Background: Methicillin-resistant Staphylococcus aureus (MRSA) has been endemic in healthcare facilities for many years and has led to the development of nosocomial infection-associated pathogen. Rapid and accurate detection of colonized individuals is critical to infection control practices. This study evaluated the performance of the second generation molecular assay (BD MAX) targeting the staphylococcal cassette chromosome (SCCmec) – right extremity junction (MREJ) region. Specifically, the performance of BD MAX was compared with a confirmed methicillin-resistant Staphylococcus aureus (MSSA) gene. These isolates were screened for the presence of mixed populations of methicillin-resistant CoNS and a drop-out strain. This study aimed to evaluate the performance of the BD MAX assay; (i) to determine the relative percentage of right extremity junction (MREJ) – MSSA, (ii) to determine the relative rate of MRSA with unrecognized MREJ region sequences. Isolates showing discrepant results regarding mecA gene were subjected to the BD MAX MRSA assay. Additional experiments and definitions: Isolates were simultaneously subjected to the BD MAX assay according to the manufacturer’s instructions. A subset of MSSA (n=903) and MSSA (n=36) isolates were subjected to the BD MAX assay. The results were recorded using a computer program targeting the mecA (co-determined by the primers targeting the Staphylococcus aureus). Next, these isolates were screened for MRSA by the BD MAX MRSA assay. Results: Among the MRSA subset (i.e. CoNS). Performance evaluations of second generation targeting the mecA gene and/or cefoxitin (MSSA) had the highest specificity and sensitivity respectively. Among the MRSA subset (i.e. CoNS). Performance evaluations of second generation (MSSA) had the highest specificity and sensitivity respectively. The BD MAX assay for detection of methicillin-resistant Staphylococcus aureus (MSSA) and methicillin-sensitive Staphylococcus aureus (MSSA) genes), results from both assays were in agreement. Moreover, an overall rate of drop-out mutants were distributed among isolates showing discrepant results. The PCR assay was performed using a multiplex approach, including primers targeting the mecA gene as an internal control. Among the MRSA subset (i.e. CoNS). Performance evaluations of second generation targeting the mecA gene and/or cefoxitin (MSSA) had the highest specificity and sensitivity respectively. The BD MAX assay for detection of methicillin-resistant Staphylococcus aureus (MSSA) and methicillin-sensitive Staphylococcus aureus (MSSA) genes), results from both assays were in agreement. Moreover, an overall rate of drop-out mutants were distributed among isolates showing discrepant results. The PCR assay was performed using a multiplex approach, including primers targeting the mecA gene as an internal control.

RESULTS

Among the 1,807 MSSA, all but two (99.3%, 1,805/1,807) were confirmed methicillin-resistant (MSSA) isolates. Two isolates were classified as methicillin-susceptible (MSSA) and resistant (MRSA) isolates were subjected to the BD MAX MRSA assay. These two negative results repeated on a second attempt, while identification was maintained. The mecA genes were not identified in these isolates. Among the MRSA subset (i.e. CoNS), two isolates were genotypically characterized as MRSA (Table 2). These two negative results repeated on a second attempt, while identification was maintained. The mecA genes were not identified in these isolates. A total of 91.1% (892/900) of MSSA isolates had BD MAX results in agreement with the mecA gene. Additionally, a high rate of drop-out mutants were detected, emphasizing the importance for accurate identification of MSSA. Among the 1,807 MSSA, all but two (99.3%, 1,805/1,807) were confirmed methicillin-resistant (MSSA) isolates. Two isolates were classified as methicillin-susceptible (MSSA) and resistant (MRSA) isolates were subjected to the BD MAX MRSA assay. These two negative results repeated on a second attempt, while identification was maintained. The mecA genes were not identified in these isolates. A total of 91.1% (892/900) of MSSA isolates had BD MAX results in agreement with the mecA gene. Additionally, a high rate of drop-out mutants were detected, emphasizing the importance for accurate identification of MSSA.

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