

In this study, the prevalence of *fim* H gene was studied among 105 *E. coli* isolates obtained from urine samples of patients attended Azadi hospital in Duhok City. The intended gene was detected in 94.3% of the isolates. Triplex PCR assay was applied and according to which the studied isolates were assigned into four groups namely A, B1, B2, and D groups which constituted 20.95 %, 3.8 %, 54.28 %, 20.95 %, respectively. Ten randomly selected isolates were subjected to SNPs *fim*H analysis with 3 reference strains of *E. coli*. The results revealed that 44 SNPs observed at 42 polymorphic sites accounting for 5.59%. All mutations were of substitutions and 29.5 % of mutations were transversions while transition type mutations constituted of 70.5 %. Ten SNPs accounting for 22.7 % of mutations gave rise to amino-acid changes (sense mutation) while the rest 34 (77.3 %) resulted in silent mutations. Moreover, twelve SNPs were singletons and among them five were with amino acid replacements. Amino acid replacements due to SNPs accounted for 1.27% of whole sequenced fragment of *fim*H. It can be concluded that there is no relationship inferred between the isolates of *E. coli* when the two phylotyping techniques are compared but the results of both can serve the purpose of genotypic characterization of uropathogenic *E. coli*.