The Relationship between Milk Urea Nitrogen and Reproductive Performance in Dairy Cattle

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Introduction

The objective of this study was to investigate the relationship between milk urea nitrogen (MUN) and first service breeding success on dairy farms.

Materials and Methods

The study population included all cows with a first service from 191 Prince Edward Island (PEI) dairy herds on monthly milk recording. Breeding data for these cows were obtained from the Atlantic Dairy Livestock Improvement Corporation (ADLIC) for June 1, 1999 to May 31, 2001. First-service breeding success (FSBS) was determined for breedings between June 1, 1999 to May 31, 2000. In order to minimize misclassification errors for FSBS, the remaining period was utilized to categorize the first services as successful or not, according to strict definitions (eg. successful = first breeding was last breeding, producing a subsequent calving 270-290 days later). MUN and milk production data for these cows were obtained from ADLIC for April 1, 1999 to August 31, 2000 in order to obtain possible covariate data for the milk production test date closest to the breeding date, and to calculate the following MUN values relative to each breeding: 1) average MUN value during the 60 days before breeding, 2) most recent MUN value before breeding, 3) MUN value that was closest to the breeding date (before or after), 4) the next MUN value after breeding, and 5) average MUN value during the 60 days after breeding. After investigation of simple associations between MUN categories and FSBS, multiple variable logistic regression was used to determine if the five categories of MUN values were related to FSBS, while controlling for possible confounders such as milk production, parity, milk protein, linear score somatic cell count (LSSCC), number of days of dry period of previous parity, days in milk on service date, and month of the year. A random variable for herd and for cow were included in the model to control for clustering of management and reproductive success of cows within herds and lactations within cows.

Results and Conclusions

In total, 6,081 first services with a determination of the pregnancy success were used in the analysis, 2,716 successful services and 3,165 unsuccessful services. There were 1180 first services that did not meet the criteria for successful or unsuccessful breeding, and therefore were excluded from the analyses. The MUN value on the test date closest to the breeding date ("MUN closest") produced the strongest statistical (and biological) relationship with pregnancy and therefore was used in the multiple variable modelling process. Simple associations showed MUN closest was significantly ($p<0.05$) related to FSBS. Without controlling for 24 hour test day milk production on the date closest to the breeding date, the final model of significant ($p<0.05$) variables included MUN closest, LSSCC for the closest test date to the breeding date, parity, and previous dry period length, with each having an inverse relationship with FSBS. When controlling for milk production, the results showed that MUN closest was still significant ($P=0.05$). A change in MUN from 10 to 20 mg/dl was associated with a 14% reduction in the odds of conception. This relationship between MUN and FSBS will be further examined using nutritional data recorded for 83 of the 191 herds.

The Distribution of *Mycobacterium avium* Paratuberculosis in the Environment Surrounding Minnesota Dairy Farms

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Introduction

Paratuberculosis, or Johne's disease, is a chronic and progressive intestinal disease in ruminants caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP). The usual route of infection is fecal-oral, with young cattle becoming infected by exposure to infected adults or their environment. The disease becomes manifest in adulthood and results in economic losses due to premature culling, reduced milk production and loss of body weight in cattle sold for slaughter. The bacterium survives for months in extreme environmental conditions. The objectives of this study were to characterize the distribution of MAP in the environment of Minnesota dairy farms and to assess the association between infected dairy herds and their environments.

Materials and Methods

One hundred and eight Minnesota dairy herds were sampled during the summer of 2002, including 80 herds known to be infected from previous testing, which participated in the Johne's Disease Control Program (JDCP) of the Minnesota Board of Animal Health (MBAH), and 28 herds known to be uninfected based on previous testing, which participated in the Voluntary Johne's Disease Herd Status Program (HSP) of the MBAH. Fecal samples were obtained from up to 100 cows in each herd and were cultured in pools of five cows based on age order. Environmental samples were obtained from each farm, with up to two samples from each of the following locations: calving area, dry cow area, cows' alleyway, manure storage, fields near cows area, edge of streams where cows have access or water runoff from the parlor, preweaned calves, postweaned calves and sick cows pen. Fecal pools and environmental samples were tested using bacterial culture for MAP at the Minnesota Veterinary Diagnostic Laboratory.

Results and Conclusions

Sixty-four of the 80 JDCP herds had at least one pool positive; 16 did not have any positive pools. The environment around the farm was found to be contaminated on 61 of the 64 herds with positive pools and in one of the 16 herds with only negative pools. The most common areas found to be contaminated on the farms were cows' alleyways (77% of herds with positive pools) and manure storage (68%). Other infected areas were the calving area (21%), sick cows pen (18%), water stream edge and water runoff (6%), and post-weaned calves area (3%). In 91% of these herds, at least one sample from cows' alleyway or/and manure storage was positive to MAP. Twenty-six herds of the HSP herds (n=28) were found to be negative, with no positive pools; two herds had one positive pool each. The environment among these herds was found to be contaminated in one herd, which had a positive pool as well. Most of the environment samples had low numbers of colonies per tube, whereas most of the fecal pools samples had high numbers of colonies per tube.

Eighty percent of supposed positive herds were positive on fecal culture; 78% were positive in environment sampling. The association between infected herds and their infected environment emphasizes the critical importance of farm management strategies for the control of Johne's disease in order to reduce environmental MAP contamination and exposure to cattle. In addition, targeting common contaminated areas in the farm environment suggests a promising alternative strategy for herd screening and Johne's infection status assessment. This strategy has the potential of saving significant economical resources in terms of cost and time.