An Epidemiologic Model to Evaluate the Risk of *B. abortus* Infected Undetected Breeding Cattle Moving out of the Designated Surveillance Areas in Idaho, Montana, and Wyoming

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Abstract:

The United States has come very close to its goal of brucellosis eradication in cattle, but persistent infection in elk and bison in the Greater Yellowstone Area provides a continued threat to cattle in areas of Idaho, Montana, and Wyoming. The purpose of this assessment is to estimate the risk of *B. abortus* being present and undetected in shipments of breeding cattle leaving the Designated Surveillance Areas (DSA) in Idaho, Montana, and Wyoming and evaluate the impact of post-movement testing and reproductive monitoring. The results demonstrate that post-movement testing and reproductive monitoring of all DSA-origin breeding cattle is not a cost-effective mitigation. While additional testing of DSA-origin animals outside of the DSA reduces the already low probability of an infected undetected shipment leaving the DSA (0.02-0.03 shipments per year or 0.01-0.025 per 1,000 breeding shipments), this small reduction comes at a high cost. It would take a very large outbreak ($100-$300 million range) and testing of DSA-origin breeding cattle for 40-60 years to break even.

Keywords:

*B. abortus*, regionalization, risk assessment model, epidemiologic model, designated surveillance area

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Brucellosis Regionalization Risk Assessment Model

An Epidemiologic Model to Evaluate the Risk of *B. abortus* Infected Undetected Breeding Cattle Moving out of the Designated Surveillance Areas in Idaho, Montana, and Wyoming

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EXECUTIVE SUMMARY

The purpose of this assessment is to estimate the risk of infected undetected breeding cattle leaving the Designated Surveillance Areas (DSAs) in Idaho, Montana, and Wyoming (Figure 1). The results demonstrate that post-movement testing and reproductive monitoring of all DSA-origin breeding cattle is not a cost-effective mitigation given the low probability of an infected shipment leaving the DSAs undetected (0.02-0.03 shipments per year or 0.01-0.025 per 1,000 breeding shipments) and the high break-even value for post-movement testing and monitoring.

The break-even value for post-movement testing and monitoring, or cost that an outbreak would have to be to equal the cost of applying the post-movement risk mitigation for as long as necessary to detect an exposure event, would be in the $100-$300 million range. The actual cost of an outbreak associated with an introduction event outside of the DSAs could not be estimated; but, historic outbreak costs—when herd prevalence in the United States was as high as 1% (1970s)—was estimated at $120 million dollars (2014 dollars).

The United States has come very close to its goal of brucellosis eradication in cattle with herd prevalence estimated as low as 0.0001 percent. Persistent infection in elk and bison in the Greater Yellowstone Area provides a continued threat to cattle in areas of Idaho, Montana, and Wyoming. The interim rule 75 CFR 81090 requires States with a known wildlife reservoir to develop a brucellosis management plan to prevent the spread of brucellosis outside of these geographic areas. Idaho, Montana, and Wyoming have complied with this rule by the development of each States’ DSA. Cattle in these areas are at higher risk of contact with infected wildlife and therefore subject to additional testing and other mitigations to prevent the spread of brucellosis to cattle outside of DSAs.

Focusing resources to areas of highest risk (i.e., DSAs), helps reduce the cost of continued implementation of the Cooperative State Federal Brucellosis Eradication Program. However, this focus on the DSAs in Idaho, Montana, and Wyoming means reduced surveillance in other parts of the country, which could result in undetected disease spread. This risk assessment helped address whether or not additional mitigation measures are necessary for breeding cattle that leave the DSAs. While additional testing of DSA-origin animals outside of a DSA reduces the already low likelihood, this small reduction comes at a high cost. It would take a very large outbreak and testing of DSA-origin breeding cattle for 40-60 years to break even.
Figure 1 - Brucellosis Designated Surveillance Areas in Idaho, Montana, and Wyoming as of January 1, 2014.
1. INTRODUCTION

1.1 Objective

To estimate the risk of exporting a shipment of breeding cattle infected with brucellosis (*Brucella abortus*) but undetected from the Designated Surveillance Areas (DSAs) in Idaho (ID), Montana (MT), or Wyoming (WY).

1.2 Background

The interim rule 75 CFR 81090 became effective in December of 2010. This rule reduced the surveillance requirements for States that have been identified as brucellosis Class Free for 5 or more years and put specific requirements on States with infected wildlife present to ensure the spread of *B. abortus* between livestock and wildlife is mitigated.

States with a wildlife reservoir are required to develop a brucellosis management plan (BMP) approved by USDA. Currently only ID, MT, and WY have a known wildlife reservoir in elk and bison. Each of these three States have a DSA that they use to implement their BMP. Outside of the DSA is considered free from brucellosis in each of these three States, which allows for reduced surveillance.

Establishment of DSAs is a method of disease control recognized as “zoning” or “regionalization” by the World Organization for Animal Health (OIE). Zoning separates animal subpopulations with distinct health status and risk based on geographical basis. Zones are identified by recognizable borders which allow epidemiologic separation of the subpopulations and all factors which present a disease risk (*OIE, 2010*). Due to the limitations on data available, the difference in risk between the cattle populations inside versus outside of the DSA zones could not be measured in this assessment. For the purpose of this risk assessment, disease is known to be present within the DSAs and disease presence outside of the DSAs is not considered.

Epidemiologic modeling is a tool which can be used in animal health to provide scientific support to decision making (*Dube et al., 2007*). Models are not necessarily predictive in nature, rather they help construct and evaluate a series of likely scenarios and compare outcomes based on the best information available. The model described here is a tool developed to provide a standard risk assessment framework, which can be applied to evaluate the risk of cattle leaving the DSAs.

The purpose of this model is to identify the risk of an infected breeding animal leaving the DSAs of Idaho, Montana, or Wyoming under current controls in place by each of these States compared to additional post movement testing and monitoring.

2. METHODS

A stochastic simulation model, which applies a modification of the OIE’s risk assessment framework, was developed by USDA:APHIS:VS. Each component of the model was reviewed by a working group consisting of animal agriculture representatives from six States (Colorado, Idaho, Montana, Texas, South Dakota, and Wyoming) and several experts within Veterinary Services. Other experts were consulted as needed.
2.1 Risk Assessment Process

The OIE’s Risk Assessment process begins with the identification of a hazard and then proceeds to four interrelated steps: 1) Entry, 2) Exposure, 3) Consequence, and 4) Risk Estimation (OIE, 2010). Because the line between entry and exposure is not as well defined in domestic risk assessments compared to import risk assessments, the delineation for these steps in this assessment has been defined as follows:

The HAZARD has been identified as *B. abortus* infected and undetected breeding cattle introduced into a herd outside of the DSAs in ID, MT, and WY.

1. The ENTRY ASSESSMENT describes the biological pathway(s) necessary for an activity to introduce pathogenic agents into a particular environment and estimates the likelihood of that occurring. **For the purpose of this model, entry assessment will estimate the number of *B. abortus* affected herds (herd with at least one infected individual) and within-herd prevalence in each affected herd in the DSA per year.**

2. The EXPOSURE ASSESSMENT describes the biological pathway(s) necessary for exposure of animals at risk to the hazards released from an affected population. **For the purpose of this model, exposure assessment will estimate the number of *B. abortus* infected breeding shipments per year leaving the DSA in each of the three States into the free portion of that State or any other State.**

3. A CONSEQUENCE ASSESSMENT describes the potential consequences of a given exposure and estimates the probability of the consequence occurring. **For the purpose of this assessment, the consequences will estimate the cost of exposure (receiving an infected shipment), weighted by the probability of receiving an infected shipment, relative to the cost of implementing post-movement testing and reproductive monitoring.**

4. The RISK ESTIMATION summarizes the overall risk from the likelihood of entry or exposure, plus the magnitude of the consequences. **For the purpose of this assessment, the risk estimation summarizes how big the consequences would need to be in order to break-even with the cost of implementing post-movement testing and reproductive monitoring.**

2.2 Model Overview

The model was broken down into several smaller components consistent with the OIE risk assessment process. Model inputs were estimated from the literature or supplied as data from the States. Uncertainty and variability in model parameters were estimated from observed data wherever possible. 1,000 iterations of the model are run to capture uncertainty and increase precision.
Figure 2. Graphic depiction of the pathways for the spread of *B. abortus* out of a DSA.
2.3 Inputs

The parameters described in this document are a representation of the current knowledge of brucellosis ecology, the brucellosis management plans provided for this assessment, and the recent review of the brucellosis management plans. The disease parameters are based on herds affected between calendar years 2002-2013. The model inputs are available in Appendix A.

3. ENTRY ASSESSMENT

For the purpose of this model, entry assessment will estimate the number of \textit{B. abortus} affected herds and within-herd prevalence of each affected herd in the DSA per year. An affected herd is a herd with at least one \textit{B. abortus} infected animal present.

\textit{B. abortus} can enter cattle herds inside DSAs of ID, MT, or WY by contact with three infected pathways:

1. Elk
2. Bison
3. Cattle movement

3.1 Entry Pathways

3.1.1 Elk

Elk are a known pathway for introduction of \textit{B. abortus} into cattle herds within the Greater Yellowstone Area (GYA) in recent years. Since 2002, all documented transmission of \textit{B. abortus} from wildlife to cattle has been attributed to elk, both by extensive epidemiologic investigation and analysis of pathogen genetics (Rhyan et al., 2013). Coarse spatial patterns and temporal trends of \textit{B. abortus} have been described for elk in the GYA (Cross et al., 2010a; Cross et al., 2010b). However, translating spatio-temporal \textit{B. abortus} dynamics in elk into a quantitative infection risk to cattle is not currently feasible. This is because of the seasonal behavior of elk, seasonal management of cattle, and surveillance for \textit{B. abortus} in elk that is not sufficient to quantify transmission to cattle. Therefore, the input into the exposure assessment from the elk entry pathway is described using only the past apparent incidence rate of affected cattle herds (affected herds per year) and apparent within-herd prevalence when the affected herds were detected within the current DSA boundaries.

The advantage of this approach is that the apparent incidence and within-herd prevalence is taken from observed transmission events that have been attributed to the elk entry pathway (Rhyan et al., 2013). The assumptions that accompany this input are that transmission from elk to cattle is restricted to within the DSA boundary and the conditions (disease in elk and cattle management) that produced transmission events since 2002 are constant. The limitations with this approach are that no spatial heterogeneity in risk within DSA can be considered, entry from infected wildlife outside the DSAs is not considered, it is not possible to evaluate the effect of specific elk mitigations, and it is not possible to evaluate the effect of specific cattle herd mitigations.

3.1.2 Bison

Transmission between bison and cattle in the GYA has not been reported (Rhyan et al., 2013). Molecular analyses support elk as the primary pathway for transmission to cattle in the GYA (Higgins et al., 2012). The geographic extent of potential bison to cattle transmission is limited to the northern
and western borders of Yellowstone National Park (YNP) and MT (Shumaker et al., 2012). In addition to having no documented historical bison-to-cattle transmission in the GYA, cattle and bison are intensively managed in these areas to maintain spatio-temporal separation of the species during the transmission risk period (Zaluski, personal communication, 2013). Therefore, this entry pathway represents negligible risk to generate cattle infection and does not contribute to the input into the exposure assessment.

### 3.1.3 Cattle Movement

*B. abortus* transmission among cattle herds is possible from co-grazing with affected herds or the introduction of latently infected or untested animals into a herd (Kellar et al., 1976; Forbes and Steele, 1989; Kadohira et al., 1997; Luna-Martínez and Mejía-Terán, 2002). Of the 18 affected herds from 2002-2013 for which epidemiologic information was available, 4 were affected as a result of introduction from cattle movement. The epidemiological data associated with the investigation indicated that these affected herds were detected as a result of traces from known affected herds with elk as the likely source of infection. Therefore, the calculation of the affected herds from the entry pathway used data from all affected herds to estimate the apparent incidence.

### 3.2 Methods

Because of the challenges with predicting future outbreaks based on the limitations of available data, affected herds are assumed to occur in the future at a rate similar to the rate from 2002-2013. This assumes that the risk within the DSA has not been altered significantly as a result of the current management plan but remains constant. The variability in the rate of affected herds each year is due to the natural variation in risk factors that bring infected elk and cattle together. Consideration was given to only using the most recent years because detection and risk may have changed over 12 years; however, statistical analysis demonstrated no evidence for a change in the rate of apparent incidence (Appendix C). Domestic bison herds were excluded because this risk assessment is specifically addressing the risk of breeding cattle leaving the DSAs. None of the affected bison herds had cattle on the premises.

#### 3.2.1 Estimation of Affected Herds per Year

A Poisson distribution was used to estimate the apparent incidence of affected herds per year. A Poisson process models the average number of events, $\lambda$, that will occur per unit of exposure, $t$ (LLC, 2013). This incidence rate is defined as the number of affected cattle herds per year. Apparent incidence ($\lambda$) was estimated from the observed number of affected herds per year (section 3.3) using direct maximum likelihood. Detailed methods of estimating $\lambda$ from data are presented in Appendix C.

#### 3.2.2 Estimation of Within-Herd Prevalence

A beta distribution was chosen to represent the within-herd prevalence and incorporate the uncertainty associated with the brucellosis transmission processes that generated variability in the observed within-herd prevalence. A data-driven approach was used to estimate the parameters of a beta distribution ($\alpha$ and $\beta$). The parameters for the beta distribution to describe within-herd prevalence were estimated from the observed within-herd prevalence 2002-2013. Detailed methods of estimating the beta distribution parameters from the observed data are presented in Appendix D.
3.3 Model Input

Assuming the rate of newly affected herds (incidence) and within-herd prevalence will occur at a rate similar to the past 12 years, these quantities were estimated based on the historic herd infection data from 2002-2013. The resulting outputs are distributions of the possible number of herds affected per year and the possible within-herd prevalence in affected herds. Details on the data and methods used to estimate these rates are described in Appendix C and Appendix D. The use of State specific parameter estimates did not have statistical support (0 and 0). However, per request from the stakeholders on the working group, State specific parameter values and associated State-specific uncertainty in model-input were used.

To incorporate uncertainty into the simulations which estimate the exposure probability (section 4), a random value for the mean number of affected herds per year (section 3.2.1) was drawn from the distribution of best fitting values to the observed apparent incidence (from within the 95% confidence limits of the maximum likelihood estimate for mean apparent incidence, \( \lambda \); Appendix C). This value was used as the mean apparent incidence in a Poisson distribution to randomly assign the number of affected herds in each iteration. The same procedure was used to assign parameters for mean within-herd prevalence randomly at each iteration of the exposure assessment simulation (beta distribution, \( \alpha \) and \( \beta \); Appendix D).

3.4 Output

3.4.1 Idaho

Five cattle herds were declared affected by USDA:APHIS:VS from 2002-2013. Many years had no affected herds identified while others had as many as two herds (Figure 3 and Appendix C).

![Figure 3. Poisson distribution and observed cases 2002-2013, Idaho.](image)
This rate is interpreted as a probability >0.65 of no affected herds in any given year; however, there is a probability of 0.28 that one affected herd will occur in any given year, and even a smaller probability of more than one.

The within-herd prevalence was calculated based on the reported number of reactor animals and the number of animals in the affected herds. A beta distribution to estimate within-herd prevalence was fit to 4 out of 5 affected herds identified in Idaho; epidemiological information for the 5th herd was not available (Figure 4 and Appendix C).

Figure 4. The within-herd prevalence distribution for Idaho. The dark bars represent the observed data; the light-gray bars represent the fit distribution (Beta (0.923, 8.974)).
3.4.2 Montana

Five cattle herds were declared affected by USDA:APHIS:VS from 2002-2013. Many years had no affected herds identified while some had two (Figure 5 and Appendix C).

![Figure 5. Poisson distribution and observed cases 2002-2013, Montana.](image)

The beta distribution to estimate within-herd prevalence was fit to 4 out of 5 affected herds identified in Montana; epidemiological information for the 5th herd was not available (Figure 6 and Appendix D).

![Figure 6. The within-herd prevalence distribution for Montana. The dark bars represent the observed data; the light-gray bars represent the fit distribution (Beta (0.676, 38.37)).](image)
3.4.3 Wyoming

Eight herds were declared affected by USDA:APHIS:VS from 2002-2013. Many years had no affected herds identified while one year had as many as three herds (Figure 7 and Appendix D).

![Figure 7. Poisson distribution and observed cases 2002-2013, Wyoming.](image1)

The beta distribution to estimate within-herd prevalence was fit to the 8 affected herds identified in Wyoming (Figure 8 and Appendix D).

![Figure 8. The within-herd prevalence distribution for Wyoming. The dark bars represent the observed data; the light-gray bars represent the fit distribution (Beta (0.981, 36.71)).](image2)
4. **EXPOSURE ASSESSMENT**

For the purpose of this model, exposure assessment will estimate the number of *B. abortus* infected breeding shipments leaving the DSA per year in each of the three States into the free portion of that State or any other State.

*B. abortus* can be introduced to cattle herds outside the DSA from:

1. elk
2. cattle movement

Limited data were available to estimate the risk of *B. abortus* infection via infected elk in cattle herds outside of the DSA. Only pathways related to cattle movement will be quantified in this assessment.

4.1 **Exposure Pathways**

4.1.1 **Cattle for Breeding Purposes**

Intact cattle are of particular concern for the spread of *B. abortus*. Last trimester abortions are the typical signal for infected animals (*Samartino and Enright, 1993*). When an infected animal enters a herd and aborts a large numbers of organisms are present in aborted fetuses and tissues (*Samartino and Enright, 1993*).

However, not all infected animals abort. Bred heifers or cows that are exposed during their last trimester may be infected without testing positive on diagnostic tests or aborting. These animals may give live births yet still shed the organism (*Cordes and Carter, 1979*). Excretion via milk does occur with the most excretion during the first week of lactation (*Cordes and Carter, 1979*).

Calves that acquire the infection vertically or by ingesting contaminated milk from seropositive cows may be a potential source of infection (*Wilesmith, 1978*). These calves may neither show clinical signs nor be identified serologically (*Lemaire et al., 2000; Neta et al., 2010*). There are reports of these calves remaining serologically negative until some point during their first pregnancy when they seroconvert and possibly abort (*Nicoletti, 1980*) during the last trimester of their pregnancy (*Samartino and Enright, 1993*). This phenomenon is historically termed the “latent heifer syndrome,” and its existence is often debated.

The “latent heifer” is of concern because of the potential for her to introduce the organism to a herd (*Catlin and Sheehan, 1986*), especially via the large numbers of organisms present in aborted fetuses and tissues (*Samartino and Enright, 1993*). Experimental studies have reported a variety of levels of prevalence for heifers from reactant dams that were seronegative until their pregnancies (*Plommet et al., 1973; Plommet, 1977; Wilesmith, 1978; Crawford et al., 1986*). It is difficult, however, to directly compare these numbers to each other based on their different methods of determining them. These varying prevalence numbers, however, do agree with the general consensus that shedding by latent heifers is variable (*Ray, 1988*). An alternative hypothesis to the “latent heifer syndrome” is that the proportion of heifers identified as seronegative earlier in life and seropositive later in life could fall within the sensitivity of the available serologic diagnostic methods.

Bulls may also become infected, developing orchitis and infertility. Many studies demonstrated that natural transmission from bull to cow is unlikely but artificial insemination with contaminated semen may be a more likely source (*Manthei et al., 1950; Rankin, 1965*).
4.1.2 Cattle for Feeding Purposes
Cattle for feeding purposes are also a potential source for introduction of *B. abortus* into another herd. Cattle moving across State lines destined for feeding channels may be subject to reduced testing or identification requirements. Many of these animals will continue in feeder channels, ultimately leading to slaughter and posing little risk to the rest of the U.S. cattle industry. However, some of these animals will be removed from feeder channels and may pose a risk for spreading of *B. abortus* or other pathogens.

According to the 2011 NAHMS feedlot study, 37% of cattle-on-feed are heifers and heifer calves. Less than 1% are cows and bulls (USDA, 2011). Less than 8% of heifers were pregnant upon arrival to the feedlot (82.1% were treated to abort). However, on average 4% of cattle placed on feed leave the feedlot for non-harvest reasons. These animals may be destined for a cow-calf operation and represent a potential pathway of brucellosis introduction.

4.1.3 Commuter Herds
Commuter herds moving between the DSAs for summer grazing and other areas of ID, MT, or WY or out of State could pose a risk of *B. abortus* introduction and spread outside of the DSAs. The testing requirements for commuter herds (and implementation of these requirements) vary by State. The primary tool for the States to reduce *B. abortus* entry into commuter herds is by setting the earliest allowed entry date.

Herds that reside in the DSAs during elk calving or abortion season may be exposed to *B. abortus* from elk. Most infective elk abortions occur Feb – May, with 95% of elk abortion events occurring by 3-June in WY (Cross et al., 2013). Normal elk calving season is thought to range from 15 May to 15 June (Vore and Schmidt, 2001; Cross et al., 2013) and the infectiousness of elk live-births from *B. abortus* infected cows is uncertain. However, normal birthing behavior of elk includes isolating themselves and cleaning of birthing materials (Barbknecht et al., 2011).

Since the earliest allowed date for commuter herds entering the DSAs is 1-2 weeks after 95% of elk abortion events and normal elk birthing behavior occur, contact is minimized. *B. abortus* entry into commuter herds, and subsequent exposure when commuter herds leave the DSAs, was therefore not considered.

4.2 Methods
A stochastic simulation model was implemented to estimate the number of infected yet undetected shipments leaving the DSAs per year. Definition of a shipment: a batch of animals leaving a single source herd (on the same day) destined for a specific premises type. The destination premises type could be another operation (direct sale) or a market. In the former case, the data (NAHMS for ID and brand inspections for WY and MT) technically break the shipments down by specific destination identity. In the latter case, a single shipment to a market could be broken down and sold to multiple buyers.

However, under the criteria used for source herd detection (detecting at least 1 infected animal), the detection probabilities are not influenced by whether the testing occurs to all animals at once, or in multiple batches because the test outcomes for individual animals are assumed independent and detecting any one infected animal triggers epidemiologic investigations to locate any other animals from that source herd. The objective of the entry and exposure assessment is to quantify the number of infected shipments leaving the DSAs.
Stochasticity was implemented by drawing random values at each iteration of the model simulation for herd-incidence rate (section 3.2.1), within-herd prevalence (section 3.2.2), the number of shipments leaving each herd (section 4.3.2), the size of each shipment leaving a herd (section 4.3.3), the probability that herd received a whole-herd test prior to shipments leaving (section 4.3.6), the probability that the shipment was tested (in the absence of a pre-shipment whole-herd test (section 4.3.6), and the diagnostic sensitivity of the testing process (section 4.3.7). One-thousand iterations of the model were run to capture the stochasticity and output was described in terms of median and 95% confidence limits of the number of infected and undetected shipments leaving the DSAs per year.

The following steps are applied to each State independently and to feeder and breeding shipments separately.

1. Generate the number of herds (DSA).
   a. Estimate the number of herds that reside in the DSA (section 4.3.1).
2. For each herd, randomly assign the number of out-shipments (section 4.3.2).
3. For each herd, randomly assign the number of head per shipment (4.3.3).
4. Calculate the number of animals shipped per herd:
   \[
   \text{Number of animals shipped per herd} = \# \text{ out-shipments} \times \# \text{ head per shipment}
   \]
5. Within the DSA, randomly assign herds as affected or not based on the herd-level prevalence derived in section 3.2..
6. For each affected herd, assign the number of infected animals shipped from a binomial distribution where \( p = \) within-herd prevalence (section 4.3.5) and \( n = \) the total number of animals shipped per herd.
7. Calculate the number of infected shipments:
   \[
   \text{Number of infected shipments} = \text{number of shipments (per affected herd)} \times \text{number of infected animals (per shipment)}
   \]
   (per affected herd) are randomly allocated a number of infected animals from the number of infected animals shipped using a uniform (min,max) distribution where min=1 and max= total number of out-shipments
8. Summarize all infected shipments per herd.
9. Estimate the probability of not detecting at least one infected shipment .

   \[
   \text{The probability of not detecting an infected shipment} = \text{Probability a shipment is not tested} + (\text{Probability a shipment is tested} \times \text{probability it is not detected})
   \]
   a. The probability of testing a shipment will vary for feeder vs. breeding/other herd shipments (see 4.3.6).
   b. Calculate the probability that the shipment is not detected:
      \[
      \text{Probability the shipment is not detected} = (1-Se)^{\text{number of infected animals}}
      \]
      \[
      \text{Whereas Se = test sensitivity (section 4.3.7)}
      \]
10. Estimate the probability of detecting at least one infected shipment in an affected herd

   \[
   \text{The probability that all shipments are not detected} = \text{The probability of not detecting an infected shipment} ^ {\# \text{ number of shipments per herd}}
   \]
11. This last probability is used as the probability of ‘failure’ (i.e., missing infected shipments) in a Bernoulli distribution.

12. Summarize all infected not detected shipments leaving the DSA.
   a. If at least one shipment from a herd is detected, no infected shipments leave that herd.
   b. Includes all infected shipments from herds where no infected shipments were detected.

13. Estimate the number of shipments that will have contact with a herd outside of the DSA.

   \[
   \text{Number of infected shipments that have contact} = \text{Number of infected shipments} \times \text{probability of contact (4.3.8)}
   \]

14. This is run for 1,000 iterations. The results of each iteration are aggregated to create a distribution of the number of infected and undetected shipments leaving the DSA per year.

### 4.3 Model Input

#### 4.3.1 Number of Herds
The total number of resident herds in the DSA (excluding commuter herds) is based on State data. Exact numbers were difficult for States to obtain and may vary over time due to changes in ownership or other business reasons.

- **Idaho**: there are 191 herds in Idaho’s DSA per the Idaho Department of Livestock (Lawrence, personal communication, 2013).
- **Montana**: the State provided data for this report indicating 296 herds within the DSA.
- **Wyoming**: previous review of Wyoming data indicates there are 432 herds in the DSA.

#### 4.3.2 Number of Out-shipments per Herd
When available, data were used directly from the State. The State brand inspection data from MT and WY provides the total number of shipments and animals per shipment. These shipments were divided into feeder or breeding channels based on purpose codes provided by the State data. Any shipment without a purpose code that had sexually intact animals was categorized into breeding channels; which is consistent with the testing protocol administered in each State. Shipments going directly to slaughter were not included.

When data were not available from the State, the number of shipments per herd was generated from a special NAHMS query for each State. The proportion of shipments destined for feeding vs breeding channels was estimated from the National Agriculture Statistics Service (NASS) Census of Agriculture and NAHMS survey data.

Detailed methods by State are presented in Appendix E.

#### 4.3.3 Number of Head per Shipment
When available, data were used directly from the State data described above by creating a distribution to fit the data. When not available, this number was generated from a special NAHMS query for each State. Detailed methods by State are presented in Appendix E.
4.3.4 Number of Affected Herds
The number of affected herds per year (incidence) is randomly assigned based on Poisson distributions fit to each States’ historical herd infection rate (section 3.4).

4.3.5 Within-Herd Prevalence
The within-herd prevalence for each affected herd is randomly assigned based on beta distributions fit to each States’ historical within-herd rates when herds were detected (section 3.4).

4.3.6 Probability of Being Tested
All shipments of breeding animals were assumed to be intact test-eligible animals; State rules require such shipments to be tested. The probability of testing breeding shipments was assumed to be 1, although this could not be verified with available data. Matching the test records to shipments, or even herds, was not possible.

Of the feeding shipments, 0.37 were anticipated to be in-tact and test eligible based on the NAHMS 2011 Feedlot Study (USDA, 2011).

4.3.7 Diagnostic Sensitivity
The testing protocol most frequently used is the Rapid Automated Presumptive Test (RAP), Complement Fixation (CF), and the Fluorescence Polarization Assay (FPA). Assuming these tests are independent, the sensitivity of each test was modeled in a testing-in-series approach. The values used to estimate the sensitivity for each test was derived from the literature (EFSA, 2006) or Veterinary Service’s (VS) internal reports.

Table 1. Sensitivity for each diagnostic test used for standard diagnosis of B. abortus

<table>
<thead>
<tr>
<th>Test</th>
<th>Parameters (Minimum, Most likely, Maximum)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rapid Automated Presumptive Test</td>
<td>0.63, 0.9, 0.97</td>
<td>VS Internal</td>
</tr>
<tr>
<td>Fluorescence Polarization Assay</td>
<td>0.981, 0.987, 0.992</td>
<td>(EFSA)</td>
</tr>
<tr>
<td>Complement Fixation Test</td>
<td>0.72, 0.96, 0.97</td>
<td>VS internal, (EFSA)</td>
</tr>
</tbody>
</table>

The resulting sensitivity of the process is a Beta (25,6.5) (Figure 9).
4.3.8 Probability of Contact with Another Herd

- **Breeding**: All shipments received for breeding purposes were assumed to have contact with another herd (p=1).

- **Feeding**: According to a recent NAHMS survey, slightly less than 4% of all cattle placed on feed left the feedlot for nonharvest reasons during each of the three study years (USDA, 2011). The probability of an animal in feeder channels contacting another herd was 0.04.

### 4.4 Outputs

The final outputs generated are (Table):

- Annual probability of exposure = Total number of infected yet undetected shipments leaving the DSA per year by State.

- Average time between infected yet undetected shipments = 1 / annual probability of exposure.

- Per shipment probability of exposure = Total number of infected yet undetected shipments leaving the DSA per year / total shipments in a year by State.

The probability that an infected breeding shipment of cattle will leave any of the three States’ DSAs undetected is low (0.027). This would average to about one infected shipment leaving any of the three States’ DSAs every 37 years, although it could be more or less frequent. When post movement testing and reproductive monitoring is added, the probability of an infected breeding shipment remaining undetected is further reduced (0.001-0.010) (Table 3).
Table 2. Output for Exposure Assessment: Number of infected breeding shipments leaving the DSA per year, by State, and by all 3 States. This assumes all States are in full compliance with their Brucellosis Management Plans (i.e., testing 100% of breeding shipments leaving the DSA).

<table>
<thead>
<tr>
<th>State</th>
<th>Estimated number of breeding shipments per year</th>
<th>Annual Probability of Exposure [99th percentile]</th>
<th>Years per 1 average exposure</th>
<th>Average exposure per 1000 shipments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Idaho</td>
<td>~250</td>
<td>0.006&lt;sup&gt;b&lt;/sup&gt;</td>
<td>167</td>
<td>0.024</td>
</tr>
<tr>
<td>Montana</td>
<td>~1000</td>
<td>0.009&lt;sup&gt;b&lt;/sup&gt;</td>
<td>111</td>
<td>0.009</td>
</tr>
<tr>
<td>Wyoming</td>
<td>~850</td>
<td>0.020&lt;sup&gt;b&lt;/sup&gt;</td>
<td>50</td>
<td>0.024</td>
</tr>
<tr>
<td>Combined DSAs</td>
<td>~2100</td>
<td>0.027&lt;sup&gt;b&lt;/sup&gt;</td>
<td>37</td>
<td>0.013</td>
</tr>
</tbody>
</table>

<sup>a</sup> Total number of infected yet undetected shipments leaving the DSAs per year destined for breeding herds.

<sup>b</sup> Calculated based on methods and inputs in Section 3.3 & 4.3

Table 3. Comparison of probability of exposure without and with post-entry testing of all shipments. The probability of exposure (and an outbreak occurring) is reduced with post-entry testing of every shipment from the DSAs.

<table>
<thead>
<tr>
<th>Average Exposure per Year</th>
<th>Exposure Assessment</th>
<th>With post-entry mitigations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Idaho</td>
<td>0.006</td>
<td>&lt;0.001 - 0.002</td>
</tr>
<tr>
<td>Montana</td>
<td>0.009</td>
<td>&lt;0.001 – 0.003</td>
</tr>
<tr>
<td>Wyoming</td>
<td>0.020</td>
<td>&lt;0.001 – 0.005</td>
</tr>
<tr>
<td>Full testing per DSA plan</td>
<td>0.027</td>
<td>0.001 – 0.010</td>
</tr>
</tbody>
</table>

5. **CONSEQUENCE ASSESSMENT**

A consequence assessment is an integral part of the risk assessment process because it puts in context the likelihood of entry and exposure of the hazard relative to alternative mitigations. Another way of stating this is that the consequence assessment quantifies the benefits of management choices, i.e., mitigations, relative to their cost. In this case the mitigation is the additional post-movement testing and reproductive monitoring and the benefit is the costs avoided by preventing brucellosis incursion (i.e., outbreak) outside the GYA.

Because brucellosis outbreaks outside of the GYA are rare, estimating biological consequences of an introduced breeding animal into a herd outside the GYA will be very imprecise, involve many assumptions, and come with much uncertainty. Therefore, the consequence assessment is focused on what can be estimated from the data available for this risk assessment with the goal of estimating a break-even value for implementing post-entry testing and reproductive monitoring. Equation 1 gives an idea of how big an outbreak must be in order to recover the costs spent on post-movement testing and reproductive monitoring of all DSA-origin breeding cattle.
5.1 Methods and Input Data

5.1.1 Break-Even Value of Mitigation

The break-even value of mitigation is defined as the point where the cost of the consequences (i.e., outbreak) equals the cost to maintain the mitigation (i.e., post-movement testing). (e.g., break-even value equal to 1, Figure 10).

![Figure 10. Conceptual diagram of weighted consequences and associated costs.](image)

Figure 10 weights the cost of mitigations by the probability that the consequences are incurred. The break-even value of the mitigation (post-movement testing) is:

\[
\text{break even value} = \frac{\text{benefits (outbreaks costs avoided)}}{\text{cost of maintaining post entry testing}} = \frac{C(c) \cdot P(e) \cdot (1 - P(m))}{C(m)} = 1
\]

Appendix G describes the values obtained of estimates for the probability of exposure \(P(e)\) the effectiveness of the mitigation \(P(m)\), and the cost of the mitigation \(C(m)\). This leaves the consequences and the cost of the consequences \(C(c)\) as the unknowns, but allows the estimation of the break-even value. Estimating biological consequences and the cost of those consequences is beyond the scope of this assessment due to the lack of readily available information on disease dynamics and the movement of cattle between herds. The best information available is the experience of reducing brucellosis from a common disease to near-eradication, but nothing on the potential spread of brucellosis as a very rare disease is available. The uncertainty in attempting to quantify this would likely be so large as to prevent any meaningful estimate in the context of this risk assessment.

Lastly, this analysis is for post-movement testing and reproductive monitoring of all shipments leaving the DSAs of the GYA States, to any other State, regardless of destination. The cost is based on the protocol currently used by the State of Texas for DSA-origin breeding cattle (Appendix F).
However, the cost of applying the mitigation is scalable based on the size, composition, and number of shipments a State received. The scaling is valid under the assumption that all potential destinations of DSA cattle have equal probability of receiving an infected and undetected animal.

### 5.2 Output

#### 5.2.1 Average Cost of Post-entry Monitoring of DSA Origin Breeding Cattle

The cost of post-entry mitigation depends on the type of breeding cattle in a shipment and is a function of how long health monitoring occurs and the number of serological tests pre- and post-calving (Appendix E).

- The expected cost to test shipments with only males is approximately $338.
- The expected cost to test shipments with bred females is approximately $1,966.
- The expected cost to test shipments with one or more un-bred females is $3,282.

The estimated total number of breeding shipments originated from all DSAs is 2,096 (see Appendix E for breakdown by type) and the total cost to test all breeding shipments is estimated to be $4.05M.

#### 5.2.2 Break-Even Value of Mitigation

The median estimate of the break-even value of an outbreak ranges from approximately $150M to $234M (Table 4). The upper and lower limits were determined based on the minimum estimate for serological sensitivity to detect one infected animal and a high detection probability based on both serological testing and direct monitoring of calving (Appendix G).

<table>
<thead>
<tr>
<th>Total Cost of Maintaining Mitigation for 1 year: $4,047,444</th>
<th>Estimated break-even value of mitigation</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean infected shipments per year: 0.027 (section 4.4)</td>
<td></td>
</tr>
<tr>
<td>Probability of detection, $P(m)$</td>
<td></td>
</tr>
<tr>
<td>Low detection (only serological sensitivity) 0.64</td>
<td>$234,227,083</td>
</tr>
<tr>
<td>High detection (direct observation and serological sensitivity) 0.99</td>
<td>$151,419,528</td>
</tr>
</tbody>
</table>

### 6. Risk Estimation/Conclusion

The risk estimation suggested that a break-even value for post-movement testing and reproductive monitoring of all DSA origin breeding cattle, weighted by the exposure and mitigation effectiveness, would be in the $100-$300 million range. In other words, this is the cost that an outbreak would have to be to equal the cost of applying the post-movement risk mitigation for as long as necessary to detect an exposure event and prevent outbreak. Based on the best available past knowledge about *B. abortus* epidemiology and surveillance, an outbreak outside the GYA would likely have to be larger than what the current slaughter surveillance is designed to detect to incur economic costs of $100M or more (Appendix G).
The primary driver of this risk estimation is the low probability that infected breeding cattle will leave the DSAs undetected. The low probability (0.02-0.03 infected undetected shipments per year) is based on the observed affected-herd prevalence, within-herd prevalence, and surveillance rate within the DSAs from 2002-2013. Since 2002 all of the observed index infections of *B. abortus* in the GYA States have been linked to infection from elk (Rhyan et al., 2013) and a key assumption of this risk estimation is that the ecological conditions that have generated the spillover from elk are relatively constant. A second key assumption underlying this risk estimation is that all risk is contained within the DSAs. However, current knowledge of GYA’s elk ecology and epidemiology of *B. abortus* points to changing distributions of elk and increasing infection in some elk herds (Cross et al., 2010a; Cross et al., 2013). All affected cattle herds since 2002 are within current DSA boundaries, but the boundaries have changed over time due to the detection of infected cattle or elk directly outside of the DSAs.

The lack of knowledge about the epidemiology of *B. abortus* and ecology of elk prevented evaluation of how variation in elk affect elk-to-cattle transmission events, as well as any inference of risk to cattle from elk outside of the current DSA boundaries. This is a major information gap that prevented any explicit incorporation of elk data in to this risk assessment (Appendix H). This data gap potentially limits the applicability of this risk model and results as conditions in the GYA change, or if infection is found in cattle outside of the DSA boundaries, as a result from elk infection.

Another limitation to the repeatability of this risk assessment framework is the limitations on State movement data. Data for movement, premises location, and testing were in different locations in each State. While some data were available electronically, linking the premises, movements, and test together was not always possible and assumptions had to be made. In many cases, the exact count of premises in the DSA or number of shipments from the DSA was unknown. It was not possible to verify that 100% of breeding shipments were tested per each States’ Brucellosis Management Plan. Without electronic data in Wyoming, paper movement records had to be hand entered, which is both costly and time consuming. Fortunately, simulations using data from NAHMS and NASS gave very similar results to the outputs using the States’ data.

The potential impact on our risk estimation of these data limitations was evaluated using a model sensitivity analysis (Appendix B). This analysis suggests that data and information limitations that influence knowledge of variation and mechanisms that potential change entry parameters have the most influence on the exposure output (the number of infected yet undetected shipments leaving the DSAs per year). That is, the limitations about epidemiology, geographic extent, and dynamics of *B. abortus* in elk have the largest impact on the applicability of this risk assessment. However, the sensitivity analysis suggests that uncertainty in the shipment characteristics have little influence on the risk estimation.

Existing knowledge did not allow for an assessment of likely biological consequences, such as time to detection, within and between herd transmission rates, number of affected herds, and spatial extent of affected herds in the event of a *B. abortus* outbreak outside the GYA. As a result the economic consequences could not be expressed as how much an outbreak would cost rather how much it would need to cost in order to equal the amount of testing necessary to detect an outbreak. This analysis

---

1 As of October 2014, Montana has increased their DSA boundaries and Wyoming has instituted additional cattle surveillance outside their DSA boundaries in response to the detection of infected elk during the 2013-2014 winter.
suggests that post-movement testing is not cost-effective given the low exposure probability (0.02-0.03 per year or 0.01-0.025 per 1,000 breeding shipments) and amount of testing necessary (40-60 years or 80,000-120,000 shipments) to prevent such a low probability event.
7. REFERENCES


LLC, E., 2013. ModelAssist for @RISK (2.0). Boulder, CO


## Appendix A. ENTRY AND EXPOSURE ASSESSMENT INPUTS

Table A 1. Inputs for entry and exposure assessments

<table>
<thead>
<tr>
<th>Variable</th>
<th>Idaho Baseline</th>
<th>Montana Baseline</th>
<th>Wyoming Baseline</th>
</tr>
</thead>
<tbody>
<tr>
<td>Affected-herd yearly incidence ($\lambda$)</td>
<td>Poisson(0.41)</td>
<td>Poisson(0.33)</td>
<td>Poisson(0.67)</td>
</tr>
<tr>
<td>(Section 3.2.1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Se (diagnostic process)</td>
<td>Beta (25,6.5)</td>
<td>Beta (25,6.5)</td>
<td>Beta (25,6.5)</td>
</tr>
<tr>
<td>(Section 4.3.7)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sp (diagnostic process)</td>
<td>Beta (599,1)</td>
<td>Beta (599,1)</td>
<td>Beta (599,1)</td>
</tr>
<tr>
<td>(Section 4.3.7)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of herds</td>
<td>179</td>
<td>296</td>
<td>432</td>
</tr>
<tr>
<td>(Section 4.3.1)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Within-herd prevalence</td>
<td>Beta (0.92,8.97)</td>
<td>Beta (0.68,38.37)</td>
<td>Beta (0.98,36.71)</td>
</tr>
<tr>
<td>(Section 3.2.2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Probability of being tested (breeding)</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>(Section 4.3.6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of breeding shipments</td>
<td>244</td>
<td>996</td>
<td>844</td>
</tr>
<tr>
<td>(Section 4.3.2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of breeding animals shipped</td>
<td>13,089</td>
<td>43,308</td>
<td>19,378</td>
</tr>
<tr>
<td>(Section 4.3.3)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Distribution of animals per shipment</td>
<td>Depends on size of operation</td>
<td>Weibull-parameters vary by field/market</td>
<td>Weibull-parameters vary by field/market</td>
</tr>
<tr>
<td>(Section 4.3.3)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Probability of being tested (feeding)</td>
<td>0.37</td>
<td>0.37</td>
<td>0.37</td>
</tr>
<tr>
<td>(Section 4.3.6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of feeder shipments</td>
<td>145</td>
<td>1,622</td>
<td>844</td>
</tr>
<tr>
<td>(Section 4.3.2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of feeder animals shipped</td>
<td>19,693</td>
<td>38,768</td>
<td>46,754</td>
</tr>
<tr>
<td>(Section 4.3.3)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Appendix B. MODEL SENSITIVITY ANALYSIS

The inputs into the entry and exposure assessment are estimated from data. There is always uncertainty in the estimation of any parameters from data. The characterization of that uncertainty and its impact on model outcomes is important to interpreting the robustness of a model. The parameters and associated uncertainty used to estimate entry and exposure risk were taken from data, to the extent possible, and a rigorous sensitivity analysis over a broad range of parameter values is presented here.

A Latin-Hypercube Sampling design (LHS) (Blower, 1994) was used to explore the effect of parameter uncertainty in the entry and exposure assessments for the parameters describing:

- herd incidence rate, \( \lambda \) (section 3.2.1; Appendix C),
- within-herd prevalence (section 3.2.2, Appendix D),
- number of out-shipments per herd (section 4.3.2; Appendix E),
- size of shipments (section 4.3.3; Appendix E),
- diagnostic sensitivity of the serological surveillance test series (section 4.3.7), and
- proportion of shipments being tested (section 4.3.6).

B.1 Parameter Value Ranges

Because there was no statistical evidence of State differences in herd incidence (\( \lambda \)) and within-herd prevalence (WIP \( \alpha \), WIP \( \beta \)), single data-derived parameter estimates for all States were used to evaluate sensitivity. The ranges of entry parameters evaluated in the sensitivity analysis included the 95% maximum likelihood confidence intervals +/- 10%: \( \lambda \) [0.28, 0.73], WIP \( \alpha \) [0.35, 1.13], and WIP \( \beta \) [15.17, 30.02] (Appendix C; Appendix D).

The number of shipments per herd and shipment size was estimated in the exposure assessment from State-specific brand inspection data. To assess sensitivity of these estimates, two scaling parameters, one for the number of shipments and the other for shipment size, were varied to assess changes of +/- 20% to the number of shipments per affected herd and the number of animals per shipment. The scaling was applied equally to breeding and feeding shipments.

The parameter values for the diagnostic sensitivity were varied by +/- 20%: Diagnostic \( \alpha \) [20, 30] and \( \beta \) [5.2, 7.8].

The value used for proportion of shipments being tested in the exposure assessment was 100%. The sensitivity was assessed for reduced proportions to 50%: [0.5, 1].

The range of values for each parameter was divided into 100 equal-probability intervals and one value was randomly sampled from each interval with uniform probability (LHS design) (Blower, 1994). Parameter sets were created by randomly combining the 100 sampled values for each parameter and simulations were run for 1,000 iterations at each parameter set. Only the shipment characteristics from Wyoming were used to assess the sensitivity because the sensitivity analysis was meant to assess the influence of parameters on the outputs and not evaluate state-specific sensitivities.
B.2 Sensitivity Output

To determine sensitivity, a partial-rank correlation coefficient (PRCC) was used with the exposure assessment output (number of infected yet undetected shipments leaving the DSAs per year) as the response variable (section 4.4). The PRCC value identifies the strength and direction of correlation between the parameter values and the response variable, accounting for the effects of variation in all other parameters. The PRCC is a non-parametric metric of sensitivity that ranges from -1 to 1, where the PRCC value corresponds to the relative strength of sensitivity and not an absolute relationship between parameter value and model output. Positive values of the PRCC indicated that increasing the parameter had a positive effect on the model output and negative values indicated a negative effect. The significance of the sensitivity was determined at the 95% level based on the t-statistics for the coefficient partial rank correlations.

The parameters with the strongest correlation to the number of infected yet undetected shipments leaving the DSAs per year were the affected-herd incidence rate and the proportion of shipments tested (Figure B-1). The affected herd incidence rate had a positive correlation with the response. That means increasing the number of affected herds per year increased the number of infected yet undetected shipments leaving the DSAs per year, accounting for the variation in all other parameters. The proportion of shipments tested had a negative response, meaning that testing a smaller proportion of shipments increased the number of infected yet undetected shipments leaving the DSAs per year, accounting for the variation in all other parameters.

The exposure output was also sensitive to the parameters that determined the distribution of within-herd prevalence (WIP $\alpha$, WIP $\beta$). While, the parameters had opposite relationship with the number of infected yet undetected shipments leaving the DSAs per year, together this can be interpreted as increasing within-herd prevalence increased the number of infected yet undetected shipments leaving the DSAs per year. Within the relative ranges of these parameters (WIP $\alpha$ << WIP $\beta$), larger values of WIP $\alpha$ increases the mean of the Beta distribution and smaller values of WIP $\beta$ increase the variance of the distribution.

The exposure output was also significantly sensitive to increasing shipment size, although the strength of that sensitivity was weak, relative to affected-herd incidence, within-herd prevalence, and shipment testing. The exposure output was not sensitive the the number of shipments nor the diagnostic sensitivity.

Finally, given the range of parameter variability used to assess sensitivity, the exposure output (the number of infected yet undetected shipments leaving the DSAs per year) ranged from 0.013 to 0.188 (Figure B-1).
Figure B-1. Partial rank correlation coefficient (PRCC) of sensitivity of exposure assessment output to uncertainty in input parameter values.

(A) The magnitude of the PRCC value indicates the relative influence of the parameter on the exposure assessment output. Positive or negative PRCC values indicate that increasing the parameter value had a positive or negative effect on the exposure assessment output, respectively. Dashed lines indicate the 95% significant cut-offs for the magnitude of the PRCC value.

(B) The range of exposure assessment output values produced from the 100 combination of input parameters. The horizontal line is the median value, the box represents the 25%-75% interquartile range, and the whiskers display the maximum and minimum values. The exposure assessment output was defined as the number of brucellosis infected and undetected shipments, leaving a single GYA State’s DSA, and destined for a breeding herd in an average year.
Appendix C. Expanded Methods: Estimating Incidence

This appendix describes the data and methods used to generate the distributions for the affected-herd incidence rate (section 3.2.1).

C.1 Data: Herd Infection Rates

The data to parameterize the distributions used to generate the affected-herd incidence rate was obtained from VS’s epidemiological investigations of confirmed brucellosis affected cattle herds from 2002-2013 (Table C-1). The year was assigned based on the calendar year when the herd was confirmed brucellosis affected by the National Veterinary Services Laboratories (NVSL).

<table>
<thead>
<tr>
<th>Year</th>
<th>Affected Herds, Idaho</th>
<th>Affected Herds, Montana</th>
<th>Affected Herds, Wyoming</th>
</tr>
</thead>
<tbody>
<tr>
<td>2002</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2003</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2004</td>
<td>0</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>2005</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2006</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2007</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2008</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2009</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2010</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2011</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2012</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2013</td>
<td>0</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>5</td>
<td>5</td>
<td>8</td>
</tr>
</tbody>
</table>

C.2 Poisson Distributions and Parameter Fitting from Data

The Poisson statistical distribution was chosen to represent the affected-herd rate and incorporate the uncertainty associated with the brucellosis transmission processes in generating variability in the number of affected herds per year. A data-driven approach was used to estimate the parameter of a Poisson distribution (\(\lambda\)) given the observed yearly affected-herd incidence from 2002-2013. The methods are outlined in two steps:

C.2.1 Estimate the Parameters Given the Data

The population of interest that a distribution is to make inference to is the herds within the DSAs that may be potentially exposed to brucellosis. The Poisson distribution estimates a rate (events per time), where the event of interest is the detection of brucellosis in cattle herds. The Poisson distribution uses a single parameter, \(\lambda\), that describes the average incidence of affected herds (Bolker, 2008). The parameter \(\lambda\) was estimated from the data using direct maximum likelihood methods (Bolker, 2013). A State specific effect (ID, MT, or ID) and a relationship with year (continuous explanatory variable) was evaluated by fitting a series of nested generalized linear models with Poisson distributed errors and using a drop-in-deviance \(\chi^2\) test to compare whether estimating parameters for more complicated generalized linear models provided a better fit to the number of affected herds per year (Table C-1).
than simpler models. The drop-in-deviance $\chi^2$ statistic tests the null hypothesis that a more complex model provides an equivalent fit to data to a simpler model; for this reason a $P$-value $< 0.05$ indicates a model with more parameters is a better fit to the data. The process begins with a full model with the interaction of year and State and sequentially tested the nested reduced models.

The full model with an interaction between year and State (different average affected-herd rates and trends with year in each State) did not provide a better fit to data than a reduced model with an additive effect of year and State (different average affected-herd rates and the same trend with year in each State; $\chi^2 = 2.5$, d.f. = 2, $P$-value = 0.28). There was no difference in the fit to data between the model with a year and State additive effect, a model with only year (no difference among States with a time trend; $\chi^2 = 1.50$, d.f. = 2, $P$-value = 0.47), or a model with only State (different average affected-herd rate among States, no trend with time; $\chi^2 = 2.7$, d.f. = 1, $P$-value = 0.60). Finally, there is also no evidence of a different affected-herd rate by State ($\chi^2 = 1.5$, d.f. = 2, $P$-value = 0.47) or by year ($\chi^2 = 0.28$, d.f. = 1, $P$-value = 0.59) when each is compared to null model with a single affected-herd rate for all States from 2002-2013. There is no statistical evidence that the rate parameters were different by State, nonetheless, at the request of stakeholders each parameter was estimated independently for each State and the increased uncertainty of the parameter estimates will be accounted for with a sensitivity analysis (Table C-2).

**Table C-2. Affected herd rate maximum likelihood estimates**

<table>
<thead>
<tr>
<th>Data</th>
<th>Average rate (A)</th>
<th>95% lower confidence limit</th>
<th>95% upper confidence limit</th>
</tr>
</thead>
<tbody>
<tr>
<td>All States</td>
<td>0.47</td>
<td>0.28</td>
<td>0.73</td>
</tr>
<tr>
<td>Idaho</td>
<td>0.41</td>
<td>0.15</td>
<td>0.90</td>
</tr>
<tr>
<td>Montana</td>
<td>0.33</td>
<td>0.10</td>
<td>0.77</td>
</tr>
<tr>
<td>Wyoming</td>
<td>0.67</td>
<td>0.30</td>
<td>1.24</td>
</tr>
</tbody>
</table>

**Limitation:** This analysis is meant to test for trends in observed rates of confirmed brucellosis affected herds only, not to make inference to true affected-herd rate that considers unobserved affected herds.

**C.2.2 Goodness of Fit**

Just because parameters can be estimated, given the data, that doesn’t mean the parameters and the assumed beta distribution accurately describes the data. A formal goodness-of-fit test was performed to confirm that the assumption of a Poisson distribution, and the estimated parameters, provide an adequate characterization of the data. The goodness-of-fit test used a $\chi^2$ that compares the observed frequency of counts (from 0 to the maximum observed affected herds in a year) of affected herds per year to the expected value from the maximum likelihood estimated Poisson rate, $\lambda$. This test evaluates the null hypothesis that the data are not different than a specified distribution. For this reason, a rejection of the null hypothesis ($P$-value $< 0.05$) indicates the distribution and estimated parameters are not reasonable to describe the data.

The $\chi^2$ goodness-of-fit test indicates the Poisson distribution is an adequate distribution to describe the frequency of affected herds per year across all States ($\chi^2 = 2.17$, d.f. = 1, $P = 0.14$). The small sample sizes of affected herds per State make formal goodness-of-fit testing unreliable, however visual inspection of the expected frequency of affected herds per year compared to the observed values indicate that the Poisson distribution is adequate (3.4).
Appendix D. Expanded Methods: Within-Herd Prevalence

This appendix describes the data and methods used to generate the distributions for within herd prevalence in the exposure assessment (section 4.3.5).

D.1 Data: Within-Herd Prevalence

The data to parameterize the distributions used to generate within-herd prevalence was obtained from Veterinary Services (VS) epidemiological investigations of confirmed brucellosis affected cattle herds from 2002-2013 (Table D-1). The year was assigned based on the calendar year the herd was confirmed brucellosis-affected by the NVSL. Within-herd prevalence data from known brucellosis affected ranched bison herds was not included. In one case, an affected cattle herd was discovered as a result of a trace-investigation from movement; the number of test-positive and exposed (herd size) was added back to the origin herd. The data for within-herd prevalence reflects the transmission from the index wildlife exposure.

Table D-1. Data used to generate within-herd prevalence distributions of *B. abortus*.

<table>
<thead>
<tr>
<th>Year</th>
<th>Test-Positive</th>
<th>Herd size</th>
<th>Year</th>
<th>Test-Positive</th>
<th>Herd size</th>
<th>Year</th>
<th>Test-Positive</th>
<th>Herd size</th>
</tr>
</thead>
<tbody>
<tr>
<td>2002</td>
<td>6</td>
<td>50</td>
<td>2007</td>
<td>NA</td>
<td></td>
<td>2004</td>
<td>40</td>
<td></td>
</tr>
<tr>
<td>2006</td>
<td>NA</td>
<td></td>
<td>2008</td>
<td>1</td>
<td>27</td>
<td>2004</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>2006</td>
<td>8</td>
<td>41</td>
<td>2011</td>
<td>6</td>
<td>204</td>
<td>2004</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2010</td>
<td>3</td>
<td>577</td>
<td>2013</td>
<td>1</td>
<td>506</td>
<td>2005</td>
<td>4</td>
<td>370</td>
</tr>
<tr>
<td>2012</td>
<td>6</td>
<td>98</td>
<td>2013</td>
<td>2</td>
<td>1505</td>
<td>2008</td>
<td>36</td>
<td>656</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2010</td>
<td>5</td>
<td>453</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2011</td>
<td>5</td>
<td>562</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2012</td>
<td>3</td>
<td>447</td>
</tr>
</tbody>
</table>

a There were 5 known affected herds in Idaho from 2002-2013; epidemiological investigation data was not available for 1 herd and it was omitted from calculation of within-herd prevalence rate

b There were 5 known affected herds in Montana from 2002-2013; epidemiological investigation data was not available for 1 herd and it was omitted from calculation of within-herd prevalence rate

c Herd size was recorded as the number of cattle potentially exposed to the known wildlife transmission.

D.2 Beta Distribution and Parameter Fitting from Data

The beta statistical distribution was chosen to represent the within-herd prevalence and incorporate the uncertainty associated with the brucellosis transmission processes that generate variability in the observed within-herd prevalence. A data-driven approach was used to estimate the parameters of a beta distribution (α and β) given the observed within-herd prevalence for 2002-2013.

D.2.1 Parameter Estimation

The population of interest a distribution makes is the herds within the DSAs that may be potentially exposed to brucellosis. The beta distribution estimates a variable probability of success based on observed affected herds, where success is an animal being infected. The beta distribution is an appropriate distribution to describe the observed patterns of within-herd prevalence. It is a continuous
value with lower and upper bounds and has a flexible parameterization of variance; the variance can be greater than the mean.

The beta parameters, $\alpha$ and $\beta$, were estimated from the data using direct maximum likelihood methods (Bolker, 2013). A State specific effect (ID, MT, or ID) on the beta parameters was evaluated by fitting a generalized linear model with beta distributed errors (Cribari-Neto and Zeileis, 2010) with State as a co-variate and using a likelihood ratio test (Bolker, 2013; Hothorn et al., 2014) to compare whether estimating parameters for each GYA State provided a better fit to the data than estimating one set of parameters of all States. The results of the LRT indicated there is not statistical evidence to suggest the within-herd prevalence differs among States (LRT $P$-value = 0.17, $d.f. = 4$) (Figure D-1).

Nonetheless, there is visual evidence to suggest that the distribution of within-herd prevalence may be different among the 3 States (3.4) and the GYA States requested each State be considered separately. Thus, beta parameters were estimated for each State independently and the increased uncertainty of the parameter estimates will be accounted for with a sensitivity analysis (Table D-2).

Figure D-1. Box and whisker plots of the observed within-herd prevalence by State, 2002-2013. The solid line indicates the median within-herd prevalence, the boxes display the 1st and 3rd quartile and the whiskers display 2.5% and 97.5% quartiles of the values.
Table D-2. Beta distribution parameter estimates of within-herd prevalence

<table>
<thead>
<tr>
<th></th>
<th>Maximum likelihood parameter estimate</th>
<th>95% lower confidence limit</th>
<th>95% upper confidence limit</th>
</tr>
</thead>
<tbody>
<tr>
<td>All States</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α</td>
<td>0.654</td>
<td>0.346</td>
<td>1.126</td>
</tr>
<tr>
<td>β</td>
<td>15.17</td>
<td>5.901</td>
<td>30.02</td>
</tr>
<tr>
<td>Idaho</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α</td>
<td>0.923</td>
<td>0.244</td>
<td>2.594</td>
</tr>
<tr>
<td>β</td>
<td>8.974</td>
<td>1.581</td>
<td>29.90</td>
</tr>
<tr>
<td>Montana</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α</td>
<td>0.676</td>
<td>0.163</td>
<td>1.851</td>
</tr>
<tr>
<td>β</td>
<td>38.37</td>
<td>3.834</td>
<td>136.7</td>
</tr>
<tr>
<td>Wyoming</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>α</td>
<td>0.981</td>
<td>0.372</td>
<td>2.113</td>
</tr>
<tr>
<td>β</td>
<td>36.71</td>
<td>8.972</td>
<td>91.68</td>
</tr>
</tbody>
</table>

Limitation: This analysis is meant to describe observed within-herd prevalence of confirmed brucellosis affected herds only. It does not make inference about mechanisms of the transmission process that considers variation in infection source (Nishi et al., 2002) or herd management.

D.2.2 Goodness of Fit

Just because parameters can be estimated, given the data, that doesn’t mean the parameters and the assumed beta distribution describe the data well. Visually, these parameter estimates do appear to provide an adequate characterization of the data (Figure, Figure 6, Figure 8). In addition, a formal Anderson-Darling (AD) goodness-of-fit test was performed (Stephens, 1974). An AD test evaluates the null hypothesis that the data are not different than a specified distribution. A rejection of the null hypothesis (P-value < 0.05) indicates that the distribution and estimated parameters are not reasonable to describe the data. The results of the AD goodness-of-fit test indicate that the estimated beta parameters for all States combined (AD P-value = 0.7) and Wyoming (AD P-value = 0.3) are statistically valid to describe the data. The small sample size of the data from Montana and Idaho do not allow formal goodness-of-fit testing. The recommendation is to use a single set of beta parameters for all three GYA States because there is no statistical evidence that the distribution of within-herd prevalence is different and the larger sample size to estimate beta parameters using all States data reduces the overall parameter uncertainty. However, to accommodate the request that the States be evaluated separately, the increased uncertainty of the State-specific parameter estimates are incorporated into a sensitivity analysis.
Appendix E. EXPANDED INPUT: EXPOSURE ASSESSMENT

E.1 Idaho

For Idaho, the available data could be used to estimate the total number of shipments leaving the DSA, but no data were available to directly estimate the number of out-shipments per herd. Therefore, the number of cattle per herd was used to indirectly estimate the number of shipments per herd. The number of cattle per herd was randomly assigned using NASS 2007 Agricultural Census data from the counties that have any area in the DSA (Fremont, Teton, Bonneville, and Caribou). NASS reports the number of herds by county and size category (1-9, 10-19, 20-49, 50-99, 100-199, 200-499, 500+). A uniform distribution was used to assign a number of animals to each herd within each size category. The upper limit of the largest size class was set at 3,300 so that the estimated inventory matched the published inventory from the NASS census. In Idaho, the number of cattle per herd was then used to estimate the number of shipments and shipment size.

E.1.1 Using NAHMS Data to Generate Number of Shipments and Shipment Size for Idaho

The 2007/2008 NAHMS Beef Study has a representative sample of beef operations from ID, MT, and WY. Data collected for each operation included the number of shipments by destination type, and the number of cattle per shipment. These data were used to estimate the number of shipments per operation and the number of cattle per shipment. Additional data considerations:

- Operations were categorized into the same size categories used by NASS.
- Within each size category, a Poisson distribution was fit to the data to model the number of shipments per operation, separately for breeding shipments and feeder shipments.
- Breeding shipments were defined as those going directly to another operation; feeder shipments were defined as those going to sales/auction or to a feedlot. Shipments going directly to slaughter were excluded.
- The parameter values for the Poisson distributions were adjusted so that the total number of breeding and feeder shipments approximated the actual numbers provided by ID.
- The number of head per shipment was estimated by shipment type (feeding and breeding) and herd size from the 2007/2008 NAHMS Beef Study. Minimum and maximum shipment sizes were estimated from the NAHMS survey responses.

To compare the number of shipments generated from the NASS and NAHMS estimates, the total number of out-of-DSA shipments were derived from a combination of Interstate Certificate of Veterinary Inspection (ICVI) data (which has been digitized by the State) and market data.

- The ICVI data contains the county of origin, State of destination, and number of animal by class for each shipment. The ICVIs originated in the Idaho counties, with any area in the DSA, were used. Because DSA is not indicated on the data provided, the proportion of DSA origin shipments was assigned proportional to the number of herds in the DSA (4.3.1) divided by the total herds reported in the DSA counties in the 2012 NASS census of agriculture.
- The market data contains the market of origin, State of destination, and number of animals by class. It is unknown how many of the market-origin animals come from the DSA versus non-
DSA areas of Idaho. According to Idaho Department of Agriculture, only Blackfoot and Idaho Falls’ markets service DSA animals. Therefore, only a portion of animals from each of these two markets will be added to the number of out-of-DSA shipments. This portion is estimated from the number of DSA brand records (269) compared to all brand records (4,529), then applying this to the proportion of all market records (6%). The total number of market records (2,658) is multiplied by 6% to get the total number of records expected from the DSA (160). This equates to approximately 27% of the shipments from these markets.

- ICVIs do not capture movements out of the DSA that stay within Idaho. Brand inspection data were used to capture these out-of-DSA movements.
  - Idaho brand inspection forms for 2013 were provided by the Idaho State Police. Only records marked “DSA” were used to estimate additional out-of-DSA movements.
  - Idaho brand inspections are not used for all movements, only change of ownership. Therefore, using brand inspection data to calculate the number of movements between the DSA and non-DSA underestimates the actual frequency of shipments.

### E.2 Montana

Montana provided three databases:

1. A premises database with all premises in the MT DSA,
2. A dataset of field brand inspections, and
3. A dataset of market brand inspections, for four markets that serve the DSA: Beaverhead, Gallatin, Madison, and Park.

**Premises database**

The number of premises in the MT DSA (296) was derived from the premises database. In order to determine shipments that originate from within the DSA, it was necessary to link the brand inspection data with the premises data. The only way to link up these datasets is by owner/seller name. It was not possible to do this electronically because seller names in the brand inspection data are inconsistent (i.e., multiple ways of specifying the same operation). Datasets were linked manually with imperfect data and exact counts were not possible. Because of this, the estimated number of shipments per farm and number of cattle per shipment from the data were used to obtain distributions for the number of shipments per farm and the number of cattle per shipment.

**Field brand inspections**

1. Estimated the number of shipments originating from within the DSA by matching seller names with names in the premises database.
2. The inspection_number defined a shipment.
3. Categorized shipments as either breeding or feeder based on the reason for the shipment and the type of cattle contained in the shipment.
4. Calculated the number of shipments for each operation by type (breed, feed) and the number of animals per shipment by type. Distributions were fit to the data. The number of shipments per operation was modeled as Lognormal, and the number of animals per shipment was modeled as Weibull (section 0).
Market brand inspections

1. Combined data from the four markets and estimated the number of shipments originating from within the DSA by matching seller names with names in the premises database.

2. This dataset was at the animal level. A shipment was defined as a group of animals from one seller on the same date.

3. The shipment type was defined based on the sex(es) of animals in the shipment.

4. Calculated the number of shipments for each operation by type (breed, feed) and the number of animals per shipment by type. Distributions were fit to the data. The number of shipments per operation was modeled as Lognormal, and the number of animals per shipment was modeled as Weibull (section 0).

E.3 Wyoming

For the inspectors that covered the DSA from 2010, brand-inspection data was maintained in paper records and forms that were hand entered:

1. “A” brand inspection forms were for cattle that were purchased directly or were being moved across county lines with retained ownership.

2. “G” forms were for cattle that were destined for markets.

“A” form processing

- All records with “slaughter” recorded as purpose were removed.
- The remaining non-slaughter records were split into shipments for feeding and breeding purposes.
- 17% of forms were recorded with breeding as the purpose and 35% of forms were recorded as feeding.
- The remaining 48% were recorded as sale (17%), feeding/grazing (11%), not specified (9%), show/exhibition (5%), other (3%), grazing (<1%), medical treatment (<1%), no data (<1%), rodeo (<1%), or transit (<1%). The records in these shipments were classified as breeding or feeding based on the type of cattle recorded in the shipment.
- Any shipments with only steers were classified as feeding shipments and any shipments with at least one bull, heifer, or cow was classified as a breeding shipment.
- This resulted in 48% of shipments classified as breeding and 52% classified as feeding for this assessment.
- The number of shipments per operation was estimated by defining premises based on the “Owner Name” data field. However, with no official premises identification or name database, the aggregation could only be done based on very close matches of the recorded owner name.

“G” form processing

- 15% of records did not have the species specified between cattle and sheep and were removed.
• The remaining non-slaughter records were split into shipments for feeding and breeding purposes.
• On >99% of the “G” form the purpose was not specified.
• Any shipments with only steers were classified as feeding shipments and any shipments with at least one bull, heifer, or cow was classified as a breeding shipment.
• This resulted in 81% of shipments classified as breeding and 19% classified as feeding for this assessment.
• The number of shipments per operation was estimated by defining premises based on the “Owner Name” data field. However, with no official premises identification or name database, the aggregation could only be done based on very close matches of the recorded owner name.

Lognormal distributions were used to estimate the number of shipments per herd and Weibull distributions were used to estimate the number of head per shipment for market shipments (“G” forms), direct shipments (“A” forms), and feeding, and breeding shipment types (section 0).

Because of the lack of consistent premises identification, the proportion of premises with both “A” and “G” forms (direct and market movements) vs. only “A” or “G” forms was not estimated. The proportion was assumed to be the same as estimated for Montana (section 0).

### E.4 Shipment Number and Size Parameter Values

**Table E-1. Distributions and parameters for number of shipments per herd and number of head per shipment estimated for Idaho.**

<table>
<thead>
<tr>
<th>Size category (number head)</th>
<th>Number shipments per farm - Poisson distribution with parameter (λ):</th>
<th>Number head per shipment – Uniform distribution with min,max:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Breeding</td>
<td>Feeder</td>
</tr>
<tr>
<td>1-9</td>
<td>0.1</td>
<td>0.1</td>
</tr>
<tr>
<td>10-19</td>
<td>0.2</td>
<td>0.2</td>
</tr>
<tr>
<td>20-49</td>
<td>0.7</td>
<td>0.5</td>
</tr>
<tr>
<td>50-99</td>
<td>1.0</td>
<td>1.0</td>
</tr>
<tr>
<td>100-199</td>
<td>3.0</td>
<td>1.5</td>
</tr>
<tr>
<td>200-499</td>
<td>5.0</td>
<td>2.5</td>
</tr>
<tr>
<td>500+</td>
<td>7.0</td>
<td>3.0</td>
</tr>
</tbody>
</table>

**Table E-2. Distributions and parameters for number of shipments per herd and number of head per shipment estimated for Montana.**

<table>
<thead>
<tr>
<th></th>
<th>Number shipments per farm - Lognormal distribution with parameters log(mean), log(sd):</th>
<th>Number head per shipment – Weibull distribution with parameters (scale, shape):</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Breeding</td>
<td>Feeder</td>
</tr>
<tr>
<td>Field brand inspections</td>
<td>0.62, 0.62</td>
<td>0.8, 0.8</td>
</tr>
<tr>
<td>Market brand inspections</td>
<td>0.68, 0.68</td>
<td>1.0, 1.0</td>
</tr>
</tbody>
</table>
Table E-3. Distributions and parameters for number of shipments per herd and number of head per shipment estimated for Wyoming.

<table>
<thead>
<tr>
<th></th>
<th>Number shipments per farm - Lognormal distribution with parameters (scale, shape):</th>
<th>Number head per shipment – Weibull distribution with parameters (scale, shape):</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Breeding</td>
<td>Feeder</td>
</tr>
<tr>
<td>Field brand inspections</td>
<td>0.31, 0.57</td>
<td>0.31, 0.57</td>
</tr>
<tr>
<td>(&quot;A&quot; forms)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Market brand inspections</td>
<td>0.34, 0.54</td>
<td>0.34, 0.54</td>
</tr>
<tr>
<td>(&quot;G&quot; forms)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

For Montana and Wyoming the proportion of herds with shipments to market only, direct sales only, and both was estimated to be: 0.35, 0.25, and 0.40.
Appendix F. **Costs Associated with Post-Entry Testing and Reproductive Monitoring**

The Texas testing process for DSA-originating cattle shipments is used to estimate the costs of post-entry testing. Figure F-1 is a flowchart showing the model used to calculate costs of the Texas testing process. In this model, the cost of testing for a shipment depends upon the composition and size of the shipment. There are three types of shipments considered:

**Type 1:** Shipments containing only males

**Type 2:** Shipments containing zero non-bred sexually-intact females and at least one bred sexually-intact female

**Type 3:** Shipments containing at least one non-bred sexually intact female

The major difference between each of these three shipment types is the number of monthly inspections that must be conducted. Type 1 shipments only require one monthly inspection; Type 2 shipments require 3-7 monthly inspections; and Type 3 shipments require 12-22 monthly inspections. These estimates for the number of required monthly inspections follow from our assumptions that females are bred 2-6 months upon entry and non-bred females are 2-12 months old upon entry and will be bred at 15 months old.

For each of these types of shipments, costs are incurred during six distinct steps in the Texas testing process:

1. Process Entry Permit
2. Place Hold Order
3. Conduct Monthly Inspections
4. Conduct Post-Entry Tests
5. Conduct Post-Calving Tests
6. Remove Hold Order

For each of the six steps in the process, costs are estimated using the input values in Table F-1. Table F-2 shows more detailed input values used to calculate the costs of producer roundup and handling for Steps 3, 4, and 5.
Figure F-1. Flowchart depicting the model used to calculate costs of the Texas testing process.
Table F-1. Input values used to calculate costs for the Texas testing process.

<table>
<thead>
<tr>
<th>Process Step</th>
<th>Data Element</th>
<th>Shipment Contains Only Males</th>
<th>Shipment Contains Zero Non-Bred Sexually Intact Females and at Least One Bred Sexually Intact Female</th>
<th>Shipment Contains at Least One Non-Bred Sexually Intact Female</th>
</tr>
</thead>
<tbody>
<tr>
<td>Process Entry Permit</td>
<td>Producer man hours [hours]</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td></td>
<td>TAHC Program Records Staff man hours [hours]</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>Place Hold Order</td>
<td>TAHC Program Records Staff man hours [hours]</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>Conduct Monthly Inspections</td>
<td>Minimum number of monthly inspections [inspections]</td>
<td>1</td>
<td>3</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>Maximum number of monthly inspections [inspections]</td>
<td>1</td>
<td>7</td>
<td>22</td>
</tr>
<tr>
<td></td>
<td>TAHC Livestock Inspector man hours [hours/inspection]</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>Producer Roundup and Handling Cost [$/head]</td>
<td>$5.72</td>
<td>$5.72</td>
<td>$5.72</td>
</tr>
<tr>
<td>Conduct Post-Entry Tests</td>
<td>TAHC Livestock Inspector man hours [hours]</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>Producer Roundup and Handling Cost [$/head]</td>
<td>$5.72</td>
<td>$5.72</td>
<td>$5.72</td>
</tr>
<tr>
<td></td>
<td>Lab Cost of Rapid Automated Presumptive (RAP) Test [$/head]</td>
<td>$7.25</td>
<td>$7.25</td>
<td>$7.25</td>
</tr>
<tr>
<td>Conduct Post-Calving Tests</td>
<td>TAHC Livestock Inspector man hours [hours]</td>
<td>0</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>Producer Roundup and Handling Cost [$/head]</td>
<td>$0.00</td>
<td>$5.72</td>
<td>$5.72</td>
</tr>
<tr>
<td></td>
<td>Lab Cost of Rapid Automated Presumptive (RAP) Test [$/head]</td>
<td>$0.00</td>
<td>$7.25</td>
<td>$7.25</td>
</tr>
<tr>
<td>Remove Hold Order</td>
<td>TAHC Program Records Staff man hours [hours]</td>
<td>0.25</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td></td>
<td>TAHC Program Records Staff Hourly Wage [$/hour]</td>
<td>$17.46</td>
<td>$17.46</td>
<td>$17.46</td>
</tr>
<tr>
<td></td>
<td>Miles Travelled By TAHC Livestock Inspector to Premises [miles]</td>
<td>103</td>
<td>103</td>
<td>103</td>
</tr>
<tr>
<td></td>
<td>Mileage Rate [$/mile]</td>
<td>$0.56</td>
<td>$0.56</td>
<td>$0.56</td>
</tr>
</tbody>
</table>

4 Source: Privately Owned Vehicle (POV) Mileage Reimbursement Rates: [http://www.gsa.gov/portal/content/100715](http://www.gsa.gov/portal/content/100715)
## Table F-2. Input values used to calculate costs for producer roundup and handling time for Steps 3, 4, and 5 of the Texas testing process

<table>
<thead>
<tr>
<th>Category</th>
<th>Data Element [Units]</th>
<th>Value (For All Shipment Types)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Representative Shipment Size [# head]</strong></td>
<td></td>
<td>25</td>
</tr>
<tr>
<td><strong>Proportion of Time Involved in Roundup and Handling</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Producer -- Manager [% of time]</td>
<td></td>
<td>65.0%</td>
</tr>
<tr>
<td>Producer -- Supervisor [% of time]</td>
<td></td>
<td>5.0%</td>
</tr>
<tr>
<td>Producer -- Laborer [% of time]</td>
<td></td>
<td>30.0%</td>
</tr>
<tr>
<td><strong>Hourly Wage Rates</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Producer -- Manager [$/hour]</td>
<td></td>
<td>$24.55</td>
</tr>
<tr>
<td>Producer -- Supervisor [$/hour]</td>
<td></td>
<td>$15.17</td>
</tr>
<tr>
<td>Producer -- Laborer [$/hour]</td>
<td></td>
<td>$10.11</td>
</tr>
<tr>
<td>Weighted Hourly Wage Rate for Roundup &amp; Handling [$/hour]</td>
<td></td>
<td>$19.75</td>
</tr>
<tr>
<td><strong>Producer Roundup and Handling Time</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Administrative Overhead [hours]</td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>Handling Overhead [hours]</td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>Roundup Time [hours]</td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Handling Time for Testing [hours]</td>
<td></td>
<td>2</td>
</tr>
<tr>
<td><strong>Producer Roundup and Handling Cost</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Administrative Overhead [$/head]</td>
<td></td>
<td>$0.98</td>
</tr>
<tr>
<td>Handling Overhead [$/head]</td>
<td></td>
<td>$0.79</td>
</tr>
<tr>
<td>Roundup Cost [$/head]</td>
<td></td>
<td>$2.37</td>
</tr>
<tr>
<td>Handling Cost for Inspection or Testing [$/head]</td>
<td></td>
<td>$1.58</td>
</tr>
<tr>
<td>Total Producer Roundup and Handling Cost [$/head]</td>
<td></td>
<td>$5.72</td>
</tr>
</tbody>
</table>

### F.1 Composition of Breeding Shipments Received Outside GYA States

The proportion of shipments that fall into the 3 breeding shipment categories and are received by an average cow-calf herd outside the GYA States was estimated from the response to question 9.a from (USDA) and the GYA States’ data on shipment size and composition (Appendix E). It was necessary to use both data sources because USDA 2009 contained specific information about animal types (i.e., bred vs. not-bred females) but lacked shipment composition data, while the State out-shipment data contained shipment composition information (i.e., number of bulls, heifers, cows, steers) but not at the resolution to differentiate between sexually intact, as well as, bred and non-bred heifers and cows.

#### F.1.1 Relative Frequency of Shipment Type

First, the proportion of shipments with at least one sexually intact and non-bred female (Type 1) was estimated as the percentage of operations that brought “beef heifers weaned but not bred” (6.2%) and “beef cows not pregnant” (2.6%) onto the operations as a proportion of operations that brought “any”
cattle or calves onto the operation (34.5%). The estimate for proportion of breeding shipments with at least 1 sexually intact and non-bred female is 0.255 = (6.2% + 2.6%) / 34.5%.

Next, the proportion of shipments with no non-bred sexually intact females (Type 2 and 3) was estimated as the complement of the proportion of Type 1 shipments, 0.745 = (1-0.255).

The proportion of shipments with bulls only (Type 3) was estimated from the GYA State data on composition of out-shipments from all 3 GYA States that had only bulls (0.096) as a proportion of Type 2 and 3 shipments (0.745) (USDA, 2003) (USDA, 2003) (USDA, 2003) (USDA, 2003) (USDA, 2003): Type 3 = 0.065 = 0.096*0.745.

The proportion of shipments with bred females and bulls was estimated as the complement to the proportion of shipments with bulls only: Type 2 = 0.673 = (1-0.096)*0.745.

Table F-3. Estimate of number, size, and composition of breeding shipments originating from the DSAs.

<table>
<thead>
<tr>
<th></th>
<th>State Brand Data</th>
<th>NAHMS Animal Type Data</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>mean breeding</td>
<td>mean bull only</td>
<td>Shipments with &gt;0</td>
<td>Shipments</td>
</tr>
<tr>
<td></td>
<td>shipment size</td>
<td>shipment size</td>
<td>unbred female</td>
<td>with bred females</td>
</tr>
<tr>
<td></td>
<td>(State brand</td>
<td>(State brand data)</td>
<td></td>
<td>&amp; 0 unbred</td>
</tr>
<tr>
<td></td>
<td>data)</td>
<td></td>
<td></td>
<td>only</td>
</tr>
<tr>
<td></td>
<td>total breeding</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>shipments (State</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>brand data)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ID</td>
<td>29.17</td>
<td>7.77</td>
<td>245</td>
<td>36.74</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>184.66</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>23.51</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Shipments size</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>by breeding</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>animal type</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1- Bulls</td>
<td>1.82</td>
<td>2.80</td>
<td>7.77</td>
<td></td>
</tr>
<tr>
<td>Type 2- Only BredFemales</td>
<td>18.16</td>
<td>26.37</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>Type 3- UnbredFemales</td>
<td>9.12</td>
<td>0.00</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>MT</td>
<td>12.34</td>
<td>1.96</td>
<td>1000</td>
<td>150.00</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>754.00</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>96.00</td>
</tr>
<tr>
<td></td>
<td>Shipments size</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>by breeding</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>animal type</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1- Bulls</td>
<td>0.77</td>
<td>1.18</td>
<td>1.96</td>
<td></td>
</tr>
<tr>
<td>Type 2- Only BredFemales</td>
<td>7.68</td>
<td>11.16</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>Type 3- UnbredFemales</td>
<td>3.86</td>
<td>0.00</td>
<td>0.00</td>
<td></td>
</tr>
<tr>
<td>WY</td>
<td>33.52</td>
<td>4.61</td>
<td>851</td>
<td>127.50</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>640.90</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>81.60</td>
</tr>
<tr>
<td></td>
<td>Shipments size</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>by breeding</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>animal type</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Type 1- Bulls</td>
<td>2.10</td>
<td>3.22</td>
<td>4.61</td>
<td></td>
</tr>
<tr>
<td>Type 2- Only BredFemales</td>
<td>20.9</td>
<td>30.3</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Type 3- UnbredFemales</td>
<td>10.5</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>
F.2 Cost of Testing by Shipment Type

Table F-4 shows the total costs of post-entry testing by shipment type estimated by this model.

Table F-4. Total costs of post-entry testing by shipment type and State

<table>
<thead>
<tr>
<th>State</th>
<th>Shipment Composition Type</th>
<th>Shipments</th>
<th>Cost Per Shipment</th>
<th>Cost</th>
</tr>
</thead>
<tbody>
<tr>
<td>Idaho</td>
<td>Type 1</td>
<td>24</td>
<td>$338.01</td>
<td>$8,112.24</td>
</tr>
<tr>
<td></td>
<td>Type 2</td>
<td>184</td>
<td>$1,966.06</td>
<td>$361,755.04</td>
</tr>
<tr>
<td></td>
<td>Type 3</td>
<td>37</td>
<td>$3,282.98</td>
<td>$121,470.26</td>
</tr>
<tr>
<td>Montana</td>
<td>Type 1</td>
<td>150</td>
<td>$338.01</td>
<td>$50,701.50</td>
</tr>
<tr>
<td></td>
<td>Type 2</td>
<td>754</td>
<td>$1,966.06</td>
<td>$1,482,409.24</td>
</tr>
<tr>
<td></td>
<td>Type 3</td>
<td>96</td>
<td>$3,282.98</td>
<td>$315,166.08</td>
</tr>
<tr>
<td>Wyoming</td>
<td>Type 1</td>
<td>82</td>
<td>$338.01</td>
<td>$27,716.82</td>
</tr>
<tr>
<td></td>
<td>Type 2</td>
<td>641</td>
<td>$1,966.06</td>
<td>$1,260,244.46</td>
</tr>
<tr>
<td></td>
<td>Type 3</td>
<td>128</td>
<td>$3,282.98</td>
<td>$420,221.44</td>
</tr>
<tr>
<td>Total Cost</td>
<td></td>
<td></td>
<td></td>
<td>$4,047,797.08</td>
</tr>
</tbody>
</table>
Appendix G. CONSEQUENCE ASSESSMENT OF BREAK-EVEN VALUE METHODS

G.1 Exposure Probability, \( P(e) \)

Exposure probability is defined as the number of undetected and infected breeding animals estimated leaving from the GYA per year. This estimate is from the entry and exposure sections of the risk assessment (sections 3 and 4).

G.2 Effectiveness of the Mitigation, \( P(m) \)

The effectiveness of the mitigation is defined as the probability that post-movement testing will detect infected breeding cattle. This is dependent on the diagnostic test sensitivities and uses the same series of tests and diagnostic series sensitivity as the exposure assessment (section 4.3.7). In addition the probability of detection depends on the number of infected animals in a shipment and is calculated as the complement of the probability of the false-negative diagnostic test results from all infected animals:

\[
P(m) = (1 - Se)^{n+},
\]

where \( Se \) is a random deviate representing the sensitivity of the diagnostic test series drawn from a beta distribution (Beta (25,6.5), section 4.3.7) and \( n+ \) is the number of infected breeding cattle in the shipment. The resulting median and 95% lower limit of detection probability increases as a function of the number of infected (Figure G-1).
Figure G-1. Median and 95% lower limit of detection probability as a function of number of brucellosis infected animals in a shipment.

For calculation of a potential range of break-even values of the mitigation, the 95% lower detection probability of detecting 1 infected animal (0.64) was used as the lower range and the upper range was set at 0.99 to reflect excellent sensitivity of veterinarian observed calving.

**G.3 Cost of Implementing the Mitigation, \( C(m) \)**

The cost of maintaining the post-movement testing depends on the size, composition, and number of shipments from the DSAs. This cost is estimated from the number and size of shipments leaving the DSAs (section 4.3.2) as well as data from the NAHMS beef cow-calf survey (USDA, 2008) to estimate the composition of breeding shipments received as herd additions outside the GYA. The total number of shipments and animals that would need to be tested and the associated costs are detailed in Appendix E.

**G.4 Percentage of DSA Origin Breeding Shipments Destined for Each State Outside the GYA**

The cost of applying the mitigation is scalable based on the size, composition, and number of shipments a State received. Likewise, the break-even value scales equally under the assumption that all potential destinations of GYA cattle have equal probability of receiving an infected and undetected animal. Table G-1 displays the estimated number of breeding shipments and proportion destined for the non-GYA risk assessment working group States.

<table>
<thead>
<tr>
<th>State</th>
<th>Breeding Shipments</th>
<th>To Texas</th>
<th>To Colorado</th>
<th>To South Dakota</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>
### G.5 Cost of Losing Class-Free Status or Implementing a Designated Surveillance Area

For further perspective, the costs of an outbreak in a class-free State could include losing brucellosis class-free status or establishing and maintaining a DSA. A range of total costs to producers was estimated based on existing estimates of costs for a State losing brucellosis class-free status (9 CFR Part 78), costs associated with an affected herd (Wilson, 2011; Roberts et al., 2012), and costs to maintain a DSA (MDOL, 2011). Where available, the high estimate of costs was used under the following categories:

- **APHIS** estimated a cost to producers of between $7.50 and $15 per head in the event of a State losing class-free status in Montana to cover necessary testing requirements.

- The State of Montana produced a detailed accounting estimate of $10.25 per head to maintain its DSA (MDOL, 2011).

- Cost to the producer of a detected herd: $40,000 to $320,000 for 400 breeding head cow-calf production herd (Wilson, 2011; Roberts et al., 2012). The upper estimate of $320,000 was used to represent a worst-case scenario (representing depopulation with compensation to the producer) and an intermediate estimate of $144,000 (for a 400 breeding head herd) was used to represent a scenario where confirmed positive animals are removed (test-and-remove) and affected herds are quarantined until three whole-herd tests are negative.

Using these estimates, the estimated economic loss to producers was generated for scenarios where 1-100 affected herds were identified; 1,000-100,000 head were included in a DSA or area that lost brucellosis class-free status; and, the costs for the affected herds were incurred in 1 year with the cost of maintaining a DSA incurred for 6 total years.\(^2\)

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\(^2\) This assumes that all affected herds are discovered in the first year and a DSA is established for that index year and 5 additional years with no further affected herds to reclaim brucellosis class-free status (CFRs).
In a scenario where a DSA is implemented with test-and-remove and quarantine for affected herds, the estimated economic loss to producers ranges from $195,520 (when there is one affected herd and 1,000 head under the DSA rules) to $19.5M (when there are 100 affected herds and 100,000 head under the DSA rules). Under the worst-case scenario where affected herds are depopulated without compensation to the producer and producers incur costs of $15 per head, the estimated economic loss to producers ranges from $395,520 (when there is one affected herd and 1,000 head under the DSA rules) to $39.5M (when there are 100 affected herds and 100,000 head under the DSA rules).

The estimates in both scenarios assume that all affected herds are discovered in year 1; there are 5 additional years of DSA costs associated with all negative tests to achieve class-free status; and, all affected herds incur average losses similar to a 400 breeding head cow-calf herd in Wyoming.

G.6 Estimated Economic Cost of Brucellosis

From the Most Recent Assessment of the Impact of Brucellosis in the United States

Finally, to provide some absolute context of what these consequences mean, the most comprehensive estimate of costs associated with brucellosis management was produced in 1977, when brucellosis was relatively common: (Beal and Kryder, 1977). Total economic loses owing to brucellosis in 1976 was approximately $121M ($30M in 1976 dollars—dairy and beef industries combined), with an estimated 0.7% animal infection rate and 1% nation-wide herd infection rate (with approx. 1.1M beef
herds and total beef inventory of 44M head), but with brucellosis mostly in southern and southwestern States.

The current USDA standard for slaughter detection is 1 in 100K or 0.00001 (USDA, 2012). These economic losses were determined from a per-infected breeding cow estimate of production losses and the average estimated at approximately $400 per infected cow (approx. $100 in 1976 dollars).
Appendix H. LIMITATIONS AND DATA GAPS

H.1 Elk

Translating spatio-temporal *B. abortus* dynamics in elk into a quantitative infection risk to cattle is not currently feasible, owing to seasonal behavior of elk, seasonal management of cattle, and surveillance for *B. abortus* in elk that is not sufficient to quantify transmission to cattle.

H.1.1 Elk Seasonality

*B. abortus* pathogenesis and transmission in elk is similar to cattle, with infective tissue and fluid expelled into the environment during an abortion or live-birth from an infected elk cow (Thorne and Morton, 1978). Thus, elk breeding biology generates highly seasonal transmission because elk breed in late September to late October (Morrison et al., 1959) and the risk of transmission from elk is primarily from abortions that occur from February to May, where elk utilize winter cattle grazing and feeding areas (Cross et al., 2013). During live birth elk cows seek seclusion and meticulously clean their birth materials, reducing potential contact with other hosts and contamination of the environment with *B. abortus* (Johnson, 1951; Barbknecht et al., 2011).

The elk populations in the GYA are a mix of migratory and non-migratory groups. Migratory elk spend the summer (May – October) at high elevations and move potentially long-distances to low-elevations during the winter (October – May) (White et al., 2010; Middleton et al., 2013). Therefore, it is during the months of February to April when the risk of elk transmission to cattle is highest because of the overlap of elk and cattle utilization of limited low-elevation habitat and most likely timing of infective elk abortions (Cross et al., 2013).

H.1.2 Cattle Seasonal Management

In the counties that are included in the GYA brucellosis DSA, 85% of operations are cow-calf producers (USDA, 2008). These producers make use of seasonal range with cattle generally exclusively grazing pasture during the summer (May - September) and utilizing pasture supplemented with hay during the winter (September – May) (Nagler et al., 2006). Not only are cattle and elk seasonally sharing low-elevation habitat during the time when brucellosis generated elk abortions are most likely (Proffitt et al., 2011), the supplemental feeding provided to cattle also is a potential attractant to elk.

In addition, cattle producers in the GYA engage in many mitigation activities to prevent exposure and transmission to their cattle including, but not limited to: vaccination, hazing elk off winter feeding lines, fencing winter feed storage, and spaying heifers (Roberts et al., 2012). Currently, very little is known about the effect that these mitigations have to prevent exposure to and transmission from elk, nor is the proportion of producers engaging in mitigations available across the GYA.

H.1.3 Elk Surveillance

There are three primary methods of surveillance for *B. abortus* in elk:

1. Passive surveillance of hunter submitted blood samples for diagnostics from elk harvested during the hunting season (generally October – December).

2. Active surveillance by State agency personnel via live-capture of groups of elk on their winter range.
3. Active surveillance by agency personnel via capture of elk on winter feedgrounds. Each surveillance method has advantages and drawbacks for determining when and to what extent elk sero-prevalence could be related to transmission of *B. abortus* to cattle.

Hunter surveillance is the most efficient way to sample elk populations over large areas. However, the timing of elk migrations to winter habitat is variable from year to year and the timing of the elk harvest seasons in the GYA target elk prior to arrival on their winter range. In addition, there is currently no way to determine if a harvested elk is part of a migratory or non-migratory group. Hunter surveillance provides a reliable way to track temporal trends in elk sero-prevalence, but cannot identify the spatial extent that hunter harvested samples translate into spatial overlap with cattle during the high-risk transmission period.

Live-capture and testing of elk on winter habitat provides the most direct measure of transmission potential to cattle and allows for intensive data collection to understand winter movement, habitat use, and overlap with cattle during the transmission season. However, this is an expensive and time intensive effort and must be used as a targeted surveillance to supplement broader-scale testing of hunter-harvested elk. Therefore, such live-capture and testing surveillance provides excellent information about transmission potential from elk to cattle in limited-areas (Anderson et al., 2010; Anderson et al., 2011; Anderson et al., 2012), but cannot provide comprehensive surveillance across the DSAs because of the expense and reality of resource-limited Fish and Game Agencies in the GYA States.

Surveillance of elk on winter feedgrounds provides the best opportunities for targeted surveillance and collection of data about potential elk contact with cattle. Much has been learned about the dynamics of brucellosis on the elk feedgrounds in the southern GYA (Cross et al., 2007; Maichak et al., 2009). However, the feedgrounds create a unique case where their presence may be simultaneously increasing transmission among elk (Etter and Drew, 2006; Cross et al., 2007) and altering movement and contact patterns between elk and cattle. Therefore, active feedground surveillance cannot be used to infer transmission potential in the rest of the GYA where there are no feedgrounds.

**H.1.4 Summary**

The boundaries of DSAs in all three States have expanded as seropositive elk are found outside of the DSAs. As recently as the 2013-2014 winter, seropositive elk have been identified outside of the DSA in Wyoming and Montana. However, correlating results from elk surveillance with detected transmission events to cattle is not currently feasible. The timing of passive hunter surveillance, relative to the timing of elk abortion events, and the mixed migratory behavior of GYA elk make inference of harvest-based passive surveillance to where cattle are exposed unachievable. While the timing of active surveillance can be performed to correspond to elk abortion timing, the resource intensive nature of active surveillance restricts the inference of any correlation between elk sero-status and transmission from elk-to-cattle to the winter elk herd that was targeted and to the year that the active surveillance was carried out.

**H.1.5 Outstanding Questions for this Risk Assessment**

- Do the DSA boundaries adequately bound areas with higher probability of wildlife to cattle transmission?
• How do the locations of hunter harvested passive elk surveillance samples translate into transmission probability to cattle?
• What are the cattle herd management risk factors associated with known affected herds?
• How effective are on-farm mitigations at reducing exposure and transmission of \textit{B. abortus} from elk?

H.2 Bison

YNP bison are known to have self-sustaining endemic brucellosis (Cheville NF, 1998). YNP bison leave the park in two main areas of Montana; north of Gardiner—Northern Management Area (NMA) and west of West Yellowstone—Western Management Area (WMA). Bison are actively managed and hazed when there is concern for public safety, property damage, and disease transmission during the winter months through the Interagency Bison Management Plan (IBMP).

\textit{Descriptions of the areas and management of YNP bison, outside of YNP, courtesy M. Zalewski (2014):}

H.2.1 Northern Management Area

The NMA has 2 small (approximately 25 head each) year-round cattle operations. Both are managed adjacent to Hwy 89.

Bison range is limited to the NMA by geographical boundaries and management actions. Specifically, a choke point to the north at Yankee Jim Canyon is an effective physical barrier that prevents bison from migrating from the Gardiner basin to Paradise Valley. This barrier was made even more effective in 2011, when a double wide "bison guard" was installed in the road. This bison guard is in place during the winter months when bison are allowed in the NMA, and is covered with steel plates after bison are returned to YNP on May 1st. Bison bulls on occasion have traveled north of Yankee Jim Canyon, but cows have done so extremely infrequently (none observed since at least 2007). Bulls that traveled north of Yankee Jim Canyon have typically been lethally removed (as was the case with one bull in 2013).

Bison are limited from commingling with the cattle operations by fencing and management actions. The Montana Department of Livestock (Franklin et al., 1975) has provided cooperative agreements funding fencing construction on both cattle properties in 2012. The Department of Livestock (DOL) responds to commingling events by working with the cattle owners to remove bison. Cattle that experienced commingling events are tested for brucellosis after the bison season.

There are summer operations that run cattle in the Cinnebar (west of the Yellowstone River) in Gardiner basin, but cattle are turned out well after bison are no longer allowed in the NMA. Year-round cattle in the NMA are managed under a herd plan, and are subject to Montana's DSA regulations.

H.2.2 Western Management Area

In the WMA, there are 4 seasonal operators (no year round cattle operations), and approximately 600 cow-calf pairs utilize the area during summer with a turnout after June 15th. Several hundred bison typically use the area in late spring with the majority of the animals utilizing Horse Butte peninsula where there are no cattle year round.
North of Hebgen Lake, approximately 300 cow-calf pairs lease pastures during the summer months. These pastures are in Zone 2, which is a tolerance area for bison until May 15th in the WMA. Montana relies on temporal separation to prevent transmission of brucellosis. The brucella organism, if deposited, is degraded by environmental factors [temperature changes, UV light] prior to cattle being turned out. This is consistent with the Bison Environmental Impact Statement (EIS) on which the Bison Record of Decision of 2000 is based and with subsequent environmental persistence of *Brucella abortus* (Aune et al., 2012).

Southwest of Hebgen Lake (still in the WMA), approximately 300 cow-calf pairs utilize the area during the summer with a turnout date after June 15th. These animals graze in Zone 3, which is a no-tolerance area for bison. While bison do occasionally enter this property, they are not tolerated by the landowner, and therefore, bison are expeditiously removed (lethally if necessary when there are cattle). Cattle in the WMA are subject to DSA regulations.

### H.2.3 Conclusion

Few cattle have any exposure to infected YNP bison. While brucellosis transmission from elk to livestock is a very rare event in Montana, transmission from bison has not been recorded during the time frame of this risk assessment.

### H.3 Epidemiological Consequences

The risk estimation (section 6) was based on economic consequences of an outbreak outside the DSAs. However, existing knowledge did not allow for an assessment of likely biological consequences, such as time-to-detection, within and between herd transmission rates, number of affected herds, and spatial extent of affected herds in the event of a *B. abortus* outbreak outside the GYA. The ability to estimate or model such epidemiological consequences of an incursion of *B. abortus* outside the DSAs is necessary to generate accurate estimates of the consequence costs (section 5).

Because data from historical incursions outside of the DSAs is not readily available, epidemiological modeling would be necessary to generate accurate estimates of consequence costs. However, the accuracy and precision of modeling outputs can only be as good as the data to inform the models and the following are several notable data gaps:

- Transmission rates within a herd and potential movement of infected animals out of a herd.
- Vaccination rates outside the GYA States and the effect that vaccination has on transmission.
- The effect of reduced national and State-level brucellosis surveillance on time to detection or subsequent spread, as all States (excluding the GYA DSAs) approach brucellosis class-free status for 5 or more years.
Brucellosis Regionalization
Risk Assessment Model

An Epidemiologic Model to Evaluate the Risk of *B. abortus*
Infected Undetected Breeding Cattle Moving out of the Designated Surveillance Areas
in Idaho, Montana, and Wyoming