O232

1-hour Oral Session

New frontiers in MALDI-TOF

Single cell MALDI-TOF based identification of strains obtained from hospitalized patients

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Objectives

Single cell MALDI-TOF is a newly developed platform, able to identify strains without previous culturing. This technique is capable of presenting bacterial cells individually to the ionization unit of the mass-spectrometer. Thus each cell produces a classifiable mass spectrum, enabling a quantitative analysis of a sample even if this contains a mix of microorganisms.
In this study we compared two typing methods to determine whether ten *Serratia marcescens* strains, collected from patients hospitalized at the Bronovo hospital in the Netherlands, were involved in an outbreak. The typing methods were: 1) AFLP, a frequently used molecular method for typing used by microbiology departments in hospitals, 2) The single cell MALDI-TOF technique (SC-MALDI-TOF).
We determined whether the rapid SC-MALDI-TOF technique was able to type ten *S. marsescens* strains as accurate compared to the molecular technique AFLP.

Methods

In total, ten *S. marsescens* strains were cultured from infected wounds (n= 5), sputum (n=3), from a positive blood (n=1) culture and from a puncture of unknown source (n=1). They were recultured on bloodagar plates for identification with AFLP (Maasstad hospital, Rotterdam). For typing with SC-MALDI-TOF, strains were recultured on TSA plates. These plates were used to prepare a liquid culture (TSB) and cultured for 24 h at 37 °C. Bacterial pellets were created by centrifugation and washing (with sterile MQ-water) 250 µL of the dense liquid culture. These pellets were resuspended in 1 mL matrix that is especially composed for this type of MALDI. This mixture was subjected to the SC-MALDI-TOF.

Results

Data of both methods were analysed. AFLP with Bionumerics and SC-MALDI-TOF with Matlab. A dendrogram was calculated using the Pearsons correlation coefficient.
The AFLP data showed two identical strains, >90%. The (biological) similarities between the other 8 strains were below the 90% and were considered not to be involved in the outbreak. All the 10 strains were completely different from the control sample. The control sample was an ESBL 2149, *Serratia fonticola*.
The clustering results of the SC-MALDI-TOF were similar to the results of AFLP. The control sample in this case was a patient related *E. coli* strain.

Conclusion

Ng-SC-MALDI-TOF is a new platform. The technique is promising and it is a rapid technique. Identification of strains can be done without culturing/isolation, so the “time-to-ID” is limited and it requires minimum lab infrastructure.
The golden standard method, AFLP and the SC-MALDI-TOF show, that the same two strains were considered identical.
This is the first experiment that indicates that SC-MALDI-TOF is as accurate for typing when compared to AFLP.