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Bayesian latent-class modelling of quarantine testing procedures for American Bison (*Bison bison*) in the Greater Yellowstone Area to determine *Brucella abortus* freedom

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OBJECTIVE
American bison (*Bison bison*) quarantine protocols were established to prevent transmission of brucellosis outside the Greater Yellowstone Area, while allowing for distribution of wild bison for conservation and cultural purposes. Quarantine standards require rigorous testing over 900 days which has led to the release of over 200 bison to Native American tribes. Standards were evaluated using 15 years of laboratory and management data to minimize the burden of testing and increase the number of brucellosis-free bison available for distribution.

ANIMALS
All bison (n = 578) from Yellowstone National Park were corralled by the National Park Service and United States Department of Agriculture.

PROCEDURES
A statistical and management evaluation of the bison quarantine program was performed. Bayesian latent-class modeling was used to predict the probability of nondetection of a seroreactor at various time points, as well as the probability of seroconversion by days in quarantine.

RESULTS
At 300 days, 1 in 1,000 infected bison (0.0014 probability) would not be detected but could potentially seroconvert; the seroconversion model predicted 99.9% would seroconvert by day 294, and 12.8% of bison enrolled in quarantine would seroconvert over time. Using a 300-day quarantine period, it would take 30 years to potentially miss 1 seroreactor out of over 8,000 bison enrolled in the quarantine program.

CLINICAL RELEVANCE
Reducing the quarantine program requirements from over 900 days to 300 days would allow management of quarantined bison in coordination with seasonal movement of bison herds and triple the number of brucellosis-free bison available for distribution.

American bison (*Bison bison*) are North America's largest mammal and the national mammal of the United States of America.[1] The largest bison herd is established in Yellowstone National Park, with 5,450 bison counted in the summer of 2021.[2] These bison are composed of a continuously free-ranging herd since prehistoric times and are an important genetic resource for breeding and conservation.[3] The Greater Yellowstone Area (GYA), as defined by the Greater Yellowstone Coordinating Committee in 1994, encompasses approximately 80,000 km^2 of state, federal, tribal, and private lands in Wyoming, Montana, and Idaho, including Yellowstone National Park and Grand Teton National Park.[4] Federal, state, and tribal entities have been involved in the conservation and management of bison in the GYA.

Bovine brucellosis, a disease caused by the zoonotic pathogen *Brucella abortus*, was first reported in Yellowstone National Park bison in 1918.[5] *Brucella abortus*, via the Bang test, was identified in serum from 2 bison females, likely due to transmission from local cattle herds.[5] Beginning in 1956, the National Brucellosis Eradication Program led to the declaration of class-free status of brucellosis (i.e., freedom-from-disease) for domestic cattle and production bison throughout the

United States in 2008.[6] Wild elk (*Cervus canadensis*) and bison in the GYA are the only known animal reservoirs of *B. abortus* in the United States,[7] and since 2012 all cases of brucellosis have been detected within the GYA.[8] An interagency management plan was created in the year 2000 to conserve a wild, wide-ranging bison population, while minimizing the spread of brucellosis to livestock in the region.[3] To mitigate the risk of spillover events from wildlife to domestic livestock, a Designated Surveillance Area was defined by Idaho, Montana, and Wyoming, with oversight by USDA-APHIS, to perform increased wildlife and livestock surveillance for brucellosis.[9–11]

Regulations regarding approved bison quarantine facilities and quarantine testing protocols were established to prevent transmission of brucellosis by the movement of wild bison outside the GYA.[12] In summary, bison undergo 3 phases of isolation and testing before they can be transferred: a "Screening Phase" during which recently corralled groups of bison are tested every 30 to 90 days, with seroreactors removed until all animals in that group are serologically negative for brucellosis; a "Quarantine Phase" that lasts at least 1 year with intermittent testing, during which female bison must be bred and give birth to calves; an "Assurance Phase," during which bison are transferred, held and tested in a separate facility for another year prior to release **(Figure 1)**.

Screening Phase

- Mixed age and sex groups captured from the wild population, and placed in isolation pens.
- Captured animals tested for brucellosis using on-site tests (CARD, BAPA, and FPA) and those testing negative placed into the quarantine facility. Positive tests are confirmed at a reference laboratory.
- Animals are placed into ITGs based on age and sex.
- An ITG moves to Quarantine Phase once all animals test negative two times at least 30 days apart.

Quarantine Phase

Male bison ITG

- The entire group must test negative entering Quarantine Phase, and again at 6- and at least 12- months from the date of the first negative test.
- All males must reach 3 years of age or older to be considered brucellosis-free for transfer to assurance testing.

Female bison ITG

- Females must be non-pregnant to enter Quarantine Phase.
    - Pregnant females in Screening Phase must calve, obtain a negative test, and then enter quarantine phase as a non-pregnant female.
- Female bison are bred with a quarantined (seronegative) male.
- Within 5 days following parturition, bison must test culture-negative via uterine swab and sero-negative to serum testing.
- The entire ITG must test negative again 6 months after the last female calved.

Assurance Phase

- ITGs are transported to Fort Peck and managed by the Fort Peck Assiniboine and Sioux Tribes in collaboration with USDA APHIS.
- ITGs must test negative at 6 months and 12 months, before being released from program for distribution to Native American tribes.

Figure 1—Summary of current quarantine and standards for brucellosis testing, quarantine, and distribution of American bison from the Greater Yellowstone Area. CARD = Card agglutination test. FPA = Fluorescence polarization assay. BAPA = Buffered acidified plate antigen. ITG = Individual test group. *Summarized from Brucellosis Eradication: Uniform Methods and Rules.[12]

The current quarantine standards for GYA bison require keeping male and female bison in captivity for approximately 930 days and 1,356 days, respectively; female bison must be bred in captivity to address potential latent *Brucella* infection. Since the completion of the feasibility assessment of the quarantine program in April 2013, which monitored 214 bison over 7 years,[13] wild American bison have been corralled in the GYA, undergone the 3-phase regime, and been redistributed to Native American tribes for breeding and conservation programs.

To manage this quarantine program, the USDA Veterinary Services works with the National Park Service, the Fort Peck Assiniboine and Sioux Tribes, Montana Department of Fish, Wildlife, and Parks, and Montana Department of Livestock. The Screening and Quarantine Phases occur at federally operated facilities at the northern border of Yellowstone National Park; the Assurance Phase occurs at the Fort Peck Reservation in Montana. After the Assurance Phase, the Fort Peck Assiniboine and Sioux Tribes and InterTribal Buffalo Council coordinate the transfer of animals to Native American tribes. To date, the program has been highly successful; there have been no positive brucellosis serological reactors detected during the Quarantine or Assurance Phases, nor spillover events following distribution of bison to Native American tribes. Using principles of adaptive management, a program and data assessment was recommended to decrease the duration of the quarantine and burden of testing for bison.

We used Bayesian latent-class time-to-event statistical models to assess the current testing standards of the quarantine program using data during 2005 through 2021 and to estimate the probability of missing a *Brucella abortus*–infected bison during specific time points of the quarantine process. These analyses with real-world laboratory testing data from quarantined bison can be used to improve the efficiency of distribution of brucellosis-free bison outside of the GYA.

Materials and Methods

Animal management and husbandry

The USDA Ruminant Health Center and National Park Service operate quarantine facilities near the northern boundary of Yellowstone National Park. In the late winter season, bison migrate outside of the northern border of Yellowstone National Park and are passively corralled into quarantine facilities for potential enrollment in the quarantine program. Bison are maintained in approximately 10- to 30-acre pens constructed according to guidelines for brucellosis quarantine,[12] including 8-foot-high double fencing separated by a minimum of 10 feet between pens. Cohorts of 10 to 50 animals are cared for with the potential for 5 ITGs to be managed at the same time during this research period; facilities have recently been expanded to manage 8 ITGs for the 2022 to 2023 season. Bison free graze in the pen with supplemental long-stem and alfalfa hay provided. During the Assurance Phase, bison are transported to Fort Peck in Montana, managed by the

Assiniboine and Sioux Tribes, in a 330-acre fenced paddock with free grazing and supplemental hay.

Laboratory testing for *Brucella abortus*

Bison sera were initially tested on-site during corralling of bison, using Card agglutination and fluorescence polarization assay (FPA). All blood sera were then forwarded to official testing laboratories (Montana Department of Livestock Diagnostics Laboratory, Bozeman, Montana, or National Veterinary Services Laboratories, Ames, Iowa) for buffered acidified plate antigen (BAPA), complement fixation (CF), and FPA testing. A bison was considered a confirmed seroreactor when a single positive CF or FPA test was identified at an official testing laboratory, based on official testing recommendations.[12] Seroreactors were culled upon detection with lymphatic tissue collected at necropsy to confirm *Brucella abortus* by bacterial culture.

Data collection, cleaning, and analyses

The USDA Ruminant Health Center and the National Park Service provided data for analyses. Data variables included signalment (year of birth, sex), management data (cohort name, date of entry into each quarantine phase, release date, identification including radio-frequency identification [RFID] tags, bangle tags, and study ID), and laboratory data (laboratory result with date and test type). R statistical software (version 4.0.3) was used to analyze data and for quality control. Management and brucellosis screening data during 2005 through 2021 were summarized and evaluated. Quarantine program data from the brucellosis quarantine feasibility study during 2006 through 2013,[13] were combined with quarantine program data during 2016 through 2021 for analyses.

Model

A Bayesian latent-class time-to-event model (infection model) was developed to evaluate the risk of nondetection of brucellosis seroreactors. The model considered 2 disease classes, infected and uninfected. An animal was estimated as infected or uninfected at the time it entered the program, and its disease status did not change. A parametric hazard function was used to evaluate the time of the first brucellosis-positive serology test for animals that were infected (seroconversion model). Uninfected animals were assumed not to exhibit a positive test.

We used a Markov chain Monte Carlo (MCMC) algorithm to simulate from the posterior distribution and estimate the unknown parameters of interest and the latent variables. Samples were drawn from the posterior distribution of each parameter and latent variable using a hybrid Gibbs sampler. Each MCMC chain was run for 500,000 iterations and thinned to ensure random mixing. All analyses were completed in program R and JAGS. A detailed specification of model parameters and likelihoods, as well as R code files with an example dataset, is provided **(Appendix)**.

Results

Bison brucellosis quarantine program summary

The National Park Service and the USDA currently select pre-reproductive (calf and yearling) animals for the quarantine program, to decrease the probability of brucellosis exposure and infection. On-site laboratory testing histories indicated that 1,403 of 3,496 (40%) corralled animals were seronegative male or female pre-reproductive animals that were eligible to enter the quarantine program **(Table 1).** Signalment and seroreactor testing information for all bison that were corralled during 2013 through 2020 are summarized **(Supplemental Table S1)**.

Animals in quarantine program

Since 2005, 578 bison have been enrolled in the quarantine program (male = 274, female = 304). The following management summary is limited to bison that have entered the program since 2016 (n = 364) after the feasibility study was completed in 2013; the feasibility study[5] (n = 214 bison) represents significant bias in summarizing the program because bison were culled due to the need for controls in the feasibility assessment (i.e., study design).

Native American tribes have received 172 adult bison from the GYA quarantine program, as well as 36 calves born during the Quarantine Phase. Excluding calves born in quarantine, male bison spent a mean of 125 days in the Screening Phase (SD = 32.0; range, 83 to 217 days) and a mean of 446 days in the Quarantine Phase (SD = 165.0; range, 363 to 1,010 days). Female bison spent a mean of 175 days in the Screening Phase (SD = 102.2; range, 82 to 483 days) and a mean of 658 days in the Quarantine Phase (SD = 148.7; range, 509 to 1,092 days). The duration of the Assurance Phase was predetermined to 365 days; therefore, male bison spent a mean 936 days (SD = 132.4; range, 811 to 1,330 days) to complete all 3 phases of the quarantine program, while female bison spent a mean 1,172 days (SD = 60.1; range, 1,120 to 1,356 days) to complete all 3 phases of the quarantine program.

Of the 364 bison that entered the program after the feasibility study, 12.4% (44 adults and 1 calf) were euthanized or died in quarantine, with negative brucellosis serology and culture. Restraint, dystocia, and trauma were specific etiologies of mortality recorded.

Table 1—Summary table of proportion of brucellosis seroreactors by age and sex for bison corralled at Yellowstone National Park during 2013 through 2020.

	Male			Female		
Age	**Adult**	**Yearling**	**Calf**	**Adult**	**Yearling**	**Calf**
Proportion positive seroreactor	68% (119/175)	39.5% (191/484)	7.3% (32/438)	65% (820/1265)	40% (184/460)	9.5% (45/473)
Seroreactor by sex	31.2% (342/1097)			47.7% (1049/2198)		

Statistical model evaluation of brucellosis seroconversion in bison

A Bayesian latent-class time-to-event model was used to evaluate the 578 bison in the quarantine program, including 76 brucellosis seroreactors; all culture-positive bison had *Brucella abortus* isolated. The latest seropositive bison were recorded at 259 days for a female bison, and 232 days for a male bison. To remove potential bias, 9 seroreactive bison were excluded from the model because they tested positive on day 0. The amount of days female and male infected bison were in quarantine before seroreactor detection, and the corresponding time-to-event model, are illustrated **(Figure 2)**.

No significant difference was found between days until seroconversion for infected male and female bison (t_{74} = 0.52, P = .6); mean days until seroreactor detection was 104 days for female bison, and 97 days for male bison. A hazard ratio calculation using the latent-class time-to-event model also revealed no significant difference in model risk between male and female bison (95% CI, 0.69 to 1.89); the data were combined for all further analyses. A combined dataset of days until seroreactors were detected and the time-to-event model for all seroreactor bison are illustrated **(Figure 3)**. Model evaluation revealed high confidence that the model fit well to the observed data **(Supplemental Figure S1)**.

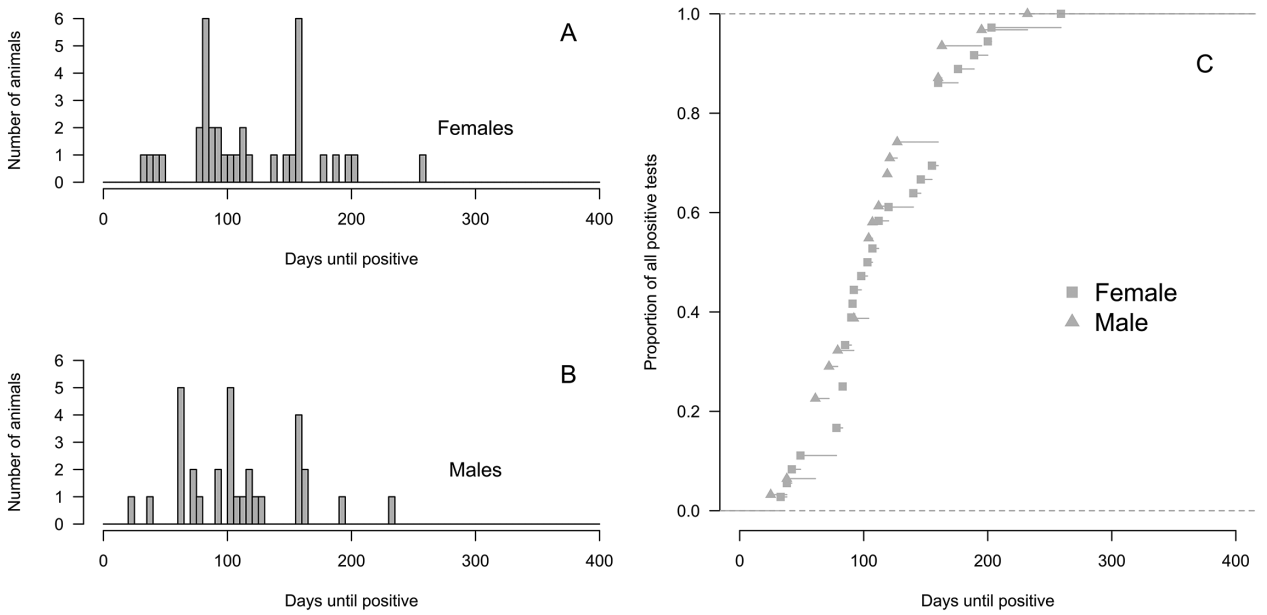

Figure 2—Days female and male infected bison were enrolled in quarantine program before seroreactor detection (A, B), and a latent-class time-to-event model of seroreactors (C), with comparisons between female and male bison. No significant difference was noted between time until detection for males and females; therefore the data were combined for all further analyses. The latest detections were at day 232 (male bison) and 259 (female bison).

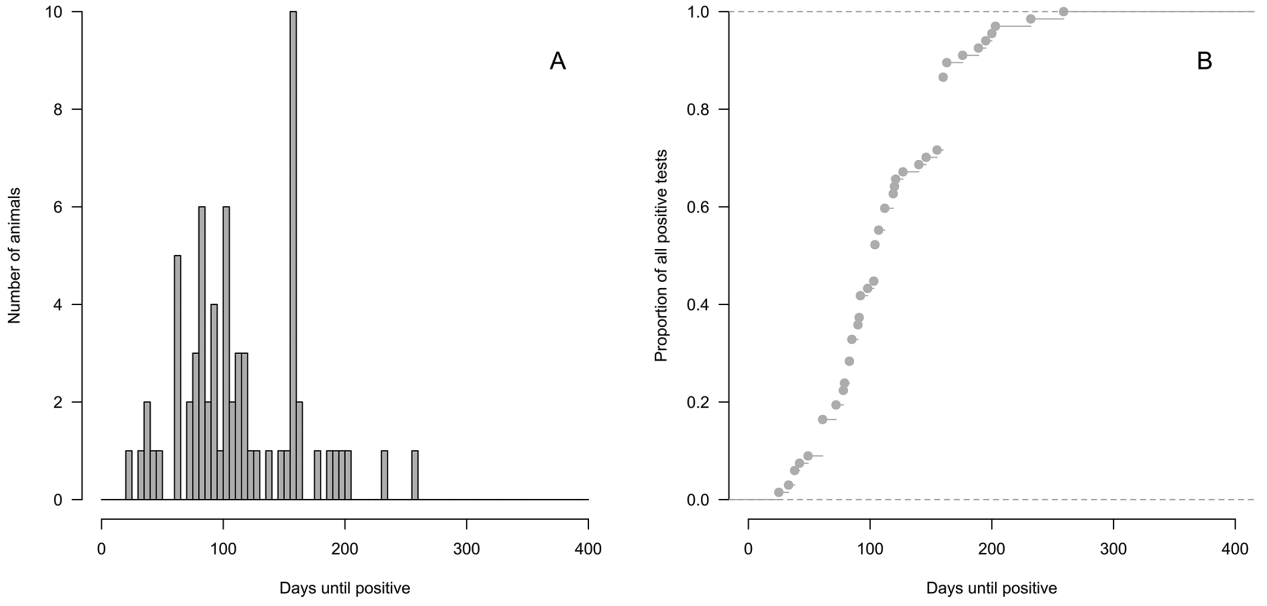

Figure 3—Days until seroreactor detection (A) and a time-to-event model (B) of all bison brucellosis seroreactors (n = 67).

Table 2—Summary of probability (95% highest posterior density [HPD]) of nondetection of seroreactor bison based on number of days in quarantine for individual infected bison and cohorts (individual testing groups [ITGs]) of 20 and 40 animals. Results are provided both as a probability and ratio for clarity. Current National Park Service and USDA facilities for quarantining bison in Yellowstone National Park would allow for a maximum of 8 ITGs to be managed per year.

Days in quarantine	Data format	Individual bison	ITG of 20 bison*	ITG of 40 bison*
270	Probability (95% HPD)	0.005 (0.00001, 0.016)	0.013 (0.000005, 0.04)	0.025 (0.000011, 0.78)
	Ratio	5 in 1,000 infected bison	1.3 in 100 ITGs	2.5 in 100 ITGs
300	Probability (95% HPD)	0.0014 (0, 0.0052)	0.0035 (0, 0.013)	0.0069 (0, 0.027)
	Ratio	1 in 1,000 infected bison	3 in 1,000 ITGs	7 in 1,000 ITGs
330	Probability (95% HPD)	0.00035 (0, 0.0016)	0.00091 (0, 0.004)	0.0018 (0, 0.0079)
	Ratio	4 in 10,000 infected bison	9 in 10,000 ITGs	2 in 1,000 ITGs
365	Probability (95% HPD)	0.000072 (0, 0.00031)	0.00019 (0, 0.0008)	0.00037 (0, 0.0016)
	Ratio	7 in 100,000 infected bison	2 in 10,000 ITGs	4 in 10,000 ITGs

*Probability one or more infected bison in an ITG will not be detected.

Risk of nondetection of seroreactors by days in quarantine (Infection Model)

To communicate the statistical trends and management options for quarantining bison, 4 time points were chosen for analyses: 270, 300, 330, and 365 days. The probability that seroreactors would not be detected for both individual bison and individual testing groups (ITGs) is shown **(Table 2)**. ITGs composed of either 20 or 40 bison were based on the capacity of National Park Service and USDA quarantine facilities; to date, 14 ITGs have entered the brucellosis quarantine program since 2013. Currently, a maximum of 8 ITGs could be managed per year; therefore, it would take over 12 years for 100 ITGs to be managed, or 120 years for 1,000 ITGs to be managed.

Seroconversion model

Based on the models generated by observed detections of infected bison in quarantine, 95% of infected bison will seroconvert by 210 days in quarantine (95% highest posterior density [HPD], 184 to 235), 99% will seroconvert by 250 days in quarantine (95% HPD, 215 to 285), and 99.9% of bison will seroconvert by day 294 (95% HPD, 248 to 343; **Figure 4**).

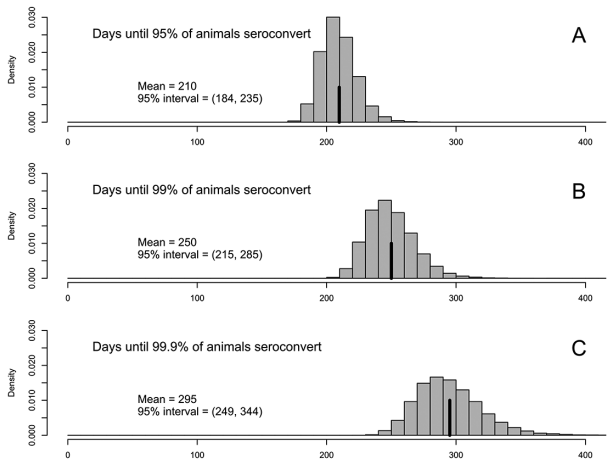

Figure 4—Modeling prediction of days until seroconversion for 95% (A), 99% (B), and 99.9% (C) of infected bison in quarantine. One in 1,000 infected bison may not seroconvert by day 294 (95% hpd, 248 to 343).

Given the natural prevalence of brucellosis in YNP bison herds and timing of exposure events when bison enter quarantine, the seroconversion model (psi parameter) predicted that 12.8% (HPD 9.9% to 15.6%) of bison enrolled into an ITG will seroconvert during the quarantine program. With the current annual management capacity of 260 bison during the Screening and Quarantine phases, this would equate to approximately 33 bison seroconverting while enrolled in the quarantine program.

Discussion

The infection model indicated the probability of not detecting an infected animal is acceptable at 300 days,[14] and negligible at the end of 1 year. At 300 days, fewer than 1 in 1,000 infected animals entering the program would be undetected; at 365 days, fewer than 7 in 10,000 infected bison would be missed.

A real-world example of risk can be illustrated by incorporating the 12.8% seroconversion model results and a maximum 260 bison (8 ITGs) management capacity. After 300 days in quarantine, it would take 30 years to potentially miss 1 seroreactor out of over 8,000 bison enrolled in the program, and 120 years until 7 out of over 1,000 ITGs had one or more potential seroreactors undetected. After 365 days in quarantine, the probability is negligible: it would take 3,052 years to potentially miss 7 bison seroreactors out of over 800,000 enrolled, or 1,250 years until 4 ITGs out of 10,000 ITGs have one or more potential seroreactors undetected. To date, successfully transferred male bison spend a mean 571 days in the Screening and Quarantine phases, while female bison spend a mean 834 days in the Screening and Quarantine phases; these bison were then required to spend an additional 365 days in the Assurance phase with follow-up testing.

Reducing testing timelines to allow animals to complete the program at 300 days would nearly triple program capacity. Testing bison by serology every 30 to 90 days until all non-negative animals are removed has been effective in identifying seroreactors. Observed data support that Screening and Quarantine Phases could become a single phase that ends at 300 days, with Assurance Phase testing ending at 365 days. Reducing the timeline would allow for National Park Service, USDA, and Native American tribes to manage

ITGs in coordination with seasonal movements of bison herds. This would also allow for approximately 226 bison to be distributed to tribes every year. Over 8 years using the current brucellosis quarantine guidelines, 172 adult bison have been distributed.

Statistical analyses revealed no significant difference in days to seroreactor detection between female and male bison enrolled into quarantine.

Female bison undergo much more rigorous quarantine procedures than male bison because of the probability of latency of brucellosis infection and its consequence in females. There have been no positive detections on post-parturition swabs during the Quarantine Phase in 108 individuals across 10 ITGs, nor any seroreactors detected 6-months post-parturition. Observed data suggest serologic screening every 30 to 90 days until all seroreactors are removed is effective to detect these cases without the need for breeding and parturition. Breeding and calving requirements lengthen time to release because females remain in the Quarantine Phase for a minimum of 26 months after all seroreactors have been removed. Animals that do not breed cannot move to the Assurance Phase. There is also inherent risk in anesthetizing and sampling female bison within 5 days of birth: animal staff are at risk of exposure to high potency opiates (e.g., etorphine) and crush injuries, and each handling event can lead to injury or death of both the cow and her calf. Reducing the breeding and calving requirements would dramatically decrease the duration of quarantine, with options including eliminating the requirement altogether, including breeding and/or calving in the Assurance Phase, and eliminating post-parturient sampling.

Male bison are currently required to be 3 years of age to finish Quarantine Phase testing before transfer to the Assurance Phase (Figure 1). This age requirement limits the enrollment of male calves (approximately 10 months of age), who would need to spend 26 months in the Screening and Quarantine Phases before moving to the Assurance Phase. There was an increased proportion of positive seroreactors for enrollment of adult male bison compared to yearlings (68% versus 40%; Table 1); enrolling younger male bison would decrease the risk of potential seroconversions while in quarantine. Changing this age requirement would increase the number of male bison that could successfully be enrolled and complete the quarantine program.

Our findings support decreasing Yellowstone National Park bison brucellosis quarantine to 300 days to seasonally manage wild bison populations and provide more brucellosis-free bison to Native American tribes. USDA Veterinary Services, the National Park Service, the Fort Peck Assiniboine and Sioux Tribes, Montana Fish, Wildlife, and Parks, and Montana Department of Livestock have successfully implemented a quarantine program to safely quarantine and monitor this national resource. The continued distribution of American bison, the national mammal of the United States, has profound cultural, economic, and genetic benefits.

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Disclaimer: The findings and conclusions in this publication are those of the authors and should not be construed to represent any official USDA or US Government determination or policy.

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Supplementary Materials

Supplementary materials are posted online at the journal website: avmajournals.avma.org

Appendix

Bayesian latent-class time-to-event model for bison brucellosis detection and seroconversion: description and code repository.

LATENT-CLASS TIME-TO-EVENT MODEL

A Bayesian latent-class time-to-event model was developed to evaluate the risk of nondetection of brucellosis seroreactors. The hierarchical model assumed an infection model to evaluate disease status and seroconversion model to evaluate the time until seroconversion.

INFECTION MODEL

Time t_0 is the time at which each individual bison was removed from the wild population and placed in isolation. Animals were assumed as infected ($z_i = 1$) or uninfected ($z_i = 0$) at time t_0. ψ was the infection probability of animals testing negative when placed in isolation. The model (likelihood) for z_i was given by

$$[z_i|\varphi] = \text{Bernoulli}\ (\varphi).$$

The model (prior distribution) for ψ was given by ψ ~ Beta (1, 1).

SEROCONVERSION MODEL

A parametric hazard function was used to evaluate the time of the first brucellosis-positive serology test. We defined t_i as the number of days since entering the quarantine facility when the i^{th} bison first exhibited a positive test. Data were right censored. When an animal tested negative through all occasions, we set t_i equal to the time of the final test. The model for t_i was given by

$$[t_i|\lambda, \alpha, \boldsymbol{\beta}, z_i = 0] = 0,$$

when an animal was not infected and

$$[t_i|\lambda_i, \alpha, \boldsymbol{\beta}, z_i = 1] = \text{Weibull}(\lambda_i, \alpha, \boldsymbol{\beta}),$$

when an animal was infected. In this model, λ_i is the seroconversion rate which varies based on sex according to

$$\lambda_i = e^{\boldsymbol{X}_i\boldsymbol{\beta}}.$$

α represents decreases in seroconversion rate over time. Our model assumed an uninfected animal ($z_i = 0$) cannot exhibit a positive test, and the probability an infected animal ($z_i = 1$) tested positive increased with time. Our model allowed for an animal exhibiting all negative tests to be

infected and undetected. The likelihood for t_i of an infected bison was given by the probability density function of the Weibull distribution,

$$\mathcal{L}(t_i|\alpha, \boldsymbol{\beta}, z_i = 1) = \exp(\boldsymbol{X}_i\boldsymbol{\beta})\ \alpha\ {t_i}^{\alpha-1} \exp\left(-\exp(\boldsymbol{X}_i\boldsymbol{\beta}) t^{\alpha}\right),$$

when seroconversion was observed, and

$$\mathcal{L}(t_i|\alpha, \boldsymbol{\beta}, z_i = 1) = \exp(\boldsymbol{X}_i\boldsymbol{\beta})\ \alpha\ {t_i}^{\alpha-1},$$

when the animal had all negative tests from one minus the cumulative distribution function of the Weibull distribution. The model (prior distribution) for α was given by log(α) ~ N(0,1000) and model for β_i by β_i ~ N(0,1000).

PREDICTING NONDETECTION

Monte Carlo integration was used to estimate the chance of false-negative classification. $p_{i,t}$ was the probability of false-negative classification for the i^{th} individual given all negative tests at time t. $p_{i,t}$ was determined by randomly selecting 100,000 values of marginal posterior distributions of each model parameter and evaluating

$${p_{i,t}}^{[\text{k}]} = \frac{\psi^{[\text{k}]} \times \exp\left(-\exp\left(\boldsymbol{X}_i\boldsymbol{\beta}^{[k]}\right) t^{\alpha^{[\text{k}]}}\right)}{\psi^{[\text{k}]} \times \exp\left(-\exp\left(\boldsymbol{X}_i\boldsymbol{\beta}^{[k]}\right) t^{\alpha^{[\text{k}]}}\right) + \left(1 - \psi^{[\text{k}]}\right)},$$

for the k^{th} iteration. The number of nondetected individuals in a test group of N individuals was simulated according to

$$\sum_{i=1}^{N} {z_{\text{sim},i}}^{[k]}, \qquad {z_{\text{sim},i}}^{[k]} = \text{Bernoulli}({p_{i,t}}^{[k]})$$

In a model without individual level covariates, the above equations simplify to

$${p_t}^{[\text{k}]} = \frac{\psi^{[\text{k}]} \times \exp\left(-\lambda^{[\text{k}]} t^{\alpha^{[\text{k}]}}\right)}{\psi^{[\text{k}]} \times \exp\left(-\lambda^{[\text{k}]} t^{\alpha^{[\text{k}]}}\right) + \left(1 - \psi^{[\text{k}]}\right)},$$

and

$${z_{\text{sim}}}^{[\text{k}]} = \text{Binomial}\left({p_t}^{[\text{k}]}, N\right).$$

MODEL IMPLEMENTATION

The joint posterior distribution was not available in closed form. We used a Markov chain Monte Carlo (MCMC) algorithm to simulate from the posterior distribution and estimate the unknown parameters of interest and the latent variables. Samples were drawn from the posterior distribution of each parameter and latent variable using a hybrid Gibbs sampler. Each MCMC chain was run for 500,000 iterations and thinned to ensure random mixing. All analyses were completed in program R and JAGS.