Final Report
Summary

Surveillance and pathotyping of Australian IBDV.

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Objectives

A To continue monitoring genetic changes occurring in circulating IBDV field strains.

B To examine the pathogenicity of selected field isolates displaying unusual amino acids changes in SPF flocks.

C To complete a feasibility study to determine whether Luminex xTAG technology can be used to detect and differentiate IBDV strains.

Background

Although both classical and variant strains of IBDV exist in Australia, they are genetically unique compared to IBDV strains isolated in other countries. For many years, classical strains predominated in NSW, WA and QLD, while variants dominated in SA and VIC. Tasmania was one of the few states to be considered free of IBDV. In 2011, we detected the first variant strain in NSW. Genetically, this strain was closely related to the SA variants. These variants rapidly spread in NSW, displacing the classical strains previously identified in NSW. However, classical strains remained in more isolated regions of NSW. The fact that variant strains were spreading in Australia was of concern, given the fact that pathogenicity trials had indicated that variant strains produced more severe disease in SPF birds compared to classical strains, including mild clinical signs in 100% of birds, lower weight gain, and greater loss of lymphocytes in the bursa.

Research

Bursal samples were sourced from commercial flocks in NSW, WA, SA, QLD, VIC and TAS. Isolates were characterised genetically (selected region of viral genome sequenced) and antigenically (ELISA, using four monoclonal antibodies). Sequences were aligned and compared to strains isolated previously in Australia and in other countries. Field isolates possessing novel amino acid substitutions were tested in SPF birds. Their pathogenicity was assessed from a number of criteria, including severity of clinical signs, histological changes in lymphoid tissues, and viral loads in the bursa and spleen. Lastly, a Luminex xTAG assay was designed to detect and differentiate important IBDV subtypes, including exotic and endemic strains based upon state of origin.

Outcomes

Monitoring of IBDV strains circulating in Australia between 2014 - 2018 has indicated no major genetic or antigenic changes in field isolates from QLD, WA or SA. However, for the first time, antigenic variants from VIC have been detected in NSW and TAS. In addition, a classical-like virus has been detected in VIC that is genetically related to classical strains isolated in NSW, but has three other genetic changes. This particular isolate also failed to react with any of our monoclonal antibodies, indicating major antigenic changes. Pathogenicity testing of selected field strains in SPF birds indicated that variant strains continue to produce clinical signs in 40%-100% of SPF birds. This was in conjunction with lower weight gain, higher lymphocyte loss in the bursa, and higher viral loads in the spleen. The Luminex xTAG assay developed was shown to rapidly detect and differentiate different IBDV subtypes within a single reaction. It did so with greater sensitivity than current methods using conventional PCR and ELISA, making it an ideal assay for IBDV surveillance.

Implications

Monitoring of IBDV strains circulating in Australia has indicated significantly greater spreading of IBDV across state boundaries between 2015 - 2017. This is particularly significant in states like NSW, which currently contains a mix of classical strains and variant strains from SA and VIC. For states like TAS, this represents the first isolation of IBDV in the region. The spreading of variants in Australia is of concern because they appear to produce more significant disease in SPF birds compared to classical strains. The data also suggest that current biosecurity measures in Australia are inadequate and may be facilitating the spread of IBDV strains in Australia. This is particularly significant in the case of an exotic IBDV incursion into Australia. Delays in detection and diagnosis could allow exotic strains to spread, making eradication more difficult.