

## RISK ASSESSMENT : RISK ASSOCIATED WITH *M. BOVIS* IN WILD WHITE-TAILED DEER IN MICHIGAN

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En 1994, un cerf sauvage de virginie (*Odocoileus virginianus*) tué à la chasse au nord du Michigan (U.S.A) a été reconnu atteint de *Mycobacterium bovis*. Les troupeaux domestiques du Michigan étaient indemnes d'infection à *M. bovis* depuis 1974. Les résultats de survie indiquent que le bétail n'était pas infecté et que l'infection se confinait à la population de cerfs sauvages. Une appréciation de risque a été demandée afin d'estimer la vraisemblance pour les animaux domestiques de contracter l'infection à *M.bovis* à partir des cerfs sauvages contaminés.

La prévalence de *M. bovis* chez le cerf a été estimée à 3.5 %. Tous les cerfs infectés ont été éliminés dans une zone de 14 miles carrés; il est supposé que le bétail de cette zone avait plus de chances d'être en contact avec les cerfs infectés. Des modèles ont été développés pour estimer le niveau de transmission de *M.bovis* dans la population de cerfs et la vraisemblance de contamination du bétail. Différents scénarios de gestion de la population de cerfs ont été simulés afin d'estimer l'effet que pourrait avoir un tel changement sur la vraisemblance du bétail à contracter l'infection à partir des cerfs. Le risque de transmission estimé est assez faible. La vraisemblance annuelle actuelle est estimée à 0.1 %. Si aucune mesure n'est prise concernant la gestion des populations de cerfs et du bétail, la vraisemblance cumulative dans les 25 prochaines années est estimée à 12 %. En simulant d'autres scénarios, la vraisemblance est plus faible, mais la prévalence de *M.bovis* chez les cerfs sauvages diminue avec le temps uniquement pour les scénarios qui postulent une réduction de la transmission d'au moins 50 %.

Cette réduction de la transmission d'au moins 50 %, afin d'éliminer *M.bovis* de la population de cerfs sauvages et éliminer le risque pour le bétail, va demander des modifications dans les mesures de gestion. Les modifications et les effets spécifiques n'ont pas été présentés dans l'appréciation du risque.

### INTRODUCTION

In 1994, a wild, hunter-killed, white-tailed deer (*Odocoileus virginianus*) from northern Michigan, U.S.A., was diagnosed with *Mycobacterium bovis* (*M. bovis* or bovine TB). Several surveys of the deer population were completed in 1995 and early 1996 to determine the prevalence of *M. bovis*, as well as the range occupied by infected deer. Domestic animals in the area were also tested. Results of these surveys indicated that domestic animals were not infected, and *M. bovis* infection was apparently being maintained in the wild deer population.

The finding of *M. bovis*, apparently maintained in a wild deer population, caused great concern. The domestic cattle population in Michigan has been free of *M. bovis* infection since 1974, and the nation-wide plan to eradicate *M. bovis* has continued to progress until there are very few remaining foci of infection. Individuals in Michigan were concerned at the possibility that cattle might contract *M. bovis* from wild deer in this area. Therefore, a quantitative risk assessment which would estimate the likelihood of that occurrence was requested.

### METHODS

In order to estimate the risk to cattle at present and into the future, it was first necessary to model the disease in the deer population. For this, two models were developed. The first was a deterministic model which estimated the past transmission in the deer population. It was assumed that *M. bovis* had entered the deer population 40 years prior to discovery of the case in 1994. The model estimated the level of transmission that had occurred in the population in order to result in the prevalence seen in the deer herd in the 1995-1996 surveys, which was approximately 3.5 percent. The second deer model used that transmission coefficient in order to project the prevalence level that could be expected in the deer population in the future (USDA, 1996).

A third model was developed to estimate the risk that domestic cattle might contract *M. bovis* from wild deer. The transmission coefficient used in the deer model was adjusted to reflect the differences between intra- and inter-species contact, and the new coefficient was used to estimate the annual likelihood that one or more cattle would contract *M. bovis* from wild deer in the area, over the next 25 years.

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The cattle model assumed that there is a single focus of infection in deer. The area encompassing the positive deer measured approximately 14 x 14 miles square, defined as the infected zone. A buffer zone was also identified, which encompassed all land within 5 miles of the location where an infected deer was discovered, not including the infected zone. It was assumed that infected deer may inhabit the buffer zone, but that was less likely than their presence in the infected zone. The area outside the infected and buffer zones was assumed to contain no infected deer. Cattle herds were assigned to the infected zone, the buffer zone, or outside those zones, based on their location. All cattle were assumed to have contact with deer, because of the pasturing of cattle which is common in the area. Because infected deer were assumed to spend most of their time in the infected zone, it was assumed that cattle in the infected zone were more likely to have contact with infected deer than cattle in the buffer zone, and therefore the likelihood of transmission from deer to cattle was assumed to be highest in the infected zone. It was assumed that cattle outside of the infected and buffer zones had negligible risk of contacting infected deer.

Different scenarios for management of the deer population were also simulated using the deer model. The results of those simulations were used in the cattle model to determine the effect that such management schemes would have on the likelihood of cattle contracting *M. bovis* from deer. Six scenarios were examined in addition to continuation of the traditional management (scenario 1): scenarios 2,3 and 4 simulated a decrease in transmission of 10 percent, 25 percent, and 50 percent respectively; scenario 5 modeled a decrease in adult survivability of 10 percent annually until the population was decreased by 50 percent; and scenarios 6 and 7 combined the two, decreasing survivability by 10 percent annually and transmission by 25 percent and 50 percent respectively.

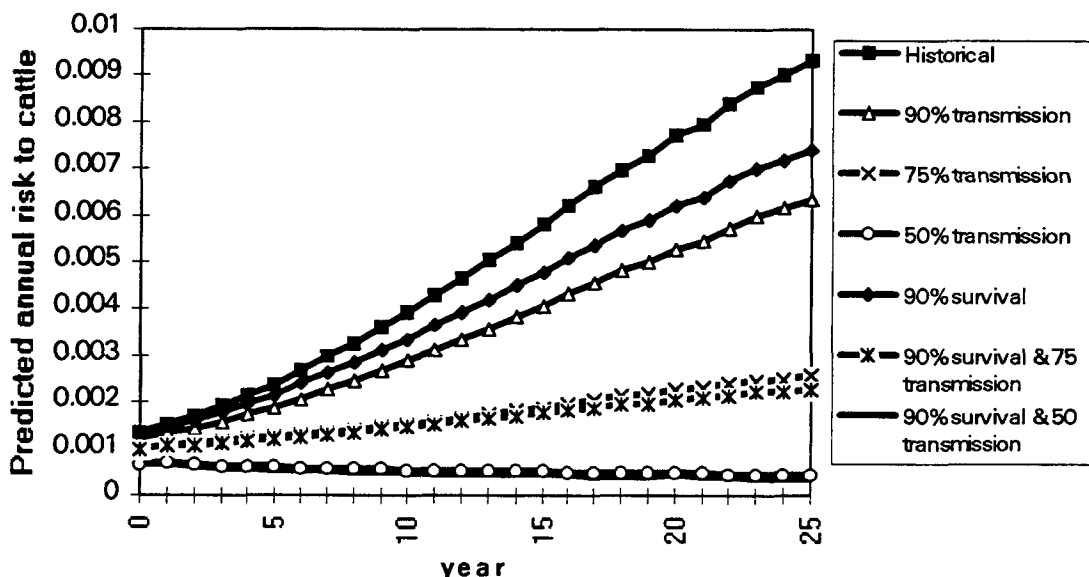
Multiple iterations of each scenario were run, using @RISK software. The annual likelihood of transmission to one or more cattle was calculated at 5 years, 10 years, and 25 years in the future. The mean was obtained for those three years, and mean values were interpolated for the intervening years to obtain a graphical representation of the estimated annual mean likelihood of transmission of *M. bovis* to cattle over time.

**RESULTS**

Prevalence in wild deer continued to increase under all scenarios except those two that included reducing transmission by 50 percent (scenarios 4 and 7). Reducing transmission by 25 percent slowed the increase in prevalence seen if historical management was continued, but, even in conjunction with an annual 10 percent decrease in survival, did not lead to decrease in overall prevalence of *M. bovis* in deer. Reducing adult survival by 10 percent annually helped to reduce disease spread, but not greatly. Therefore, under most scenarios, *M. bovis* was still present in the deer population 25 years into the future.

The risk to cattle from deer was estimated to be quite low. The current annual likelihood that one or more cattle would contract TB from a wild deer was estimated to be 0.1 percent (Figure 1). That risk would continue to rise if no changes were made in deer or cattle management, to an annual likelihood of 0.9 percent in 25 years. The cumulative likelihood for the next 25 years under the historical management scenario was estimated to be 12 percent. Under other scenarios, the likelihood was lower, but the risk to cattle decreased over time only in the scenarios where deer prevalence decreased over time (scenarios 4 and 7).

**Figure 1**  
Annual mean likelihood that one or more cattle will contract bovine TB from wild white-tailed deer over the next 25 years in the defined area of Michigan



## DISCUSSION

The cattle model estimated that the risk to cattle in the area is quite low. And, at the time the risk assessment was completed, there were no definite cases of *M. bovis* identified in cattle in or from the affected area (infected and buffer zones). However, in order to reduce the risk to cattle to a negligible level, the prevalence of *M. bovis* in deer must be decreased. The models indicate that this can be accomplished only by a serious decrease in transmission, of at least 50 percent. How that may be accomplished was not addressed in the model.

The risk of transmission of *M. bovis* from deer to cattle mirrors the risk of transmission between deer, because the model did not consider the effects of changes in cattle management. That is, under scenarios where deer-to-deer transmission is greater, greater numbers of deer are infected and the risk to cattle rises. Where deer-to-deer transmission is decreased, the risk to cattle decreases. As long as there are any infected deer, the risk to cattle remains, although it may be very small.

It was difficult to estimate the degree of inter-species transmission that might occur. There were no published reports of transmission of *M. bovis* from a free-ranging deer population to domestic cattle that did not include complicating interactions, such as the presence of infected brush-tailed possums in New Zealand. Therefore, an estimate was made of the amount of deer-to-cattle contact that would be expected, compared to the amount of deer-to-deer contact that would be expected. Based on those estimates, the probability of transmission from deer to cattle was estimated. The predicted fairly low likelihood of transmission to cattle is primarily due to the low level of social contact between the two species, and the difficulty in transmission of *M. bovis* through pasture contamination. However, contamination of pastures or feeders might occur when deer and cattle share feeding grounds, even if the different species are present at different times. Contamination of pasture by deer, subsequently used by cattle, was assumed to be a difficult way to transmit *M. bovis*, based on the high doses of bacteria needed for oral transmission. However, it is possible that *M. bovis* could be transmitted via contaminated feeding areas, either by oral inoculation, or perhaps more likely, by inhalation of contaminated secretions.

If contaminated pastures, or other elements of cross-species exposure that were not considered, prove to be important in the estimate of inter-species transmission, the omission of these factors from consideration will have a profound effect on the likelihood of infection that was estimated. For example, if the estimate of cross-species transmission is incorrect by one order of magnitude, the cumulative likelihood that one or more cattle will contract TB from wild deer over the next 25 years, under the scenario assuming no changes to deer or cattle management, rises to 60 percent.

While all cattle in the infected and buffer zones in Michigan were assumed to have direct contact with deer in the simulations, it is acknowledged that some types of management may increase or diminish such contact. Cattle kept close to buildings are less likely to have regular contact with deer than cattle pastured at a distance from buildings. Domestic animals on pasture may be less likely to suffer from significant contamination of their feed source than animals fed supplemental feed in an area that may be attractive to deer. The model did not consider the effects of changing cattle management. Instead, it focussed on the deer population because only eradication of the disease in deer could be expected to remove the risk from all cattle in this area. In addition, the deer population is managed as a group by the Michigan Department of Natural Resources. Cattle herds are managed individually, which makes management changes concerning the entire cattle population difficult to predict or model. However, an individual farmer could reduce the chances that his or her cattle would contract *M. bovis* by decreasing the level of contact between the two species. Changing feeding or pasturing practices, or judicious use of hunting on the property may decrease the contact between species and therefore the risk to individual cattle. Farmers are allowed to obtain special permits to shoot deer seen eating with cattle on their property.

The models used did not allow determination of which management changes in the deer population might effect the changes described in the different scenarios (i.e., decreasing transmission by 50 percent); however, wildlife managers in the area have already begun to make management changes where possible to attempt the necessary decreases in transmission. Therefore, the estimates produced by scenario 1 are no longer appropriate. Time will tell what effect the management changes will have on *M. bovis* in the deer population. It is expected that the model will be modified as updated information becomes available.

## NEW INFORMATION

Additional testing has been done in the deer population since the risk assessment was completed. Of particular note is the change in distribution of *M. bovis* infected deer. Infected deer have been found outside the infected zone. In most cases, the deer were found within one mile of the border of the infected zone, but several deer were found farther outside the zone. This is not believed to represent spread of the disease outside of the originally infected population, but rather to represent additional case finding. The area surveyed in 1996-97 was larger than the area surveyed previously, and infected deer were found in areas that had not been previously surveyed. Next year the survey will include additional territory not surveyed yet, and we will await the results. The results from this year, however, indicate that additional domestic cattle are exposed to *M. bovis* infected wild deer, which increases the likelihood above that reflected in the original risk assessment. No calculations have been done to estimate that increased likelihood more precisely. The prevalence of infected deer diagnosed in the survey during the 1996-97 hunting season appears to be similar to the prevalence seen in the surveys from 1995 and early 1996.

## BIBLIOGRAPHY

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