Analysis of the Molecular Epidemiology of Staphylococcus epidermidis Clinical Isolates from USA Hospitals

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INTRODUCTION

Staphylococcal species are among the most genetically diverse and complex pathogenic bacteria. Isolates belonging to this species are associated with chronic infections in hospital and other health care settings. The overall rate of methicillin (oxacillin) resistance among the species is relatively low. However, the presence of methicillin resistance causes a significant issue due to the lack of specific treatments and the potential for nosocomial transmission.

RESULTS

- Among the S. epidermidis isolates, 27/39 were linezolid-resistant (71.8%); 12/39 were MIC >4 mg/L, and 15/39 were MIC ≤4 mg/L. The total number of resistant isolates was 12/39 (30.8%)
- Among the 2-I type isolates, there were 10/21 (47.6%) linezolid-resistant. Among the CC2-II isolates, 3/39 (7.7%) were linezolid-resistant.
- Analysis of SmaI PFGE patterns clustered the isolates into seven major clonal complexes (CC) (CC2; 60/69; 87%), two minor CCs (23 and 32 [2/69; 2.9%], ST7 [5.8%] and ST59 [5.8%]). Other STs had occurrences lower than 5% (8.7%), ST83 (8.7%), ST2 (17.4%) were most commonly detected, followed by ST83
- The vast majority of CC2-I strains (17/21; 80.9%) were multidrug-resistant (resistant to at least four classes of antimicrobial agents). The vast majority of CC2-II strains (33/39; 84.6%), CC2-II-5 (33/39; 84.6%), CC2-II-6 (2/39; 5.1%), CC2-II-85 (2/39; 5.1%) and CC2-II-89 (2/39; 5.1%; Table 1).
- Molecular typing has been proposed that cluster 2-II can be further subdivided into four groups, represented in this study by 2-II-16, 2-II-5, 2-II-85, and 2-II-89. The vast majority of CC2-II strains (33/39; 84.6%), CC2-II-5 (33/39; 84.6%), CC2-II-6 (2/39; 5.1%), CC2-II-85 (2/39; 5.1%) and CC2-II-89 (2/39; 5.1%) were linezolid-resistant. Lower methicillin resistance rates were observed among CC2-II (27/39; 69.2%) and other CCs (6/15; 40.0%; Tables 1 and 2).

CONCLUSIONS

- Based on the PFGE analysis, a great degree of genetic diversity (PFGE profile) was observed within the clonal complexes of S. epidermidis. This data suggests that S. epidermidis isolates possess an enhanced capacity for acquisition of foreign DNA. In addition, the presence of mutations in the 23S rRNA may confer a lower fitness cost for CC2-II, which may be more adapted to survive in the hospital and/or its environment than other CC2 clusters.

MATERIALS AND METHODS

Electron microscope analysis was part of 18,000 clinical isolates collected during the 2010-2011 timeframe for the SENTRY Program. The study was approved by the Ethics Committee of the University of Nebraska Medical Center. IRB approval was obtained (10-7006).

Methods

- A total of 69 S. epidermidis strains were selected. Representative of each clonal complex (CC) and subtype were picked for analysis. The isolates were from 37 USA sites combining 27 USA states in 36 cities. Eleven strains, seven from each of the 37 sites, were selected and typing was performed by broth microdilution methods.
- Linezolid-resistant strain were screened for all of the isolates in the 2009 linezolid disc experiment and typing was performed by broth microdilution methods.
- All susceptible strains were selected for susceptibility testing by CLSI methods. The study was approved by the Ethics Committee of the University of Nebraska Medical Center. IRB approval was obtained (10-7006).

Molecular typing

- Multilocus sequence typing (MLST) was performed including in this study.
- It has been proposed that cluster 2-II can be further subdivided into four groups, represented in this study by 2-II-16, 2-II-5, 2-II-85, and 2-II-89. The vast majority of CC2-II strains (33/39; 84.6%), CC2-II-5 (33/39; 84.6%), CC2-II-6 (2/39; 5.1%), CC2-II-85 (2/39; 5.1%) and CC2-II-89 (2/39; 5.1%) were linezolid-resistant. Lower methicillin resistance rates were observed among CC2-II (27/39; 69.2%) and other CCs (6/15; 40.0%; Tables 1 and 2).
- Based on the PFGE analysis, a great degree of genetic diversity (PFGE profile) was observed within the clonal complexes of S. epidermidis. This data suggests that S. epidermidis isolates possess an enhanced capacity for acquisition of foreign DNA. In addition, the presence of mutations in the 23S rRNA may confer a lower fitness cost for CC2-II, which may be more adapted to survive in the hospital and/or its environment than other CC2 clusters.

SELECTED REFERENCES