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Article
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IDENTIFICATION OF ARTHROPODS BY THE MALDI TOF TEHNIQUE

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Abstract

MALDI-TOF mass spectrometry is a relatively new diagnostic technique that has revolutionised clinical microbiology by accurately identifying species of bacteria, filamentous fungi and yeasts. Recently, new applications to identify parasites and arthropods of medical interest have been developed, but few have developed MALDI-TOF analysis protocols for characterizing arthropod species. Thus, there is a need for a standardization in terms of the anatomical part(s) to be used according to arthropod families (head, thorax, legs) and the steps for protein extraction and homogenization. In this study we created a bank of 47 specimens including the following species: *Aedes caspius, Anopheles hyrcanus, Anopheles maculipennis, Coquillettidia richiardii*, *Culiseta annulata*, *Culex pipiens.* Thus, the aim of this study was to compare the quality of spectra and of results in the identification between different anatomical parts of mosquitoes, head, thorax (with wings) and legs, in order to optimize the use of the MALDI-TOF spectrometry tool. We evaluated the bank using the "bank versus bank" test (database provided by the laboratory of parasitology and mycology of Paris, Sorbonne University), each specimen had 4 deposits of protein extracts and the identification threshold log(score) was set to 1.7. Identifications were confirmed by morphological identification keys. There were differences in the protein profiles between each anatomical part. Leg spectra had the lowest number of high intensity peaks compared to those of the head or thorax.

Key words: Maldi Tof mass spectrometry; database; arthropod;