

MOLECULAR CHARACTERIZATION OF EXTRAIESTINAL PATHOGENIC *ESCHERICHIA COLI* FROM HUMANS IN SOUTHERN THAILAND

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Abstract. Extraintestinal pathogenic *Escherichia coli* (ExPEC) is an important pathogen causing diverse damages to extraintestinal organs. Thirty-one percent of *E. coli* isolates from healthy volunteer fecal samples ($n = 100$) were identified as ExPEC, with 94% carrying *kpsMTII*, 87% *iutA* and 10% *afa*. Fifty-two percent of ExPEC strains belonged to phylogenetic group B2, 29% to group D, 16% to group A, and 3% to group B1. ExPEC-associated genes carried by ExPEC strains were *cnf1* (encoding cytotoxic necrotizing factor 1) (6%), *fimH* (encoding type 1 fimbrial tip) (94%), *kpsMTK1* (encoding K1 capsular antigen, responsible for neonatal meningitis) (23%), and *traT* (encoding conjugal transfer surface exclusion protein) (58%). All 31 ExPEC strains belonged to 4 serogroups, namely, O1 (7 strains), O6 (2 strains), O25 (5 strains), and O164 (3 strains), with the remaining being untypeable O serogroup. Antibigram profile showed 42% of ExPEC strains were multi-drug resistant. ESBL gene detection showed that 29% of ExPEC carried *bla*_{TEM} and 3% carrying both *bla*_{CIX-M} and *bla*_{TEM}. BOX-PCR profiles demonstrated ExPEC O6 and O164 strains within each serogroup were identical in their fingerprint, while ExPEC O1 and O25 strains displayed two profiles each, with 78% and 98% genetic similarity, respectively. These findings provide information on existence and virulence of commensal ExPEC strains in healthy human intestinal microbiota in southern Thailand, which should be of benefit to an underearning of potential public health problems in this region of the country.

Keywords: extraintestinal pathogenic *Escherichia coli*, human, phylogenetic group, seroprevalence, Thailand

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