ABSTRACT

Multidrug resistant (MDR) *Escherichia coli* (*E. coli*) is disseminating resistance in humans and animals by incorporating into food chain. *E. coli* has contaminated natural water bodies and wild fishes. In the present study, we detected and identified MDR genes in *E. coli* that was isolated from wild carps. Total 32 samples of riverine carp were collected from Chenab River (Head Punjnad & Head Trimmu) and screened for *E. coli*. Biochemical confirmation of isolates for *E. coli* was done by biochemical tests (oxidase, catalase, glucose fermentation, indole and citrate) and selection of these tests were done by using Bergey's Manual of Determinative Bacteriology. About 23/32 (71.8%) isolates were confirmed in biochemical tests. Molecular confirmation of *E. coli* was done by detecting *uspA* gene in polymerase chain reaction (PCR). About 18/32 (56.25%) isolates were confirmed as *E. coli* by PCR. Eight antibiotics (erythromycin, tetracycline, amoxicillin, ciprofloxacin, vancomycin, cefoparazone, gentamicin and chloramphenicol) from different classes were subjected to positive isolates of *E. coli*. Antibiotic sensitivity test (AST) was performed by Kirby Bauer disk diffusion method. Isolates of *E. coli* showed resistance to five antibiotics (erythromycin, tetracycline, amoxicillin, ciprofloxacin and vancomycin). Three antibiotics (cefoparazone, gentamicin and chloramphenicol) were effective against isolates of *E. coli*. Antibiotic resistance genes; *ermB*, *tetA*, *CTX-M* and *qnrB* were observed. Culture sensitivity showed 88.8% isolates were resistant to tetracycline, 83.3% were resistant to amoxicillin, 55.5% were resistant to erythromycin, 44.4% were resistant to ciprofloxacin and 100% were resistant to vancomycin. Molecular detection of resistance genes showed 83.3% isolates had tetracycline resistance gene *tetA*, 72.2% isolates had amoxicillin resistance gene *CTX-M*, 38.8% isolates had erythromycin resistance gene *ermB*, 16.6% isolates had ciprofloxacin resistance gene *qnrB*. Genotypic MDR of all isolates was recorded. About 16.6% isolates had only one resistance gene, 55.5% had 2 genes, 16.6% had 3 genes, 5.55% had 4 genes and no gene was detected in 5.55% isolates. Results of present study have given valuable knowledge in terms of misuse of antibiotics and unhygienic practices.

Key words: *Escherichia coli,* antibiotic susceptibility, resistant genes, MDR prevalence, health risk