Risk of removal and effects on milk production associated with paratuberculosis status in dairy cows

Jason E. Lombard, DVM, MS; Franklyn B. Garry, DVM, MS, DACVIM; Brian J. McCluskey, DVM, PhD, DACVP; Bruce A. Wagner, PhD

Objective—To determine effects on production and risk of removal related to Mycobacterium avium subsp paratuberculosis (MAP) infection at the individual animal level in dairy cattle.

Design—Longitudinal study.

Animals—7,879 dairy cows from 38 herds in 16 states.

Procedure—A subset of dairy cattle operations that participated in the National Animal Health Monitoring System Dairy 2002 study was evaluated via a serum ELISA for antibodies against MAP and categorized according to ELISA score. Dairy Herd Improvement Association records were obtained to collect current and historical lactation data and removal (ie, culling) information. Production variables were evaluated on the basis of serum ELISA category.

Results—Cows with strong positive results had mature equivalent (ME) 305-day milk production, ME 305-day maximum milk production, and total lifetime milk production that were significantly lower than cows in other categories. No differences were observed for ME 305-day fat and protein percentages, age, lactation, and lactation mean linear somatic cell count score between cows with strong positive results and those with negative results. After accounting for lactation number and relative herd-level milk production, cows with strong positive results were significantly more likely to have been removed by 1 year after testing.

Conclusions and Clinical Relevance—Without management changes designed to reduce the farm-level prevalence of MAP infection, paratuberculosis will continue to reduce farm income by decreasing milk production and potentially increasing premature removal from the herd. (J Am Vet Med Assoc 2005;227:1975–1981)

Paratuberculosis is a bacterial disease of many domestic and wild animals that primarily affects the intestines. The causative agent is Mycobacterium avium subsp paratuberculosis (MAP), and clinical disease is characterized by weight loss and the progression of intermittent to constant diarrhea. The incubation period can be long, and clinical effects may not be seen within the productive life of the animal.

Several studies have evaluated effects on production of MAP infection via organism identification, ELISA, or both, with variable outcomes. On the basis of organism identification techniques, dairy cattle that were identified as infected produced from 15% to 18% less milk, compared with noninfected cattle. Reduced linear somatic cell counts and increased cull rates in known infected cows were also reported in 1 study. In addition to reduced milk production, results of another study indicated that significantly less milk fat and protein were produced by infected cows.

Result of studies evaluating production differences on the basis of ELISA results have been mixed, with increased milk production associated with higher anti-MAP antibody concentrations, no association, and decreased milk production with increased anti-MAP antibody concentrations. A study evaluating serum ELISA and bacteriologic culture of feces in parallel found no differences in milk, fat, or protein production. Another published report demonstrated that serum ELISA–positive cows had 28 more days to conception (days open), compared with serum ELISA–negative animals.

Results of the National Animal Health Monitoring System (NAHMS) Dairy 1996 study indicated that, on the basis of decreased milk production and removal (ie, culling) costs, the cost of MAP infection was > $200/cow in the herd for herds with > 10% of removed cows with clinical signs and with at least 2 of 25 to 40 randomly sampled cows that had positive results of serum ELISA. That study included serum ELISA testing and historical herd information from 1,004 operations.

Studies evaluating the association between paratuberculosis test status, herd removal rate, mortality rate, and reduced value at time of removal from the herd have revealed increased removals, decreased value for animals with positive test results, and increased mortality rates. Although some studies have evaluated the effect of MAP infection on production in individual dairy cattle, most are restricted to a small region of the United States and a fairly small number of operations. Many of the studies have reported production findings relative to test status that are contradictory to other studies. The only national study to evaluate the cost of paratuberculosis was performed at the herd level. It is widely cited that differences in the adjusted annual value of dairy production reported in that study were directly attributable to the effects of MAP infection. Although herds with MAP infection had substan-

From the USDA Animal and Plant Health Inspection Service, Centers for Epidemiology and Animal Health, 2150 Centre Ave, Bldg B-2E7, Fort Collins, CO 80526 (Lombard, McCluskey, Wagner); and the Department of Clinical Sciences, College of Veterinary Medicine and Biological Sciences, Colorado State University, Fort Collins, CO 80523 (Lombard, Garry). Completed as partial fulfillment of a Master of Science degree by the senior author, College of Veterinary Medicine and Biological Sciences, Colorado State University. Supported by the USDA Animal and Plant Health Inspection Service Veterinary Services.

The authors thank Drs. Lindsey Garber and Stephen Ott for technical assistance.

Address correspondence to Dr. Lombard.
tial economic losses, compared with those without, it cannot be determined whether the losses were primarily attributable to the disease or to other herd features not related to paratuberculosis.

The objective of the study reported here was to determine production differences and risk of removal related to MAP infection at the individual animal level in dairy cows. The opportunity to perform this study in conjunction with the NAHMS study allowed evaluation of many operations of various sizes and production practices from across the United States.

Materials and Methods

State and operation selection—States included in the NAHMS Dairy 2002 study were selected to represent at least 70% of the dairy cattle and producer populations in the United States. The National Agricultural Statistics Service random sample frame was used to determine the major US dairy states on the basis of dairy cattle populations. Final selection for the Dairy 2002 study included 21 states from 4 regions of the United States and accounted for > 80% of dairy cattle and operations.18

Herd selection was based on the National Agricultural Statistics Service sampling frame. A stratified random sample of herds in the participating states was selected on the basis of the number of dairy cows on the operation and the management's willingness to participate in each subsequent study.19

A subset of operations (n = 106) was invited to participate in testing to determine the within-herd prevalence of anti-MAP antibodies for the Dairy 2002 study. Of the operations that consented to prevalence testing, those enrolled in Dairy Herd Improvement Association (DHIA) testing were encouraged to participate in the production analysis by providing access to production records. Thirty-eight operations from 16 states (regions) participated in this production analysis including California, Colorado, New Mexico, Texas, and Washington (west); Indiana, Michigan, Minnesota, Missouri, Ohio, and Wisconsin (midwest); New York, Pennsylvania, and Vermont (northeast); and Florida and Virginia (southeast). States not included in the production analysis were Kentucky, Idaho, Iowa, Illinois, and Tennessee because operations in those states declined the invitation to participate.

Herd-level variables included in the analysis were location (region), herd size, and operation. Operation was nested within region for analysis.

Cow selection—The initial survey and sampling of individual cows for anti-MAP antibody testing was a cross-sectional study performed in the 21 participating states. Cows in the second or greater lactation were targeted for testing, with no other restrictions on which cows could be sampled (eg, lactating, dry [nonlactating], sick, or those to be removed). At the time of sample collection, all cows were body condition scored (thin, normal, or fat). Operations with ≤ 500 cows in at least the second lactation tested all eligible cows in the herd (census sample). A convenience sample of cows was tested on larger operations. The number of cows tested in large herds was based on herd size by use of statistical subset sampling.19 Only cows from operations with DHIA records were included in this study.

Sample collection and testing procedures—Blood samples from dairy cows were collected from March 25, 2002, to September 25, 2002, by personnel from USDA:Animal and Plant Health Inspection Service:Veterinary Services and shipped to the National Veterinary Services Laboratories in Ames, Iowa. Serum was separated and stored at −20°C until tested. All serum samples were tested for antibodies against MAP by use of a commercially available ELISA9 according to manufacturer's recommendations, with the exception that samples were only tested in a single well. Test results were categorized as negative or positive on the basis of the kit manufacturer's recommendations.9 To further categorize test results, ELISA scores were calculated for each sample by subtracting the mean optical density of the negative control from the optical density of the test sample and multiplying the difference by 10. The ELISA scores were converted to categorical results (negative, inconclusive, positive, and strong positive) on the basis of guidelines from the University of Wisconsin (Appendix).

Production data—The DHIA records, which contain numerous production-related variables as well as information on removal of individual cows from herds, were obtained directly from the Dairy Record Processing Center on a monthly or bimonthly basis. Production data were collected for the entire lactation in which each cow was tested. Commercially available dairy management software packages4,5,9 were used to extract data from complete herd records. The mature equivalent (ME) 305-day milk (MEM), ME 305-day fat percentage (%MEF), and ME 305-day protein percentage (%MEP) production values, which take into account age, breed, herd location, season of calving, and milking frequency, were used to measure current lactation milk production and quality. These variables are calculated by all Dairy Record Processing Centers by use of the same method.4 Other production variables collected for analysis included lifetime maximum MEM (in the lifetime of an individual cow), the highest predicted MEM (%MEP), total lifetime milk production (actual cumulative milk production of the cow), months of age, lactation number, mean days nonpregnant, relative herd milk production (herd rating), and lactation mean linear somatic cell count score. Information for each cow used in the analysis was collected for the last test day of the lactation or last test day prior to removal from the herd. If a cow was culled during the lactation when ELISA testing was performed, the actual removal date or date of last test was used as the culling date for risk analysis regarding removal.

Statistical analysis—Production variables were analyzed for association with ELISA results by use of a software program.4 The production variables were the dependent variables in the 9 models, which were current MEM, maximum MEM, lifetime milk production, %MEF, %MEP, months of age, lactation number, days nonpregnant, and lactation mean linear somatic cell count score. The serum ELISA result, lactation number, body condition score, breed, and region were explanatory variables in the models. Cows were nested within farm, which was also nested within region, to account for clustering within a herd. The balance of the explanatory variables was fixed in the model. The model with the smallest Akaike information criterion was chosen. A value of P ≤ 0.05 was considered significant in determining differences in the production variables.

Two logistic regression models were developed by use of commercially available software4 to determine the risk of herd removal for each ELISA result category. The software accounted for the potential clustering effects of removal within herds. The first model accounted for cattle removed prior to the herd owner receiving individual cow results. The second model accounted for herd removals that occurred within 365 days of testing, including the time after which test results were reported to herd owners.

Breed, body condition score, lactation number, relative herd milk production (herd rating), serum ELISA result, herd size, and region as well as all 2-way interactions were evaluated as initial explanatory variables in the removal models. A stepwise backward selection process was used to construct the final models with a Wald P value of ≤ 0.05 considered significant. Main effects were not removed from the model if they were included in an interaction, regardless of P value. Model fit was evaluated on the basis of the Hosmer-Lemeshow χ² test P value.
Revenue differences for MEM, determined by use of current MEM of test-negative cows as the base, were calculated for each test classification category by use of MEM and the 2002 mean milk price for the United States. The 2002 mean milk price of $12.19/100 lb, obtained from the National Agricultural Statistics Service, was rounded to the nearest whole dollar ($12.00) for the partial revenue calculations.

**Results**

Cows—A total of 7,879 female dairy cattle from 38 dairy operations in 16 states were included in the study.

More than 27,000 dairy cows were represented by the 38 operations, but because all cows within a herd were not necessarily tested, only cattle with serum ELISA results and DHIA record information were included in the analysis. The overall cow-level prevalence of ELISA-positive cattle in the study population was 3.8%. The within-herd seroprevalence for the 38 operations in this study ranged from 0% to 14.8%.

Holsteins accounted for the majority (90.6%) of cattle, but other breeds such as Jersey and Brown Swiss were also included (Table 1). Cows in their third or greater lactation comprised the majority (52.0%) of cattle, whereas cows in second lactation accounted for 38.7%. Only 9.3% of cows tested were in their first lactation because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

More than 27,000 dairy cows were represented by the 38 operations, but because all cows within a herd were not necessarily tested, only cattle with serum ELISA results and DHIA record information were included in the analysis. The overall cow-level prevalence of ELISA-positive cattle in the study population was 3.8%. The within-herd seroprevalence for the 38 operations in this study ranged from 0% to 14.8%.

Holsteins accounted for the majority (90.6%) of cattle, but other breeds such as Jersey and Brown Swiss were also included (Table 1). Cows in their third or greater lactation comprised the majority (52.0%) of cattle, whereas cows in second lactation accounted for 38.7%. Only 9.3% of cows tested were in their first lactation because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

More than 27,000 dairy cows were represented by the 38 operations, but because all cows within a herd were not necessarily tested, only cattle with serum ELISA results and DHIA record information were included in the analysis. The overall cow-level prevalence of ELISA-positive cattle in the study population was 3.8%. The within-herd seroprevalence for the 38 operations in this study ranged from 0% to 14.8%.

Holsteins accounted for the majority (90.6%) of cattle, but other breeds such as Jersey and Brown Swiss were also included (Table 1). Cows in their third or greater lactation comprised the majority (52.0%) of cattle, whereas cows in second lactation accounted for 38.7%. Only 9.3% of cows tested were in their first lactation because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.

Least square means for the evaluated production variables were determined for each herd by use of curvilinear regression because this study targeted cows in their second or greater lactation. Body condition scores were recorded as normal for 85.4% of cows. Of all cows in the study, 70.8% were from herds with > 500 head, whereas only 4.5% of the cows were from herds with < 100 head. The west region contributed the majority (57.6%) of cows in the study. A subset of cows and herds had complete historical production records available for determination of maximum MEM and lifetime milk production.
Current lactation MEM was approximately 3,000 lb less for cows with strong positive results, compared with cows with negative results, which resulted in approximately $360 less in gross milk revenue (Table 2). Cows with positive results had current MEM of 880 lb less than cows with negative results, which resulted in $105 in decreased gross milk revenue. Sensitivity analysis was performed to evaluate changes in milk price and associated decreased gross revenue from cows that had positive or strong positive results. Comparison of the change in gross revenue at $10.00 milk prices to the 5-year high in 1998 of $15.50 indicated that gross revenue loss associated with decreased MEM in the current lactation ranged from $88 to $136 for cows with positive results and from $300 to $466 for cows with strong positive results.

Gross revenue differences among serum ELISA result categories were also calculated on the basis of pounds of fat and protein and somatic cell count by use of US mean 2002 milk component pricing. The revenue differences were approximately the same as values calculated by use of the $12/100 lb of milk to calculate the change in gross milk revenue, suggesting that either method of estimating the change in gross revenue was feasible.

Prior to producer knowledge of test outcome (mean, 122 days; range, 85 to 177 days), cows with positive or inconclusive ELISA results, but not strong positive, were at increased risk of being removed from the herd after accounting for relative herd milk production (Table 3). Cows with strong positive test results were 1.8 times as likely to be removed as cows with negative results, although this was not significant ($P = 0.07$). Only herd rating and positive ELISA result were significant in the model. Cows that produced milk at ≤80% of herd average were at significantly increased risk of removal in both models. The Hosmer-Lemeshow $\chi^2 P$ value of 0.82 suggested good model fit.

After test results were reported to producers, only cows with strong positive test results were at significantly increased risk of removal in the model. Herd rating was also significant in the model that included removals to 365 days after testing, with lactation having a $P$ value of 0.051. A nonsignificant Hosmer-Lemeshow $\chi^2 P$ value of 0.38 was also obtained for the second logistic model, which suggested a good model fit.

Discussion
Veterinarians and producers need firm evidence of the production-related effects and costs associated with MAP infection in dairy operations to develop the most efficient and profitable way to manage and control infection. Removing cows with positive test results by any test may be a component of MAP control programs with the rationale of decreasing spread of the agent, but simulation models suggest this method is not the most cost-effective, compared with other management changes. The production-related effects of MAP infection as reported here give more evidence to veterinarians and producers that infected dairy cows can substantially affect the potential gross income of an operation, thus providing more rationale for implementation of control measures to reduce the prevalence of MAP in a herd.

Results of this study suggest that negative effects on milk production may occur throughout the productive lifetime of those cows that produce sufficient antibodies to cause a positive or strong positive ELISA result. Decreased current MEM, maximum MEM, and lifetime total milk production observed in cows with strong positive ELISA results, compared with cows in the other result categories, suggested that the disease does not progress linearly in all cows. Although cows with strong positive ELISA results are thought to be in the later stages of disease, production losses occurred throughout their lifetimes, suggesting that the disease affects those cows differently than cows with positive results. The reduction in current MEM is consistent with Nordlund et al, who also reported a decrease in milk yield in serum ELISA-positive cows, compared with ELISA-negative cows.

McNab et al have speculated that cows with a higher production potential that remain in the herd are more likely to be removed because of MAP infection.

Table 3—Odds ratios and 95% confidence intervals (CI) for removal of dairy cows prior to producer’s knowledge of ELISA results for MAP infection (Prior) and 1 year after testing (After) on the basis of certain model variables.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Prior Odds ratio 95% CI</th>
<th>After Odds ratio 95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>ELISA result</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Strong positive</td>
<td>1.8</td>
<td>1.0–3.5</td>
</tr>
<tr>
<td>Positive</td>
<td>1.9</td>
<td>1.1–3.3</td>
</tr>
<tr>
<td>Inconclusive</td>
<td>1.9</td>
<td>1.0–3.3</td>
</tr>
<tr>
<td>Negative</td>
<td>Referent</td>
<td>Referent</td>
</tr>
<tr>
<td>Lactation number</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Continuous</td>
<td>NR</td>
<td>NR</td>
</tr>
<tr>
<td>Herd rating (%)*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>&gt; 110</td>
<td>0.3</td>
<td>0.1–0.5</td>
</tr>
<tr>
<td>101 to 110</td>
<td>0.3</td>
<td>0.2–0.4</td>
</tr>
<tr>
<td>91 to 100</td>
<td>0.4</td>
<td>0.3–0.7</td>
</tr>
<tr>
<td>81 to 90</td>
<td>0.8</td>
<td>0.5–0.7</td>
</tr>
<tr>
<td>≤ 80</td>
<td>Referent</td>
<td>Referent</td>
</tr>
</tbody>
</table>

Bolded odds ratio and 95% CI represent significant ($P < 0.05$) findings.
*As a percentage of herd mean milk production.
NR = Not retained in the model.
The maximum MEM results from our study suggest that is incorrect. After the infection has progressed to a certain level and antibody response is extremely high, milk production substantially decreases and the cows are more likely to be removed from the herd.

Mature equivalent percentages of milk fat and protein were not significantly different between cattle with strong positive versus negative results. These findings concur with Nordlund et al. and Johnson et al., who also reported no difference in %MEF and %MEP between testing groups.

Finding no significant differences in linear somatic cell count among tested cows was consistent with Wilson et al. Reproductive efficiency as defined by days nonpregnant was significantly different; cows with strong positive results had less days nonpregnant than cows with negative results. These results are opposite of the results found in another study. Although there are logical nutritional theories for MAP-infected cows to have infertility problems, there are many poorly defined influences on dairy cow reproduction that could have influenced results in this and the other study.

Alternatively, cows with strong positive results in this study may have been selectively removed by herd owners on the basis of test results, which could have biased the estimate of days nonpregnant.

In general, cattle with MAP infection are believed to be removed at a younger age than uninfected herdmates. Early removal could be caused by the effects of disease or the use of diagnostic test results to assist in making removal decisions. Our findings of a non-significant decrease in months of age did not suggest that MAP-infected cattle are prematurely culled. Survivor bias could have been introduced into these results because MAP-infected cows that were poor producers may have been removed for subclinical disease (decreased milk production) during the first lactation or prior to having positive test results.

Cows with positive or inconclusive test results, compared with cows with negative results, had increased odds of removal prior to results being released to producers, even after accounting for relative herd milk production. Because many producers make decisions about removals with the use of anti-MAP antibody test results, it was appropriate to determine the increased risk of removals attributable to the effect of infection alone and then with producer knowledge of test results. However, because contact with herd owners was not allowed because of the nature of NAHMS studies, it was not known whether test results from other sources were available prior to the release of NAHMS results. If operations were performing routine testing in addition to this study, it is possible that decisions were made with knowledge of MAP status; however, the low risk of removal of cows with strong positive results suggests that results from other sources were not used by many operations.

After the test results were known, relative milk production and strong positive test results were significantly associated with removal. Producers may have used test results to make removal decisions because recommendations are frequently made to remove cows with positive results. Alternatively, it is also plausible that clinical signs of disease may have appeared by 1 year after testing, necessitating removal regardless of herd owners' awareness of test results. Reports indicate that cows with strong positive results are more likely to be infected, and it is more likely for the cow to have clinical signs within 1 year of testing.

The variability of results from previous studies with respect to the effects of MAP infection on production is most likely attributable to individual herd prevalence of disease, management levels, and test characteristics and subsequent misclassification of cows within a test group. Herd-level prevalence of MAP likely affects the amount of exposure and the subsequent dose of the organism ingested. Results of a previous study indicate that an increased dose of MAP decreases the time to clinical disease. This suggests that herds with different prevalence values have different costs associated with an individual case of MAP infection because of the timing of clinical disease. Heavily infected herds would potentially have more individuals with clinical signs of disease at a younger age, thus leading to greater financial losses.

Although there was no significant association between body condition scores and serum ELISA results, it is possible that some clinically affected cows could have been tested and influenced outcomes of this study. Because all eligible cows were tested on operations with ≤ 500 cows in at least second lactation, there was not an opportunity for clinically affected cows to be selectively chosen over clinically normal cows. On larger operations, the large number of cows tested would avoid having a few clinically affected cows influence the overall results. Additionally, the authors would expect operations with infected cows to remove them from the herd soon after developing clinical signs.

The purpose of this study was to evaluate production losses associated with ELISA results and not to promote entire-herd testing for MAP infection. Production losses from MAP infection can be substantial at the herd level, but these are losses to potential revenue and not out-of-pocket expenses. The additional cost of testing may not be justified for the purpose of removing cows with positive results because removals represent additional costs to the producer, whereas decreased milk production only results in a loss of potential revenue. Also, a cow with strong positive test results that is producing 3,000 lb/y less milk than expected could still be a positive revenue contributor in the herd.

It seems reasonable to consider the economic cost to the producer to identify cows with positive ELISA results. A 1,000-cow herd with a 5% within-herd seroprevalence of MAP infection could be considered because most cows in this study were from herds with > 500 cows. The serum ELISA costs approximately $8 for sample collection and testing. If the owner of the herd tested all cows and identified the 50 cows with positive results, the cost to identify each cow would be $160 (1,000 cows x $8)/50 test-positive cows). The same testing cost per identified infected cow would be true for any herd with > 20 cows with similar seroprevalence. As within-herd prevalence decreases, the cost associated with identifying test-positive cows increases. This addi-
tional testing cost would have to be added to the losses already incurred from decreased production.

To justify the expense of testing and removing cows, producers would have to recover the testing cost per identified cow ($160) in additional salvage value at the time of removal, compared with removing the cow after the onset of clinical signs (disregarding the opportunity costs of replacements). Results of previous studies\cite{16} evaluating the difference in market value of clinically and non-clinically affected cows suggest that the testing costs could not be recouped by early removal, but changes in market price and subsequent value would have to be evaluated prior to investing in the testing program. Whole-herd testing would have to be justified by benefits other than a decrease in production losses after removing cows with positive results.

Although not evaluated in this study, the likelihood for continual contamination of the environment and disease transmission by infected cows with positive or strong positive results is potentially more costly than the production effects on an individual cow on the basis of transmission models reported by van Roermund et al.\cite{29} If reducing transmission is the only real benefit of removing cows with positive results, this benefit would have to outweigh production losses, testing costs, reduced salvage value, and opportunity cost of replacements.

Without management changes designed to reduce the faecal excretion of MAP, paratuberculosis will continue to reduce farm income by decreasing milk production and potentially increasing premature culling from the herd. The risk and associated costs of MAP transmission from maintaining infected cattle in a herd need to be further evaluated.

### References


### Appendix

Classification and interpretation of results of an ELISA* for antibodies against *Mycobacterium avium* subsp. *paratuberculosis* (MAP) in dairy cows.

<table>
<thead>
<tr>
<th>Result</th>
<th>ELISA score</th>
<th>Explanation and recommendation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Negative</td>
<td>0.00 to 0.49</td>
<td>Antibodies against MAP were not detected. Cows are either not infected or not producing antibodies.</td>
</tr>
<tr>
<td>Inconclusive</td>
<td>0.50 to 0.99</td>
<td>Cows are more likely to be infected than cows with negative results. Retesting is recommended.</td>
</tr>
<tr>
<td>Positive</td>
<td>1.00 to 3.49</td>
<td>Cows are approximately 30 to 75 times as likely to be infected with MAP as are cows with negative results.</td>
</tr>
<tr>
<td>Strong positive</td>
<td>≥ 3.50</td>
<td>Cows are approximately 175 to 200 times as likely to be infected with MAP as are cows with negative results. Cows have a higher probability of developing clinical paratuberculosis in the next 12 months than cows with lower scores.</td>
</tr>
</tbody>
</table>

Adapted from Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin–Madison, Interpretation Chart.

---

**Selected abstract for JAVMA readers from the American Journal of Veterinary Research**

**Effects of long-term dietary supplementation with clinoptilolite on incidence of parturient paresis and serum concentrations of total calcium, phosphate, magnesium, potassium, and sodium in dairy cows**

Panagiotis-Dimitrios Katsoulos et al

**Objective**—To determine whether dietary supplementation with clinoptilolite affects the incidence of parturient paresis and serum concentrations of total calcium (tCa), inorganic phosphorus (PO$_4^{2-}$), magnesium (Mg$^2+$), potassium (K$^+$), and sodium (Na$^+$) in dairy cattle.

**Animals**—52 dairy cows.

**Procedure**—Cows were placed into 3 groups. The first 2 groups (group A [$n = 17$] and group B [$17$]) were offered a concentrate supplemented with 1.25% and 2.5% clinoptilolite, respectively. The third group C ($n = 18$) served as a control and was offered the concentrate alone. The experiment started 1 month before parturition and lasted until the beginning of the next nonlactating period. Around the time of calving, all cows were monitored for the development of parturient paresis. Blood samples were taken at the commencement of the experiment, on the day of calving, and thereafter at monthly intervals to measure serum tCa, PO$_4^{2-}$, Mg$^2+$, K$^+$, and Na$^+$ concentrations.

**Results**—The incidence of parturient paresis in group B cows was significantly lower, compared with group C cows. However, serum concentrations of tCa, PO$_4^{2-}$, Mg$^2+$, K$^+$, and Na$^+$ were not significantly affected by long-term supplementation with clinoptilolite.

**Conclusions and Clinical Relevance**—In the context of this experiment, clinoptilolite supplementation at 2.5% appeared to have reduced the incidence of parturient paresis in dairy cows, suggesting that its effectiveness depends on the amount incorporated in the ration of cows. Addition of clinoptilolite in the concentrate of dairy cows during the nonlactating period could be used as a cost-effective preventive treatment for parturient paresis. *(Am J Vet Res 2005;66:2081–2085)*