

Short Communication

Evaluation of phenotypic methods for methicillin resistance characterization in coagulase-negative staphylococci (CNS)

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Coagulase-negative staphylococci (CNS) are the major cause of nosocomial infections. Methicillin-resistant strains are particularly important because they narrow therapeutic options. Detecting methicillin resistance among CNS has been a challenge for years. The objective of this study was to determine the accuracy of an agar screening test (0.6 and 4 µg oxacillin ml⁻¹), disc diffusion and the automated MicroScan system to characterize methicillin resistance among CNS. One hundred and seventy five strains were analysed: 41.1 % *Staphylococcus epidermidis* and 59.9 % other species; 69.1 % were *mecA*-positive. The results showed that the methods have optimal correlation with the detection of *mecA* gene for *S. epidermidis*, *Staphylococcus hominis* and *Staphylococcus haemolyticus*. However, accuracy of the tests is impaired when less common species are analysed. The only 100 % accurate test was agar screening with 4 µg oxacillin ml⁻¹.

Introduction

Coagulase-negative staphylococci (CNS) have been the major cause of nosocomial infections (Marshall *et al.*, 1998; Yamazumi *et al.*, 2001). Methicillin resistance among CNS is particularly important due to cross-resistance to virtually all β -lactam agents and other antimicrobial classes. As a result, therapeutic approaches are restricted to glycopeptide and new antimicrobial agents as linezolid (Woods *et al.*, 2002). Therefore, an accurate analysis of methicillin resistance may allow the provision of better antimicrobial therapy and avoid the selection of vancomycin-resistant strains.

The rates of methicillin resistance have increased in the last two decades, according to the National Nosocomial Infectious Surveillance System (NNIS, 2001). In Brazil, a multi-centre study showed that 87.7 % of CNS isolated from blood cultures were resistant to methicillin (Sader *et al.*, 1999). The most common mechanism of methicillin resistance is the production of a penicillin-binding protein (PBP) with low affinity for β -lactams, PBP2a. PBP2a is coded by the *mecA* gene and can be detected by PCR, which is considered the gold-standard test to identify methicillin resistance (Chambers, 1997; Swenson *et al.*, 2001).

The detection of methicillin resistance among CNS isolates has been a challenge for years (Gradelski *et al.*, 2001) because these micro-organisms present an hetero-resistant pattern (Chambers, 1997). Although recent breakpoints (NCCLS, 1999) have shown an acceptable correlation with the presence or absence of the *mecA* gene in *Staphylococcus epidermidis*, *Staphylococcus hominis* and *Staphylococcus haemolyticus* isolates, species with borderline MICs (Hussain *et al.*, 2000; Gradelski *et al.*, 2001; Ferreira *et al.*, 2003) and less common species impair test accuracy. Thus, the aim of this study was to verify the accuracy of the agar screening test (0.6 and 4 mg oxacillin ml⁻¹), disc diffusion and the automated MicroScan system in the detection of methicillin resistance among CNS isolates.

Methods

This study included 175 consecutive CNS strains collected from hospitalized patients in southern Brazil. The samples were identified through MicroScan, panel Positive Combo 13 (Dade Behring). Methicillin resistance was characterized through an agar screening test, disc diffusion (NCCLS, 2003) and automated MicroScan system. For the agar screening test, strains were plated on tryptic soy agar with 5 % sheep blood and a 0.5 McFarland standard suspension was prepared for each sample. Mueller–Hinton agar plates (Oxoid) supplemented with 4 % (w/v) NaCl were used and two oxacillin concentrations were tested: 0.6 µg ml⁻¹ (Kohner *et al.*, 1999) and 4 µg ml⁻¹ (Ferreira *et al.*, 2003).

Abbreviations: CNS, coagulase-negative staphylococci; PBP, penicillin-binding protein.

The plates were inoculated using Steer's replicator, incubated at 35 °C and screened after 24 and 48 h incubation. The growth of more than one colony on the plates indicated oxacillin-resistant strains.

Disc-diffusion test was performed according to NCCLS (2003) guidelines. Methicillin susceptibility testing with MicroScan was performed according to the manufacturers' instructions. The NCCLS (2003) breakpoints and MICs for methicillin susceptibility were used to analyse resistance through disc diffusion and MicroScan.

The results were compared to PCR for the detection of the *mecA* gene (Santos *et al.*, 1999). *Staphylococcus aureus* ATCC 33591 (methicillin-resistant) and *S. aureus* ATCC 25923 (methicillin-susceptible) were included as control organisms.

Results and Discussion

Table 1 shows the CNS species distribution and the methicillin susceptibility profile, considering the presence or absence of *mecA* gene. According to MicroScan identification 72 (41.1%) were *S. epidermidis*, 36 (20.6%) *S. hominis* subspecies *hominis*, 6 (3.4%) *S. hominis* subspecies *novobioceticus*, 41 (23.4%) *S. haemolyticus*, 5 (2.9%) *Staphylococcus warneri*, 5 (2.9%) *Staphylococcus simulans*, 3 (1.7%) *Staphylococcus capitis* subspecies *urealyticus*, 2 (1.1%) *Staphylococcus auricularis*, 2 (1.1%) *Staphylococcus saprophyticus*, 1 (0.6%) *Staphylococcus sciuri*, 1 (0.6%) *Staphylococcus cohnii* subspecies *cohnii* and 1 micro-organism not identified by MicroScan. The presence of the *mecA* gene was detected in 69.1% of strains (121/175).

The results of phenotypic methods are shown in Table 2. The disc-diffusion test showed that 112 out of 121 strains were *mecA*-positive (92.5% sensitive). On the other hand, 49 out of 54 *mecA*-negative strains were susceptible to methicillin (90.7% specific) by disc-diffusion test.

The agar screening test containing 0.6 µg oxacillin ml⁻¹ showed that 119 out of 121 *mecA*-positive strains were resistant (98.3% sensitive). Only one *S. saprophyticus* *mecA*-negative strain was methicillin-resistant (98.1% specific). The agar screening test containing 4 µg oxacillin ml⁻¹ was totally accurate.

MicroScan characterized 120 out of 121 strains as methicillin-resistant. The system classified 46 out of 54 *mecA*-negative strains as susceptible (85.1% specific). All strains but one *S. epidermidis*, described as false-positive, presented borderline MICs (Table 3).

As a result of the difficulty of characterizing methicillin resistance among CNS, phenotypic methods have been constantly studied. Except for the agar screening test containing 4 µg oxacillin ml⁻¹, all the other methods misclassified resistant and susceptible strains. The false-negative results may have occurred due to an extremely heterogeneous expression of resistance (Gerberding *et al.*, 1991; Chambers, 1997).

On the other hand, the false-positive results may have been the result of overproduction of penicillinase, or super-expression/alterations of constitutive PBPs. It is known that penicillinase-resistant penicillins may show some degree of lysis when such enzymes are present. The super-expression and alterations of constitutive PBPs generate a higher concentration of free transpeptidase which will synthesize the bacteria's cell wall (Chambers, 1997).

Even though researchers have shown that an agar screening test containing 6 µg oxacillin ml⁻¹ is not efficient towards CNS (Tenover *et al.*, 1999), and it is no longer recommended for CNS (NCCLS, 1999), comparative studies to assess the

Table 1. Identification of CNS isolates and the methicillin susceptibility profile based on the presence or absence of *mecA* gene

Species	% (no./total)	<i>mecA</i>	
		Positive (%)	Negative (%)
<i>S. epidermidis</i>	41.1 (72/175)	51 (70.8)	21 (29.2)
<i>S. hominis</i> subsp. <i>hominis</i>	20.6 (36/175)	18 (50.0)	18 (50.0)
<i>S. hominis</i> subsp. <i>nov.</i>	3.4 (6/175)	6 (100)	–
<i>S. haemolyticus</i>	23.4 (41/175)	37 (90.2)	4 (9.8)
<i>S. warneri</i>	2.9 (5/175)	1 (20.0)	4 (80.0)
<i>S. simulans</i>	2.9 (5/175)	3 (60.0)	2 (40.0)
<i>S. capitis</i> subsp. <i>urealyticus</i>	1.7 (3/175)	1 (33.3)	2 (66.6)
<i>S. auricularis</i>	1.1 (2/175)	2 (100)	–
<i>S. saprophyticus</i>	1.1 (2/175)	–	2 (100)
<i>S. sciuri</i>	0.6 (1/175)	1 (33.3)	–
<i>S. cohnii</i> subsp. <i>cohnii</i>	0.6 (1/175)	–	1 (100)
Unidentified organism	0.6 (1/175)	1 (100)	–
Total	100 (175/175)	121 (69.1)	54 (30.9)

Table 3. Results of MICs obtained by the automated MicroScan system for false-positive strains compared to PCR for the *mecA* gene

Strain no.	Species	MIC ($\mu\text{g ml}^{-1}$)	Disc diffusion	Agar screening 0.6 $\mu\text{g ml}^{-1}$
101	<i>S. epidermidis</i>	>2	–	–
180	<i>S. cohnii</i> subsp. <i>cohnii</i>	0.5	False-positive	–
172	<i>S. haemolyticus</i>	1	False-positive	–
87	<i>S. saprophyticus</i>	0.5	False-positive	False-positive
74	<i>S. saprophyticus</i>	0.5	–	–
195	<i>S. warneri</i>	0.5	False-positive	–
198	<i>S. warneri</i>	0.5	False-positive	–
93	<i>S. hominis</i> subsp. <i>hominis</i>	1	–	–

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