

ANTIMICROBIAL RESISTANCE, INTEGRON, VIRULENCE GENE, AND MULTILOCUS SEQUENCE TYPING OF *ESCHERICHIA COLI* ISOLATES FROM POSTWEANING PIGLETS WITH AND WITHOUT DIARRHEA

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Abstract. Pathogenic *Escherichia coli* is a major cause of diarrhea in postweaning piglets. Virulence genes, antimicrobial resistance, integrons, and genetic diversity of *E. coli* were determined in 100 rectal swab samples collected from postweaning piglets with and without diarrhea (5-7 weeks of age) in a farm in a central province of Thailand. Of 246 *E. coli* isolates, 141 were positive for at least one virulence gene determined by multiplex PCR, the most commonly found from both groups of piglets being *astA*, while *lt*, *F4*, *F18*, and *F41* only from diarrheal piglets. More than 80% of *E. coli* isolates were resistant to 7 of 12 antimicrobial agents. One hundred and fifty-seven *E. coli* isolates carried class 1 and/or 2 integron(s). Integron-positive isolates are significantly associated with strains resistant to kanamycin, oxytetracycline, streptomycin, sulfamethoxazole/trimethoprim and tetracycline. Phylogenetic analysis by multilocus sequence typing revealed that the 31 representative *E. coli* isolates were genetically diverse, especially those from diarrheal piglets suggesting that *E. coli* from postweaning piglets were not derived from a single clone. Sequence type (ST)10, ST641 and ST1114 were most commonly found in both groups of piglets. No correlation was observed among ST, presence of integron and antimicrobial resistance. The study suggests that swines in a farm could be a reservoir and possible spread of diarrheagenic *E. coli* including strains with antimicrobial resistance genes.

Keywords: *Escherichia coli*, diarrhea, multilocus sequence typing, postweaning piglet, virulence gene

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