Evaluation of Novel Genes for Detecting Methicillin-Resistant *Staphylococcus aureus*: Clinical and Epidemiological Aspects

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant pathogen that has emerged over the last four decades, causing both nosocomial and community-acquired infections. Such endemic MRSA are difficult to eradicate, and they most likely further increase the number of infections, the costs, and the length of hospital stays. Thus, rapid and accurate detection of methicillin resistance in *S. aureus* is important for the use of appropriate antimicrobial therapy and for the control of nosocomial spread of MRSA strains.

Molecular methods for the rapid identification of MRSA are generally based on the detection of an *S. aureus*-specific gene and the *mecA* gene[1]. Such methods cannot be applied for the detection of MRSA from non-sterile specimens because these samples often contain both coagulase-negative staphylococci (CoNS) and *S. aureus*, either of which can carry *mecA*.

In this study, we describe a multiplex PCR assay which allows the detection of MRSA from clinical samples. To evaluate primer sets selected by bioinformatic approaches, 290 clinical samples were tested and primers used in this study had 95.96% specificity and 96.6% positive predictive value. All target gene-positive MRSA isolates were analyzed by repetitive extragenic palindromic-PCR (rep-PCR) and SCC*mec* typing method. Using this PCR method based on novel genes, we can discriminate MRSA from other bacterial species including methicllin-resistant CoNS and simultaneously classified by strain as well as analysis whether community-acquired or hospital-acquired *S. aureus*. [This work was supported by Medigenes Co.]

Reference

1. Kobayashi N, Wu H, Kojima K, Taniguchi K, Urasawa S, Uehara N, Omizu Y, Kishi Y, Yagihashi A, Kurokawa I □ Detection of *mecA*, *femA*, and *femB* genes in clinical strains of staphylococci using polymerase chain reaction□ (1994) Epidemiol Infect. 113(2), 259-266.