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Distribution of sul genes and their variants in uropathogenic Escherichia coli isolated from two hospitals of Sabah

Abstract

Sulphonamides resistant strains are highly prevalent in uropathogenic *Escherichia coli* (UPEC) isolates. *Sul* genes encode sulphonamide resistance and are present on transferrable plasmids. Integrons (IGNs) are genetic elements containing integrase gene, *attI* site and gene cassettes which carry multiple antibiotic resistant genes. Class 1 integrons have been extensively studied because these were most prevalent among clinical isolates. In this study, UPEC isolates were determined for the antibiotic susceptibility patterns to four antibiotics commonly used for urinary tract infections, which include co-trimethoxazole (TMP-STX). Distribution of *sul* genes and integrase1 gene (*intI1*) was studied in TMP-STX resistant UPEC isolates by using multiplex polymerase chain reaction (mPCR). *Sul* genes variants were investigated by DNA sequencing of the whole open reading frame of *sul1* and *sul2* genes and PCR product of *sul3* gene. *Sul1*, *sul2* and *sul3*genes were prevalent in 37 (24.7%) of 150 UPEC isolates. *IntI1* is positive in 22 *sul* genes positive isolates. Of six isolates positive with *sul2* genes, *sul*2(a) and *sul2*(b) variants, which were described in the previous study, in the four isolates and the two isolates respectively were observed. This is the first mPCR which investigates the prevalence of three *sul* genes and *intI1* in the UPEC clinical isolates from two hospitals of Sabah.