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P0448 MALDI-TOF MS for automated detection of KPC-producing *Enterobacteriaceae*: beyond *Klebsiella pneumoniae*

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Background: KPC enzymes are the most globally widespread and clinically significant carbapenemases associated with *Enterobacterales*. Although initially KPC appeared, evolved and spread in *Klebsiella pneumoniae*, reports of KPC-production in other species of enterobacteria are increasing worldwide.

Recently, the automated detection of the KPC-related peak at 11,109 m/z in the MALDI-TOF MS spectra of *K. pneumoniae* was described, enabling the instant identification of particular KPC-producing strains during identification process.

In this study we evaluated the possibility to extend the real-time automated detection of the KPC-related peak to other species of enterobacteria.

Material/Methods: MALDI-TOF mass spectra of n=9440 enterobacteria isolates (n=3591 *Escherichia coli*, n=2716 *Enterobacter cloacae* complex, n=434 *Klebsiella aerogenes* (formerly *Enterobacter aerogenes*), n=1465 *K. oxytoca*, n=663 *Citrobacter* spp., n=541 *Serratia marcescens* and n=30 *Klebsiella variicola*) were investigated for the presence of the KPC-specific peak.

Spectra were acquired from 2009 to 2018 in Bologna, Italy and Dortmund, Germany, including carbapenem-resistant (n=687) and -susceptible isolates (n=8753), with a Microflex LT mass spectrometer (Bruker Daltonik, Germany).

For each species, a specific algorithm for the automated detection of the KPC peak was developed and evaluated, in order to be implemented into commercially available software.

Results: The new algorithm detected the KPC-specific peak in 175/196 (89.3%) of the *E. coli* spectra. The number of KPC-producing *E. coli* rose from 1 in 2011 to 66 in 2017, and the prevalence of the KPC-peak positive strains among all the KPC-producing circulating clones achieved the 96%.

The KPC peak was also detected in 8/10 *E. cloacae* complex, 11/15 *K. aerogenes*, 5/7 *K. oxytoca*, 10/11 *C. freundii*, and 4/7 *S. marcescens*, 3/3 *K. variicola* KPC-producers.

The peak was not detected in the n=9191 non-KPC strains but 1 *C. freundii* strain.

Conclusion: We developed specific algorithms for automated detection of KPC-producing enterobacteria other than *Klebsiella pneumoniae*. Our study shows overall a high sensitivity (86.7%) and excellent specificity (99.99%), similar to the established KPC detection in *K. pneumoniae*. Integration of these algorithms into the MALDI routine could allow fast detection of these worriesome isolates during standard identification process, helping the improvement of therapy and application of infection control measures.