

MALDI-TOF mass spectrometry-based identification of bacterial pathogens in China

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Aims: According to the need of clinic diagnosis, communicable diseases control and prevention and food safety use, a database and related software for MALDI-TOF Mass Spectrometry-based identification of bacterial pathogens should be set.

Methods: grant amount of reference strains and isolates of bacterial pathogens were got, identified by classical and molecular methods, and tested by MALDI-TOF Mass Spectrometry. All the peptide mass fingerprinting data was analysis by bio-informatics, the new computerized algorithm and related database were set. The new algorithms and database were tested compared with 16S rRNA sequence analysis and the identification by other software (such as Biotyper system or SARAMIS database).

Results: A new database and software, named MicroID, was set up, and successfully used in bacterial pathogens identification. The results (such as for the identification of *Helicobacter spp.*, *Acinetobacter spp.*, and so on) shown that a more accurate and quick method of MALDI-TOF Mass Spectrometry-based Identification of bacterial pathogens was set.

Conclusion: Based on the MicroID software system, a more accurate and quick method of MALDI-TOF Mass Spectrometry-based Identification of bacterial pathogens was set in China.

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