was determined to be positive in samples from cow alleyways (77% of the herds), manure storage (68%), calving area (21%), sick cow pen (18%), water stream edge and water runoff (6%), and postweaned calves area (3%), but not in preweaned calves or fields near cow area. There was an association between maximum level of colonies per tube from cow alleyways and manure storage and fecal pool prevalence. Herds with both areas cultured negative were estimated to have 0.3-4% fecal pool prevalence. Herds with both areas having a heavy load of bacteria were estimated to have 53-73% fecal pool prevalence.

Significance

Targeted common and contaminated areas in the farm environment, specifically cow alleyways and manure storage (especially lagoons), suggest a promising alternative strategy for herd screening and JD infection status assessment and for estimating herd fecal prevalence. This strategy has the potential of saving significant economical resources in terms of cost and time.

Effect of Management Related Disease Control Methods on the Development of Johne's Disease in Dairy Cattle in Texas.

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Introduction

With the primary objective of evaluating long-term effectiveness and feasibility of management-related disease control methods in large dairies and on beef operations on the development of Johne's disease (JD) in cattle in Texas, USDA-APHIS and Texas A&M University have initiated the Johne's Disease Control Demonstration Project for the Texas dairy and beef industries. The epidemiological and production analysis of one of the dairy demonstration herds (n=3534) is presented, and the effect of JD on the herd's production parameters is evaluated.

Materials and Methods

A retrospective epidemiological study was conducted from April 2001 until December 2003 on the lactating herd. Serum samples were collected from cows after they had been confirmed pregnant and prior to lactation cessation. The serum samples were tested using an ELISA test (IDEXX Laboratories). Test results >0.25 S/P value were considered positive for JD. Production parameters (305 days milk production, somatic cell counts, total fat, total protein) and reproduction parameters (times bred, days open and times aborted per lactation) were collected. The herd was then stratified and JD-positive cases were compared to negative cases for production and reproduction parameters using T-test and Mann-Whitney Rank Sum Test using Sigma Stat (SPSS, 2001). A colostrum management strategy of using colostrums only from test-negative cases was implemented at the beginning of the study (April, 2001), and results of the serological analysis were incorporated into each cow file and considered during treatment decisions on digestive disorders and when making culling decisions. Cow replacement of home-reared animals with purchased cows was also implemented.

Results

Laboratory analysis indicated 116 positive cases (8.51%) of a total of 1362 analyzed samples during 2001, 36 positive cases (7.89%) of a total of 456 analyzed samples during 2002 and 83 positive cases (5.61%) of a total of 1477 analyzed samples during 2003.

Prevalence of JD in home-reared cows was 11.73%, and 6.12% and in purchased cows. Cows in lactation one showed no statistically significant differences in any parameter analyzed. Statistically significant differences in 305 days milk (P=0.037), 305 days mature equivalent milk (P=0.006), total fat (P=0.001) and total protein (P=<0.001) were found for cows in lactation two and three. No significant differences in the parameters analyzed occurred in cows in their third or later lacation. The presence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) in fecal material was deter-

mined as positive (22/45) by fecal culture in September 2001.

Significance

Results indicated a significant detrimental effect on milk production (expressed as 305 days milk) and milk quality (total fat, total protein), which were reduced in cows with subclinical Johne's disease, during second and third lactation. This effect began at an average age of 5.41 years, which corresponds with the known chronic nature of JD. The lack of a difference in older animals may be due to the relatively small numbers in this population or that heavily infected cows were previously removed from the herd. The reduction in prevalence of JD observed up to this point is indicative of a younger, purchased herd. Calves raised under the colostrum management program are now entering the herd, and the prevalence in this subpopulation will be monitored to determine if the management strategy has been effective in reducing the prevalence of the disease in home-reared animals.

Salmonella Antimicrobial Resistance Patterns on Midwest and Northeast Dairy Farms

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Introduction

Potential impact of antimicrobial use in livestock on the development of antimicrobial-resistant zoonotic pathogens is an ongoing and controversial public health issue. Our objective was to determine the prevalence of antimicrobial resistance among *Salmonella* isolates collected from dairy farms.

Materials and Methods

Thirty-two organic farms and 97 conventional farms in Michigan, Minnesota, New York, and Wisconsin were enrolled in the study. Herds were selected without regard to prior history of *Salmonella* infections. Environmental and cattle fecal samples were collected on each farm at two-month intervals from August 2000 to October 2001. *Salmonella* isolates were tested for susceptibilty to amikacin, amoxicillin/clavulanic acid, ampicillin, ceftiofur, ceftriaxone, cephalothin, chloramphenicol, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline and trimethoprim/sulfamethoxazole using a broth dilution method. Isolates were classified as susceptible or having decreased susceptibility (intermediate or resistant) for each antimicrobial based on minimum inhibitory concentrations.

Results

There were 63 distinct antimicrobial resistance patterns, but seven patterns accounted for greater than 90% of the isolates. A median of 75% of isolates shared the dominant pattern within farm for 60 farms, with at least four isolates tested. The most frequent pattern was susceptible to all 15 antimicrobials, with 91 farms having at least one isolate pan-susceptible and 50% of farms having two-thirds or more of isolates susceptible to all antimicrobials tested. There were 13 farms where the majority of isolates had decreased susceptibility to five or more antimicrobial agents. Strains with decreased susceptibility to 10 or 11 drugs were found on 12 farms. The most frequent patterns among these isolates were decreased susceptibility to amoxicillin/clavulanic acid, ampicillin, ceftiofur, cephalothin, chloramphenicol, gentamicin, kanamycin, streptomycin, sulfamethoxazole, tetracycline, and +/- ceftriaxone (eight farms).