عنوان مقاله:

Antimicrobial Resistance Pattern in Relation to Virulence Genes and Clonal Groups Among Uropathogenic Escherichia coli in Iran

محل انتشار:

بیست و یکمین کنگره بین المللی میکروب شناسی ایران (سال: 1399)

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خلاصه مقاله:

Background and Aim : Uropathogenic Escherichia coli (UPEC), is one of the most important etiologic agent of urinary tract infection (UTI). Investigating the relationship between different characteristics of UPEC strains is advantageous for epidemiological surveillance of high-risk clones.Methods : PCR, the Kirby Bauer disk diffusion method and MLST were used to characterize and correlate among the clonal groups, virulence genes and antimicrobial resistance pattern in ۱۰۱ UPEC strains.Results : The fimH, pai, and traT genes were highly prevalent among UPEC strains isolated from patients in our region. Among ۹ different Sequence-types, ST۱۳۱ was the most prevalent clonal group that significantly correlated with the pai gene. ۷۰.۳% of the tested population were multidrug-resistant and the majority of the isolates were resistant to Ampicilin and trimethoprim/sulfamethoxazole.Conclusion : Clonal groups showed no significant differences in terms of antibiotic resistance patterns. There was no significant difference between virulence genes and antibiotic resistance patterns in the studied clonal groups. These findings suggest that the relationship between virulence and antimicrobial resistance pattern can vary according to different genetic and environmental factors and Understanding these relationships requires deep molecular research and may help in the future to manage .the spread of infectious diseases

کلمات کلیدی:

Antimicrobial Resistance Pattren, Virulence Genes, Clonal Groups

لینک ثابت مقاله در پایگاه سیویلیکا: