

Study of phylogenetic background and antibiotic resistance of *Escherichia coli* isolates obtained from healthy household dogs and their owners in Kerman city

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Abstract

The dogs' relationship with their owners has made them one of the most popular pets. They can be a reservoir of many microbial pathogens, so they are important for public health. This study was performed to determine the phylogenetic backgrounds and antimicrobial resistance of *E. coli* isolates from healthy household dogs and their owners in Kerman province, Iran. Samples were taken regardless of antibiotic usage in the dogs. Based on the history of the animals, 90% of them had not used antibiotics during the few months before the study. 168 *E. coli* strains belonging to feces of healthy household dogs (n=49), their owners (n=49) and the people without a pet (n=70) were studied; phylogenetic sequences including *chuA*, *yjaA* and *TspE4.C2* were screened by conventional polymerase chain reaction (PCR). The isolates were investigated phenotypically for antimicrobial resistance against 11 commonly used antibiotics in dogs which were erythromycin, streptomycin, enrofloxacin, oxytetracycline, cefotaxime, ampicillin, trimethoprim-sulfamethoxazole, amoxicillin-clavulanic acid, ceftazidime, ceftriaxone and kanamycin. *E. coli* isolates were classified into A, D, B1 and B2 phylogroups with the prevalence of 55.9%, 30.3%, 7.1% and 5.3%, respectively. Considerably, antimicrobial resistance to erythromycin and oxytetracycline were predominant while the lowest frequency of antibiotic resistance was detected against ceftriaxone, ceftazidime, amoxicillin-clavulanic acid and kanamycin. This study was performed on apparently healthy dogs so it could determine their carrier role for antibiotic-resistant *E. coli* strains. This research revealed that healthy household dogs should be considered as the significant reservoir of resistant *E. coli* isolates especially to erythromycin, oxytetracycline, streptomycin, enrofloxacin, cefotaxime and ampicillin which these resistant strains were mostly belonging to A and D phylogenetic groups.

Key words: *Escherichia coli*, Dog, Owners, Antimicrobial resistance, Phylogenetic

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