



V 18 Species identification of ticks by whole-animal mass spectrometry

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Identification and characterization of microorganisms by intact cell matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has become very popular in recent years. The hallmarks of this technique, which is also referred to as MALDI-typing, are minimal sample preparation protocols, high speed, high-throughput capability, low cost, and high informative value, which make it an almost ideal tool for this purpose. In an effort to apply MALDI-typing to screen for tick-borne pathogens, it was necessary to analyze the mass spectra of the host animal as a first step. Consequently, MALDI-typing was applied to extracts from whole ticks (whole-animal mass spectrometry, WAMS), and its potential regarding the differentiation of tick species was explored. A simple protocol for the MALDI-TOF MS and PCR-compatible extraction of whole animal homogenates was developed, and a reference database with MALDI-TOF mass spectra from 88 samples comprising 7 tick species was constructed. Using commercially available software for the comparison of sample spectra with the references in the database, unambiguous species identification was possible for all species. Correctness of species assignments were checked by sequence analysis of 16S rRNA. Cluster analysis of mass spectra originating from *Ixodes ricinus* revealed that eggs, larvae, nymphs, and adult ticks produced spectra specific for the respective developmental stages. Moreover, males and females formed distinct clusters indicating that sex is a determinant for WAMS. Depending on the amount of blood that was taken, species identification from ticks that had had a blood meal was hampered but possible in a number of cases. We suggest WAMS as a simple, rapid, cost-effective, precise, and PCR-compatible tool for the determination of tick species.