Abstract

Molecular characterization of ESBL-related bla genes including blaTEM, blaSHV, and blaCTX-M has been performed for Escherichia coli isolated from urine and collected from three cities in Kurdistan region/Iraq (Erbil, Sulaimani, and Duhok). One hundred sixty nine isolates of E. coli have been identified and their production of ESBLs enzymes have been determined using phenotypic methods. All these isolates were successfully amplified producing a single band of the uidA locus in all strains with a molecular weight of about 670bp in order to confirm at molecular level that all these isolates were E. coli. One hundred sixty ESBL E. coli isolates out of 169 appeared to have one or more ESBLs genes accounting for 94.7 %. CTX-M constituted the high prevalent type of ESBLs genes compared to the others represented by 94.1% of all isolates in all the three cities of Kurdistan region followed by TEM and SHV in a percentages of 43.8% and 2.5 %, respectively. In Duhok, TEM showed the higher prevalence (60.8 %) in comparison to the other two cities in percentages of 36.2 % for Sulaimania while Erbil represented by 25 %. Furthermore, it was clear that SHV type of ESBLs had the lower prevalence of all types and there were only four isolates out of 160 appeared to carry this type of gene representing 2.5 %. The presence and/or absence of the three genes in all isolates were also investigated and it was shown that 86/160 isolates (53.75%) had the CTX-M gene only while the rest of genes were lacking. Moreover, 69/160 isolates had both CTXM and TEM. Interestingly, 3/160 harbored all three involved genes. The isolates characterized by the presence only TEM gene and those that had both CTX-M and SHV, shared the same percentage (0.6%). after taking sequencing of the PCR product of studied genes for 12 E coli isolates into consideration, it was obvious that all the PCR products of CTX-M were belonged to type CTXM-15; while TEM-1 type appeared predominant among all sequences PCR product for TEM gene. Finally, from the three isolates which revealed positive PCR amplification for the SHV gene, two isolates showed 100% similarity to the SHV-12 genome type while the rest single isolate was similar (99%) to SHV11.

Keywords: PCR assay, ESBLs, Escherichia coli