Methicillin-Resistant *Staphylococcus pseudintermedius* Infection in a Bone Marrow Transplant Recipient

Vincenzo Savini, a Daniela Barbarini, b Klaudia Polakowska, c Giovanni Gherardi, d Anna Bialecka, e Andzej Kasprowicz, e Ennio Pollilli, e Roberta Marrollo, a Giovanni Di Bonaventura, f Paolo Fazii, f Domenico D’Antonio, f Jacek Miedzobrodzki, f Edoardo Carretto f

Spirito Santo Hospital, Pescara, Italy; Fondazione IRCCS Policlinico San Matteo, Pavia, Italy; Jagiellonian University, Kraków, Poland; Campus Biomedico University of Rome, Rome, Italy; Center for Microbiological Research and Avitavaccines, Kraków, Poland; G. d’Annunzio University of Chieti-Pescara, Chieti, Italy; IRCCS Arcispedale Santa Maria Nuova, Reggio Emilia, Italy

*Staphylococcus pseudintermedius* is a veterinary pathogen that has seldom been described as an agent of human disease. Features of this probably underreported coagulate-positive *Staphylococcus* species are depicted here through the description of a graft-versus-host disease-related wound infection caused by a multidrug-resistant strain.

**CASE REPORT**

A 65-year-old male patient who had received (3 years previously) an allogeneic bone marrow transplant (BMT) for chronic lymphoblastic leukemia was admitted to the Pescara Civic Hospital (Italy) because of a wound infection, located in the periumbilical region and showing two different purulent discharges. The lesion was due to chronic graft-versus-host disease (GvHD) that complicated the BMT. The patient affirmed that he lived in proximity to a pet dog and farm cows.

Pus staining revealed Gram-positive cocci within leukocytes, while cultures yielded a massive growth of mannitol-nonfermenting coagulase-positive staphylococci (CPS). Based on colony aspect (brightness of the white-gray color), two different isolates (named S32 and S33) were recognized, sharing a double-zone hemolysis on the sheep blood agar plate (Fig. 1). They were identified as *Staphylococcus intermedius* by both the Vitek2 and the API system (bioMérieux, Marcy l’Etoile, France). However, *S. intermedius* is the only species belonging to the so-called *Staphylococcus intermedius* group included in these systems’ databases. The *S. intermedius* group includes *S. intermedius*, cultured from a wide variety of animals, *Staphylococcus pseudintermedius*, which recent studies indicate is the prevalent *S. intermedius* group species harbored by dogs and cats, and *Staphylococcus delphini*, first isolated from dolphins but later collected from several terrestrial animals (1, 2). Thus, we did not consider this identification as conclusive. Moreover, since the absence of mannitol fermentation, along with the double-zone hemolysis, was highly suggestive for *S. pseudintermedius* rather than *S. intermedius*. Among genotypic assays, 16S rRNA sequencing did not provide a definitive discrimination among *S. intermedius*, *S. pseudintermedius*, and *S. delphini*. The isolates were then analyzed through automated ribotyping (RiboPrinter; Qualicon DuPont, USA). The instrument provided identical fingerprints for all of the strains and identified them as *S. intermedius*. A specific multiplex PCR was performed, as previously described (3). The isolates were identified as *S. pseudintermedius*, since a clear band was obtained at 926 bp (Fig. 2). This finding was finally confirmed by analyzing the *tuf* (4) and *rpoB* (5) genes, the latter allowing better discrimination than the *tuf* analysis alone. The isolates showed a high degree of similarity with the fully sequenced genome of *Staphylococcus pseudintermedius* ED99 (GenBank accession number CP002478.1); the *rpoB* sequence we obtained was submitted to GenBank.

The antimicrobial susceptibility profiles, obtained through the Vitek2 system, were then confirmed using both a disc diffusion method and MIC test strips (Liofilchem, Roseto degli Abruzzi, Italy). According to the EUCAST (version 2.0) interpretative breakpoints for *Staphylococcus aureus*, all of the isolates were resistant to benzylpenicillin, oxacillin, fluoroquinolones, macrolides, clindamycin, and cotrimoxazole and susceptible to tetracycline, chloramphenicol, rifampin, tigecycline, daptomycin, glycopeptides, and linezolid. Again, S32 and S33 showed gentamicin susceptibility, whereas all the other isolates displayed resistance to the aminoglycoside.

As cefoxitin sensitivity was observed in spite of the oxacillin resistance, the mecA gene was searched with an in-house method using the mecA primers and the conditions described in the paper of Oliveira and de Lencastre (6). We confirmed the results using the Gene X-pert system (Cepheid, Sunnyvale, CA, USA). Both techniques showed that the genetic element was harbored by all isolates.

To evaluate the genome relatedness between wound strains and those from nose and skin, random amplification of polymorphic DNA (RAPD) was performed, using a previously described protocol (7). Four different arbitrary primers were used, along with a specific multiplex PCR, and the results were submitted to GenBank (accession number KF896023).

**Address correspondence to Vincenzo Savini, vincenzo_savini@libero.it.**

V.S. and E.C. contributed equally to this article.

Copyright © 2013, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JCM.03310-12

---

Received 16 December 2012 Returned for modification 14 January 2013 Accepted 6 March 2013

Published ahead of print 13 March 2013

Copyright © 2013, American Society for Microbiology. All Rights Reserved.
with a control strain of veterinary origin. All the strains gave the same fingerprint with the different primers. Although it was clear then that we had a single \textit{S. pseudintermedius} clone (confirmed by RAPD analysis and ribotyping), both isolate S32 and isolate S33 were deposited to the DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen, GmbH) collection, Germany, under accession numbers DSM 25713 and DSM 25714, respectively.

A 10-day course of topical gentamicin (twice a day) led to sterilization of the ulcer; afterward, complete lesion healing was obtained by employing platelet-rich plasma gel (3 applications at 5-day intervals).

(A preliminary version of this clinical case was presented at the Gram Award [9 to 10 February 2012, Rome, Italy], a scientific event promoted by Novartis Farma S.p.A. The presentation was sponsored by Novartis Farma S.p.A. on behalf of IntraMed Communications S.r.L.)

The CPS of medical interest are mainly represented by \textit{S. aureus}, which is highly prevalent in humans although increasingly isolated from different animals species (most of all, pets), and by the microorganisms belonging to the \textit{S. intermedius} group.

Recently, CPS other than \textit{S. aureus} have gained importance in veterinary medicine, as molecular techniques have allowed a better understanding of them, leading to a deep revision of their taxonomy and pathogenicity. In particular, the spread of multidrug-resistant (MDR) strains, mostly within the \textit{S. pseudintermedius} species, has been reported more and more frequently, and the role of the mutual transmission of bacteria and/or virulence determinants between animals and their owners has been emphasized (2, 8, 9). In animals, \textit{S. intermedius} group organisms are frequently isolated as colonizers, although they may cause diseases. In humans, it is not known whether \textit{S. delphini} shows a zoonotic potential; conversely, \textit{S. intermedius} has been related to bacteremia, pneumonia, brain abscesses, and wound infections (mostly of canine-inflicted wounds). \textit{S. pseudintermedius} has been recognized on a few occasions as a pathogen (a case of rhinosinusitis, a catheter-related bacteremia, and an implantable cardioverter-defibrillator infection were previously published) (10–12).

To our knowledge, we are reporting the second methicillin-resistant \textit{S. pseudintermedius} (MRSP) infection in a human host (10), although it is clear from the published literature that current knowledge of the \textit{S. intermedius} group is fragmentary, requiring further revisions. In particular, it may be hypothesized that a large number of strains previously identified as \textit{S. intermedius} may be \textit{S. pseudintermedius}, and a wide majority of reported \textit{S. intermedius} human infections might actually be due to \textit{S. pseudintermedius} (1, 2).

Based on current knowledge, however, this case expands the spectrum of \textit{S. pseudintermedius} diseases to wound infections and emphasizes the risk of zoonoses in compromised subjects; in particular, the underlying GvHD-related immunosuppression and skin damage reasonably played a pivotal role in the development of the disease.

From a laboratory point of view, clinical microbiologists should not hastily label and dismiss mannitol-nonfermenting microorganisms as coagulase-negative staphylococci but carefully perform a coagulase test if the hemolysis on blood agar plates is suggestive for an \textit{S. intermedius} group organism. Typically, a complete inner band (β-hemolysis) is observed, while the outer one is incomplete (α-hemolysis), although it becomes complete at 4°C (hot-cold hemolysis). Among the mannitol-nonfermenting staphylococci, this double zone has been known to be pathognomonic of \textit{S. intermedius} and \textit{S. pseudintermedius} (Fig. 1) (13).

Although some phenotypic features have been employed in the past decades to discriminate within the \textit{S. intermedius} group, these do not actually appear to be conclusive (2, 14). Also, in the context of the newest approaches to microbial identification, matrix-assisted laser desorption ionization–time of flight mass spectrometry...
try (MALDI-TOF MS) libraries have recently been shown not to be adequate, as yet, to reliably characterize S. intermedius group strains (15). Therefore, molecular methodologies are mandatory to provide a correct species identification.

Similarly, we did not obtain a conclusive characterization either by 16S rRNA sequencing or through the automated ribotyping; it is known in fact that the first method cannot always distinguish among such closely related species (those belonging to the S. intermedius group), while S. pseudointermedius profiles are not included in the riboPrinter reference databases. Ribotyping data for these organisms should be obtained, along with MALDI-TOF MS data.

Like other authors (15), we finally achieved a good identification through the multiplex PCR proposed by Sasaki et al. (3) and the rpoB gene analysis (5).

Concerning the antibiotic susceptibility testing, it has to be emphasized that the isolates were susceptible to cefoxitin but resistant to oxacillin; this result can be misleading, as cefoxitin screening is widely used in clinical laboratories as a marker for methicillin resistance in S. aureus. The mecA gene was detected through molecular methods, and this finding was not surprising, since the spread of MRSP has been previously and widely reported, although in the veterinary context (2, 8). In our opinion, it is critical that methicillin/oxacillin resistance in CPS (other than S. aureus) should as a routine practice be screened through different methods, including molecular tools, pending specific criteria for in vitro testing and interpretation of the activities of drugs against S. intermedius group members.

It is likely that human and veterinary S. pseudintermedius isolates have been misidentified as S. aureus, S. intermedius, and S. delphini in the past (1, 2). Nevertheless, when a patients’ history includes contact with pets (mostly dogs or cats), the potential role of S. pseudintermedius (rather than S. intermedius) as the agent of zoonoses has to be taken into account, and a correct identification may be performed only by using molecular techniques.

The real prevalence and incidence of S. pseudintermedius (as a colonizer or pathogen) in the human population is surely underestimated, and more accurate phenotype- and genome-based investigations are warranted to further highlight the behavior of this organism as an emerging human pathogen in the future.

**Nucleotide sequence accession number.** The rpoB sequence of strain S32 was deposited in GenBank and assigned accession number KC680229.

**ACKNOWLEDGMENTS**

The project was partially supported by grant no. N N401 017740 from the Polish Ministry of Science and Education (to J.M.) and by a grant from the Scientific Committee of the IRCCS Arcispedale Santa Maria Nuova, Reggio Emilia (to E.C.).

We thank Cecilia Passeri and Ornella Iuliani (Department of Transfusion Center, Spirito Santo Hospital, Pescara, Italy) and Giorgia Mancini (Department of Hematology, Ospedali Riuniti of Ancona, Ancona, Italy) for providing us with details about the patient’s history and follow-up and for their interest in this case.

**REFERENCES**