

POSTER PRESENTATION

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DNA microarray analysis reveals variability of accessory genes among isolates recovered during an MRSA outbreak

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Introduction / objectives

Although MRSA outbreaks might have significant consequences on patients and/or health care resources, few data are available about the microevolution of a strain during a single outbreak. In this study, our aim was to characterize the variability of accessory genes among isolates recovered during a local MRSA outbreak.

Methods

Ten MRSA isolates recovered during a large outbreak occurring at the Lausanne University Hospital (Switzerland) were characterized using a DNA microarray (StaphyType, Alere Technologies, Germany) that targets approximately 180 genes including several resistance and virulence genes. Each isolate belonged to the South German clone (ST-228-SCC*mec* I) and had been recovered between September 2008 and December 2009.

Results

As expected during the clonal dissemination of a strain, the 10 isolates shared identical presence/absence for most of the *c.a.* 180 genes tested. Nevertheless, variation was observed for several resistance and virulence genes. These included the beta lactamase operon genes (*blaZ*, *blaI*, *blaR*), genes involved in the resistance to Trimethoprim and Mupirocin (*dfrA* and *mupR*, respectively), a gene encoding unspecific efflux pump conferring resistance to a variety of antiseptic such as chlorhexidine (*qacA*), and genes potentially involved in virulence (*lukX*, *lukY*, *aur*). This variability affected at least 5 of the ten isolates.

Conclusion

Our results indicate the gain/loss of resistance and virulence genes during a local outbreak, suggesting that the biological characteristics of the strain might vary through time.

Disclosure of interest

None declared.

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