عنوان مقاله:

Correlation between antibiotic resistance and phylogenetic types among multidrug-resistant Escherichia coli isolated from urinary tract infections

محل انتشار:

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خلاصه مقاله:

Objective(s): Emergence of multidrug resistance has reduced the choice of antimicrobial regimens for UTIs. To understand the association of phenotype and genotype among uropathogens. Materials and Methods: Six hundred and twenty-eight (۶۲λ) urine samples were collected and analyzed. Antibiotic sensitivity pattern was determined by the Kirby-Bauer Disc Diffusion Method and minimum inhibitory concentration (MIC) was tested by the E test. Fluoroquinolone resistant mutations in QRDR of gyrA and ParC, phylogenetic groups, and PAlusp subtype were detected by PCR.Results: Most prevalent uropathogens were Escherichia coli (ΔΨ.Υ%) followed by Klebsiella pneumoniae (Υ1%). Multidrug- resistance was observed in > Δο% cases for third-generation cephalosporins and ciprofloxacin and lowest in meropenem. E. coli (۶۶.Υ%) and K. pneumonia (۶۴.۴%) were extended-spectrum β-lactamases (ESBLs) producers. MIC to trimethoprim-sulfamethoxazole was highest in E. coli (>10.10.17 μg/ml). In λο (Υ۴%) of the ΨΨ۴ E. coli isolates analyzed in detail, Δ۴ fluoroquinolones (FQ) resistant isolates carried mutations (SλΨL, DλγN, SλοΙ, Ελ۴V) in QRDR of gyrA and ParC. Out of Δ۴ FQ-resistant isolates, ۴Ψ (Υ1.9.%) isolates belonged to the phylogenetic group BY, and 11(Υο. F%) belonged to group D. Isolates belonged to group BY, ΨΛ (λλ. F%) of the FΨ

isolates carried PAlusp subtype IIa and high frequency of mutation EAFV in ParC was detected in TY (9Y.F%). Other mutations, such as SAoI, SATL in gyrA and DAYN in ParC were found in all resistant isolates. Conclusion: Correlations between phenotype and genotype provided a basis to understand the resistance development in uropathogens, and .PAlusp subtyping indicated that E. coli belonged to the BY group

کلمات کلیدی: Escherichia coli, ESBL, MDR, PCR, UTI

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