RESUMO - PROTOZOOLOGIA E PATÓGENOS TRANSMITIDOS POR VETORES

OCCURRENCE OF CRYPTOSPORIDIUM PARVUM AND OTHER ENTEROPATHOGENS IN CALVES WITH NEONATAL DIARRHEA IN PARANÁ BRAZIL

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Neonatal calf diarrhea (NCD) is one of the leading causes of calf mortality, resulting in significant productive and economic losses in dairy herds. This study aimed to identify the pathogens involved in an NCD outbreak in a high-producing dairy herd in Paraná, Brazil, and to molecularly characterize Cryptosporidium spp. Fecal samples from calves aged 7 to 14 days, with diarrhea (DC) and

without diarrhea (NDC), were analyzed using molecular and bacterial methods. The investigated agents included Cryptosporidium spp., Eimeria spp., rotavirus A (RVA), bovine coronavirus (BCoV), bovine viral diarrhea virus (BVDV), and diarrheagenic Escherichia coli (DEC) pathotypes.

Total genomic DNA from fecal samples was extracted using the commercial kit NucleoSpin Tissue (Macherey-Nagel, Düren, Germany), following the manufacturer's protocol. To verify the presence of DNA of Cryptosporidium spp., a nested PCR was performed using primers targeting the 18S rRNA gene of Cryptosporidium spp. Cryptosporidium subtyping was performed by PCR and sequencing of the gene gp60. A conventional PCR assay was performed for the detection of Eimeria spp. using primers targeting the ITS1 rDNA region. The presence of RVA and bovine viral diarrhea virus (BVDV) RNA was investigated using reverse transcription polymerase chain reaction (RT-PCR) assays, whereas BCoV RNA was detected by a semi-nested RT-PCR assay. Isolation of E. coli was performed on agar supplemented with 5% defibrinated sheep blood and on MacConkey agar, with incubation at 37 °C for 24 h. Among diarrheic calves, the most frequently detected agents were Cryptosporidium spp., RVA, and enteropathogenic E. coli, often occurring as co-infections. Eimeria spp. was detected in 25% of the samples. Cryptosporidium spp. was identified in 62.5% of the fecal samples, including 87.5% of samples from the DC group and 37.5% (3/8) from the NDC group. Molecular analysis identified Cryptosporidium parvum subtypes IIaA19G1R1 and IIaA20G1R1. These results reinforce the multifactorial etiology of NCD, highlighting the importance of mixed infections in calves with and without diarrhea.

Palavras-chave: calves; cryptosporidium spp; escherichia coli; eimeria spp; rotavirus a.