

Identification and Differentiation of Food-related Bacteria: A Comparison of FTIR Spectroscopy and MALDI-TOF Mass Spectrometry

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The food industry requires easy, accurate, and cost-effective techniques for microbial identification to ensure safe products and identify microbial contaminations. In this work, FTIR spectroscopy and MALDI-TOF mass spectrometry were assessed for their suitability and applicability for routine microbial diagnostics of food-related microorganisms by analyzing their robustness according to changes in incubation time and medium, identification accuracy and their ability to differentiate isolates down to the strain level [1]. For MALDI-TOF MS the microflex LT spectrometer (Bruker Daltonics, Bremen, Germany) and the MALDI Biotyper 3.0 database were used. FTIR spectroscopy was done using a Tensor 27 spectrometer coupled to the HTS-XT high-throughput device (both Bruker Optics, Ettlingen, Germany) and spectra were identified using the in-house database of the Technical University Munich.

Changes in the protocol lead to a significantly impaired performance of FTIR spectroscopy, whereas they had only little effects on MALDI-TOF MS. Identification accuracy was tested using 174 food-related bacteria (93 species) from an in-house strain collection and 40 fresh isolates from routine food analyses. For MALDI-TOF MS, weaknesses in the identification of bacilli and pseudomonads were observed; FTIR spectroscopy had most difficulties in identifying pseudomonads and enterobacteria. In general, MALDI-TOF MS obtained better results (52-85% correct at species level), since the analysis of mainly ribosomal proteins is more robust and seems to be more reliable. FTIR spectroscopy suffers from the fact that it generates a whole-cell fingerprint and intraspecies diversity may lead to overlapping species borders, which complicates identification. In the present study values between 56% and 67% correct species identification were obtained. Using fresh isolates from routine diagnostics, both techniques performed well with 88% (MALDI-TOF) and 75% (FTIR) correct identifications at species level, respectively.

On the opposite, the high sensitivity of FTIR spectroscopy may also be an advantage, as it offers the opportunity of typing below the species level. This is of major importance for epidemiologic studies and the tracing of contamination routes. Using the Biotyper software, MALDI-TOF MS was not able to discriminate different strains of the same species, whereas this was achieved rather easily using FTIR spectra and hierarchical cluster analysis. However, with the use of a different type of software (ClinProTools) it was possible to exploit also MALDI-TOF spectra for strain typing purposes.

References

- [1] M. Wenning, F. Breitenwieser, R. Konrad, I. Huber, U. Busch, S. Scherer, *J. Microbiol. Methods* 103, 44-52 (2014).