Genotyping in surveillance and outbreak investigations of methicillin resistant Staphylococcus aureus- Can DNA microarrays replace conventional methods?

HV Aamot1, HS Alhassani2, A Hashi3, S Samata, S Moncke4, K Helmerssen4, A Blomfield1
1Department of Microbiology and Infectious Control, Akershus University Hospital, Lørenskog, Norway
2Faculty of Health Sciences, Oslo and Akershus University College of Applied Sciences, Oslo, Norway
3Institute for Medical Microbiology and Hygiene, Technical University of Dresden, Dresden, Germany and Alere Technologies GmbH, Jena, Germany
4Department of Research, Section for Clinical Molecular Biology and Laboratory Sciences (EpiGen), Akershus University Hospital, Lørenskog, Norway

*have contributed equally to the project

1. Introduction
In Norway, a national aim is to prevent methicillin resistant Staphylococcus aureus (MRSA) from establishing and becoming a permanent part of the bacterial flora in hospitals and nursing homes [1]. Genotyping methods are important in MRSA surveillance and outbreak investigations. Staphylococcus protein A (spa) typing is frequently used as first-line method. However, when isolates belong to identical, closely related clones of subtypes, traditional genotyping methods may be necessary to differentiate between the isolates.

2. Aim
Evaluate which of the following genotyping methods are best suited to discriminate between spa-types in MRSA outbreak investigations:

1. MLVA - Multiple-Locus Variable number of tandem repeat Analysis
2. PFGE - Pulse Field Gel Electrophoresis
3. DNA microarray

3. Materials and methods
A selection of previously spa-typed MRSA isolates (n=44) related to 16 different outbreaks analysed at Akershus University Hospital, Norway were included. An outbreak was defined as two or more individuals having MRSA that belonged to the same bacterial strain and had a temporal and spatial connection.

Outbreaks with rare (10/1509), fairly frequent (22/3), frequent (1002, 10/24) and closely related (1004, 10/44) spa-types were selected (Table 1). The outbreaks occurred over a time span of several years (2006-2013) in different geographic locations. The isolates were analysed with PFGE [2], MLVA using genes [3] and S. aureus DNA microarray covering >70 S. aureus-specific genes including resistance and virulence markers (Alere technologies, Jena, Germany).

4. Results
The results are presented in Tables 2a-d. MLVA and PFGE clustered according to the previously defined outbreaks except for the five 2233 outbreaks, where MLVA gave five different clusters and PFGE only two clusters. Also, MLVA and PFGE did not differentiate between outbreaks 12 and 16 (Table 2). In addition, MLVA distinguished between the isolates from two outbreaks with both 1006 and 0241 spa-type, DNA microarray differentiated more than spa-typing, MLVA and PFGE and also showed different variants within several outbreaks.

5. Discussion and Conclusion
Genotyping in surveillance and outbreak investigations of MRSA is important for targeted infection control interventions and will be of great practical relevance for the patients in the future. Costs and time per analysis are also important parameters.

6. References

Table 1. An overview of included spa-types

Table 2a. Results of MLVA, PFGE and DNA microarray analyses of 44 MRSA isolates collected from 16 epidemiologically defined MRSA outbreaks

Table 2b. Sample ID Sample date Outbreak ID MLVA PFGE DNA microarray

Table 2c. Sample ID Sample date Outbreak ID MLVA PFGE DNA microarray

Table 2d. Sample ID Sample date Outbreak ID MLVA PFGE DNA microarray

6. References