Significance

In summary, this was the first report to characterize multiple cp BVDV isolates within 1 herd of PI animals. Cytopathic BVDV viruses isolated from 13 of the PI animals showed a cellular DnaJ insertion in the NS2-3 junction of the viral sequences. The insertions were identical in all cp viruses with common insertion sites indicating that 1 animal likely developed a cp virus that then progressively spread to the other 12 animals. A larger number of nucleotides changes were observed

in the insertion region of the cp isolates compared to the 3' flanking viral sequences and the same region of the ncp isolates. This may support the idea that cp BVDV could not tolerate changes in this viral area of the genome while changes in the insertion area, which were not essential for the viral replication, would be less critical. In herds with multiple cases of MD, a single CP mutant maybe responsible for entire outbreak of MD. This is consistent with cases where PI cattle have been vaccinated with a CP BVDV vaccine and developed MD where the CP vaccine virus was isolated.

Program outcomes from the Atlantic Johne's Disease Initiative

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Introduction

Johne's disease is an incurable, chronic, infectious enteritis of domestic and wild ruminants. It is caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). It has been identified as one of the top health priorities of the Canadian dairy industry by the Dairy Farmers of Canada. The Atlantic Johne's Disease Initiative (AJDI) was launched in 2011 as a voluntary, long-term farm strategy with the overall objective of reducing the prevalence and impact of Johne's disease in Atlantic Canada. This report outlines program implementation statistics, prevalence data, risk assessment scores, and management plan recommendations for the AJDI.

Materials and Methods

Annual herd testing was conducted using an environmental culture (EC) procedure modeled on the USDA Voluntary Bovine Johne's Disease Control Program. Six mixed manure samples were collected from prescribed locations by trained technical staff. The fresh samples were cultured at the Atlantic Veterinary College using the *para-JEM* broth culture system (Thermo Fischer). A PCR (VetAlertTM, Tetracore) was used to confirm cultures that were positive for growth through the TREK incubator sensor or were acid-fast positive after incubation. Veterinarians certified through AJDI delivered the herd results, conducted a farm-specific risk assessment, developed a management plan (RAMP), and assessed management plan adherence for each herd. A risk assessment workbook, designed using the Canadian na-

tional standards for risk assessment, was used for the RAMP process. During the second RAMP, the certified veterinarian assessed management plan adherence by completing a Management Plan Implementation survey.

Results

Four hundred and sixty three of the region's 664 herds (70%) enrolled in the AJDI. Year 1 (Y1) results indicated that 88 of 457 herds (19.3%) were EC positive, whereas 90 of 414 year 2 (Y2) herds (21.7%) were EC positive. When interpreted in series, 121 herds (26.5%) tested positive in at least 1 of the 2 years. To date, RAMPs have been completed and entered into the database for 422 Y1 herds and 201 Y2 herds. The overall proportion of maximum risk score was 0.46 (95% confidence interval (CI) of 0.45-0.47) for Y1 herds and 0.42 (CI 0.40-0.43) for Y2 herds. The proportion of maximum risk score was 0.45 (CI 0.44-0.46) for Y1 negative herds and 0.50 (CI 0.48-0.52) for Y1 positive herds. The proportion of maximum risk score was 0.41 (CI 0.40-0.43) for Y2 negative herds and 0.44 (CI 0.41-0.47) for Y2 positive herds. Veterinarians were able to make a maximum of 3 management recommendations at each RAMP. The best management practice of "animals are not purchased" was recommended 302 of 1630 total recommendations (18.5%), and "calves are removed from the dam within 30 minutes" was recommended 10.8% of the time (176/1630). At the time of the Y2 RAMP, the certified veterinarians assessed the adherence to the Y1 management plan recommendations for 198 herds to be 4.1 (CI 3.9-4.3), using a 7-point Likert scale.

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Significance

Program participation of 70% of regional dairy herds was achieved. Herd prevalence of Johne's disease was comparable to other regions in Canada, but lower than reported herd prevalence in the United States. RAMP scores were significantly higher for Y1 herds than Y2 herds and higher for EC positive herds compared to EC negative herds. It is encouraging that RAMP scores

decreased in year 2, suggesting that the AJDI had an impact on the Johne's disease risk. This decrease was more pronounced for EC positive versus EC negative herds, despite the veterinarians indicating that management plan recommendations were only moderately implemented. In the future, specific efforts to improve the adherence to program recommendations may further improve Johne's disease control.

Risk factors in beef cattle for terminal rectal mucosa colonization of *Escherichia coli* O157:H7

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Introduction

Escherichia coli O157:H7 (STEC O157) is an important foodborne pathogen of humans. Cattle are sub-clinically colonized with STEC O157 at the terminal rectal mucosa (TRM). Live cattle serve as an important reservoir for human exposure, but it is unknown if health or performance characteristics of cattle predict their risk for colonization. Our objective was to test if disease during the finishing phase, growth performance, or carcass quality measurements at harvest increased the odds of E. coli TRM colonization at the time of slaughter.

Materials and Methods

Data were analyzed from 751 steers assigned to 94 pens (8 animals/pen) from 2 separate vaccine randomized controlled trials in which TRM samples taken at slaughter were cultured for STEC O157. Health records from the day of arrival at the feedlot until slaughter were obtained, as well as growth performance and carcass quality characteristics. Data were analyzed using mul-

tilevel multivariable logistic regression in a generalized linear mixed model with random effects of study and pen. Vaccination against STEC O157 was treated as a fixed effect to adjust for potential confounding.

Results

We found no difference in the odds for TRM colonization related to hot carcass weight (p = 0.33), feedlot-ending live weight (p = 0.27), marbling score (p = 0.71), longissimus muscle area (p = 0.29), or liver abscess score (p = 0.49). Also, there was no significant difference in the odds for TRM colonization related to respiratory disease treatment (p = 0.35) or foot rot (p = 0.40). Vaccination against STEC O157 did significantly explain the odds for TRM colonization (OR= 0.40, p = 0.003).

Significance

These findings suggest that colonization of cattle with STEC O157 is not explained by their health or performance characteristics.