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Prevalence of CTX-M Variants in ESBL Producing Multidrug-Resistant *Enterobacteriaceae* from Outpatients in Karachi, Pakistan

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***SUMMARY*. Globally, CTX-M variant is the dominant genotype in extended spectrum β-lactamase producing *Enterobacteriaceae* (ESBL-E) particularly in uropathogenic *Escherichia coli.* The objective of present investigation was to assess the prevalence rate of CTX-M in ESBL-E isolated in Karachi, Pakistan between January and December 2015 and their association with a few risk factors. A total of 84 isolates of ESBL-E collected during one year of time period, were included in the study. Genotype identification of beta-lactamases and antimicrobial susceptibility tests were performed. Risk factors were analyzed statistically by *chi*-square test at $p < 0.05$. Of 84 ESBL-*Enterobacteriaceae* CTX-M was found in 50 isolates. The presence of CTX-M in females was higher than in men [70% (35/50)], although differences were non-significant ($p > 0.05$). In uropathogens Non-significant association was found among CTX-M presence and urinary tract infections [82% (41/50)] ($p = 0.105$, OR 2.179, 95% C.I 0.787-6.031, RR 1.212). Out of 50 CTX-M ESBLs, 45 were detected in *E. coli* ($p = 0.149$, OR 2.333, 95% C.I 0.673-8.086, RR 1.133). Ninety four percent of CTX-M ESBLs were carried by multidrug resistant bacteria, but this was a non-significant association (OR 2.701, 95% CI 0.600-12.158, RR 1.102). A relative risk of concomitant fluoroquinolone resistance was found. ESBL-E were frequently *in vitro* susceptible to piperacillin/tazobactam, imepenem, fosfomycin and amikacin. The CTX-M genotype was the most prevalent variant in ESBL-E and was frequently associated with fluoroquinolone resistance.**

RESUMEN. A nivel mundial, la variante CTX-M es el genotipo dominante en *Enterobacteriaceae* (ESBL-E) productora de β-lactamasa de espectro extendido, particularmente en *Escherichia coli* uropatogénica. El objetivo de la presente investigación fue evaluar la tasa de prevalencia de CTX-M en las ESBL-E aisladas en Karachi, Pakistán entre enero y diciembre de 2015 y su asociación con algunos factores de riesgo. Un total de 84 aislamientos de ESBL-E recolectados durante el período de un año se incluyeron en el estudio. Se realizó la identificación genotípica de betalactamasas y pruebas de susceptibilidad antimicrobiana. Los factores de riesgo se analizaron estadísticamente mediante la prueba de *chi*-cuadrado a $p < 0,05$. De 84 ESBL-*Enterobacteriaceae* CTX-M se encontró en 50 aislamientos. La presencia de CTX-M en las mujeres fue mayor que en los hombres [70% (35/50)], aunque las diferencias no fueron significativas ($p > 0.05$). En uropatógenos no se encontró asociación significativa entre la presencia de CTX-M y las infecciones del tracto urinario [82% (41/50)] ($p = 0.105$, OR 2.179, 95% C.I 0.787-6.031, RR 1.212). De las 50 ESBL CTX-M, se detectaron 45 en *E. coli* ($p = 0.149$, OR 2.333, 95% C.I 0.673-8.086, RR 1.133). Noventa y cuatro por ciento de las ESBL CTX-M fueron portadas por bacterias resistentes a múltiples fármacos, pero esto no fue una asociación significativa (OR 2.701, IC 95% 0.600-12.158, RR 1.102). Se encontró un riesgo relativo de resistencia a las fluoroquinolonas concomitantes. Las BLEE-E fueron frecuentemente *in vitro* susceptibles a piperacilina/tazobactam, imepenem, fosfomicina y amikacina. El genotipo CTX-M fue la variante más prevalente en la ESBL-E y se asoció con frecuencia a la resistencia a la fluoroquinolona.

KEY WORDS: CTX-M, *Enterobacteriaceae*, ESBLs, *Escherichia coli,* UTIs

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