Evaluation of a Fully Automated System (RAISUS) for Rapid Identification and Antimicrobial Susceptibility Testing of Staphylococci


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RAISUS is a system for rapid bacterial identification and antimicrobial susceptibility testing. RAISUS and VITEK showed 97.8% and 75.9% agreement in identification of 45 Staphylococcus aureus strains and 58 coagulase-negative staphylococci (CoNS), respectively, and RAISUS and CLSI (formerly NCCLS) methods showed 87.2% and 87.9% agreement in the MICs for S. aureus and CoNS, respectively. RAISUS provided these data within 3.75 h, suggesting its utility for clinical bacteriological laboratories.

Methicillin-resistant Staphylococcus aureus (MRSA) is one of the principal pathogenic bacteria that cause hospital infections in Europe and the United States (3, 4, 7, 11), and the number of methicillin-resistant coagulase-negative staphylococci (MR-CoNS) has been increasing recently. Consequently, this has had an adverse effect on treatment of nosocomial infections, including catheter infections.

It is important to select proper antibacterial agents for these pathogens (6, 10), but many clinical laboratories currently spend from 48 to more than 72 h to obtain results from susceptibility testing. If resistant bacteria (methicillin-resistant or vancomycin-resistant bacteria) could be identified at an earlier stage, the use of ineffective antibiotics could be avoided, and a choice could be made of the most suitable antibacterial agents for patients with infections caused by a given bacterium. Moreover, immediate reports are likely to lead to avoidance of the emergence of new resistant bacteria, and such information is also likely to be useful for clinicians.

RAISUS is a fully automated system of identification and susceptibility developed by Nissui Pharmaceutical Co., Ltd. The RAISUS system is a fully automated instrument from sample inoculation onto a microtiter plate, culture, identification, and MIC determination to collection of the test device within 2 dilutions for the two methods. In addition, the measured MIC was classified into three categories: susceptibility (S), intermediate resistance (I), and resistance (R), according to CLSI criteria (12). Agreement in clinical category (ACC) was evaluated using three criteria: very major error (VME), major error, and minor error (5).

Agreement between RAISUS and VITEK for identification of S. aureus was 97.8% (44/45), and the methods showed disagreement for only one strain. In identification of CoNS, RAISUS and VITEK showed agreement for 75.9% of the strains (44/58) and gave different results for 14 strains. Among the 14 strains, 10 strains identified as Staphylococcus capitis by RAISUS were identified as Staphylococcus epidermidis by VITEK. These strains were studied by DNA-DNA hybridization by the method of Ezaki et al. (2), which confirmed that all these strains were identified correctly by RAISUS.

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The essential agreement of MICs within 2 dilutions for the two methods for *S. aureus* was lowest at 62.2% for AMC and highest at 100% for CLI, VAN, and LVX (Table 1). The lowest agreement in clinical category was 66.7% for AMC, and the highest was 100% for CLI, VAN, and SXT. For OXA, which is essential for MRSA identification, the MIC agreement was 84.4% (38/45) and ACC was 100% (45/45). Moreover, 95.8% (23/24) of strains identified as MRSA and 95.2% (20/21) identified as methicillin-sensitive *S. aureus* by CLSI methods were identified as MRSA and methicillin-sensitive *S. aureus* by RAI-SUS within 5 h after the measurements were started. The remaining two strains required 6.25 h for identification (Fig. 1).

The essential agreement of MICs within 2 dilutions for the two methods for CoNS was the lowest at 75.9% for PEN and the highest at 100% for VAN (Table 2). On the other hand, the lowest ACC was 84.5% for MEM, and the highest was 100% for VAN. Very major errors were observed in three, four, two, and two strains for PEN, AMC, MEM, and LVX, respectively. Regarding OXA, which is essential for identification of MR-CoNS, the essential agreement was 82.8% (48/58) and ACC

![FIG. 1. RAISUS detection times for identification and susceptibility of *S. aureus* and CoNS. Data represent the time required to determine the antimicrobial susceptibilities of *S. aureus* and CoNS to nine antibiotics.](image-url)
TABLE 2. Comparison between the MICs determined by RAISUS and the reference microdilution method and category errors for CoNS (n = 58)a

<table>
<thead>
<tr>
<th>Antimicrobial agent</th>
<th>No. of MICs from RAISUS within the indicated log2 reference MIC</th>
<th>Essential agreementb (%)</th>
<th>Minor error</th>
<th>Major error</th>
<th>Very major error</th>
<th>ACC</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>≤−4</td>
<td>−3</td>
<td>−2</td>
<td>−1</td>
<td>Same</td>
<td>1</td>
</tr>
<tr>
<td>Penicillin G</td>
<td>2</td>
<td>23</td>
<td>15</td>
<td>6</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Oxacillin</td>
<td>0</td>
<td>4</td>
<td>6</td>
<td>23</td>
<td>0</td>
<td>0</td>
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<tr>
<td>Amoxicillin-CLA</td>
<td>0</td>
<td>2</td>
<td>7</td>
<td>23</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Meropenem</td>
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<td>3</td>
<td>1</td>
<td>9</td>
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<tr>
<td>Erythromycin</td>
<td>0</td>
<td>2</td>
<td>5</td>
<td>35</td>
<td>10</td>
<td>2</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>48</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Vancomycin</td>
<td>0</td>
<td>0</td>
<td>13</td>
<td>36</td>
<td>9</td>
<td>0</td>
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<tr>
<td>SXT</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>43</td>
<td>5</td>
<td>7</td>
</tr>
<tr>
<td>Levofloxacin</td>
<td>0</td>
<td>3</td>
<td>16</td>
<td>36</td>
<td>3</td>
<td>0</td>
</tr>
</tbody>
</table>

a For abbreviations, see Table 1 footnotes.
b Values are numbers of MICs.

was 96.6% (56/58), with two strains showing a major error and none showing a VME or minor error. We closely investigated these two strains using the method for detection of the mecA gene by enzymatic detection of PCR products (13). Both strains were presumed to be methicillin-sensitive CoNS (MS-CoNS) because the presence of mecA was not detected. In addition, 82.2% (37/45) of MR-CoNS and 69.2% (9/13) of CoNS identified by CLSI methods were identified as MR-

The total times for RAISUS identification and antimicrobial susceptibility testing using OXA were about 5 h for S. aureus and about 7 h for CoNS. The difference in identification times between S. aureus and CoNS might simply result from the large number of CoNS strains that developed slowly. We conclude that RAISUS shows excellent accuracy in identification of staphylococci and that rapid and effective reports can be achieved from RAISUS susceptibility data. Therefore, RAISUS can provide the necessary information for selection of appropriate antibacterial agents in a shorter time frame.

REFERENCES