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# Molecular Typing of *Staphylococcus aureus*: Understanding and Controlling Epidemic Spread

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## Abstract

Methicillin resistant *Staphylococcus aureus* (MRSA) infections continue to spread worldwide. From an epidemiological perspective, risk factors for hospital acquired (HA) infections are most associated, but not limited to, with invasive medical devices, prolonged hospitalization, and surgical procedures. Strains causing infections in patients without risk factors for MRSA are known as community acquired (CA-MRSA). The line between HA- and CA-MRSA is blurring and clones of this pathogen are spreading across geographical borders due to international travel. Strain typing is an important component of epidemiological investigations that should be done to identify outbreak-related strains and hence to control new waves of MRSA infections both locally and internationally.

**Keywords:** MRSA; CA-MRSA; ST80-MRSA-IV; Typing

*S. aureus*is a well-recognized human pathogen of worldwide distribution. In Europe the most common CA-MRSA strain is CC80:ST80-IV [1,2]. In Denmark, CC80:ST80-IV was found to be the predominant cause of CA-MRSA infections in patients with family relationships in the Middle East. Studies conducted by Tokajian et al. in Lebanon [3] and Jordan [4] confirmed the notion that this clone was originally introduced in Denmark and possibly other parts of Europe from the Middle East. Hence, determining the disease burden, genotype, and clonal distribution are all important components that should be integrated in sound epidemiological investigations that should be implemented in developed and underdeveloped countries.

This requires routine strain typing to follow and identify outbreak-related strains and to distinguish epidemic from endemic or sporadic isolates [5].This however, should be combined with the establishment of a sequence-based network in the Middle East to generate easily comparable typing data in electronic, portable form to be used by infection control units locally and internationally. This network could mimic the initiative of the currently available Seqnet.org which includes 44 laboratories from 25 European countries and one from Lebanon [6].

The most reliable typing methods with *S. aureus* are multilocus sequence typing (MLST) and pulse-Field gel electrophoresis (PFGE) [7]. MLST groups strains into sequence types (STs), and BURST (Based Upon Related Sequence Types) analysis is then used to group them into clonal complexes (CCs) [8,9]. PFGE has been found difficult to reproduce between laboratories and is limited in speed of analysis. MLST is usually preferred as a general typing technique because the data can be exchanged between different laboratories. However, major disadvantages of MLST are that it is expensive, laborious and time-consuming [8]. *spa*-typing of *S. aureus* is also an important sequence-based tool in the study of strain origin, clonal relatedness and epidemiology of *S. aureus* outbreaks. Protein A is a cell wall linked protein of *S. aureus*, and the X region of its gene (*spa*) consists of a variable number of direct repeats exhibiting an extensive polymorphism [10]. Sequencing of the repeat region generates informative typing results, hence allowing the grouping of the isolates into different *spa* types [11]. The BURP (Based Upon Repeat Pattern) algorithm is then used to group various *spa*-types into *spa*-CCs. *spa*-typing, unlike the others, can be used to study both the molecular evolution and hospital outbreaks of MRSA [8]. Sequencing of a single locus specific for *S. aureus* makes it the least tedious, expensive and time-consuming amongst the 3 methods. The technique's reliability on a single locus however, can be limiting with respect to discriminatory power due to same or related *spa* loci in different clonal lineages or to related repeat successions in different lineages [8].

There is an urgent need to standardize sampling regimen and typing of MRSA in the Middle East for epidemiological purposes. Real-time synchronization of typing data will help to: elucidate how strains that cause epidemics evolve, restrict CA-MRSA infections, and define the specific conditions that lead to the increased risk of spread of infections associated with foreign travel. Finally, a "search-and-destroy" policy as the one employed in Scandinavian countries should be implemented to ultimately restrict the effect of *S. aureus* infections.

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