
Damien Dubois, Christine Segonds, Marie-Françoise Prere, Nicole Marty and Eric Oswald

Published Ahead of Print 10 April 2013.

Updated information and services can be found at: http://jcm.asm.org/content/51/6/1861

These include:

**REFERENCES**

This article cites 50 articles, 35 of which can be accessed free at: http://jcm.asm.org/content/51/6/1861#ref-list-1

**CONTENT ALERTS**

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: http://journals.asm.org/site/misc/reprints.xhtml
To subscribe to another ASM Journal go to: http://journals.asm.org/site/subscriptions/

Damien Dubois,a,b Christine Segonds,a,b Marie-Françoise Prere,a,b Nicole Marty,a,b Eric Oswald,a,b

Laboratoire de Bactériologie-Hygienè, Institut Fédératif de Biologie, Centre Hospitalo-Universitaire, Toulouse, France; Université Paul Sabatier-Toulouse III, Toulouse, France

**Discrimination between *Streptococcus pneumoniae* and its close relatives of the viridans group is a common difficulty in matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry–based identification. In the present study, the performances of the Vitek MS MALDI-TOF mass spectrometry system were assessed using 334 pneumococci, 166 other *S. mitis* group streptococci, 184 non-*S. mitis* group streptococci, and 19 related alpha- and nonhemolytic aerobic Gram-positive catalase-negative coccal isolates. Pneumococci had been identified by means of optochin susceptibility and bile solubility or serotyping, and other isolates mainly by use of RapidID32 Strep strips. In case of discordant or low-discrimination results, genotypic methods were used. The sensitivity of the Vitek MS for the identification of *S. pneumoniae* was 99.1%, since only three bile-insoluble isolates were misidentified as *Streptococcus mitis/Streptococcus oralis*. Conversely, two optochin-resistant pneumococci were correctly identified (specificity, 100%). Three *Streptococcus pseudopneumoniae* isolates were also correctly identified. Among nonpneumococcal isolates, 90.8% (*n* = 335) were correctly identified to the species or subspecies level and 2.4% (*n* = 9) at the group level. For the remaining 25 isolates, the Vitek MS proposed a bacterial species included in the list of possible species suggested by genotypic methods, except for 4 isolates which were not identified due to the absence of the species in the database. According to our study, the Vitek MS displays performance similar to that of the optochin susceptibility test for routine identification of pneumococcal isolates. Moreover, the Vitek MS is efficient for the identification of other viridans group streptococci and related isolates, provided that the species are included in the database.**

*Streptococcus pneumoniae* is responsible for upper respiratory tract infections (otitis and sinusitis) as well as severe diseases (pneumonia, bacteremia, and meningitis) associated with high morbidity and mortality rates (1). More than 90 capsular serotypes have been characterized, with an unequal distribution in systemic infections (2). The species *S. pneumoniae* belongs to the *S. mitis* group streptococci, which are part of the so-called viridans streptococci group, which also includes the *S. salivarius, S. mutans*, *S. anginosus*, and *S. bovis* groups (1, 3). In contrast to pneumococci, nonpneumococcal viridans group streptococci colonizing the upper respiratory tract are rarely responsible for systemic infections like endocarditis (1). Given these differences in clinical significance, accurate identification of *S. pneumoniae* is essential.

Both the biochemical systems and the commercial antigen detection tests available for pneumococcal identification (ID) are recognized as unsatisfactory (1, 4). The simplest and most reliable tests for *S. pneumoniae* ID in clinical laboratories are optochin susceptibility and/or bile solubility. However, optochin-resistant and bile-insoluble pneumococcal isolates and optochin-susceptible nonpneumococcal alpha-hemolytic streptococci have been reported (1, 4–9). Another pitfall of using optochin susceptibility testing is the differentiation of *S. pseudopneumoniae* isolates (10). Detection and determination of capsular polysaccharides of *S. pneumoniae* with type-specific antisera is a valuable second-line ID test but remains mainly an epidemiologic tool and entails the problem of untypeable pneumococci (1, 11, 12). To overcome problems in phenotypic pneumococcal ID, pneumococcus-specific PCRs targeting anonymous DNA fragments or genes encoding virulence factors like pneumolysin (*plyA*), autolysin (*lytA*), an oxidative stress resistance component (*psaA*), and capsular biosynthesis (*cpsA*) have been developed (13–20). Partial sequence analysis or specific nucleotide signatures of various housekeeping genes have been also proposed as an alternative approach for discriminating pneumococci and viridans streptococci (21–26). However, *S. pneumoniae* and other *S. mitis* group streptococci may share a high degree of DNA sequence identity due to the high frequency of genetic transformation of these bacterial species (27–29). In addition, these numerous molecular methods, which display variable specificity and reliability, remain inconvenient for routine diagnostic use.

Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS)-based systems are increasingly replacing conventional phenotypic methods for routine ID of bacteria due to their fast, easy-to-use, cost-effective, and thus high-throughput performances (30–37). However, one of the main limitations reported for MALDI-TOF MS systems remains the
lack of discrimination between S. pneumoniae and other closely related alpha-hemolytic streptococci (30, 33, 36–40). Conversely, two previous studies from Martiny and coworkers and our laboratory tested the Vitek MS (bioMérieux, France), a MALDI-TOF mass spectrometry-based ID system, and reported the apparent appropriate species ID of S. pneumoniae and other viridans group streptococci. Nonetheless, these studies were based on only a few isolates (34, 35). In the present study, we evaluated the performances of the Vitek MS system on a large and representative clinical collection of 334 pneumococci, 166 other S. mitis group streptococci, 184 non-S. mitis group streptococci, and 19 related alpha- and nonhemolytic aerobic Gram-positive catalase-negative coccal isolates.

MATERIALS AND METHODS

Bacterial isolates. A set of 334 nonredundant isolates of S. pneumoniae recovered in the Midi-Pyrénées region of France in 2009 as part of the regional epidemiological surveillance of S. pneumoniae (n = 300) or randomly chosen from our 2011 laboratory collection (n = 34) were analyzed (2). Pneumococcal strains originated from 193 blood cultures, 55 acute otitis media samples, 38 respiratory samples, 28 cerebrospinal fluids, 15 pleural effusions, two conjunctivitis samples, one joint fluid sample, one vaginal sample, and one skin lesion. Moreover, all nonredundant non-pneumococcal isolates recovered in our laboratory during the first 9 months of 2011 (n = 369, except 30 Streptococcus anginosus and 30 Streptococcus constellatus isolates randomly chosen), encompassing 166 other S. mitis group and 184 other non-S. mitis group viridans group streptococci, as well as 19 isolates belonging to six related genera were also included in this study. All isolates were cultured on 5% sheep blood Columbia agar (bioMérieux) for 18 h to 48 h at 35°C under a 5% CO₂ atmosphere.

Optochin susceptibility test. A 5-μg optochin disk (6-mm disks; MAST ID Optochin Discs, MAST, United Kingdom) was placed on sheep blood Columbia agar plates inoculated under 5% CO₂, or ambient atmosphere when stated. Optochin susceptibility was defined as an inhibition zone of ≥14 mm.

Bile solubility test. The bile solubility test was performed with the tube method, with preparation of bacterial suspensions in 1 ml of 0.9% NaCl equivalent to a McFarland 1.0 standard. A 0.5-ml portion of 2% deoxycholate was added to a 0.5-ml suspension of each isolate prepared in 0.9% NaCl and incubated at 35°C for 1 h. A positive test was indicated by visible clearing of the suspension. A negative control for each isolate was similarly performed with 0.5 ml of 0.9% NaCl added to a 0.5 ml suspension of each isolate prepared in 0.9% NaCl.

Serotyping method. Pneumococcal capsular polysaccharide serotype was determined by agglutination with specific antisera (Statens Serum Institut, Copenhagen, Denmark).

Phenotypic identification systems. Rapid ID32 Strep strips or the Vitek 2 system. This technical efficiency for analysis of Gram-positive cocci, as well as 19 isolates belonging to six related genera were also included in this study. All isolates were cultured on 5% sheep blood Columbia agar (bioMérieux) for 18 h to 48 h at 35°C under a 5% CO₂ atmosphere.

Plate preparation, mass spectrum collection, and database searching. Mass spectrometry was carried out with a unique deposit for 94.3% of the isolates (n = 663; Table 1), including 17 of 22 (77%) mucoid pneumococci. The mass spectrometry of the database and the result was recorded as “no ID.” In the case of warning messages generated by poor-quality spectra, LD results, and no-ID results, the deposits were read again, and when required, the isolates were tested again with a single deposit. In case of persistent LD results or poor-quality spectra, a protein extraction step was performed, as previously described (43).

Reference identifications and result management. Presumptive pneumococcal isolates were tested for optochin susceptibility and bile solubility or serotype. S. pneumoniae isolates were defined as optochin susceptible (inhibition zone of ≥14 mm) under a CO₂ atmosphere and bile insoluble or typeable. Bile-insoluble or nontypeable isolates exhibiting an optochin inhibition zone of >6 mm and ≤14 mm under a CO₂ atmosphere but of >14 mm under an ambient atmosphere in a complementary test were considered S. pseudopneumoniae (10). Other isolates were identified using the Rapid ID32 Strep system, except for S. bovis group and Helcococcus kunzii isolates, which were identified using the Vitek 2 system. S. mitis group isolates were confirmed to be optochin resistant.

In the case of discordant results between Vitek MS and conventional phenotypic methods, or low-discrimination results with conventional phenotypic methods, including discordant results between optochin susceptibility tests and bile solubility tests or serotypeability, or absence of ID (no ID) with the Vitek MS system, genetic IDs were performed, and the results were considered the reference ID. For management of discordant results, different partial gene sequencing was performed according to presumptive ID: recA sequencing, currently one of the most reliable genotypic tools for proper ID to species level of pneumococci and closest related species (26); 16S rRNA gene sequencing for catalase-negative nonstreptococcal isolates; and sodA sequencing for others. For informative purposes, partial gyrB gene sequencing was also performed in some cases with inconclusive IDs according to sodA sequencing. Moreover, bile solubility testing was carried out, along with ply-, ltyA-, psaA-, and MFP-specific PCR assays for discrimination between S. pneumoniae and the most closely related species, for informative purposes.

RESULTS AND DISCUSSION

Technical efficiency. MALDI-TOF MS-based IDs were efficiently carried out with a unique deposit for 94.3% of the isolates (n = 663; Table 1), including 17 of 22 (77%) mucoid pneumococci. This technical efficiency for analysis of Gram-positive cocci with a single deposit without an extraction procedure is consistent with previous reports regarding the Vitek MS and Anstroms MALDI-TOF MS-based systems in contrast to the BioMasy system (Bruker) (30, 31, 34, 35, 37, 39). A second deposit performed with 5.7% of the isolates (n = 40) resolved half of the IDs (Table 1). The six persistent no-ID results were considered...
true absences of ID. An extraction step followed by a unique deposit was performed for persistent LD results \((n = 9)\) and poor-quality spectra \((n = 5)\); the latter corresponded to mucoid pneumococci that account for 23% of all the mucoid pneumococcal isolates tested. The extraction step resolved all IDs but one, which remained an LD between *Gemella morbilorum* and *Gemella haemolytica*. Low-confidence values, LD results, and requirement of a second deposit or of an extraction step were not related to particular species, except that 23% of mucoid pneumococcal isolates needed an extraction step.

Inconsistent results occurred for three isolates, identified as coagulase-negative staphylococci or *β*-hemolytic *Streptococcus*. Performing a second deposit allowed us to successfully identify two isolates, the other one belonging to a species that was outside the scope of the database. These outright inconsistent IDs emphasize the fact that bacteriological technical expertise remains essential to avoid major misidentifications.

**S. pneumoniae identification performances.** A large diversity of pneumococci was assessed in this study, which includes 267 isolates belonging to 22 different serogroups. The sensitivity of the Vitek MS system for the ID of *S. pneumoniae* was 99.1%, with three of the 334 isolates being misidentified as *Streptococcus mitis* or *oralis* (Table 2) according to partial *recA* gene sequencing analysis. These three misidentified *S. pneumoniae* were isolated from respiratory samples and are atypical pneumococci, since all three isolates were bile insoluble, and two of them were negative for MFP and *psaA* amplifications. These PCRs have been recently reported to be among the most reliable species-specific PCRs to appropriately discriminate *S. pneumoniae* and the most closely related species, like *S. pseudopneumoniae* (13, 17). Conversely, the specificity of the Vitek MS system for *S. pneumoniae* ID was 100% (Table 2), with two optochin-resistant, bile-soluble, and typeable pneumococci correctly identified. One of these two isolates, originating from a blood culture, was *psaA* and *lytA* negative. In contrast to previous reports related to other MALDI-TOF systems (30, 33, 36–40), the Vitek MS system allows good discrimination between the *S. pneumoniae* species and other viridans streptococcal species. This is probably linked to its particular algorithm, which may efficiently detect the specific mass/charge peak profiles of *S. pneumoniae* and the most closely related species, as recently highlighted by Werno and coworkers (44).

Of note, the good performances of the Vitek MS for the ID of *S. pneumoniae* were obtained from pure culture on agar media. Viridans group streptococci form minuscule to small colonies, frequently requiring the use of more than one colony to perform the deposit of intact whole bacteria on the MALDI-TOF MS target. Since viridans group streptococci can have similar colony morphologies, performing a deposit with more than one colony to detect *S. pneumoniae* isolates directly from a possibly polymicrobial culture, like those frequently originated from respiratory samples, remains very hazardous.

**Nonpneumococcal identification performances.** Among nonpneumococcal isolates, 90.8% \((n = 335)\) were correctly identified to the species or subspecies level (Table 2). Isolated from respiratory samples without any other pathogenic bacteria recovered, all three *S. pseudopneumoniae* isolates were correctly identified. The three isolates were *psaA* negative, and two isolates were *ply* positive, which is consistent with the reported specificity of the *psaA* PCR for *S. pneumoniae* ID and the frequent *ply*-positive PCRs among *S. pseudopneumoniae* isolates (10, 13, 45).

Four nonpneumococcal isolates (1.1%) were not identified due to the absence of these species in the database (Streptococcus *massiliensis*, *Facklamia tabacinalis*, *Facklamia ignava*, and *Aerococcus sanguinicola*) (Table 2). The *sodA* gene sequence of the *S. massiliensis* isolate displayed only 94.2% identity with the sequence of the reference strain 4401825, which harbors a 27-bp duplication. In contrast, the partial *gyrB* sequence showed 100% identity with the one of the reference strain (46). The partial *sodA* and *gyrB* sequences of this *S. massiliensis* isolate from peritoneal fluid had been deposited in the EMBL Nucleotide Sequence Database into the accession numbers HF677578 and HF677579, respectively.

Nine nonpneumococcal isolates (2.4%) were correctly identified to the group level but misidentified at the species or subspecies level, including five *S. mitis* group, one *S. anginosus* group, and three *S. bovis* group isolates. The five *S. mitis* group isolates were five *Streptococcus australis* isolates identified as *Streptococcus parasanguinis* or *Streptococcus sanguinis* (Table 2). These *S. australis* misidentifications may be due to the close relationships of *S. australis* with *S. sanguinis* and *S. parasanguinis* (46), together with the absence of *S. australis* in the database of the Vitek MS.

Reference IDs using genotypic methods were obtained only at the group level for 5.7% \((n = 21)\) of nonpneumococcal isolates, including five *S. mitis* group, nine *S. anginosus* group, five *S. bovis* group, and two related-genus isolates. The Vitek MS proposed a bacterial species included in the list of possible species suggested by *sodA* or 16S rRNA gene sequence analysis for 19 isolates and no ID for two isolates (Table 2). The latter were an *S. mitis* group isolate for which the *sodA* gene sequence was similar to *S. mitis* group species absent from the Vitek MS database (*S. australis*, *S. infantis*, and *S. peroris*), and a *Granulicatella* isolate for which partial 16S rRNA gene sequencing suggested species present in the Vitek MS database (*G. adiacens* and *G. elegans*) or absent in the Vitek MS database (“*Granulicatella para-adiacens*”).

In the *S. anginosus* group, considerable genetic similarity has been previously reported, which adds to the complexity of defining species, despite an apparent biochemical heterogeneity (1, 47, 48). By sequencing four different housekeeping genes, Glazunova and coworkers showed that some *S. anginosus* group isolates were identified as either *S. anginosus* or *S. constellatus*, depending on which gene sequence was analyzed (47). For informative purpose, *gyrB* gene sequencing was performed for two randomly chosen isolates. The *gyrB* gene sequence confirmed the identification ob-

### TABLE 1 Distribution of result categories among all 703 isolates tested, according to identification attempts

<table>
<thead>
<tr>
<th>Result</th>
<th>No. of isolates (%) with result after:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Single deposit</td>
</tr>
<tr>
<td>Good ID</td>
<td>663 (94.3)a</td>
</tr>
<tr>
<td>LD</td>
<td>17 (2.4)</td>
</tr>
<tr>
<td>No ID</td>
<td>13 (1.9)</td>
</tr>
<tr>
<td>Warning messages</td>
<td>10 (1.4)</td>
</tr>
</tbody>
</table>

- a Including 17 of 22 (77%) mucoid pneumococcal isolates.
- b Corresponding to or including 5 of 22 (23%) mucoid pneumococcal isolates.
- c Corresponding to an LD result between *Gemella morbilorum* and *Gemella haemolytica*.
- d ND, not done (after two deposits with a no-ID result, the isolates were considered outside the scope of the database).

June 2013 Volume 51 Number 6 jcm.asm.org
### TABLE 2 Relevant phenotypic and genotypic test results for the 703 strains studied

<table>
<thead>
<tr>
<th>Reference ID (no. of isolates)(^a)</th>
<th>Vitek MS ID</th>
<th>Optochin CO(^2)</th>
<th>BS test(^c)</th>
<th>Pneumococcal capsule identification</th>
<th>PCR result</th>
<th>No. of isolates with sequencing</th>
<th>No. of isolates (%) with Vitek MS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pneumococcal isolates (334)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. pneumoniae (292)</td>
<td>S. pneumoniae</td>
<td>S</td>
<td>ND</td>
<td>Yes</td>
<td></td>
<td></td>
<td>331 (99.1)</td>
</tr>
<tr>
<td>S. pneumoniae (37)</td>
<td>S. pneumoniae</td>
<td>R (R)</td>
<td>Not soluble</td>
<td>No or ND(^d)</td>
<td></td>
<td></td>
<td>37</td>
</tr>
<tr>
<td>S. pneumoniae (1)</td>
<td>S. pneumoniae</td>
<td>R (R)</td>
<td>Soluble</td>
<td>3</td>
<td>+ + + +</td>
<td></td>
<td>11</td>
</tr>
<tr>
<td>S. pneumoniae (1)</td>
<td>S. mitis/S. oralis</td>
<td>S (S)</td>
<td>Not soluble</td>
<td>2.3F</td>
<td></td>
<td></td>
<td>11</td>
</tr>
<tr>
<td>S. pneumoniae (1)</td>
<td>S. mitis/S. oralis</td>
<td>S (S)</td>
<td>Not soluble</td>
<td>37</td>
<td></td>
<td></td>
<td>11</td>
</tr>
<tr>
<td>S. pneumoniae (1)</td>
<td>S. mitis/S. oralis</td>
<td>S (S)</td>
<td>Not soluble</td>
<td>ND</td>
<td></td>
<td></td>
<td>11</td>
</tr>
<tr>
<td>Non-pneumococcal isolates (369)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Other mitis group streptococci (166)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. pseudopneumoniae (1)</td>
<td>S. pseudopneumoniae</td>
<td>R (S)</td>
<td>Not soluble</td>
<td>No</td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. pseudopneumoniae (1)</td>
<td>S. pseudopneumoniae</td>
<td>R (S)</td>
<td>Not soluble</td>
<td>ND</td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. pseudopneumoniae (1)</td>
<td>S. pseudopneumoniae</td>
<td>R (S)</td>
<td>Not soluble</td>
<td>ND</td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. mitis/S. oralis (126)(^e)</td>
<td>S. mitis/S. oralis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>126</td>
</tr>
<tr>
<td>S. gordonii (7)</td>
<td>S. gordonii</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>7</td>
</tr>
<tr>
<td>S. cristatus (1)</td>
<td>S. cristatus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. sanguinis (7)</td>
<td>S. sanguinis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>7</td>
</tr>
<tr>
<td>S. parasanguinis (11)</td>
<td>S. parasanguinis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>11</td>
</tr>
<tr>
<td>S. australis (3)</td>
<td>S. australis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>3</td>
</tr>
<tr>
<td>S. australis (2)</td>
<td>S. australis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>S. massilicense (1)</td>
<td>No ID</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. oralis/S. parasanguinis (1)</td>
<td>S. parasanguinis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. mitis group (4)</td>
<td>2 S. mitis/ oralis, 3 S. parasanguinis, 1 no ID</td>
<td>R</td>
<td>Not soluble</td>
<td>4</td>
<td></td>
<td></td>
<td>4</td>
</tr>
<tr>
<td>Non-mitis group streptococci (184)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. salivarius group (39)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. salivarius subspp. salivarius (35)</td>
<td>S. salivarius</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>35</td>
</tr>
<tr>
<td>S. vestibularis (4)</td>
<td>S. vestibularis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4</td>
</tr>
<tr>
<td>S. mutans group (2)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. mutans (2)</td>
<td>S. mutans</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2 (100)</td>
</tr>
<tr>
<td>S. anginosus group (111)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. constellatus (57)</td>
<td>S. constellatus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>101 (91)</td>
</tr>
<tr>
<td>S. anginosus (49)</td>
<td>S. anginosus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>37</td>
</tr>
<tr>
<td>S. constellatus/S. anginosus (5)</td>
<td>S. constellatus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>5</td>
</tr>
<tr>
<td>S. anginosus (4)</td>
<td>S. anginosus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4</td>
</tr>
<tr>
<td>S. intermedius (16)</td>
<td>S. intermedius</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. bovis group (32)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>S. gallolyticus subspp. gallolyticus (4)</td>
<td>S. gallolyticus subspp. gallolyticus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>24 (75)</td>
</tr>
<tr>
<td>S. gallolyticus subspp. pasteurianus (18)</td>
<td>S. gallolyticus subspp. pasteurianus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>18</td>
</tr>
<tr>
<td>S. gallolyticus subspp. pasteurianus (2)</td>
<td>S. gallolyticus subspp. pasteurianus</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2</td>
</tr>
<tr>
<td>S. bovis (1)</td>
<td>S. bovis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. lactis/S. bovis/S. equinus (1)</td>
<td>S. bovis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>S. lactis/S. bovis/S. equinus (4)</td>
<td>S. lactis</td>
<td>R</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>4</td>
</tr>
</tbody>
</table>

\(^a\) Reference ID (no. of isolates) refers to the number of isolates of the specific strain.

\(^b\) Vitek MS ID refers to the identification of the isolate using the Vitek MS system.

\(^c\) Optochin CO\(^2\) and BS test refer to specific phenotype tests for the identification of the isolate.

\(^d\) No or ND\(^d\) refers to the result of the phenotype test, indicating no reaction or not determined.

\(^e\) S. mitis/S. oralis refers to the identification of the isolate as S. mitis or S. oralis.

\(^f\) S. mitis/S. oralis refers to the identification of the isolate as S. mitis or S. oralis.

\(^g\) S. salivarius subspp. salivarius refers to the subspecies identification of S. salivarius.

\(^h\) S. vestibularis refers to the identification of the isolate as S. vestibularis.

\(^i\) S. mutans refers to the identification of the isolate as S. mutans.

\(^j\) S. constellatus refers to the identification of the isolate as S. constellatus.

\(^k\) S. anginosus refers to the identification of the isolate as S. anginosus.

\(^l\) S. intermedius refers to the identification of the isolate as S. intermedius.

\(^m\) S. bovis refers to the identification of the isolate as S. bovis.

\(^n\) S. lactis refers to the identification of the isolate as S. lactis.

\(^o\) S. vestibularis refers to the identification of the isolate as S. vestibularis.

\(^p\) S. mutans refers to the identification of the isolate as S. mutans.

\(^q\) S. constellatus refers to the identification of the isolate as S. constellatus.

\(^r\) S. anginosus refers to the identification of the isolate as S. anginosus.

\(^s\) S. intermedius refers to the identification of the isolate as S. intermedius.

\(^t\) S. bovis refers to the identification of the isolate as S. bovis.

\(^u\) S. lactis refers to the identification of the isolate as S. lactis.

\(^v\) S. vestibularis refers to the identification of the isolate as S. vestibularis.

\(^w\) S. mutans refers to the identification of the isolate as S. mutans.

\(^x\) S. constellatus refers to the identification of the isolate as S. constellatus.

\(^y\) S. anginosus refers to the identification of the isolate as S. anginosus.

\(^z\) S. intermedius refers to the identification of the isolate as S. intermedius.

\(^{1}\) S. bovis refers to the identification of the isolate as S. bovis.

\(^{2}\) S. lactis refers to the identification of the isolate as S. lactis.

\(^{3}\) S. vestibularis refers to the identification of the isolate as S. vestibularis.

\(^{4}\) S. mutans refers to the identification of the isolate as S. mutans.
In conclusion, according to our study, the Vitek MS displays performances similar to that of the optochin susceptibility test for routine ID of pneumococcal isolates. Provided that the species are included in the database, this system is an efficient method for the ID of nonpneumococcal viridans streptococci to the group level and in most cases to the species level.

ACKNOWLEDGMENTS

We thank the outstanding clinical bacteriology laboratory technologists at the Centre Hospitalier Universitaire de Toulouse, France, for their help in collecting and analyzing isolates of this study. We also thank the biologists from the Observatoire Régional du Pneumocoque Midi-Pyrénées 2009 for providing most of the Streptococcus pneumoniae isolates and the Centre National de Référence des Pneumocoques, headed by Emmanuelle Varon, Hôpital Européen Georges Pompidou, AP-HP, Paris, for serotyping of most pneumococcal isolates.

REFERENCES


Dubois et al.


