

MALDI-TOF mass spectrometry for the detection of antimicrobial resistance mechanisms

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Matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS) is routinely used for the identification of bacteria and fungi and has the potential to be applied in complex diagnostic processes. Because MALDI-TOF MS is capable of detecting a broad spectrum of molecules, including structural modifications at the molecular level, the detection of different mechanisms of resistance to antimicrobials may soon become available. Two main approaches can be used for this purpose: 1) the identification of molecular epidemiological markers specific to drug-resistant cells and 2) the detection of the destruction or modification of antibiotic molecules. The former approach has been used for the detection of methicillin-resistant strains of *Staphylococcus aureus* and for the elucidation of polymyxin resistance in Gram-negative bacteria resulting from structural changes in their lipopolysaccharides. The latter approach was first applied for detecting the modification of beta-lactams by beta-lactamases. Methods for the detection of carbapenemases based on the hydrolysis of meropenem or ertapenem were recently validated. MALDI-TOF MS was able to detect small changes in carbapenem molecules (e.g., sodium salt variant of these antibiotics). Therefore, it can be hypothesised that assays for the detection of modifications of other antibiotic molecules (e.g., aminoglycosides) can be rapidly developed. The greatest challenge in determining the mechanisms of drug resistance is the quantification of antibiotic concentrations. In general, the quantification of molecules using MALDI-TOF MS may be difficult but is possible. This method could be helpful in the study of efflux and porins. I believe that MALDI-TOF MS can provide many new applications that will be applicable not only in research on drug resistance mechanisms but also the development of routine microbiological diagnostics.