

Title Safety of raw meat and shellfish in Vietnam: An analysis of *Escherichia coli* isolations for antibiotic resistance and virulence genes

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Citation International Journal of Food Microbiology, Volume 124, Issue 3, 10 June 2008, Pages 217-223

Keywords *Escherichia coli*; Food; Antibiotic resistance; Resistance gene; Virulence gene

Abstract

This study was conducted to examine a current baseline profile of antimicrobial resistance and virulence of *Escherichia coli* isolated from foods commonly sold in the market place in Vietnam. *E. coli* were isolated from 180 samples of raw meat, poultry and shellfish and also isolated from 43 chicken faeces samples. Ninety-nine *E. coli* isolates recovered from all sources were selected for the investigation of their susceptibility to 15 antimicrobial agents by the disk diffusion method. Eighty-four percent of the isolates were resistant to one or more antibiotics, and multi-resistance, defined as resistance to at least 3 different classes of antibiotics, was detected in all sources. The rates of multi-resistance were up to 89.5% in chicken, 95% in chicken faeces and 75% in pork isolates. Resistance was most frequently observed to tetracycline (77.8%), sulfafurazole (60.6%), ampicillin (50.5%), amoxicillin (50.5%), trimethoprim (51.5%), chloramphenicol (43.4%), streptomycin (39.4%), nalidixic acid (34.3%) and gentamicin (24.2%). In addition, the isolates also displayed resistance to fluoroquinolones (ciprofloxacin 16.2%, norfloxacin 17.2%, and enrofloxacin 21.2%), with chicken isolates showing the highest rates of resistance to these antibiotics (52.6–63.2%). Thirty-eight multi-resistant isolates were selected for further the examination of antibiotic resistance genes and were also evaluated for virulence gene profiles by multiplex and uniplex polymerase chain reaction. The beta-lactam TEM gene and tetracycline resistance *tetA*, *tetB* genes were frequently detected in the tested isolates (84.2% and 89.5% respectively). Genes which are responsible for resistance to streptomycin (*aadA*) (68.4%), chloramphenicol (*cmlA*) (42.1%), sulfonamides (*sulI*) (39.5%), trimethoprim (*dhfrV*) (26.3%) and kanamycin (*aphA-1*) (23.7%) were also widely distributed. Plasmid-mediated *ampC* genes were detected in *E. coli* isolates from chicken and pork. The isolates were tested for the presence of 58 virulence genes for adhesins, toxins, capsule synthesis, siderophores, invasins and others from different *E. coli* pathotypes. All of the tested isolates contained at least one virulence gene and there were 16 genes detected. Virulence genes detected were *fimH* (92.1%), *bmaE* (84.2%), TSPE4.C2 (42.1%), *aida* AIDA-I (*orfB*) (31.6%), *east1* (26.3%), *traT* (23.7%), and others including *fyuA*, *iutA*, *chuA*, *yjaA*, *iss*, *iroN*_{*E. coli*}, *ibeA*, *aah* (*orfA*), *iha* and *papG* allele III (10.5–2.6%). Typical toxin genes produced by enterohemorrhagic and enterotoxigenic *E. coli* pathotypes (a heat-stable toxin (ST), heat-labile toxin (LT) and Shiga toxin *stx1*, *stx2*) were not detected in any of these 38 isolates. The study has revealed that *E. coli* in raw foods is a significant reservoir of resistance and virulence genes.