عنوان مقاله:

Distribution of antimicrobial resistance and some widespread extended-spectrum beta-lactamase genes in different phylogroups of Shiga toxin-producing Escherichia coli (STEC) isolates of ruminant origin

محل انتشار:

دوفصلنامه علوم و فنون دامپزشکی ایران, دوره 15, شماره 1 (سال: 1402)

تعداد صفحات اصل مقاله: 9

نویسندگان:

Rwida Tomeh - *Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.*

Mahdi Askari Badouei - *Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran*

Gholamreza Hashemi Tabar - *Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.*

Hamideh Kalateh Rahmani - *Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.*

خلاصه مقاله:

Limited data is available on the prevalence of extended-spectrum beta-lactamase (ESBL) genes in Shiga toxin-producing Escherichia coli (STEC) isolates of ruminant origin. This study determined the molecular prevalence of ESBL-encoding genes (blaCTX-M, blaTEM, blaSHV and blaOXA) and antimicrobial-resistance (AMR) of ۵۸ STEC isolates recovered from cattle (n= ۳۲), sheep and goats (n= ۲۶). In the current study, ESBL genes were identified by the molecular technique, while phenotypic AMR against six antibiotics (amoxicillin-clavulanic acid, tetracycline, neomycin, florfenicol, enrofloxacin and sulfamethoxazole-trimethoprim) were tested by disc diffusion method. Phylogenetic groups were also determined by a PCR scheme. Isolates were categorized into five phylogroups (A, B۱, C, D and E) and B۱ was the most prevalent phylogenetic group (۴۳; ۷۴.۱%). Statistical analysis revealed significant association between phylogroup D and small ruminants (sheep and goats, p= ۰.۰۱۴). Moreover, the highest rates of antimicrobial resistance were related to tetracycline (۲۵.۹%) and neomycin (۲۲.۴%). Resistant isolates to tetracycline (p= ۰.۰۰۱), trimethoprim-sulfamethoxazole (p= ۰.۰۱۳) and neomycin (p= ۰.۰۰۰) were significantly prevalent among strains recovered from cattle. In addition, the majority of MDR strains were also had a significant distribution among cattle isolates (p= ۰.۰۰۱). In the current study, prevalence of ESBL positive STEC was ۱۲.۰۶% (۷/۵۸). Genes blaCTX-M and blaTEM were detected separately and in combination in bovine isolates. However, only one STEC strain of small ruminants harbored blaTEM. In conclusion, it seems that cattle isolates are notable sources of different AMR traits which could be a threat to veterinary sections, public health and food hygiene, in particular.

کلمات کلیدی:

E. coli, STEC, antimicrobial resistance (AMR), ESBL, blaCTX-M, blaTEM, Phylogroup