# Isolation of fimbriated F18 and Shiga-toxin producing *Escherichia coli* associated with oedema disease in post-weaned pigs in Malaysia

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#### Introduction

Oedema disease (ED) is an enterotoxemic disorder caused by specific pathotypes of Escherichia coli (E. coli) which affects primarily rapidly-growing nursery and weaned pigs. ED in pigs is associated with the colonization and adherence of the intestine cells by hostspecific highly-adapted pathogenic E. coli strains with F18 fimbriae. The fimbriae are encoded by fedab<sup>+</sup> and fedac<sup>+</sup> genes predominantly found in ED strains of E. coli and diarrhoea-causing enterotoxigenic E. coli (ETEC) respectively (3). ED strains in addition, possess stx2e genes located in plasmids that produces Shiga toxins (1, 2). On absorption of the Shiga toxins from the intestinal lumen into the blood vessels, vascular cell damage occurs leading to oedema in particular the submucosa of the stomach and mesocolon, ataxia and sudden death.

### **Materials and Methods**

A survey was conducted to identify Shiga-toxin producing E. coli (STEC) isolates in post-weaners in Malaysia from February to April 2013. Faecal and organ samples were collected from 19 farms with about 500 standing sow population in 6 states in Malaysia namely Penang, Perak, Selangor, Melaka, Johor and Sarawak. The targeted animals were post-weaners (3-14 days post weaning), where there is sudden death in healthy pigs with swollen eyelids and/or with ataxia. Samples such as mesenteric lymph nodes, tonsils, jejunum with content, spleen, kidney and brain stem were tested for bacterial isolation and nucleic acid extraction then followed by multiplex PCR. Samples were cultured on MacConkey and on sheep blood agar. A total of 377 representative E. coli strains on blood agar were purified, determined for haemolysis and identified. PCR was conducted on the haemolytic E. coli for the presence of STEC (stx2e (2)). Positive Shiga-toxin E. coli strains were then analyzed for the presence of the *fedab* and *fedac* genes (1).

#### Results

A total of 59 haemolytic E coli isolated from 8 farms were subjected to a singleplex PCR-based method for  $stx2e^+$  and a multiplex PCR-based method for the detection of  $fedab^+$  and  $fedac^+$ . 7 of the 8 farms with haemolytic E. coli were found to be positive for stx2e genes. A total of 5 farms were positive for stx2e,  $fedab^+$  and  $fedac^+$  genes (Table 1).

**Table 1**. Microbiological and PCR findings

Farm	Haemolytic	stx2e	fedab		fedac	
	E. coli	+ve	+ve	-ve	+ve	-ve
A	0	0	0	0	0	0
В	8	1	0	1	0	1
С	0	0	0	0	0	0
D	0	0	0	0	0	0
E	5	4	2	0	2	0
F	2	2	2	0	2	0
G	0	0	0	0	0	0
H	0	0	0	0	0	0
I	0	0	0	0	0	0
J	0	0	0	0	0	0
K	9	3	1	2	1	2
L	0	0	0	0	0	0
M	26	9	7	2	7	2
N	4	3	0	0	0	2
0	0	0	0	0	0	0
P	2	0	0	0	0	0
Q	3	3	1	0	1	0
R	0	0	0	0	0	0
S	0	0	0	0	0	0
Total	59	25	13	5	13	7

# Discussion

This study demonstrated that Shiga-toxin producing *E. coli* (STEC) carrying *fedab*<sup>+/-</sup> and *fedac*<sup>+/-</sup> genes were detected from haemolytic *E. coli* associated with clinical findings of oedema disease (ED) in post-weaned pigs. This finding concludes that virulence genes were present in certain pig farms in Malaysia which leads to ED.

## References

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