Identification of Pasteurellaceae by Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry

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Objectives

The taxonomic systematic of Pasteurellaceae is a difficult topic. Some species has been reclassified from the genus Haemophilus to Aggregatibacter (e.g. Aggregatibacter aphrophilus and paraaphrophilus). Other species left the genus Pasteurella and new genus were defined (e.g. Avibacterium or Gallibacterium). In daily routine in the microbiology lab many of them are difficult to identify in commercially available systems using biochemical parameters. Matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry is a rapid and accurate tool for the identification of many microorganisms. We assessed this technology for more than 30 Pasteurellaceae species from the Medical Culture Collection Marburg (MCCM). In addition we determined the presence of ß-lactamases in the strains, an important marker for effective treatment recommendations.

Materials and Methods

Pasteurellaceae strains were grown on blood or chocolate agar under aerobic or microaerophilic conditions between 24 to 72 hours. Identification with mass spectrometry was done by smear preparations (direct inoculation of the target from the plate) and after a protein extraction protocol. The results were compared to the MCCM database and all identifications were confirmed by 16S-rDNA sequencing. In addition the presence of ß-lactamases was determined by MALDI-TOF using a modification of our recently described protocol for carbapenemase detection (Burckhardt et al., JCM 2011).

Conclusions

1. MALDI-TOF is a fast and reliable method to identify Pasteurellaceae in daily lab routine.
2. The presence of ß-lactamases can be investigated on the mass spectrometer.