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Paper Poster Session I

Recent advances in molecular bacterial typing

Multicentre validation of standardized MALDI-TOF based typing of ESBL-producing *Escherichia coli* outbreak isolates

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Introduction: Rapid determination of strain relatedness is crucial for outbreak control. Matrix-assisted laser desorption/ionization-time of flight mass-spectrometry (MALDI-TOF) has the potential to become a high-resolution and fast typing method. However, the reproducibility and performance of MALDI-TOF based typing has not been thoroughly assessed.

Methods: We have established a standard operating procedure (SOP) to conduct MALDI-TOF based typing. To test for inter-laboratory reproducibility, we distributed 12 extended spectrum beta-lactamase (ESBL)-producing *E. coli* strains to four laboratories. The strains derived from two independent outbreaks as well as from non-outbreak related isolates. All laboratories were blinded regarding the strain relatedness and followed the SOP for work-up and analysis. Every center used a Microflex MALDI-TOF system (Bruker) and determined peaks >1000 intensity units of individual strains in triplicates with flexAnalysis software (Bruker) to generate a peak list. Next, we analysed the results from all centers to evaluate the reproducibility of MALDI-TOF based typing results from all centers. Pulsed-field gel electrophoresis was used as gold standard.

Results: The participating centers identified between 9 and 17 peaks for each strain. Each center could clearly identify specific peaks to correctly allocate the strains to the two outbreaks and the non-outbreak related strains. The strains from the first outbreak had a specific peak at 6537 m/z (median, IQR: 6536-6539) and the strains of the second outbreakat 9714 m/z (median, IQR: 9710-9714). The variability of these peaks determined by the various centers was below 4 Daltons. The reproducibility between centers for identification of the specific peaks was 100%.

Conclusion: Here we show that a standardized procedure allows a highly reproducible identification of specific peaks within ESBL-producing *E. coli* strains with MALDI-TOF based typing. The peak list analysis enabled the correct allocation of outbreak-related and non-outbreak related strains. This suggests a global application of MALDI-TOF based typing in outbreak settings. Due to its high reproducibility, the specific peaks could be exchanged between centers for epidemiological purposes.