Application of MALDI-TOFMS in the Rapid Detection and Differential Identification of Microbial Spores and Cells Isolated from Various Environments

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In light of recent world events, fast, sensitive, and selective microbial detection methodology has become a priority in the scientific community. Matrix-Assisted Laser Desorption/ Ionization Time of Flight Mass Spectrometry (MALDI-TOFMS)-based microbial detection technology has recently been evaluated to rapidly detect and discriminate microbial species. Analysis of whole bacterial cells and spores with this technique has given rise to unique protein fingerprints that can be used for identification at the strain level. Current challenges for MALDI of whole bacteria cells include identification of mixed bacterial populations, variability of spectra, and the detection limits, which restricts the technique to cultured or concentrated bacterial samples.

MALDI-TOFMS was performed on a Bruker Daltonics Reflex II Mass Spectrometer with delayed extraction. Vegetative cells and purified spores of Bacillus subtilis 168, B. pumilus FO-036b and ATCC 7061 were analyzed via MALDI-TOFMS. Matrix and solvent combinations were varied to produce spectra with the highest signal to noise ratios in concert with the maximum number of peaks observable. Recently available AnchorChip^{TM} technology was utilized, in addition to the common stainless steel plate, as a sample support for the MALDI analysis.

Spectra obtained from each spore and vegetative cell sample gave a distinct mass fingerprint, which allows for identification and speciation of the different spores and vegetative cells studied. In addition, the optimum matrix and solvent combinations have been evaluated for extraction of proteins from whole bacterial cells and spores. The use of the AnchorChip^{TM} as a sample support lowered the limit of detection. The MALDI-TOFMS, in conjunction with AnchorChip^{TM} technology, allows for more sensitive and selective bacterial analysis. Decreased limits of detection increase the sensitivity while an increase in the number of distinct peaks per species improves selectivity. Sample preparation is minimized through the use of whole cells and spores as opposed to protein extracts, leading to fast identification of bacterial species.