

MALDI-TOF MS for Rapid Analysis of Bacterial Pathogens Causing Urinary Tract Infections in the Riyadh Region

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Abstract: The successful treatment of bacterial disease is relied on selecting a suitable drug based on the type of bacteria and antimicrobial susceptibility testing. The study's objective was to identify bacterial isolates from urine samples of patients from the community, followed by antimicrobial susceptibility testing of the isolated bacteria. A total of seventy urine samples were received in the clinical microbiology laboratory; out of which 18 culture-positive cultures and by direct identification using MALDI-TOF MS (Matrix Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry) were identified. Of 18 identified bacteria, 17 (94%) were pathogenic. The culture demonstrated that the major species detected in urine samples were *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, and *Aeromonas caviae*. *E. coli* (72.2%) was the most common bacterium retrieved from urine samples followed by *K. pneumoniae* (16.6%). Interestingly, all the isolates, except *Enterococcus faecalis*, were resistant to erythromycin. The isolates 8 of 13 (61.5%) were resistant to both of the cotrimoxazole and tetracycline. We performed MLST (Multi-locus Sequence Typing) typing of 13 *E. coli* isolates to study their genetic relatedness and diversity. MLST typing of *E. coli* showed a total of nine different STs (Sequence Types), which showed the diversity among them. ST 129 was the most common ST found in three *E. coli* isolates. In our study, two isolates with ST 1126 and ST 1432 represented the global clonal complex 155. MALDI-TOF MS provided dependable results for identifying the bacteria up to species level from urine samples by indirect culture methods. Such local surveillances are highly recommended for empirical therapy awareness and determining isolates' level of resistance.