عنوان مقاله:

Determination of antibiotic resistance genes in relation to phylogenetic background in Escherichia coli isolates from fecal samples of healthy pet cats in Kerman city

محل انتشار:

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خلاصه مقاله:

The aim of this study was to determine antibiotic resistance genes, phylogenetic groups and anti-microbial resistance patterns of Escherichia coli isolates from fecal samples of healthy pet cats in Kerman city. Ninety E. coli isolates were recovered from obtained rectal swabs. Antibiotic resistance pattern of the isolates against seven selected antibiotic was determined using disc diffusion method. Phylogenetic background of the isolates was determined according to the presence of the chuA, yjaA and TspE۴C۲ markers. Theisolates were examined to determine a selection of antibiotic resistance genes including tetA, tetB, aadA, sulI and dhfrV by polymerase chain reaction. Forty two isolates (۴۶.۶%) were positive at least for one of the examined genes. Phylotyping revealed that the isolates are segregated in phylogenetic groups A (۶۶.۷%), B۱ (۱.۲%), B۲ (۱۳.۴%) and D (۱۸.۹%). Among ۹۰ isolates, ۲۶.۶% were positive for tetB gene, ۱۰.۰% for cqnrS gene, ۱۲.۳% for sulI and aadA genes, ۸.۹% for tetA and ۲.۲% for dhfrVgene. None of the E. coli isolates were positive for qnrA and qnrB genes. Sixteen combination patterns of antibiotic resistance genes were identified which belonged to four phylogroups. Maximum and minimum resistant isolates were recorded against to tetracycline (۸۲.۳%) and gentamycin (۱.۲%), respectively. Fifteen antibiotic resistance patterns were determined in different phylo-genetic groups. In conclusion, feces of healthy pet cat in Kerman could be a source of antibiotic resistant E. coli isolates, whereas these isolates were distributed all over the main phylogroups.

کلمات کلیدی:

Antibiotic resistance genes, Cat, Escherichia coli, Phylogenetic group

لینک ثابت مقاله در پایگاه سیویلیکا: