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PROTEINS ON MICROBIAL IDENTIFICATION: PAST ACHIEVEMENTS, PRESENT STATE-OF-THE-ART, AND FUTURE CHALLENGES

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The use of chemical analysis of microbial components, including proteins, became an important achievement in the 80's of the last century to the microbial identification. This led a more objective microbial identification scheme, called chemotaxonomy, and the analytical tools used in the field are mainly 1D/2D gel electrophoresis, spectrophotometry, high-performance liquid chromatography, gas chromatography, and combined gas chromatography-mass spectrometry. The Edman degradation reaction was also applied to peptides sequence giving important insights to the microbial identification. The rapid development of these techniques, in association with knowledge generated by DNA sequencing and phylogeny based on rRNA gene and housekeeping genes sequences, boosted the microbial identification to an unparalleled scale.

The recent results of mass spectrometry (MS), like Matrix-Assisted Laser Desorption/Ionisation Time-of-Flight (MALDI-TOF), for rapid and reliable microbial identification showed considerable promise. In addition, the technique is rapid, reliable and inexpensive in terms of labour and consumables when compared with other biological techniques. At present, MALDI-TOF MS adds an additional step for polyphasic identification which is essential when there is a paucity of characters or high DNA homologies for delimiting very close related species. The full impact of this approach is now being appreciated when more diverse species are studied in detail and successfully identified. However, even with the best polyphasic system, identification of some taxa remains time-consuming and determining what represents a species remains subjective.

The possibilities opened with new and even more robust mass spectrometers combined with sound and reliable databases allow not only the microbial identification based on the proteome fingerprinting but also include *de novo* specific proteins sequencing as additional step. These approaches are pushing the boundaries in the microbial identification field.