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Next-Generation Sequencing for Typing and Detection of ESBL and MBL *E. coli* causing UTI

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Abstract

Next-generation sequencing (NGS) has the potential to provide typing results and detect resistance genes in a single assay, thus guiding timely treatment decisions and allowing rapid tracking of transmission of resistant clones. We can be evaluated the performance of a new NGS assay during an outbreak of sequence type 131 (ST131) Escherichia coli infections in a teaching hospital. The assay will be performed on 100 extended-spectrum- beta-lactamase (ESBL) *E. coli* isolates collected from UTI during last 5 years. Typing results will be compared to those of amplified fragment length polymorphism (AFLP), whereby we will be visually assessed the agreement of the Bio-Detection phylogenetic tree with clusters defined by AFLP. A microarray will be considered the gold standard for detection of resistance genes. AFLP will be identified a large cluster of different indistinguishable isolates on adjacent departments, indicating clonal spread. The BioDetection phylogenetic tree will be showed that all isolates of this outbreak cluster will be strongly related, while the further arrangement of the tree also largely agreed with other clusters defined by AFLP. With these experiments we will detect the ESBL and MBL strains and the patient can be prescribed the antibiotics accordingly.