ABSTRACT

Extended spectrum β-lactamases (ESBLs) are enzymes commonly produced by the family Enterobacteriaceae. They exhibit wide spectrum activities against penicillins, first-, second-, and third-generation cephalosporins, and monobactam, aztreonam (but not the cephamycins or carbapenems), but inhibited by β-lactamase inhibitors. CTX-M β-lactamases were discovered at the beginning of 1990s. They are now replacing TEM and SHV mutants in *E. coli* isolates from both community and hospital sources worldwide. Genes encoding CTX-M β-lactamases are found on plasmids commonly harboring multidrug resistant genes. Multidrug resistant organisms cause profound effects on patients and complicate medical treatment. In Palestine, a paucity of information is available regarding this significant topic. The aim of this study was to determine phenotypic and molecular epidemiology of ESBLs among *E. coli* isolates from various clinical sources. Preliminary screening of ESBL-producers was achieved by utilizing 1 μg/ml cefotaxime containing MacConkey plates and double disk synergy tests. The suspected ESBL-producers were confirmed by Combination disk test and molecular PCR technique. Agar dilution method was used to determine MICs to all ESBL isolates using different antimicrobial agents. Occasionally, faecal carriage of ESBL-producing *E. coli* was evaluated in patients with urinary tract infection caused by the same organisms. A rate of 18.2% (77/423) of *E. coli* isolates were designated as ESBL producers. All ESBL isolates exhibited 100% susceptibility to meropenem, while 30% (23/77) were multidrug resistant to non-β-lactam agents; gentamicin, levofloxacin and sulfa drugs.

CTX-M was detected in all ESBL isolates (100%) while TEM and SHV β-lactamases were found to be 59.7%, (46/77) and 1.3% (1/77) respectively. Analyses of CTX-M amplicons revealed that 80.5%, (62/77) and 19.5%, (15/77) were CTX-M group 1 and group 9 respectively.

ESBL-producing *E. coli* was detected in faecal samples of eight patients with urinary tract infection due to the same organism. These ESBL isolates had similar genotype and susceptibility profile to the third generation cephalosporins except in one case where CTX-M was not detected. Our findings indicate that CTX-M-15 like allele which belongs to group 1 is the most common CTX-M type detected which agree with many studies conducted worldwide. The ESBL detection rate described in this study was comparable to worldwide studies, tends to be towards the upper end of the spectrum, and is therefore a major cause for concern.