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Staphylococcal Cassette Chromosome *mec* (SCC*mec*) in Methicillin-Resistant *Staphylococcus aureus*: An Overview

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Introduction

Methicillin resistant *Staphylococcal aureus* (MRSA) is a major pathogen of nosocomial and community acquired infections associating with significant morbidity and mortality rates of 15-60% [1]. Resistance to methicillin is conferred by the expression of PBP 2a protein, which is encoded by the methicillin resistance gene (*mec*A gene), which is situated on a unique mobile genetic element known as the staphylococcal cassette chromosome *mec* (SCC*mec*) [2].

The emergence of MRSA from methicillin susceptible *S.aureus* (MSSA) is due to site-specific integration of SCC*mec* into the orfX locus in the chromosome of a susceptible isolate. This type of resistance was termed as intrinsic resistance, because it was not due to destruction of the antibiotic by β-lactamase [3].

SCC*mec* elements are highly diverse in their structural organization and genetic content and have been classified into types and subtypes. SCC*mec* consists of three regions: a *mec* complex carrying *mec*A and, if present, its regulatory genes *mec*I and *mec*R1, a *ccr* complex carrying cassette chromosome recombinase (*ccr*) genes which encodes site specific recombinases, namely *ccr*A/B that mediate the integration and excision of SCC*mec* from the recipient chromosome and are, therefore, responsible for its mobility and a series of variable junkyard or J regions (J1, J2 and J3), which constitute nonessential components of SCC*mec*; although, in some cases, these regions carry additional antibiotic resistance determinants [4]. SCC*mec* elements can be typed firstly by identifying the *mec* and *ccr* type, and then identifying genes in the J-regions [5].

Significant geographic variations have been found in the structural organization of the SCC*mec* and these variations have been used to classify the SCC*mec* types [6]. Following the first report of the SCC*mec* element, many structurally distinct elements have been identified. To date, nucleotide sequences of more than 80 SCC*mec* elements have been determined in staphylococcal species. The SCC*mec* elements identified in *S.aureus* are classified various into types depending on the combination of two essential components, the *mec* gene complex and the *ccr* gene complex.

Eleven types have been reported so far based on the criteria suggested by IWG-SCC [7], but only type I-V are globally distributed, whilst others appear to exist as local strains in the country of origin [8, 9]. The updated list and the classification of SCC*mec* are available at http://www.SCCmec.org or http://www.staphylococcus.net. Polymorphism in J regions (mainly J1) have been described and used for the definition of SCC*mec* type IV subtypes (IVa- IVg) [10, 11].

Finally, the global emergence of MRSA has turned into a serious public health problem. Monitoring and limiting the spread of MRSA strains requires the use of rapid and precise epidemiologic typing systems. MRSA typing is essential for the establishment of national and international surveillance networks. In MRSA typing, both phenotypic and genotypic methods are used. These methods vary greatly in their discriminatory power, reproducibility of the results and the cost and efforts required. Molecular typing is a powerful tool that can provide information about genetic characteristics of a specific clone. A large number of molecular methods have been developed for typing of MRSA strains. SCC*mec* typing is an important molecular tool and it is also of a potential clinical and epidemiologic interest for the analysis of MRSA [12]. Thus, characterization of SCC*mec* types can be a good marker to reveal the epidemiological change of MRSA infection [13].

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