**Abstract**

Urinary Tract Infection (UTI) is mainly due to the entry of microorganisms and start developing to multiply in the urinary bladder. Cystitis and Urethritis are the two most common UTI among infected patients and mostly affect the bladder and urethra. The UTIs contribute significantly to the cost of providing health care in economically developed countries and it may be symptomatic or asymptomatic. Several studies such as multi-drug resistant strain, Extended Spectrum Beta Lactamase producing strain, recurrent urinary tract infection, symptomatic *Shigella sonnei*,UTI in pregnancy, polymicrobial septicemia etc. had been conducted with reference to *Shigella flexneri*. However, a study on Uropathogenic and their molecular typing and characterisation of *Shigella flexneri* using 16s r RNA gene sequencing is scanty. In the present study, the investigators were isolated *Shigella* species from the UTI patient and identified using standard microbiological procedures. The isolated strain was further confirmed by 16S rRNA gene sequencing. The sequenced strain has been submitted to GENBANK, USA and received gene accession number (JX444058). The Electropherogram report has been generated by Quality Control of Applied Biosystem, Hyderabad and reported that the *Shigella flexneri* ST-02 consist of 939 base pairs. Finally the sequenced strain was subjected to bioinformatic tools such as BLAST and phylogenetic tree for explorative and comparative studies. To the best of our knowledge, this constitutes the first report in which *Shigella flexneri* clinical strain had been isolated for UTI patient and was characterized by molecular typing using 16s ribosomal RNA gene partial sequencing analysis.