

An Outbreak of neonatal diarrhea associated to rotavirus type C

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Introduction

Neonatal diarrhea is one of the main causes of preweaning mortality worldwide. Diarrhea is the result of the combination of several factors, including infectious agents, host immunity, environment and management procedures (7). Newborn piglets are susceptible to infection by several enteric microorganisms, including virus, bacteria and protozoans (7). Among viruses, in Argentina porcine rotaviruses (PoRV) groups A, B and C and transmissible gastroenteritis coronavirus (TGEV) has been described associated with subclinical or severely diarrheic outbreaks (4,6). Rotaviruses have a dsRNA genome that contains 11 segments. They are classified into 10 serogroups (A-J) through cross-reactivity of antigens on the VP6 protein that makes up the intermediate layer of the tripe-layer capsid shell of the virus (7). Rotavirus group A, B and C are ubiquitous in swine population; however, group A is the most extensively found on neonatal diarrhea. We perform a multidisciplinary approach in order to clarify an outbreak of a neonatal diarrhea.

Materials and Methods

The outbreak occurred in a multisite farrow-to-finish herd of 7500 sows with AIAO management. Control of neonatal diarrhea included sows vaccination against E. coli and feed-back practice in gilts. In August 2018, 2 to 4 days-old piglets exhibited a watery diarrhea affecting 50 % to 60 % litters with 10% to 15 % mortality rates. Diarrhea persisted for 2 weeks. The study involved 30 acute diarrheic fecal samples from piglets less than 3week-old and pathological studies from 4 euthanized piglets. Segments of ileum and jejunum were fixed in 10 % buffered formalin and stained with H&E. Viral dsRNA was obtained from fecal samples previously diluted 1/4 in PBS Tween 0,05 % using a combination of guanidinium thiocyanate and phenol/chloroform nucleic acid extraction methods. All diarrheic fecal samples were tested by 5 % polyacrylamide gel electrophoresis (PAGE) followed by ethidium bromide staining to verify the presence of porcine rotavirus groups A, B, and C (2). Identification of PoRV was conducted using RT-PCR according with the procedure described by Gouvea et al (1). The RT-PCR (PoRVA and PoRVC) products were analyzed using 2 % agarose gel electrophoresis, stained with ethidium bromide, and visualized under UV light. In addition, studies for the detection of TGEV, E. coli and Cystoisospora suis were carried-out.

Results

Histopathological study showed a mild multifocal villus atrophy in small intestine with low cuboidal to flattened surface epithelium, mild lymphoplasmacytic infiltrate in lamina propria and lymphangiectasia. By PAGE analysis 5 samples (16.6 %) presented a PoRVC electropherotype. The same samples were identified as PoRV group C positive while the remaining 25 samples (83.32 %) were negative. No bacterial or parasitic pathogens were identified.

Discussion and conclusions

PoRV group C has been reported as a cause of diarrhea in piglets under 7 days-old (7) in accordance with our study. A 16.67 % of samples were only positive to group C that was an unexpected finding. Previous studies in Argentina showed only 5 % of PoRV group C prevalence of infection in herds (4). The high rates of morbidity/mortality reported by others suggested the involvement of a mixed PoRV groups or other enteric viruses or bacteria (3). However, in our study, this was ruled-out by complementary studies. Besides, single infections of PoRVC occur more commonly in piglets less than 3 days-old as our reported outbreak (7). Microscopic lesions corresponded with those of a viral infection although, by histopathology, rotaviral from coronaviral infection cannot be distinguished (7). PAGE is the most practical and low-cost method used for PoRV diagnoses; however, it has a low sensitivity. Further, the use RT-PCR assay increased the frequency of detection of PoRV as single or mixed infections (5). The study highlights the importance of PoRV group C alone as a causative agent of neonatal diarrhea.

Acknowledgements

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