

DETECTION OF *mec*-REGULATORY GENES IN *STAPHYLOCOCCUS* *spp.*
STRAINS ISOLATED OF NOSOCOMIAL INFECTION

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The *mecA* gene that encodes methicillin (oxacillin) resistance in *Staphylococcus spp.* may be regulated by the *mecR1* and *mecI* genes, and this region has been referred to as the *mec* complex. The distribution of the *mec* complex that regulates the expression of methicillin resistance was investigated by PCR in 27 clinical staphylococci of hospital origin. An analysis of these regulatory genes has found two classes of *mec* complexes in these strains. Nineteen isolates (17 *S. aureus* and 2 coagulase-negative staphylococci (CoNS)) contain the class A *mec* complex with the complete regulatory region (*mecA-mecR1-mecI*). Eight isolates probably contain a variant of Class A, the Class A1 *mec* complex, with a complete *mecI* gene but with a deletion in a segment of the *mecR1* gene encoding the protein's membrane-spanning domain. All isolates analysed were oxacillin susceptible as detected by disc diffusion, using 1 µg oxacillin, and by the oxacillin agar dilution method (with 6µg/mL oxacillin in Mueller-Hinton agar supplemented with 4% NaCl). Our findings support the global spread of epidemic clones and confirm the close relationship between the class A *mec* isolates and the N315 isolate found in Japan. The elucidation of the genetic basis for methicillin resistance *Staphylococcus* creates an epidemiologic base for the study of the evolutionary biology of these isolates.