## Materials and Methods

A literature search was performed to identify studies evaluating the effectiveness of bovine herpesvirus-1 (BHV-1), bovine respiratory syncytial virus (BRSV), bovine viral diarrhea virus (BVDV), and parainfluenza-type 3 (PI3) vaccination in cattle. Literature inclusion criteria included appropriate allocation of experimental units to treatment groups and blinding of evaluators. Studies were categorized as natural exposure or challenge studies, and the challenge studies were further divided by the viral antigen evaluated, and whether the product was a modified-live (MLV) or inactivated vaccine.

## Results

Thirty-one studies with 88 trials were included; however, few trials (n = 9) were natural exposure in beef calves. The natural exposure trials showed reduced risk of BRDC in vaccinated calves. Evaluation of commercially available BHV-1 and MLV BVDV vaccines using challenge models demonstrated reduced morbidity risk; however, trials evaluating MLV BRSV and PI3 vaccines in challenge settings failed to demonstrate evidence of reduced morbidity and mortality risk in vaccinated calves.

## Significance

Published literature regarding viral vaccine efficacy in the face of natural challenge was sparse, but provided some information that vaccination mitigated disease risk. The literature did not provide evidence for determining which viral components are necessary to include in a vaccination program to reduce BRDC risk.

# Characterization of the 13 cytopathic BVDV strains from mucosal disease cases from a single herd

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## Introduction

Bovine viral diarrhea virus (BVDV) is a positive single-stranded RNA virus belonging to the Pestivirus genus of the Flaviviridae family. BVDV has a wide host range that includes most ruminants. Noncytopathic (ncp) BVDV may establish lifelong persistent infections in calves following infection of the fetus between 40 and 120 days of gestation. Cytopathic (cp) BVDV strains arise from ncp strains via mutations. The most common cp mutations are insertions of RNA derived from either host or a duplication of viral sequences into the region of the genome coding for the NS2/3 protein. Superinfection of a persistently infected animal with a cp virus can give rise to mucosal disease (MD), a condition that is invariably fatal.

## Materials and Methods

A herd of 136 bred first-calf heifers was studied. These heifers gave birth to 36 PI animals of which 13 succumbed to mucosal disease. We characterized the ncp and cp viruses isolated from these 13 animals. The viruses were isolated and the polymerase chain reaction was used to characterize the type of insertions in the cp viruses. We then sequenced the virus and compared the sequences of the 13 ncp and cp both to the pair isolated from the calf but also to the isolates from the other calves.

## Results

All viruses belonged to the BVDV-2a genotype and were highly similar. All the cp viruses contained an insertion in the NS2/3 coding region consisting of the sequences derived from the transcript encoding a DnaJ protein named Jiv90. Comparison of the inserted DnaJ regions along with the flanking viral sequences in the insertion 3' end of the 13 cp isolates revealed sequence identities ranging from 96% to 99% with common borders. This suggested that 1 animal likely developed a cp virus that then progressively spread to the other 12 animals.

## 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 (VetAlert™, 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 national 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.