Methods Thirty two virulence factors including adhesions group, protectin related genes, common toxins related to UPEC, phylogenic typing, Pathogenicity Island and miscellaneous genes which are involved in Escherichia coli pathogenicity mechanisms were examined by PCR.

Results The PCR assay results identified vat (96 vs. 4%), PAI IVS365 (85 vs. 41%), PAI ICF703 (78 vs. 25%), kpsMTII (71 vs. 42%), ompT (68 vs. 53%), usp (52 vs. 3%), sat (47 vs. 3%), pucU (41 vs. 1%), PAI ICF703 (58 vs. 13%), PAI I536 (57 vs. 7%), fucC (H7 vs. 9%), hydD (22 vs. 2%), focG (21 vs. 3%), cnf1 (21 vs. 0%), gafD (20 vs. 2%), cdh1 (19 vs. 7%), bmaE (17 vs. 5%), PAI I J96 (11 vs. 3.5%) were more frequent virulence markers in urinary E.coli isolates than commensal E. coli, respectively. The frequency of sfa (7 vs. 10%), fliH (92 vs. 97%), kpsMT K1 (41 vs. 57%), kpsMT III (11 vs. 5%), frr (LPS O4) (9 vs. 2%), PAI I IS36 (20 vs. 24%), PAI I IS56 (3 vs. 0%), PAI I J96 (53 vs. 43%), hbaC (17 vs. 26%) markers were almost similar in both of them. cvaC (64 vs. 18%) was most frequent marker in commensal E. coli. PCR phylotyping revealed higher prevalence of commensal E. coli in groups A and D while uropathogenic strains were mainly found in subgroup B2.

Conclusion Based on these results, the potential for Commensal E. coli to act as human UPEC or as a reservoir of virulence genes for UPEC should be considered.