C-172. Evaluation of MALDI-TOF MS for Identification of *Acinetobacter* Species

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Background: Identification of acinetobacters to species level is difficult. Neither reference phenotypic methods nor genotypic identification methods are suited for routine diagnostic microbiology labs. Commercially available identification systems for manual use such as API 20 NE (bioMérieux) perform poorly for identification of *Acinetobacter* species, and automated identification systems can identify only a few species. MALDI-TOF MS (Matrix-Assisted-Laser-Desorption/Ionization-Time-Of-Flight-Mass-Spectrometry) is becoming a popular tool for rapid identification of microorganisms. **Methods**: We evaluated the combination of MALDI-TOF MS with the SARAMIS software for identification of 552 well-characterized *Acinetobacter* strains representing 15 different species (*A. calcoaceticus*, n=13; *A. baumannii*, 27; *Acinetobacter* genomic species 3, 116; *Acinetobacter* genomic species 13TU, 23; *A. hemolyticus*, 33; *A. junii*, 39; *A. johnsonii*, 73; *A. lwoffii*, 98; *Acinetobacter* genomic species 10, 20; *Acinetobacter* genomic species 11, 30; *A. radioresistens*, 35; *Acinetobacter* genomic species 13BJ_14TU, 9; *Acinetobacter* genomic species 15TU, 7; *A. schindleri*, 13; *A. ursingii*, 16). Isolates had been identified to species level by the reference phenotypic method, AFLP, ribotyping, and ARDRA, respectively. **Results**: The strains of most of the genomic species were separated from each other at levels ranging from 20-40% with the exception of strains of the *A. calcoaceticus - A. baumannii* complex and of genomic species 10 and 11 that clustered more closely together. The strains of each of the genomic species formed a separate cluster at a cut-off level >60%, only strains of *A. calcoaceticus* and genomic species 15TU show a greater variation and cluster at 52% and 57% respectively. The method is robust, and involves simple handling, low use of consumables, high speed and high-throughput capability. **Conclusion**: The SARAMIS-MALDI-TOF MS application represents a promising tool for rapid identification of the most important species of the diverse genus *Acinetobacter* and may offer significant advantages over currently available methods.