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NEONATAL PIGLET DIARRHEA IN FRANCE: WHICH PATHOGENS ARE INVOLVED?

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Introduction

Neonatal diarrhea is common in pig farms and induces economic losses because of poor technical performances and increased mortality of the affected piglets, as well as increased frequency of antimicrobial use. The aim of this study was to establish the prevalence of potential pathogens in affected French farms and the frequency of histological lesions that could be attributed to these pathogens.

Material and Methods

From 2015 to mid-2017, 283 analyses were performed on feces samples from diarrheic piglets. All samples were subjected to bacterial culture and genotyping of pathogenic isolates combined with viral analyses by PCR (Polymerase Chain Reaction). In addition, in 84 of these analyses, histological examination was carried out on samples of gut walls.

Results

No *Clostridium perfringens* type C or TGE (Transmissible Gastro Enteritis) or PED (Porcine Epidemic diarrhea) coronaviruses were found. The prevalence of pathogens in investigated herds was as follows (in parentheses: isolation prevalence and histological lesion frequency, respectively): *Clostridium perfringens* type A (84% and 33%), *Enterococcus hirae* (63% and 49%), *Clostridium difficile* (48% and 12%), rotavirus type A (26% and 26%) and enterotoxic *Escherichia coli* (18% and 20%). Histological results seemed influenced by the age of the sampled piglets. For 28% of the 84 diagnosis with histological examination, it was impossible to identify an etiological cause of disease because there were contradictions between the bacterial and/or viral findings and the observed histological lesions. For the other 72%, bacteria belonging to normal gut microbiota were commonly involved (alone or jointly): *Enterococcus hirae* (47%) and *Clostridium perfringens* type A (29%).

Discussion and Conclusion

Understanding under what conditions commensal bacteria become pathogenic would help to solve many neonatal diarrhea cases.