

Prevalence of postweaning diarrhea caused by *Escherichia coli* in Spain

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Introduction

Post-weaning diarrhoea (PWD) caused by *Escherichia coli* (*E coli*) remains a major cause of economic losses for the pig industry due to mortality, morbidity, decreased growth rate and cost of medication.¹ PWD usually occurs a few days after weaning causing dehydration, loss of body conditions and mortality.² However, in case of Spain, there has been a shift in the dynamic of infection, and clinical signs are mainly observed between the second and the third weeks after weaning.

Material and methods

A total of 193 pig farms with acute cases of PWD were sampled between January 2018 (n = 53) and December 2019 (n = 140). These farms were located in Spain. Animals were selected based on PWD clinical signs (diarrhoea, dehydration and increased mortality). A total of 579 four to eight-week old pigs within the first 24 hours of the acute phase of the disease were sampled and three rectal swabs were collected from three different pigs on each farm. Swabs with fecal matter were inserted into Amies transport medium in airtight screw cap plastic vials and were submitted to the laboratory (Exopol; Zaragoza, Spain) for *E coli* diagnosis. A multiplex PCR was carried out directly from 3 pooling of fecal samples contained in rectal swabs. PCR was performed to detect adhesion factor and toxin genes, including F4 (K88) and F18 fimbriae, adhesin involved in diffuse adherence (AIDA-1), heat-stable and heat-labile enterotoxins (STa, STb, LT), shigatoxin (STx2e), enteroaggregative heat-stable toxin (EAST-1) and, *E coli* attaching and effacing (eae).

Results

Only 1.6% (3 out of 193) of farms were negative for all the *E coli*'s virulence factor genes. The total prevalence of genes for adhesion factors and toxins of *E coli*, Rotavirus type A and PEDV among 193 farms with PWD cases in 2018 and 2019 are shown in Table 1. AIDA-1 gene was the most commonly found (70.1%) followed by F18 (61.8%) and F4 (48.8%). The most prevalent toxin was EAST-1 (97.4%) followed by STb (86.1%) and STa (78.0%). Rotavirus type A

was found in 64.6% of the PWD cases and PEDV in 11.4%. Enteropathogenic *E coli* (EPEC) was present in 75.8% of isolates.

Discussion and conclusion

The present study searched for F4, F18 and AIDA-1 adhesion factor genes. Results showed that the most prevalent adhesin gene was AIDA-1 (70.1%) followed by F18 (61.8%) and F4 (48.8%). In relation to F4 and F18 fimbriae, another Spanish study carried out in 2015 found that F18 gene was the most prevalent in comparison to F4, F5, F6 and F41.³ The most prevalent enterotoxin gene has been EAST-1 (97.4%). Other studies are in accordance with the present study and showed EAST-1 as the most prevalent.⁴ The present study shows the high prevalence of ETEC pathotype, which is able to cause PWD. There is a high degree of variability in the *E coli* virulence factors within country as well as differences between countries. It is necessary to conduct a rigorous diagnosis in order to characterize the *E coli*'s virulence factors and find the most appropriate solution in each PWD case, since it is described that some virotypes are more severe and show a higher resistance to certain antibiotics.⁵

References

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Table 1: Total prevalence (%) of genes for adhesion factors and toxins of *E coli*, rotavirus type A and porcine epidemic diarrhea virus (PEDV) among 193 farms with PWD cases between 2018 and 2019.

Pathogen	Virulence factor								
	Adhesion factor			Toxins					
	F4	F18	AIDA	Sta	Stb	LT	Stx2e	EAST-1	eae
Percentage of <i>Escherichia coli</i> 's virulence factors	48.8	61.8	70.1	78.0	86.1	66.8	22.4	97.4	75.8
Percentage of rotavirus A					64.6				
Percentage of PEDV					11.4				

