ePoster Viewing
MALDI-TOF

COMPARISON OF MALDI-TOF MS AND AFLP FOR STRAIN TYPING OF ESBL-PRODUCING ESCHERICHIA COLI ISOLATES COLLECTED DURING AN OUTBREAK IN A DUTCH NURSING HOME

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Objectives

Theintroduction of Matrix-assisted laser desorption/ionisation time-of-flight massspectrometry (MALDI-TOF MS) in hospital laboratories has revolutionised routineidentification of micro-organisms. Future applications include the use of spectraldata for strain typing, thus potentially providing an efficient on-site method tomonitor the spread of antimicobial-resistant bacteria and to rapidly detectoutbreaks.

We comparedtyping results generated by MALDI-TOF MS to those by Amplified Fragment Length Polymorphism(AFLP) in a collection of ESBL-producing E. coli isolates cultured from Dutch nursinghome residents during an ongoing outbreak of ST131 E. coli.

Methods

In 2consecutive cross-sectional surveys, we collected faecal samples from allresidents, and hand cultures from health-care workers. ESBL-producing E. coliwere isolated using selective culture methods. For each patient, every firstnon-duplicate ESBL isolate (based on phenotypic resistance patterns) wasincluded in the collection. To obtain MALDI-TOF MS spectra, single colonies of isolatesgrown on Columbia agar at 37°C for 24h were collected and suspended in 70%ethanol. Four replicate samples were prepared for each strain (1 µL ofsuspension each) and measured on a VITEK MS RUO system (bioMérieux, France), usingstandard settings as for routine identification. The resulting spectra wereused to compute consensus spectra for each strain in SARAMIS. To increaseresolution in cluster analyses, an exclusion list was created that containedpeaks common to all or most spectra. Type specific peaks or peak patterns wereidentified by aligning strain spectra with a tolerance of 800 ppm.

In addition,all ESBL E. coli isolates were typed by AFLP. PCRs were used to detectST131-specific sequences and to assign the isolates to one of the E.coliphylogroups (PGs). All analyses were performed in a blinded fashion.

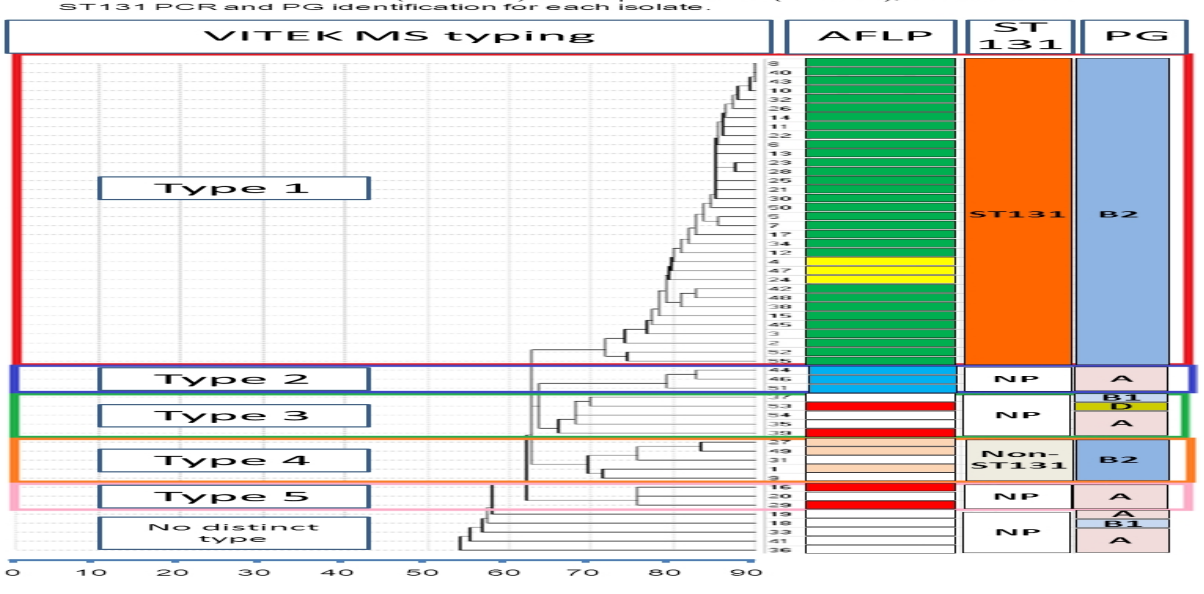
Results

Among 56 E.coliisolates, 5 different strain types could be distinguished based on theMALDI-TOF spectra. Five isolates had no distinct spectral type (Figure 1). Thelargest group consisted of 34 isolates, all ST131 and PG B2. All these isolateswere found in 2 (of 5) adjacent departments, wherethe prevalence of ESBL carriage was approximately 40%. Largely inagreement with these results, AFLP identified five clusters in this set of isolates(indicated by colours in figure 1), whilst 12 isolates were considered unique(indicated in white). Three isolates belonging to spectral type 1 (the largestcluster) were collected from a separate location, and identified as a separatecluster by AFLP (indicated in yellow). Further differentiation of the isolatesin this group using MS spectra may be possible but this has not been tested yet.

Conclusion

The performance of MALDI-TOFMS for typing of E. coli is promising, showing good agreement with typingresults obtained by AFLP. Its performance needs to be evaluated in larger testcollections from different locations.

Figure 1. Tree diagram based on VITEK MS spectra. The 3 columns on the right indicate the AFLP cluster (in colour) or unique isolates (in white), results of the ST131 PCR and PG identification for each isolate.



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