DRECA DAIRY RESEARCH SUMMARY

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Evolution and Dynamics of Bovine Viral Diarrhea Virus (BVDV)

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Why is BVDV important?

Among cattle in Canada bovine viral diarrhea virus (BVDV) causes significant financial loss for dairy producers because infections result in immunosuppression which leads to digestive, respiratory and reproductive tract disorders. Many times diseased, weak or dead calves are a prominent finding. BVDV also causes lethal mucosal disease.

The main source of BVDV circulation in herds is persistently infected (PI) calves, which contracted the infection via the placenta. Such calves shed large quantities of viral particles their entire life, and keep the virus circulating in the herd.

Elimination of PI calves is the main focus of BVDV eradication programs and vaccination is an important tool in these strategies. As with many viruses BVDV is not a static virus because it changes over time. But we know very little about how the virus evolves over the years and we also do not know if the vaccine still protects animals sufficiently against these changing field viruses?

What are we doing?

We collect as many strains of BVDV that we can find in Canada for evaluation. We can then identify PI animals on farms and sample all tissues and fluids from these animals. We have also evaluated almost all viruses that were stored in the freezers of Canadian diagnostics labs.

We want to know how BVDV has spread and changed within Canada over the last 40 years, by studying archived viruses. All of these viruses have been genetically characterized and we are studying the structures of the components of the virus that are recognized by the cow's immune system. With this information we will compare the variability of field BVDV strains to vaccine-induced immunity. We try to understand how the immune system recognizes BVDV following vaccination.

These findings will:

- assist farmers in implementing more efficacious BVDV control programs (e.g. control programs that are closely related to the field situation),
- benefit vaccine producers so that they can create better vaccines,
- assist researchers who are exploring the pathogenesis and transmission of BVDV. With this information we aim to predict the future of BVDV, (e.g. how it will look in 5 or 10 years from now, how it will spread between farms and regions), so we will be ready for new virus variants.



A BVDV persistently infected animal with mucosal disease lesions

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Alberta Agriculture and Rural Development, Alberta Milk, the University of Alberta, and the University of Calgary

A partnership in dairy research, extension and education activities

agric.gov.ab.ca albertamilk.com afns.ualberta.ca vet.ucalgary.ca

What did we find?

So far we have collected about 250 different BVDV strains that represent the viruses that have circulated in Canada over the last 40 years. We were able to find Pl's on dairy farms that did not vaccinate their herds against BVDV in the last few years. The tissues and fluids of over ten Pl's derived from dairy farms were examined and we compared the within-animal diversity of this virus.

We found a large variability of the virus within an individual PI indicating that these animals are the drivers behind the change of the virus. Examination of viruses derived over the years showed relatively small genetic changes, however the immune system wasn't in all cases able to recognize the virus anymore.

The large number of BVDV strains that we are currently analysing will help us to determine the transmission and introduction of viruses over time. This will show what routes pathogens can take when introduced into herds and therefore we can prepare for new disease causing agents that will be entering Canada in the future.



BVDV persistently infected animals are difficult to recognize, this animal was found in the milking herd

What does this mean?

BVDV is still circulating in dairy herds with non-vaccinating herds having an especially high chance of becoming infected. This can have significant economic consequences.

Our findings also indicate that even a small genetic variation of BVDV will have consequences at the surface of the virus and the way it is recognized by the immune system. We are also trying to determine if the small genetic variation in BVDV has an impact on the ability of current vaccines to provide the appropriate protection to prevent the infection of an animal or herd.

Summary Points

- BVDV is still circulating in herds in Alberta, all persistently infected (PI) animals were found on farms that did not vaccinate their animals
- Viruses change quickly, BVDV is no exception.
- Vaccines need to use an up to date BVDV strain to ensure optimal protection

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