

# ***Going Deep in the Inter- and Intraspecies Differentiation of Clinically Relevant Bacteria by MALDI-TOF MS and FTIR***

Ângela Novais

REQUIMTE@UCIBIO. Faculty of Pharmacy, University of Porto, Porto, Portugal

Identification of particular pathogenic and/or multidrug resistant species and bacterial lineages is critical for clinical management and infection control in the hospital setting. In the last decades, these taxonomic units have been increasingly defined and detected by DNA-based methods, which, despite significant improvements, lack sufficient speed and resolution or are not thoroughly accessible.

Alternatively, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) and Fourier-Transform Infrared Spectroscopy (FTIR) revealed to be promising high-throughput analytical methods in a plethora of applications in clinical microbiology and biomedical research, including bacterial identification at the species level. More recently, their potential for resolution of closely related bacterial species (*Acinetobacter baumannii* complex), clinically relevant clones (within *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*) or subclonal variants (within *Escherichia coli*) was demonstrated by analysis of particular cellular fractions by multivariate data analysis (1-4). The discriminatory potential of these methods is preferentially linked to the content in peptides/proteins (MALDI-TOF MS) or carbohydrates (FTIR) corroborating genomics data, and is associated with variable resolution for the different bacterial species. Interestingly, besides the taxonomic interest, these methods provided insights into key biomolecules associated with bacterial evolution, virulence or other adaptive features.

We are certainly at the beginning of an exciting era, where the application of technologies with higher sensitivity, accuracy and resolution and more sophisticated bioinformatics tools to bacterial characterization will potentiate global and integrative approaches with the potential to revolutionize the speed of clinical diagnosis and the knowledge on the pathophysiology of bacterial pathogens.

## References

- [1] Â. Novais et al.. MALDI-TOF mass spectrometry as a tool for the discrimination of high-risk *Escherichia coli* clones from phylogenetic groups B2 (ST131) and D (ST69, ST405, ST393). *Eur J Clin Microbiol Infect Dis.* 33(8), 1391-9 (2014).
- [2] C. Sousa, Â. Novais et al.. Diverse high-risk B2 and D *Escherichia coli* clones depicted by FTIR. *Sci Rep.* 20;3, 3278 (2013).
- [3] C. Sousa, L. Silva, F. Grosso, J. Lopes, L. Peixe. Development of a FTIR-ATR based model for typing clinically relevant *Acinetobacter baumannii* clones belonging to ST98, ST103, ST208 and ST218. *J Photochem Photobiol B.* 133, 108-14 (2014).
- [4] C. Rodrigues, R. Branquinho, C. Sousa, L. Andrade, E. Machado, A.L. Darini, Â. Novais, L. Peixe. Identification of diverse capsular types in multidrug-resistant (MDR) *Klebsiella pneumoniae* clones using *wzi* sequencing and FTIR. Poster presentation. 6th Congress of European Microbiologists (FEMS 2015). June 2015.