deer (Odocoileus virginianus) are reservoirs for Mycobacterium bovis in northeast Michigan, USA. Production of nitric oxide (NO) by activated macrophages is a potent mechanism of mycobacterial killing. The capacity of macrophages to produce NO, however, varies among mammalian species. The objective of this study was to determine if mononuclear cells from white-tailed deer produce nitrite as an indication of NO production and, if so, is NO produced in response to stimulation with M. bovis antigens. Supernatants were harvested from adherent peripheral blood mononuclear cell (PBMC) cultures that had been stimulated with either Mannheimia haemolytica lipopolysaccharide (LPS) or media alone (i.e., no stimulation). Nitrite levels within M. haemolytica LPS-stimulated culture supernatants exceeded ($P < 0.05$) those detected within supernatants from non-stimulated cultures as well as those detected within
supernatants from cultures receiving an inhibitor of NO synthase in addition to M. haemolytica LPS. In response to stimulation with M. bovis antigens, nitrite production by PBMC from M.bovis-infected deer exceeded ($P < 0.05$) the production by PBMC from non-infected deer. The response of PBMC from infected deer to M. bovis antigens exceeded ($P < 0.05$) the response of parallel cultures from the same deer receiving no stimulation. The response of PBMC from M. bovis-infected deer to M. avium antigens did not differ from that of PBMC from M. bovis infected deer to no stimulation or from that of PBMC from non-infected deer to M. avium antigens. These findings indicate that adherent PBMC from white-tailed deer are capable of NO production and that mononuclear cells isolated from M. bovis-infected white-tailed deer produce NO in an antigen-specific recall response.

Key Words

bovine tuberculosis, lipopolysaccharide, Mannheimia haemolytica, mononuclear cells, Mycobacterium bovis, nitric oxide, Odocoileus virginianus, reactive nitrogen intermediates, white-tailed deer

Citation

Waters, W. R., M. V. Palmer, T. C. Thacker, K. Orloski, P. Nol, N. P. Harrington, S.C. Olsen, and B. J. Nonnecke. 2008. Blood culture and stimulation conditions for the diagnosis of tuberculosis in cervids by the Cervigam assay. Veterinary Record 162:203-208.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Mitogen- and antigen-induced interferon-y (IFN-y) responses of peripheral blood leucocytes from cervids were evaluated by a commercial whole-blood assay. The assay was applied to Mycobacterium bovis-infected white-tailed deer and reindeer, M bovis BCG-vaccinated white-tailed deer and elk, and unvaccinated, uninfected white-tailed deer, fallow deer, elk and reindeer. The responses of the M bovis-infected white-tailed deer to pokeweed mitogen (PwM) varied with time and between individuals. The responses of the M bovIs-infected reindeer to PWM and M bovis purified protein derivative (PPD) were positively associated. Samples from tuberculosis-free captive herds in various parts of the USA were also evaluated.Four per cent of fallow deer, 20 per cent of elk, 44 per cent of white-tailed deer, and 91 per cent of reindeer had responses to PWM exceeding 025 A optical density, that is, PWM stimulation minus no stimulation. The specificity of the responses to M bovis PPD and a Mycobacterium tuberculosis complex-specific antigenrESAT-6:CFP-1O, excluding animals not responding to PWM, ranged from 78 per cent to 100 per cent and was dependent upon the species and the positive response cut-off value. The results show that the commercial assay is valid for the detection of TB in reindeer; however, further development of the assay will be required before it is used in surveillance programmes for white-tailed deer, fallow deer, and elk.

Key Words Diagnosis, cervids, cervigram assay, surveillance,

Citation

Whiting, T. L. and S. V. Tessaro. 1994. An abattoir study of tuberculosis in a herd of farmed elk. Canadian Veterinary Journal 35:497-501.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

The purpose of this study was to examine the prevalence and distribution of grossly visible lesions of tuberculosis in a herd of 344 North American elk (Cervus elaphus) depopulated during a three-month period in 1991. Abattoir inspection detected mycobacterial lesions in 134 (39.8%) of the 337 animals received for slaughter. The prevalence of lesions increased with the age of the animals. Lesions were predominantly suppurative rather than caseous, and mineralization was less evident than in tuberculous lesions in cattle. Lesions occurred predominantly -in lymph nodes, and lungs were the only organs in which mycobacterial lesions were found. The distribution of lesions suggested that aerosol transmission was the most significant means of spread of the disease within the herd. Giant liver flukes (Fascioloides magna) were observed in approximately 80% of the adult elk.

Key Words

abattoir, elk, cervus elaphus, liver flukes, prevalence, visible lesions

Citation

Wilkinson, D., R. Bennett, I. McFarlane, S. Rushton, M. Shirley, and G.C. Smith. 2009. Cost-benefit analysis model of badger (Meles meles) culling to reduce cattle herd tuberculosis breakdowns in Britian, with particular reference to badger perturbation. Journal of Wildlife Diseases 45(4):1062-1088.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (TB) is an important economic disease. Badgers (Meles meles) are the wildlife source implicated in many cattle outbreaks of TB in Britain, and extensive badger control is a controversial option to reduce the disease. A badger and cattle population model was developed, simulating TB epidemiology; badger ecology, including postcull social perturbation; and TB-related farm management. An economic cost-benefit module was integrated into the model to assess whether badger control offers economic benefits. Model results strongly indicate that although, if perturbation were restricted, extensive badger culling could reduce rates in cattle, overall an economic loss would be more likely than a benefit. Perturbation of the badger population was a key factor determining success or failure of control. The model highlighted some important knowledge gaps regarding both the spatial and temporal characteristics of perturbation that warrant further research.

Key Words

badger, bovine tuberculosis, cattle, economics, Meles meles, Mycobacterium, bovis, spatial model

Citation Williams, R. S. and W. A. Hoy. 1930. The viability of B. tuberculosis (bovinus) on pasture land, in stored faeces and in liquid manure. The Journal of Hygiene. 30(4):413-419.

Abstract Only ☐

No Abstract ☑

Article Type Journal Article

Abstract

Key Words Pasture, feces, manure, viability

Citation Wint, G.R.W., T.P. Robinson, D.M. Bourn, P.A. Durr, S.I. Hay, S.E. Randolph, and D.J. Rogers. 2002. Mapping bovine tuberculosis in Great Britian using environmental data. Trends in Microbiology 10(10):441-444.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract The incidence of bovine tuberculosis (BTB) is increasing in Great Britain, exacerbated by the temporary suspension of herd testing in 2001 for fear of spreading the much more contagious foot and mouth disease. The transmission pathways of BTB remain poorly understood. Current hypotheses suggest the disease is introduced into susceptible herds from a wildlife reservoir (principally the Eurasian Badger) and/or from cattle purchased from infected areas, while the role of climatic factors in transmission has generally been ignored. Here,we show how remotely sensed satellite data, which provide good indicators of a variety of climatic factors, can be used to describe the distribution of BTB in Great Britain in 1997, and suggest how such data could be used to produce BTB risk maps for the future.

Key Words bovine tuberculosis, Great Britian, mapping

Citation

Witmer, G. W., R. B. Sanders, and A. C. Taft. 2003. Feral swine- are they a disease threat to livestock in the United States. Proceedings of the Wildlife Damage Management Conference 10:316-325.

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

Feral swine populations provide both benefits and liabilities to citizens of the United States. Their expanding range and increasing densities, however, have raised concern over the adverse environmental and agricultural effects and the increased risk of disease transmission between feral swine and livestock. We discuss the role of feral swine in the transmission of wildlife diseases and, in particular, in diseases of national significance to the livestock industry. We also discuss available management tools and strategies for reducing feral swine populations, minimizing damage or disease occurrences and eradicating populations when deemed appropriate. Finally, we note areas of research that may provide valuable management tools in the future.

Key Words

bovine tuberculosis, brucellosis, exotics, feral swine, invasive species, livestock, pseudorabies, Sus scrofa, trichinosis, vesicular stomatitis

Citation

Witmer, G., A.E. Fine, J. Gionfriddo, M. Pipas, K. Shively, K. Piccolo, and P. Burke. 2010. Epizootiological survey of Mycobacterium bovis in wildlife and farm environments in northern Michigan. Journal of Wildlife Diseases 46(2):368-378.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Bovine tuberculosis (bovine TB), caused by Mycobacterium bovis, has reemerged in northern Michigan, with detections in white-tailed deer (Odocoileus virginianus) in 1994 and in cattle in 1998. Since then, significant efforts have been directed toward reducing deer densities in the area in the hopes of reducing the bovine TB prevalence rate in deer and eliminating spill-over of the disease into cattle. Despite the success of the efforts to reduce deer densities, additional cattle herds have become infected. Other mammals can be infected with M. bovis and some carnivores and omnivores had been found to be infected with the disease in northern Michigan. We conducted a multi-year surveillance effort to detect bovine TB in wild species of mammals in the Michigan outbreak area. From 2002 to 2004, tissue samples from 1,031 individual animals of 32 species were collected, processed, and cultured for M. bovis. Only 10 (1.0%) were culture positive for M. bovis (5 raccoons [Procyon lotor], 4 opossums [Didelphis virginiana]), and 1 grey fox [Urocyon cinereoargenteus]). We also found 2 raccoons and 4 opossums to be positive for M. avium. We collected 503 environmental samples from cattle farms recently identified as bovine TB positive; none yielded positive M. bovis culture results. Finally, we used infrared cameras to document wildlife use of 4 barns in the area. Many avian and mammalian species of wildlife were observed, with raccoons being the most commonly observed species. This surveillance study identified no new wildlife species that should be considered significant reservoirs of bovine TB in the outbreak area in northern Michigan. However, the relatively high apparent bovine TB prevalence rates in some carnivorous and omnivorous species, their relatively long lifespan, and their frequent use of barns, suggests that removal of raccoons, opossums, foxes, and coyotes (Canis latrans) should be considered when a newly infected farm is depopulated of cattle.

Key Words

bovine tuberculosis, disease transmission, environmental contamination, farm management, Mycobacterium bovis, prevalence rate, surveillance, wildlife management

Citation

Witmer, G., T. DeLiberto, K. VerCauteren, P. Butchko. 2003. Mycobacterial Diseases in Wildlife. Proceedings of the Wildlife Damage Management Conference 10:310-315.

Abstract Only ☐

No Abstract ☐

Article Type Proceedings

Abstract

Mycobacterium infections occur in numerous wildlife species worldwide and this bacterial genus can also cause disease in humans and livestock. Two Mycobacterium species and one subspecies that infect wildlife are important from a wildlife damage management perspective. Mycobacterium avium, avian tuberculosis, is a ubiquitous and cosmopolitan disease of wild and domestic birds. Wild and domestic ruminants are host to M. avium paratuberculosis, also known as Johne's disease. Finally, Mycobaterium bovis, bovine tuberculosis, is primarily associated with domestic and wild bovines and ungulates, but also infects many other species of mammals. Eradicating these diseases from wildlife populations is very difficult if not impossible. Preventing spill-over into domestic livestock herds is also problematic. We review the Mycobacterial diseases in wildlife and discuss their implications to livestock and human health. Our emphasis is on bovine tuberculosis and the current outbreak in northern Michigan, USA.

Key Words

Avian tuberculosis, bovine tuberculosis, Johne's disease, livestock disease, Mycobacterium, wildlife damage management, wildlife disease

Citation

Wittenberg, E. and C. Wolf. 2007. 2006 Michigan Dairy Farm Business Analysis Summary. Staff Paper 2007-08. Department of Agricultural Economics, Michigan State University, East Lansing, MI.

Abstract Only ☐

No Abstract ☐

Article Type Report

Abstract

This report summarizes the financial and production records of 139 dairy farms from throughout Michigan in 2006. To be included, the farms must have produced at least 50 percent of gross cash farm income from milk and dairy animal sales. The records came from Michigan State University's TelFarm project and the Farm Credit Service system in Michigan. The values were pooled into averages for reporting purposes. The farms are larger than would be the average of all dairy farms in Michigan. While considerable variation in the data exists, average values are reported in the summary tables and discussion that follows.

Key Words bovine tuberculosis, cost, dairy farms, Michigan

Citation

Wobeser, G. 2009. Bovine tuberculosis in Canadian wildlife: An updated history. The Canadian Veterinary Journal 50:1169–1176.

Abstract Only ☑

No Abstract ☐

Article Type Journal Article

Abstract

Mycobacterium bovis infection in wild animals attracted little attention in Canada until the disease was almost eliminated from domestic livestock. Tuberculosis was endemic in plains bison and occurred in elk, moose, and mule deer in Buffalo National Park (BNP), Alberta during the 1920s and 1930s. Bison were moved from BNP to Wood Buffalo National Park (WBNP), where tuberculosis became, and remains, endemic in bison, posing a risk to efforts to restore bison in northern Canada. Tuberculosis was found in a white-tailed deer in Ontario in 1959, and in an infected elk near Riding Mountain National Park (RMNP), Manitoba in 1992. Intense surveillance has resulted in detection of 40 elk, 8 white-tailed deer, and 7 cattle herds infected between 1997 and 2008 in the RMNP area. The strains of M. bovis in the RMNP area are different from strains tested from cattle and bison elsewhere in Canada. Management of tuberculosis in cattle and wild animals is challenging because of uncertainty about the ecology of the disease in various species, difficulty in obtaining samples and population data from wildlife, lack of validated tests, overlapping jurisdictions and authority, and conflicting values and opinions among stakeholders.

Key Words

wild, Cnada, bison, elk , moose, mule deer, Buffalo National Park, Alberta, Riding Mountain National Park, management, cattle, ecology

Citation

Woodroffe, R., C. A. Donnelly, D. R. Cox, F. J. Bourne, C. L. Cheeseman, R. J. Delahay, G. Gettinby, J. P. Mcinerney, and W. I. Morrison. 2006. Effects of culling on badger Meles meles spatial organization: implications for the control of bovine tuberculosis. Journal of Applied Ecology 43:1–10.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. The incidence of bovine tuberculosis (TB) in British cattle has risen markedly over the last two decades. Failure to control the disease in cattle has been linked to the persistence of a reservoir of infection in European badgers Meles meles, a nationally protected species. Although badger culling has formed a component of British TB control policy for many years, a recent large-scale randomized field experiment found that TB incidence in cattle was no lower in areas subject to localized badger culling than in nearby areas where no experimental culls occurred. Indeed, analyses indicated that cattle incidence was higher in culled areas.
2. One hypothesis advanced to explain this pattern is that localized culling disrupted badgers' territorial behaviour, potentially increasing the rate of contact between cattle and infected badgers. This study evaluated this hypothesis by investigating badger activity and spatial organization in 13 study areas subjected to different levels of culling. Badger home ranges were mapped by feeding colour-marked baits at badger dens and measuring the geographical area in which colour-marked faeces were retrieved.
3. Badger home ranges were consistently larger in culling areas. Moreover, in areas not subjected to culling, home range sizes increased with proximity to the culling area boundary. Patterns of overlap between home ranges were also influenced by culling.
4. Synthesis and applications. This study demonstrates that culling badgers profoundly alters their spatial organization as well as their population density. These changes have the potential to influence contact rates between cattle and badgers, both where culls occur and on adjoining land. These results may help to explain why localized badger culling appears to have failed to control cattle TB, and should be taken into account in determining what role, if any, badger culling should play in future control strategies.

Key Words

bait marking, bovine TB, European badger, Krebs trial, Mycobacterium bovis, perturbation, randomized badger culling trial, reservoir host, wildlife disease, zoonosis

Citation

Woodroffe, R., C. A. Donnelly, G. Wei, D. R. Cox, F. J. Bourne, T. Burke, R. K. Butlin, C. L. Cheeseman, G. Gettinby, P. Gilks, S. Hedges, H. E. Jenkins, W. T. Johnston, J. P. McInerney, W. I. Morrison, and L. C. Pope. 2009. Social group size affects Mycobacterium bovis infection in European badgers (Meles meles). Journal of Animal Ecology 78:818–827.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

1. In most social animals, the prevalence of directly transmitted pathogens increases in larger groups and at higher population densities. Such patterns are predicted by models of Mycobacterium bovis infection in European badgers (Meles meles).
2. We investigated the relationship between badger abundance and M. bovis prevalence, using data on 2696 adult badgers in 10 populations sampled at the start of the Randomized Badger Culling Trial.
3. M. bovis prevalence was consistently higher at low badger densities and in small social groups. M. bovis prevalence was also higher among badgers whose genetic profiles suggested that they had immigrated into their assigned social groups.
4. The association between high M. bovis prevalence and small badger group size appeared not to have been caused by previous small-scale culling in study areas, which had been suspended, on average, 5 years before the start of the current study.
5. The observed pattern of prevalence might occur through badgers in smaller groups interacting more frequently with members of neighbouring groups; detailed behavioural data are needed to test this hypothesis. Likewise, longitudinal data are needed to determine whether the size of infected groups might be suppressed by disease-related mortality.
6. Although M. bovis prevalence was lower at high population densities, the absolute number of infected badgers was higher. However, this does not necessarily mean that the risk of M. bovis transmission to cattle is highest at high badger densities, since transmission risk depends on badger behaviour as well as on badger density.

Key Words bovine tuberculosis, cattle TB, wildlife disease, wildlife host

Citation

Woodroffe, R., C. A. Donnelly, H. E. Jenkins, W. T. Johnston, D. R. Cox, F. J. Bourne, C. L. Cheeseman, R. J. Delahay, R. S. Clifton-Hadley, G. Gettinby, P. Gilks, R. G. Hewinson, J. P. McInerney, and W. I. Morrison. 2006. Culling and cattle controls influence tuberculosis risk for badgers. Proceedings of the National Academy of Sciences 103(40):14713–14717.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Human and livestock diseases can be difficult to control where infection persists in wildlife populations. In Britain, European badgers (Meles meles) are implicated in transmitting Mycobacterium bovis, the causative agent of bovine tuberculosis (TB), to cattle. Badger culling has therefore been a component of British TB control policy for many years. However, large-scale field trials have recently shown that badger culling has the capacity to cause both increases and decreases in cattle TB incidence. Here, we show that repeated badger culling in the same area is associated with increasing prevalence of M. bovis infection in badgers, especially where landscape features allow badgers from neighboring land to recolonize culled areas. This impact on prevalence in badgers might reduce the beneficial effects of culling on cattle TB incidence, and could contribute to the detrimental effects that have been observed. Additionally, we show that suspension of cattle TB controls during a nationwide epidemic of foot and mouth disease, which substantially delayed removal of TB-affected cattle, was associated with a widespread increase in the prevalence of M. bovis infection in badgers. This pattern suggests that infection may be transmitted from cattle to badgers, as well as vice versa. Clearly, disease control measures aimed at either host species may have unintended consequences for transmission, both within and between species. Our findings highlight the need for policymakers to consider multiple transmission routes when managing multihost pathogens.

Key Words wildlife, badgers, meles meles, causative agent, culling, cattle

Citation

Woodroffe, R., P. Gilks, W. T. Johnston, A. M. Le Fevre, D. R. Cox, C. A. Donnelly, F. J. Bourne, C. L. Cheeseman, G. Gettinby, J. P. McInerney, and W. I. Morrison. 2008. Effects of culling on badger abundance: implications for tuberculosis control. Journal of Zoology 274:28–37.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

Culling is often considered as a tool for controlling wildlife diseases that can also infect people or livestock. Culling European badgers Meles meles can cause both positive and negative effects on the incidence of bovine tuberculosis (TB) in cattle. One factor likely to influence the outcome of different badger-culling strategies for cattle TB is the reduction in badger population density achieved. However, this reduction is difficult to measure because badgers, being nocturnal and fossorial, are difficult to count. Here, we use indices of badger abundance to measure the population impacts of two culling strategies tested in Britain. The densities of badger setts and latrines recorded before culling were correlated with the densities of badgers captured on initial culls, suggesting that both were indices of actual badger abundance. Widespread 'proactive' culling was associated with a 73% reduction in the density of badger latrines, a 69% reduction in the density of active burrows and a 73% reduction in the density of road-killed badgers. This population reduction was achieved by a coordinated effort entailing widespread and repeated trapping over several years. However, this strategy caused only modest reductions in cattle TB incidence in culled areas and elevated incidence in neighbouring unculled areas. Localized 'reactive' culling caused a 26% reduction in latrine density, a 32% reduction in active burrow density and a 10% reduction in the density of road-killed badgers, but apparently increased the incidence of cattle TB. These results indicate that the relationship between badger population reduction and TB transmission to cattle is strongly non-linear, probably because culling prompts changes in badger behaviour that influence transmission rates. These findings raise serious questions about the capacity of badger culling to contribute to the control of cattle TB in Britain.

Key Words

badger, culling, Meles meles, Mycobacterium bovis, perturbation, randomized badger culling trial, tuberculosis, wildlife disease

Citation

Wyss, D., M. Giacometti, J. Nicolet, A. Burnens, G.E. Pfyffer, and L. Audige. 2000. Farm and slaughter survey of bovine tuberculosis in captive deer in Switzerland. The Veterinary Record 147:713-717.

Abstract Only ☐

No Abstract ☐

Article Type Journal Article

Abstract

In 1998, a survey was conducted by postal questionnaire to gather basic knowledge about the management, health and productivity of captive deer in Switzerland. In addition, lymph nodes were collected from slaughtered deer from 124 of the 262 holdings surveyed, and tested for Mycobacterium bovis and Mycobacterium tuberculosis. The total farmed deer population was 8389 animals kept on 485 holdings; 87 per cent were fallow deer, 8 per cent red deer, 4 per cent sika deer, and there were small numbers of other species. The median herd sizes were 12 for fallow deer and eight for red deer. Few owners had handling facilities or crushes. In none of the lymph nodes examined were lesions typical of bovine tuberculosis observed, and neitherM bovis nor M tuberculosis was cultivated from any of the samples.

Key Words bovine tuberculosis, captive deer, farm, slaughter, survey