Risk of cattle shipments exported from the United States containing bluetongue virus-viremic animals.

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Summary:
The major impact of bluetongue virus (BTV) infection for many countries is its effect on international trade of livestock and germplasm. Using Monte Carlo simulation, we modeled the probability of exporting BTV-viremic cattle from the United States. For shipments undergoing 0- or 28-day quarantines, the model simulated that shipments originating from the northeast had the lowest probability of exporting a viremic animal, while those originating from the southwest had the highest probability. For all regions, our model simulated that shipments undergoing 100-d quarantine had zero probability of containing viremic animals. The risk of introducing an exotic strain of BTV into a country by importing infected cattle from the United States was found to be remote.

Introduction:
Bluetongue (BT) is an economically important disease in the United States primarily because of trade restrictions that limit the ability to export to bluetongue virus (BTV)-free countries. In 1998, 66 countries imposed 159 BT-based import measures on US ruminants and their products (Kahrs, 1998). Most import protocols require serologic tests to document lack of recent exposure to BTV (Kahrs, 1998).

Exporting antibody-positive animals that are not viremic does not pose a biological risk of exporting BTV; viremia is essential for transmission of BTV, and duration of viremia in an animal species has a direct relation to the importance of that species in the epidemiologic characterization of BT. Therefore we created a model to simulate the probability that shipments of cattle originating from various regions in the United States contain BTV-viremic animals.

Materials and Methods:
Data on number of animals and month of shipment of cattle exported from the United States from January 1994 to March 2002 were obtained from the United States Department of Agriculture. The United States was divided into six geographic zones, allowing for regional delineation of risk (Hoar et al, 2003). The regions were designated as northeast (Connecticut, Delaware, Indiana, Maine, Maryland, Massachusetts, Michigan, New Hampshire, New Jersey, New York, Ohio, Pennsylvania, Vermont, Virginia, and West Virginia), north-central (Illinois, Iowa, Minnesota, Nebraska, North Dakota, South Dakota, and Wisconsin), northwest (Idaho, Montana, Oregon, Washington, and Wyoming), southeast (Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee), south-central (Arkansas, Colorado, Kansas, Louisiana, Missouri, New Mexico, Oklahoma, and Texas), and southwest (Arizona, California, Nevada, and Utah).
Records were analyzed to determine the number of animals per shipment exported from each region during each month. Cumulative distribution functions (CDFs) were fitted to the data using a probability fitting software package (BestFit, Palisade Corp., Newfield, NY). Parameters were derived by use of maximum-likelihood estimation, and fit of the data was optimized by use of the Levenberg-Marquardt method (Press et al., 1990). Fitted distributions were evaluated quantitatively by use of $\chi^2$, Kolmogorov-Smirnov, and Anderson-Darling goodness-of-fit test statistics. Fit of the distributions was also evaluated by visual inspection.

National estimates for state-specific apparent prevalence (AP) of BTV-antibody were obtained from the literature (Pearson, 1992; Metcalf, 1981). The sensitivity (SE) and specificity (SP) of the agar gel immunodiffusion test (AGID) were described by using the best-fitting distributions based on expert opinion as described previously (Hoar et al., 2003). Beta distributions chosen were as follows: SE ($a = 99.70, b = 6.19$); SP ($a = 80.47, b = 3.04$). These distributions have mean values of 94.2 and 96.4%, respectively. We then converted observed AP to estimated true prevalence (TP), by use of the following equation (Marchevsky, 1974):

$$TP = \frac{(AP + [SP – 1])}{(SE + [SP – 1])}.$$ 

Duration of viremia was estimated using previously published data (Singer et al., 2001). The probability that an imported animal was viremic was calculated, based on the simulated number of days between infection and export.

The number of viremic animals within a shipment was calculated as a binomial distribution of shipment size and individual probability of viremia.

Results:

Data for 19,216 shipments containing 528,918 cattle over the study period were analyzed. The AP of antibodies for each state used in the models ranged from 0.5% (Massachusetts) to 81% (Nevada).

Median shipment sizes simulated by the model were 3 (northwest), 4 (northeast and south-central), 5 (north-central), 11 (southeast), and 20 animals (southwest). The model simulated that shipments originating from the northeastern United States had the lowest probability of exporting a viremic animal (0.002% and 0.009% of shipments contained 1 or more viremic animals with a 28- or 0-day quarantine respectively), while those originating from the southwestern United States had the highest probability (0.727% and 3.778% of shipments contained 1 or more viremic animals with a 28- or 0-day quarantine, respectively). For all regions, our model simulated that shipments undergoing 100-d quarantine had zero probability of containing viremic animals.

Discussion:

To protect native animals from infection with an exotic strain of BTV, an importing country must consider the distribution and prevalence of infection in the exporting country, the presence of potential vectors in its own country, and the presence of susceptible hosts in its own country and their relationship to potential vectors (Roberts et al., 1993). In this study we modeled the probability that a shipment of cattle originating from one of six regions within the United States contained one or more viremic animals. Our model demonstrates the low probability
that export shipments originating in the United States contain cattle viremic with BTV. The current OIE recommendations for testing and quarantine are adequate to protect cattle in importing countries from BTV.

We used a beta distribution to model the probability of viremia for an individual animal. The beta distribution provides conservative estimates because it ensures that a non-zero probability results, therefore we believe the true probability of a viremic animal in a shipment would be less than what our model predicts.

The risk assessment model presented here is essentially a release assessment and thus it considers only the export of BTV-viremic animals and not subsequent exposure and consequences to ruminants in the importing country. It must be emphasized that the importation of a viremic animal does not imply that secondary transmission is likely to occur. There still must be competent vectors that are capable of transmitting this imported strain of virus. Current research as well as epidemiological data suggests that vectors and viruses may have co-evolved over time such that it would be unlikely for a local vector to be competent for exotic strains of BTV (Gibbs and Greiner, 1994).

References:


