

New neonatal porcine diarrhoea. II. aspects on etiology

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Introduction

A new neonatal porcine diarrhoea (NNPD) of uncertain origin has affected piglets globally during the last decade. As *E coli* is an important microbe associated to neonatal diarrhoea, the role of *E coli* was scrutinized in piglets with diarrhoea in a herd affected by NNPD.

Materials and Methods

The herd had been affected by neonatal diarrhoea of unknown origin since a year. No antibiotic was added to the food, but piglets affected by NNPD were individually medicated.

The offspring to 31 sows that farrowed within three days in a farrowing batch was studied in detail (1). Fecal samples were collected from 23 piglets clinically diagnosed with NNPD at the day of birth, as well as from 11 apparently healthy piglets at that day. All samples were collected before any medical treatment was initiated.

The fecal *E coli*-flora was biochemically fingerprinted using the pheny-plate system (2), and the diversity of the flora was defined in each pig. Thereafter, the floras of the pigs with diarrhoea were compared with the floras of the apparently healthy piglets.

Results

The diversity of the fecal *E coli* flora was high in both healthy piglets and in piglets affected by NNPD (Table 1). In total, 8 different dominant clones of *E coli* were identified in the 11 healthy piglets and 17 dominant clones were identified in the 23 piglets affected by NNPD. In both groups, this corresponded to 0.73 dominant clones identified per piglet investigated.

One out of the 17 clones identified from the piglets diagnosed with NNPD was defined as OX46, an unofficial serotype of *E coli* that occasionally have been diagnosed in Sweden since the 70ies. The remaining 16 clones did not belong to any serotype that was included in the panel. Nor did the panel identify any specific serotype from 5 out of the 8 dominant clones identified in the healthy piglets (Table 1).

Table 1. Diversity of the fecal *E. coli*-flora at the day of birth in healthy piglets and in piglets affected by NNPD.

The table also shows the number of dominant clones of *E. coli* identified as well as the serotypes of these clones

	Healthy (n=11)	NNPD (n=23)	
Diversity Index	0.67 ± 0.30	0.83 ± 0.26	NS
Dominant clones	8	17	
<i>Serotyping of clones</i>			
O8 and O141	2 / 8	-	
O157	1 / 8	-	
OX46	-	1 / 17	
O?	5 / 8	16 / 17	

Discussion

The diversity of the flora of pigs with diarrhoea induced by *E coli* will be very low due to the impact of the causative strain which will dominate the intestinal flora (3). Therefore the results obtained suggest that *E coli* not is responsible for NNPD, as also previously concluded (4). This conclusion was further strengthened by the lack of a common dominating clone of *E coli* in the 23 piglets diagnosed with NNPD.

In this herd, an initial treatment success of NNPD with penicillin-G had to be altered to Trim-sulfa (1). As the two substances have different antimicrobial spectras, the unclear cause of NNPD was further elucidated. We are suspecting a viral etiology for this syndrome, where an agent has been recognised and work is in progress to establish the correlation between it and the syndrome in question.

References

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