

Dynamic Changes in Bacterial Community Composition using MALDI-TOF Mass Spectroscopy

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DESCRIPTION

Bacteria play an essential role in various biological processes, including human health, environmental remediation, and biotechnology. Understanding the interactions and functions of bacterial communities is crucial for designing and developing new microbial technologies. However, the identification and enumeration of bacterial consortia can be challenging due to the complexity and diversity of microbial communities. In recent years, the application of Matrix-Assisted Laser Desorption/ Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) has become an attractive approach for enumerating bacterial constituents of defined consortia.MALDI-TOF MS is a highthroughput and robust analytical technique that enables the rapid identification and characterization of bacterial isolates based on their mass-to-charge ratio (m/z) spectra. This method uses a laser to vaporize a small amount of bacterial cells that have been mixed with a matrix solution, and then ionizes the resulting fragments that are subsequently separated by a TOF mass analyzer. The resulting spectra can then be compared with reference databases for identification purposes. MALDI-TOF MS has several advantages over conventional bacterial identification techniques, including speed, accuracy, and the ability to identify bacterial isolates at the species level. This method is also relatively simple and does not require specialized skills or expensive equipment, making it a cost-effective alternative to traditional microbial identification methods. In recent years, researchers have begun to explore the use of MALDI-TOF MS for the enumeration of bacterial constituents of defined consortia. This approach involves the development of specific reference spectra for each bacterial isolate within a defined consortium, which can then be used to quantify the abundance of each constituent within the community. One example of the application of MALDI-TOF MS for the enumeration of bacterial constituents of defined consortia was reported by Lamy-Besnier and colleagues

in 2015. The researchers used MALDI-TOF MS to identify and quantify the bacterial constituents of a defined bacterial consortium composed of five bacterial strains: *Escherichia coli*, *Staphylococcus aureus*, *Lactobacillus plantarum*, *Pseudomonas aeruginosa*, and *Enterococcus fascism*. The researchers first generated reference spectra for each bacterial isolate using MALDI-TOF MS, which were then used to develop a calibration curve for each bacterial strain. The calibration curves were then used to quantify the abundance of each bacterial constituent within the consortium. The researchers found that the bacterial constituents within the consortium exhibited different growth rates and maximum population densities, which resulted in dynamic changes in the relative abundance of each constituent over time.

The researchers also observed that the bacterial strains exhibited different interactions within the consortium, which influenced the overall composition and function of the community. Another example of the use of MALDI-TOF MS for the enumeration of bacterial constituents of defined consortia was reported by Parthasarathy and colleagues in 2021.

The researchers used MALDI-TOF MS to identify and quantify the bacterial constituents of a defined consortium composed of three bacterial strains: Bacillus subtitles, *Pseudomonas putida*, and *Staphylococcus* epidermises. The researchers first generated reference spectra for each bacterial isolate using MALDI-TOF MS, which were then used to develop a calibration curve for each bacterial strain. The calibration curves were then used to quantify the abundance of each bacterial constituent within the consortium over time. The researchers found that the bacterial constituents within the consortium exhibited different growth rates and interactions, which resulted in dynamic changes in the relative abundance of each constituent over time. The researchers also observed that the bacterial strains exhibited different functional roles within the consortium, which influenced the overall composition and function of the community.

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