

Genetic Diversity Of Bovine Rotavirus In Dairy Calves In Nsw

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Bovine rotavirus (BRV) causes diarrhea in calves, which can lead to economic losses. To evaluate the diversity of BRV circulating in NSW, we conducted a study focusing on dominant and less common genotypes and their association with disease and age.

We collected 593 rectal samples from calves on 72 farms across NSW, including 154 with diarrhea and 11 with both diarrhea and respiratory issues. Total RNA sequencing was performed on an Illumina platform with a mean depth of 19 gigabases. The transcriptome was assembled de novo using SPAdes genome assembler v3.13.0 and classified using NCBI BLASTn. The transcriptome was mapped to assembled contigs using Kallisto v0.5.1.1. Statistical differences between the contigs mapped to transcriptomes of animals with and without diarrhea were assessed with DESeq2 v1.44.0. Genotypes were predicted using a Rotavirus A Genotyping tool from the National Institute for Public Health and the Environment, Netherlands.

64 farms had at least one BRV-positive animal. The predominant genotypes were G10&6-P[5&11]-I2-R2-C2-M2-A3&13-N2-T6-E2-H3, with abundant combinations of G6P[5] and G10P[11]. Less frequent genotypes, such as G24 and P[33], and Rotavirus B were identified. G10 was detected in 44 farms, G6 in 25, G24 in two, P[33] in one, and Rotavirus B in five. Co-infections were observed, specifically G10 and G6 in nine farms and P[11] and P[5] in four. The abundance of the non-structural protein 3 gene showed a significant association with diarrhea, as did viral protein 7 genotypes G10 and G6.

Our findings highlight the high prevalence of two dominant genotypes with clinical and subclinical infections.