

MALDI-TOF/TOF and diagnosis of bacterial UTIs

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Abstract:

Urinary tract infections (UTIs) are the most common form of bacterial infections in the community and in hospitals, so fast and reliable microbial pathogen identification in human urine samples is required for clinical microbiology laboratory, especially for the world with more prevalent antibiotic resistance. In our study we analyzed 20 outpatient human urine samples with microbiologically proved presence of more than 10⁵ CFU/ml with Matrix Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF/TOF). As a reference for bacterial diversity selected urine samples were determined using 16S rRNA gene sequencing.

The direct approach, without step in which the microorganisms are isolated and grown, provided successful identification of bacteria at the genus and species levels, especially for monobacterial samples of *Citrobacter koseri*, *Escherichia coli*, *Klebsiella spp.*, and *Proteus spp.* The results of this study demonstrate that we could identify different pathogen with MALDI-TOF/TOF from fresh or frozen, not cultivated human urine samples. In order to address problems encountered with hypothetical proteins during bioinformatics analysis with ProteinPilot we have developed our in-house software based on natural language processing.

Keywords:

native urine sample, pathogen identification, proteomics, genomics, bioinformatics

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