Infection (2019) 47:853–856
https://doi.org/10.1007/s15010-019-01276-8

CASE REPORT

A case of a surgical-site infection with *Staphylococcus condimenti*

Mercedeh Tajdar[1] · **Marijke Reynders**[1] · **Jens Van Praet**[2] · **Maria Ángeles Argudín**[3] · **Stefaan J. Vandecasteele**[2] · **Eric Nulens**[1]

Received: 27 November 2018 / Accepted: 31 January 2019 / Published online: 5 April 2019

Abstract

Introduction Coagulase-negative staphylococci (CNS) are considered to have a medium or low pathogenic capacity when compared to *S. aureus*. Among the more harmless, CNS are those that are used in the food industry, represented by *S. carnosus*, whose genome has extensively been studied. Its genome was found to contain several genomic sequences that have a virulent function in the pathogenic *S. aureus*. Even though these genes are probably not virulent in *S. carnosus*, their presence might indicate a more virulent potential. We report the third clinical case associated with a surgical-site infection with *S. condimenti*, which belongs to these food industry related CNS. It corresponds to a blood stream infection, secondary to a surgical-site infection.

Results Antibiotic susceptibility testing indicated a resistance to erythromycin and rifampicin, which was partly confirmed by the presence of a macrolide resistance gene by PCR screening for *S. aureus* virulence factors. Although no other putative virulence factors were detected, this organism managed to cause a severe post-operative wound infection.

Conclusion This case shows that CNS that are currently used in the food industry may play a role in human infection. With technologies such as MALDI–TOF, pathogens that are regarded non-pathogenic could be identified more often. Therefore, the risk of different *Staphylococcus* strains used in the food industry must be better assessed.

Keywords Surgical-site infection · Coagulase-negative staphylococci · Non-pathogenic · Virulence · *S. condimenti*

Introduction

Staphylococci are a heterogeneous group of pathogens that can cause low grade and—especially in the case of *Staphylococcus aureus*—severe life-threatening infections. In a recent publication, *Staphylococcus* species were classified according to their pathogenic capacity [1, 2]. *Staphylococcus aureus* is accepted as the only highly pathogenic species followed by medium and low pathogenic coagulase-negative staphylococci (CNS). Infections by CNS are mostly caused by *S. epidermidis, S. hominis*, and *S. haemolyticus*. However, some species are also considered responsible for *S. aureus*-like infections such as *S. lugdunensis*. Furthermore, a small group within the CNS consists of species that currently are not associated with infections, but find their application in the food industry in the production of fermented products such as meat, soy, and milk [1].

This last group is represented by *S. carnosus*. In an extensive genome study, this species was found to contain many sequences already known as virulence factors in *S. aureus*. These sequences may have a bivalent nature, and are assumed to have a non-virulent function in *S. carnosus*, or were deactivated by truncation of regulatory genes. Furthermore, these functions are thought to be lost by adaptation to an unchallenging nutrition-rich habitat [2, 3].

Recent technology developments and the increasing availability of bacterial identification systems allow for a more specific microorganism detection, due to a better discriminatory power of these techniques. These include matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI–TOF), 16S rRNA gene amplification, and

---

✉ Mercedeh Tajdar
mercedeh.tajdar@azsintjan.be

[1] Department of Laboratory Medicine, AZ Sint-Jan Brugge AV, Ruddershove 10, 8000 Bruges, Belgium

[2] Department of Nephrology and Infectious Diseases, AZ Sint-Jan Brugge AV, Ruddershove 10, 8000 Bruges, Belgium

[3] National Reference Centre, Staphylococcus aureus, Department of Microbiology, Hôpital Erasme, Université Libre de Bruxelles, Route de Lennik 808, 1070 Brussels, Belgium

whole genome sequencing [4]. One of such newly identified pathogens is *Staphylococcus condimenti* [5], which was initially classified as a subgroup of *S. carnosus*, and is now considered a separate species [6]. *Staphylococcus condimenti* was originally isolated from soy sauce mash and detected in a meat starter culture "condiment" [6, 7]. There are only a few clinical publications of *S. condimenti* infections, most notably a soft tissue and a catheter-related infection [5, 8]. Interestingly, Gabrielsen et al. showed that *S. condimenti* contained a number of putative virulence factors such as adhesins and leucocidin-like toxins, which could have contributed to the severity of the disease. However, they did not investigate to what extent these factors were actually expressed [8]. Nevertheless, in these cases, *S. condimenti* remained susceptible to antimicrobials [5, 8]. These recent clinical publications underline our lack of knowledge on the virulence potential of this species.

Case description

In this manuscript, we report the third clinical case associated with an *S. condimenti* infection. It corresponds to a blood stream infection, secondary to a surgical-site infection in a male patient of 49 years. The patient underwent a surgical procedure at the General hospital AZ Sint-Jan Brugge (Bruges, Belgium) for a lumbar discus hernia at L5–S1 level with osteosynthesis of the vertebrae. Seven days after surgery, the patient developed severe headache, neck stiffness, fever, and serious pain radiating from the surgical site to the legs. Redness and swelling surrounding the wound indicated a post-operative wound infection. Spondylodiscitis was excluded by Magnetic Resonance Imaging (MRI). In the following days, three pairs (aerobe/anaerobe) of blood cultures were drawn (BD BACTEC™ FX, Becton, Dickinson & Company, Belgium, Erembodegem). Subsequently, deep and superficial tissues were taken during a surgical exploration. Empiric therapy with vancomycin (2.3 g/24 h) and high-dose ceftazidime (6 g/24 h) was initiated in continuous infusion. The next day, Gram stain of the blood cultures showed that from two pairs, the anaerobic bottles were positive with Gram-positive cocci, and growth on Columbia blood agar showed 2 mm cream-colored, non-haemolytic, clumping factor negative colonies (Pastorex, BIO-RAD, CA, USA). The isolates were identified as *S. condimenti* by MALDI–TOF MS with an average log score of 1.91 (Bruker Daltonics, Bremen, Germany). A pure culture of the same organism was also isolated from the superficial and deeper tissue samples. The strain was confirmed by the National Reference Center for Staphylococci in Brussels (Belgium) as *S. condimenti* by rpoB typing and 16S sequencing as described elsewhere [9, 10]. Antibiotic susceptibility testing was performed with Phoenix (Becton & Dickinson, Erembodegem, Belgium) according to the manufacturer's guidelines using EUCAST breakpoints. The isolate was susceptible to oxacillin and all other tested antibiotics in the panel except for erythromycin and rifampicin. It initially showed intermediate susceptibility to rifampicin, but was later confirmed as resistant by the National Reference Center with the broth dilution method according to EUCAST [11]. The strain was screened by PCR for the presence of typical *S. aureus* virulence factors, as well as for the presence of antimicrobial resistance genes as previously described [9, 12, 13]. The full-screening results are displayed in Table 1. The *S. condimenti* strain was negative for all the genes tested, except for the macrolide resistance gene *msr*(A).

Thereafter, the therapy was switched to high-dose (2 g × 6/24 h) intravenous flucloxacillin for 14 days, and continued with oral moxifloxacin (400 mg o.d.) and rifampicin (600 mg o.d.) at discharge, because the foreign material was retained. However, 3 days later the patient again developed pain, swelling, and induration at the incision site. An MRI identified a 2×2.5 cm collection around the processus spinosus of L3 and S1. This was not judged to be an abscess, but an infection could not be fully excluded. After readmission for another 11 days on intravenous flucloxacillin therapy, the patient was discharged for the second time. Oral therapy with cotrimoxazole (960 mg bid) was continued, since by that time, the pathogen was confirmed as rifampicin resistant. A fever that developed in the next 2 weeks was attributed to an allergic reaction to cotrimoxazole, and therapy was switched once more, this time to amoxicillin/clavulanic acid (875/125 mg t.i.d.). Clinical and biochemical evolution was favorable, and the therapy could be stopped after 2 months. Nine months after the initial surgery, the patient had fully recovered. Regarding the background of the patient, no other risk factors were identified, except for alcohol abuse (weekly consumption of at least 20 alcohol units). No further investigation was performed on the source of the *S. condimenti* infection. Samples from likely sources, such as skin or gut, were not available, and little was known on external conditions such as special dietary habits, except that the spouse of the patient worked in a butcher shop.

Discussion

There are several reasons that make this case stand out above the routine post-operative infections that deal with implanted foreign bodies. First of all, surgical-site infections in the presence of foreign material, especially by staphylococci, are a known entity [1]. *Staphylococcus condimenti*, however, is considered to belong to the group of non-pathogenic CNS, and in addition, no obvious virulence factors were found that could explain its apparent pathogenicity. In a more extensive investigation by Gabrielsen et al., using genome sequencing,

Table 1 Full-screening results on this *S. condimenti* strain, for common virulence factors by the Belgian National Reference Laboratory

Detection of exotoxines	
PCR PVL	Neg
PCR TSST-1	Neg
PCR eta	Neg
PCR etb	Neg
PCR etd	Neg
Detection of enterotoxines	
PCR sea	Neg
PCR seb	Neg
PCR sec	Neg
PCR sed	Neg
PCR see	Neg
PCR seg	Neg
PCR she	Neg
PCR sei	Neg
PCR sej	Neg
PCR sek	Neg
PCR sel	Neg
PCR sem	Neg
PCR sen	Neg
PCR seo	Neg
PCR sep	Neg
PCR seq	Neg
PCR ser	Neg
PCR ses	Neg
PCR set	Neg
PCR seu	Neg
Resistance MLS	
PCR ermA	Neg
PCR ermB	Neg
PCR ermT	Pos
Methicillin resistance	
PCR mecA	Neg
PCR mecC	Neg
Immune evasion gene cluster	
PCR sak	Neg
Pcr chp	Neg
Pcr scn	Neg
Pathogenicity island	
PCR arcA	Neg

multiple putative virulence factors were identified for *S. condimenti*, in contrast to our investigation. As shown by Rosenstein, however, the mere presence of virulence genes does not necessarily mean the expression of a virulent function, which makes it even harder to indicate the origin of virulence in this clinical case [2, 7]. Second, infections by CNS are often challenging to treat because of the presence of methicillin resistance [1], which is absent in both our case and the earlier case reports on *S. condimenti* [5, 8]. However, resistance to two antibiotics was detected in the isolate. One of these resistance genes was found to originate with the msr(A) gene that is usually plasmid-related. As far as we know, this is the first report of an *S. condimenti* strain that shows resistance to antibiotics and may underline the capacity of this species to acquire resistance. A third remark is related to the development of the clinical picture. CNS are often associated with delayed or low-grade infections and may develop after weeks to months, which contrasts with this case. Such an early infection is commonly associated with highly virulent pathogens such as *S. aureus* [1, 14].

Based on these considerations and other factors that might facilitate an infection with *S. condimenti*, no obvious reasons can initially be given why this bacteria has the capacity to cause this early and manifest infection. Therefore, patient-related and procedure-related factors should also be taken into account, as they may affect the risk of a surgical-site infection [15, 16].

Although rare, CNS that are commonly associated with the food industry may play a role in human infection. However, these species are not regularly known to colonize skin and mucous membranes [1], but we hypothesize that microorganisms are transmitted from meat to persons working in specialized food industry. Apart from case reports for *S. condimenti*, clinical cases were described for *S. equorum, S. lentus, S. pasteuri*, and *S. xylosus* [1, 7]. It is noteworthy that no cases of infections with S. *carnosus* are known, despite its much more frequent use in the food industry.

Conclusion

We should keep in mind that the low prevalence of infections with less common CNS could be accounted for by the limited detection possibilities in the past. With the arrival of more advanced technologies such as MALDI–TOF, rare pathogens that were previously regarded as non-pathogenic will probably be identified more often as causal pathogens in clinically apparent cases. With this upcoming knowledge, the potential risk of the different *Staphylococcus* strains used in the food industry must be better assessed.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

References

1. Becker K, Heilmann C, Peters G. Coagulase-negative staphylococci. Clin Microbiol Rev. 2014;27:870–926.

2. Rosenstein R, Götz F. What distinguishes highly pathogenic staphylococci from medium- and non-pathogenic? Curr Top Microbiol Immunol. 2013;358:33–89.
3. Rosenstein R, Götz F. Genomic differences between the food-grade *Staphylococcus carnosus* and pathogenic staphylococcal species. Int J Med Microbiol. 2010;300:104–8.
4. Argemi X, Riegel P, Lavigne T, Lefebvre N, Grandpré N, et al. Implementation of matrix-assisted laser desorption ionization-time of flight mass spectrometry in routine clinical laboratories improves identification of coagulase-negative staphylococci and reveals the pathogenic role of *Staphylococcus lugdunensis*. J Clin Microbiol. 2015;53:2030–6.
5. Misawa Y, Yoshida A, Okugawa S, Moriya K. First reported case of *Staphylococcus condimenti* infection associated with catheter-related bacteraemia. New Microbes New Infect. 2015;3:18–20.
6. Probst AJ, Hertel C, Richter L, Wassill L, Ludwig W, et al. *Staphylococcus condimenti* sp nov, from soy sauce mash, and *Staphylococcus carnosus* (Schleifer and Fischer 1982) subsp *utilis* subsp nov. Int J Syst Bacteriol. 1998;48:651–8.
7. Zell C, Resch M, Rosenstein R, Albrecht T, Hertel C, et al. Characterization of toxin production of coagulase-negative staphylococci isolated from food and starter cultures. Int J Food Microbiol;127:246–51.
8. Gabrielsen C, Kols NI, Øye C, Bergh K, Afset JE. Characterization of the virulence potential of *Staphylococcus condimenti* isolated from a patient with severe soft tissue infection. New Microbes New Infect. 2017;18:8–14.
9. Argudín MA, Dodémont M, Vandendriessche S, Rottiers S, Tribes C, Roisin S, de Mendonça R, Nonhoff C, Deplano A, Denis O. Low occurrence of the new species *Staphylococcus argenteus* in a *Staphylococcus aureus* collection of human isolates from Belgium. Eur J Clin Microbiol Infect Dis. 2016;35:1017–22.
10. Lane DJ. 16S/23S rRNA sequencing. In: Stackebrandt E, Goodfellow M, editors. Nucleic acid techniques in bacterial systematics. New York: Wiley; 1991. pp. 115–76.
11. EUCAST. Breakpoint tables for interpretation of MICs and zone diameters. Version 7.1, 2017. http://www.eucast.org. Accessed 16 Mar 2017.
12. Deplano A, Vandendriessche S, Nonhoff C, Dodémont M, Roisin S, Denis O. National surveillance of *Staphylococcus epidermidis* recovered from bloodstream infections in Belgian hospitals. J Antimicrob Chemother. 2016;71:1815–9. https://doi.org/10.1093/jac/dkw086.
13. Vandendriessche S, Kadlec K, Schwarz S, Denis O. Methicillin-susceptible *Staphylococcus aureus* ST398-t571 harbouring the macrolide-lincosamide-streptogramin B resistance gene *erm*(T) in Belgian hospitals. J Antimicrob Chemother. 2011;66:2455–9. https://doi.org/10.1093/jac/dkr348.
14. Trampuz A, Zimmerli W. Prosthetic joint infections: update in diagnosis and treatment. Swiss Med Wkly. 30;135:243–51.
15. Ban KA, Minei JP, Laronga C, Harbrecht BG, Jensen EH, Fry DE, Itani KM, Dellinger EP, Ko CY, Duane TM. American College of Surgeons and Surgical Infection Society: surgical site infection guidelines, 2016 update. J Am Coll Surg. 2017;224:59–74.
16. Cooper RA. Surgical site infections: epidemiology and microbiological aspects in trauma and orthopaedic surgery. Int Wound J. 2013;10:3–8.