

Abstract

Staphylococci are common part of human flora but also they are a dangerous pathogen. Among staphylococci strains, methicillin resistance is widespread. The *mecA* gene, organized in *mec* complex, is responsible for methicillin resistance. The *mec* complex is part of mobile genetic element – staphylococcal chromosome cassette *SCCmec*. *SCCmec* is large variable mobile genetic element and it is always composed of three parts – *mec* complex, *ccr* complex and J regions. Complex *mec* consists of *mecA* gene and its regulatory genes *mecR1* and *mecI*. Complex *ccr* encodes recombinase genes, they are responsible for excision and insertion of *SCCmec*. J regions are remaining parts of *SCCmec*, which include other mobile genetic elements that directly influence methicillin resistance genes expression or carry genes for resistance to other antimicrobial agents. *SCCmec* or its parts can be transferred by horizontal gene transfer between staphylococci both intraspecific and interspecific, although mechanism of its transfer is still unknown. Eleven types of *SCCmec* have been described so far. In this thesis, I summarized the findings about molecular composition of *SCCmec*, horizontal gene transfer of the genes encoding methicillin resistance and molecular evolution of *SCCmec*. Mobile genetic elements play a key role in evolution and adaptation of bacteria. Understanding of these mechanisms is important for control of methicillin resistance spread.