Characterization of the virulence potential of Staphylococcus condimenti isolated from a patient with severe soft tissue infection

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Abstract

The coagulase-negative bacterium Staphylococcus condimenti and closely related species are commonly isolated from or found in starter cultures of fermented sausage as well as fish and soy sauces, and have traditionally been considered nonpathogenic. Recently, however, a case of catheter-related bacteraemia caused by S. condimenti was reported. In the present study we identified and characterized a strain of S. condimenti isolated from a patient with a severe soft tissue infection, comparing it to S. condimenti and S. carnosus type strains in order to elucidate the virulence potential of the clinical strain. Genome comparison showed high degree of conservation between the clinical strain and the type strain used in food industry, as well as with S. carnosus. The genome of the clinical S. condimenti strain contains few horizontally transferred regions and 37 putative virulence genes, including genes with similarity to leucocidin and genes involved in immune evasion, proinflammatory and cytolytic activity. However, it remains to be tested whether these putative virulence genes are expressed and functional. Although uncommon, S. condimenti may cause severe infection in previously healthy persons.

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Keywords: Coagulate negative, genome, S. condimenti, soft tissue infection, staphylococci, virulence

Original Submission: 22 December 2016; Accepted: 21 March 2017
Article published online: 8 April 2017

Introduction

The genus Staphylococcus consists of more than 50 species, which have traditionally been grouped in coagulase-positive and coagulase-negative staphylococci (CoNS). The majority of CoNS are commonly found on human and animal skin and mucous membranes, and these have been regarded as nonpathogenic or less virulent compared to the coagulase-positive staphylococci, most notably S. aureus. However, some CoNS, especially S. epidermidis and S. haemolyticus, are major nosocomial pathogens frequently causing biofilm-associated infections related to prosthetic and other indwelling devices [1]. S. carnosus, S. piscifermentans and S. condimenti make up a phylogenetic subgroup of CoNS that are commonly isolated from or are used in starter cultures of fermented sausage as well as fish and soy sauces [2,3]. These species have until recently not been associated with human disease. The first reported case of a human infection caused by S. condimenti was catheter-related bacteraemia in a 17-year old female patient with severe dilated cardiomyopathy [4]. Given their role in food production, investigating the potential pathogenicity of these species is of importance.

In this study, we identified and characterized a strain of S. condimenti isolated from a patient with a severe soft tissue infection, comparing it to the S. condimenti type strain DSM 11674 and the related S. carnosus TM300 in order to elucidate the virulence potential of the clinical strain.
Case Presentation

While on holiday, a 7-year-old girl from a Central European country with no history of disease was admitted to St Olavs University Hospital in August 2014. The patient had a laceration after cutting her left knee on a fragment of glass in a plastic swimming pool the previous evening. Debridement of the wound and irrigation of the knee were performed, and the patient was discharged the following day without antibiotics.

At follow-up 4 days later, the patient presented with a temperature of 39°C, a painful knee and foul-smelling discharge from the wound. Blood samples showed C-reactive protein of 199 mg/L, erythrocyte sedimentation rate of 108 mm/h, and normal leukocyte count. The patient was readmitted, and revision surgery was performed promptly. A synovial fluid aspirate and deep biopsy samples from infected tissues were collected and submitted for microscopy and culture. After surgery, intravenous antibiotic treatment was initiated with dicloxacillin and gentamicin.

Synovial fluid and deep tissue samples from the left knee were cultured on aerobic and anaerobic media as well as media for the cultivation of mycobacteria. Microscopy of the samples showed presence of Gram-positive cocci. White catalase-positive and coagulase-negative morphologically similar colonies grew abundantly from synovial fluid and all tissue samples on 5% bovine blood agar and chocolate agar after an incubation period of 2 days. A representative isolate was identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) to the genus level, with the best hit being Staphylococcus (log scores ranging from 1.27 to 1.99), while biootyping gave an unattainable profile identification (API ID 32 Staph profile 375152000), the nearest significant taxon being Staphylococcus chromogenes, S. caprae, S. carnosus and S. simulans. 16S rRNA gene sequencing analysis did not provide sufficient discrimination towards related species (99.8% sequence similarity with S. carnosus and S. piscifermentans). PCR analyses for mecA, nuc, TSST-1, ETA and ETB genes were negative. The isolate was found to be susceptible to all antibiotics tested (Table 1).

After an incubation period of 10 weeks, growth of acid-fast bacteria was not detected. Staphylococcus was not recovered in S. condimenti and S. simuliens. PCR analyses for mecA, nuc, TSST-1, ETA and ETB genes were negative. The isolate was found to be susceptible to all antibiotics tested (Table 1).

Throughout the hospital stay, a total of 12 revision surgeries were performed due to severe infectious myositis with extensive involvement of the soft tissues of the right thigh up to the ischial tuberosity, and also involvement of the contralateral hip and thigh. Between revisions, the surgical wounds were left open. On the basis of results of antimicrobial susceptibility testing, antibiotic treatment was adjusted to intravenous clindamycin and dicloxacillin from day 7.

Two weeks after the first revision surgery, the surgical wounds were closed. The patient was discharged after 4 weeks’ hospitalization with dicloxacillin tablets for 20 days’ treatment. Clinical follow-up was to be scheduled in her home country.

Materials and Methods

Bacterial strains and typing

The bacterial strains used in this study were the clinical isolate of Staphylococcus condimenti from the described case, hereafter referred to as StO 2014-01, and the StO 2014-01 type strain (CCUG 39902T) isolated from soy sauce mash. Bacterial cultures were identified by MALDI-TOF MS (Bruker Daltonics) with MALDI Biotyper software. Identification to the species level was defined as log scores ≥2.0, and identification to the genus level on log scores between 1.7 and 1.9, based on the manufacturer’s guidelines. Antibacterial susceptibility testing was performed with agar disc diffusion and minimum inhibitory concentration testing by agar gradient diffusion. Interpretation of results was based on EUCAST/NordicAST breakpoints for staphylococci. 16S rDNA was sequenced with PCR primers covering V1–V9 and Sanger sequencing using BigDye Terminator v 3.1 and ABI Hitachi 3130 XL Genetic Analyser (Applied Biosystems).

Whole genome sequencing and assembly

Bacterial cells were cultured with proteinase K (2 mg/mL) and lysostaphin (0.1 mg/mL) for 15 minutes with shaking at 37°C, before heating for 15 minutes at 65°C. Genomic DNA was isolated using the Qiagen MagAttract DNA Mini M48 kit on
Qiagen BioRobot M48. Illumina sequencing libraries were prepared using the Nextera XT sample prep kit, and were sequenced on the MiSeq platform with 300 bp paired-end reads (MiSeq Reagent Kit v3). MinION libraries were prepared from genomic DNA sheared by G-tube (Covaris) using the SQMAP-004 kit (Oxford Nanopore Technologies). The MinION library was sequenced on a R7.3 flow cell using the MinION sequencer (Oxford Nanopore Technologies). Raw data were basecalled using Metrichor software (r7.X 2D Basecalling rev 1.12), and extracted using Poretools [5]. Data from two Nextera XT libraries and one MinION library (2D filtered reads) were hybrid assembled using the SPAdes Genome Assembler (v3.5.0) [6]. Contigs were assembled and circularized using the Geneious Assembler (Biomatters). The complete genome was annotated using the Rapid Annotation using Subsystem Technology (RAST) [7]. The StO 2014-01 chromosome and plasmid sequences were deposited in DDBJ/ENA/GenBank (RAST) [7]. The plasmid (named pStO 2014-01) identified in S. condimenti StO 2014-01 displays very little sequence similarity (maximum 25% alignment length) to known sequences in National Center for Biotechnology Information’s nucleotide collection, and thus appears to be a new plasmid.

Comparative genomics and identification of virulence factors

Accessions of the reference genome sequences used in this study are provided in Table 2. BRIG [8] was used for whole genome comparison. Proteins were considered to be homologs having at least 90% sequence identity over at least 60% alignment length. ClustalX2 [9] and FigTree v1.4.2 were used for sequence alignments and phylogeny. Putative virulence factors were identified by protein sequence blast against the Virulence Factors Database using BLAST+ and PfamScan against the Pfam-A database. Putative horizontally transferred pathogenicity islands were identified using Alien Hunter [10].

Results

The genome of S. condimenti StO 2014-01 was sequenced and assembled into a complete 2 665 650 bp chromosome and a 35 235 bp plasmid. The genome encodes a total of 2535 protein-encoding genes, of which 1866 (73.6%) were assigned to a function and 669 (26.4%) were defined as hypothetical, based on RAST. The plasmid (named pStO 2014-01) identified in S. condimenti StO 2014-01 displays very little sequence similarity (maximum 25% alignment length) to known sequences in National Center for Biotechnology Information’s nucleotide collection, and thus appears to be a new plasmid.

Comparative genomics of S. condimenti and closely related species

We selected genomes of the most closely related species to S. condimenti for comparisons. These are strains originally isolated from food sources and are thus not known to be pathogenic. Furthermore, we selected genomes of more distantly related species such as S. simulans, S. massiliensis, S. epidermidis and S. aureus to include in whole genome comparisons (Table 2).

Whereas ribosomal gene (16S and 23S rDNA) alignments could not discriminate sufficiently between these staphylococcal species (results not shown), an alignment of the sodA gene encoding superoxide dismutase, which is commonly used for species-level identification of coagulase-negative staphylococci [11], provided discrimination between the closely related S. condimenti and S. carnosus strains (Fig. 1).

Alignments of the chromosomes of S. condimenti StO 2014-01 and S. carnosus TM300 (Fig. 2) indicate a high degree of synteny and sequence identity between these two species. Between the two S. condimenti strains StO 2014-01 and DSM 11674, there is an even higher degree of synteny and sequence identity, indicating that apart from a few horizontally transferred regions, the genomes are highly conserved in both structure and function.

Horizontally transferred genomic regions in S. condimenti StO 2014-01

Identification of putative horizontal gene transfer (HGT) regions in S. condimenti StO 2014-01 (Table 2, Fig. 2) revealed that

| Strain | Source | Type | RefSeq accession no. | Size (Mb) | GC% | Protein | rRNA | tRNA |
|--------|--------|------|----------------------|-----------|-----|---------|------|------|
| S. condimenti StO 2014-01 | Human soft tissue infection | Complete | NZ_CP018776-7 | 2.70 | 34.6 | 2535 | 15 | 58 |
| S. condimenti DSM 11674 | Soy sauce mash | Complete | NZ_CP015114 | 2.66 | 34.7 | 2427 | 18 | 58 |
| S. carnosus subsp. carnosus TM000 | Meat starter culture | Complete | NC_012121 | 2.57 | 34.6 | 2357 | 15 | 58 |
| S. carnosus subsp. utilis LT47013 | South Tyrolean Ham | Contigs | NZ_LAUL00000000 | 2.63 | 34.4 | 2399 | 12 | 57 |
| S. carnosus 336 | Beef trim | Contigs | NZ_LSIV00000000 | 2.67 | 34.4 | 2467 | 12 | 57 |
| S. simulans ACS-120-V-Schl | Human reproductive tract | Scaffolds | NZ_AGZ2X00000000 | 2.67 | 36.0 | 2399 | 14 | 55 |
| S. simulans FDAARGOS_124 | Human blood | Complete | NZ_CP014016 | 2.65 | 36.0 | 2390 | 18 | 59 |
| S. massilienii CCUG 55927 | Human brain abscess | Scaffolds | NZ_AKGE00000000 | 2.37 | 36.5 | 2106 | 3 | 55 |
| S. massilienii 546 | Healthy human skin | Contigs | NZ_AMQ00000000 | 2.45 | 36.3 | 2231 | 7 | 53 |
| S. epidermidis ATCC 12228 | Reference strain | Complete | GCF_00007645 | 2.56 | 32.1 | 2482 | 16 | 60 |
| S. aureus NCTC 8325 | Conjunctiva, corneal ulcer | Complete | GCF_000031425 | 2.82 | 32.9 | 2767 | 16 | 61 |

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FIG. 1. Midpoint rooted neighbour-joining phylogenetic tree based on sodA alignment (606 bp). Bootstrapping values (1000 resamplings) are displayed for each node. The sodA gene of *Staphylococcus condimenti* StO 2014-01 displays 100% pairwise sequence identity to sodA of *S. condimenti* DSM 11674, 96.54% identity to *S. carnosus* LTH7013 and *S. carnosus* 336, and 96.38% identity to sodA of *S. carnosus* TM300. Identity to *S. simulans* strains is 90.05%, to *S. massiliensis* strains 81.05% and to more distantly related *S. aureus* and *S. epidermidis* strains from 78 to 83%.

FIG. 2. Whole genome comparison of the chromosome of *Staphylococcus condimenti* StO 2014-01 to the chromosomes of *S. carnosus* TM300 and *S. condimenti* DSM 11674 created using BRIG [8]. Sequence identity is indicated by coloured key as specified. Putative horizontally transferred genomic regions identified in *S. condimenti* StO 2014-01 are marked on the outer circle in black.
this strain contains a GroEL-integrated genomic island (SeR-FusB-like) that appears to be related to several phage-related regions previously described in S. epidermidis [12]. The genomic island however lacks the region encoding the FusB gene providing resistance to fusidic acid. The clinical strain also contains a staphylococcal chromosomal cassette (SCC) that is 99% identical to SCCM1 of S. aureus M1 [13]. The strain furthermore contains a 41.7 kb prophage similar to S. aureus phage 37 [14] as well as the well-characterized intercellular adhesion (ica) operon which is involved in biofilm formation [15]. Two other genomic regions (HGT 2 and HGT 3) identified as potentially horizontally transferred appear to be involved in adherence.

**Putative virulence factors identified in S. condimenti StO 2014-01**

We identified 37 putative virulence factors in S. condimenti StO 2014-01, most of which were also found in either S. condimenti DSM 11674 and to a lesser extent in S. carnosus TM300 (Table 4). Notably, S. condimenti StO 2014-01 encodes two proteins containing leukocidin domains that may form a putative bicomponent β-barrel toxin and have close homologs in S. condimenti DSM 11674. The S. condimenti clinical strain furthermore contains a number of genes which appear to encode functions related to immune evasion and suppression (Table 3). These include proteins encoding domains conserved in staphylococcal superantigens and toxins involved in modulation of T-cell responses [16], immunoglobulin-binding domain B of staphylococcal protein A (SpA), as well as a putative staphopain, extracellular fibrinogen-binding protein (Efb), staphylococcal complement inhibitor (SCIN) and secreted von Willebrand factor–binding protein (VWbp). As is common in staphylococci, S. condimenti StO 2014-01 encodes a number of cell wall–anchored proteins, including microbial surface components recognizing adhesive matrix molecules (MSCRAMMs) [17]. The strain furthermore encodes two putative phenol-soluble modulins (PSMs), which have been implicated in proinflammatory and cytolytic activity, as well as in biofilm-associated infections [18].

**Discussion**

In this study we have identified, sequenced the genome of and identified putative virulence traits of a strain of *S. condimenti* which caused severe soft tissue infection with extensive and prolonged inflammation of the leg and thighs in a patient with no known immune defects or underlying disease. This is the first reported genome of a *S. condimenti* strain involved in human disease. We compared the genome of the clinical strain with those of closely related staphylococci, i.e. the *S. condimenti* type strain DSM 11674 and three strains of *S. carnosus*, all of which have been isolated from food sources and have been considered to be nonpathogenic, in an attempt to elucidate which virulence traits contributed to the severity of disease observed in this case.

*S. condimenti* was isolated in pure culture from both synovial fluid and several soft tissue samples collected via biopsy during the first revision surgery 4 days after the first treatment for knee injury. *S. condimenti* must therefore be considered as the definite cause of infection in this case. The infection must also be classified as a severe, life-threatening condition because it progressed, necessitating multiple surgical revisions despite adequate intravenous antibiotic treatment. The 7-year-old patient did not have any known underlying disease or history of infections indicating primary immunodeficiency which could explain her susceptibility to a low-virulent bacterium, in contrast to the recently reported case of catheter-related bacteraemia in a patient with severe dilated cardiomyopathy [4].

Except the single case of infection mentioned earlier, *S. condimenti* has not previously been reported as a cause of infection in humans. This could reflect the low virulence of the
species, but it may also be a consequence of the difficulty in identifying the species by phylogenetic methods available in routine laboratories before matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) was recently introduced [19]. Regardless, S. condimenti seems to be a rare cause of infections in humans. In a study including 8388 CoNS identified by MALDI-TOF MS from clinical samples in a hospital in France, only three isolates were identified as S. condimenti [19]. Similarly, this bacterial species was recently introduced [19]. Regardless, S. condimenti seems to be a rare cause of infections in humans. In a study including 8388 CoNS identified by MALDI-TOF MS from clinical samples in a hospital in France, only three isolates were identified as S. condimenti [19]. Similarly, this bacterial species was recently introduced [19]. Regardless, S. condimenti seems to be a rare cause of infections in humans. In a study including 8388 CoNS identified by MALDI-TOF MS from clinical samples in a hospital in France, only three isolates were identified as S. condimenti [19]. Similarly, this bacterial species was recently introduced [19].

Comparative genomic analysis of strain StO 2014-01 with genomes of related species shows high degree of conservation between the two S. condimenti genomes with few horizontally transferred genomic regions, although the low number of available genomes for comparison makes interpretation of results uncertain. Two of the pathogenicity islands, SCCM1 and serRifuS-like, had a high degree of similarity to pathogenicity islands in S. aureus and S. epidermidis respectively.

In this study we have identified a number of putative virulence factors in S. condimenti StO 2014-01 which may have contributed to the observed severity of disease. Among these were proteins with similarity to leukocidin, involved in immune evasion, and with proinflammatory and cytolytic activity. However, to what extent these putative virulence factors are expressed and functional was not tested. In a previous study of CoNS isolated from food and starter cultures, no toxin production was found in the two S. condimenti strains tested; however, one strain displayed moderate haemolytic activity on human blood agar [2]. Since most of the putative virulence genes identified in the strain StO 2014-01 were also present in

**TABLE 4. Putative virulence factors and associated protein domains identified in Staphylococcus condimenti StO 2014-01 and their presence or absence in S. condimenti DSM 11674, S. carnosus TM300, S. carnosus subsp. utilis LTH7013 and S. carnosus 336**

| Protein | Function and location | Presence in strain |
|---------|-----------------------|--------------------|
| Locus | Domains | Putative function | Location | Group | StO 2014-01 | DSM 11674 | TM300 | LTH 7013 | 336 |
| 87310–86201 | Glyco_tranf_2, 3(D) | Biofilm | Ica region | PIA | + | + | – | – | – |
| 93302–90869 | SdrG_C, C(D), Fn_bond(R), Gram_pos_anchor(F) | Adhesion (Fn binding) | MSRAMMs | + | + | – | – | – | – |
| 124775–125395 | Gram_pos_anchor(F) | + | + | – | – | – | – | – | – |
| 128041–129885 | YIRSK_signal(M) | + | + | – | – | – | – | – | – |
| 236818–240156 | Gram_pos_anchor(F), SdrG_C, C(D) | Adhesion (Fn binding) | MSRAMMs | + | + | + | + | – | – |
| 236867–363578 | Gram_pos_anchor(F) | + | + | – | – | – | – | – | – |
| 381063–374938 | Gram_pos_anchor(F) | HGT 2 | MSRAMMs | + | + | – | – | – | – |
| 386132–387114 | Gram_pos_anchor(F) | HGT 2 | MSRAMMs | + | + | – | – | – | – |
| 387835–388607 | YIRSK_signal(M) | HGT 2 | MSRAMMs | + | + | – | – | – | – |
| 387841–396902 | YIRSK_signal(M), Collagen(R) | Adhesion (Collagen binding) | HGT2 | + | – | – | – | – | – |
| 401777–397014 | YIRSK_signal(M), Gram_pos_anchor(F) | Adhesion (Collagen binding) | MSRAMMs | + | + | – | – | – | – |
| 440878–445341 | Cna_B(F), Gram_pos_anchor(F) | Adhesion (Collagen binding) | MSRAMMs | + | + | – | – | – | – |
| 533345–532070 | Gram_pos_anchor(F) | + | + | – | – | – | – | – | – |
| 58179–582465 | Wzz(F) | + | + | – | – | – | – | – | – |
| 607337–608196 | Wzz(F) | + | + | – | – | – | – | – | – |
| 610182–615804 | Gram_pos_anchor(F) | Adhesion | HGT 3 | + | + | – | – | – | – |
| 616174–616500 | YIRSK_signal(M) | HGT 3 | + | + | – | – | – | – |
| 1108237–1106822 | B(D) | Immune evasion | Spa | + | + | – | – | – | – |
| 1169228–1163152 | Virul_facs_Brkb(F) | + | + | – | – | – | – | – | – |
| 153049–1559167 | Virulence_fact(F) | + | + | – | – | – | – | – | – |
| 1730473–1729709 | SSL_O(D), Stap_Strp_tox_C,F | Exotoxin/supraantigen-like | Toxins | + | + | – | – | – | – |
| 1732147–1730576 | Coagulase(D) | + | + | – | – | – | – | – | – |
| 1774244–1769928 | Gram_pos_anchor(F) | Adhesion | MSRAMMs | + | + | – | – | – | – |
| 1859938–1857904 | Phage_fammo(F) | Haemolysis | PSIs | + | + | – | – | – | – |
| 1860988–1859954 | Phage_fammo(F) | Haemolysis | PSIs | + | + | – | – | – | – |
| 186469–1864199 | efb-c(D) | Adhesion/immune evasion | + | + | – | – | – | – | – |
| 2081226–2082389 | Staphopain_pro(D), Peptidase_C7(F) | Immune evasion | Staphopains | + | + | – | – | – | – |
| 2082420–2082479 | Staphopain_B(D) | + | + | – | – | – | – | – | – |
| 2193344–2196078 | Staph_Strp_tox_C,F | Exotoxin/supraantigen-like | Toxins | + | + | – | – | – | – |
| 2513714–2513393 | YIRSK_signal(M) | + | + | – | – | – | – | – | – |
| 2589085–2588090 | Leukocidin(D) | Leukocidin | Toxins | + | + | – | – | – | – |
| 2590970–2589087 | Leukocidin(D) | Leukocidin | Toxins | + | + | – | – | – | – |
| 2597744–2596648 | Complinhb_SCIN(F) | Immune evasion | SCIN | + | + | – | – | – | – |
| 2631010–2628557 | YIRSK_signal(M) | + | + | – | – | – | – | – | – |
| 2644455–2640147 | YIRSK_signal(M) | + | + | – | – | – | – | – | – |
| 8288–6513 | Strept_67kDa_ant(F) Plasmid | + | + | – | – | – | – | – | – |
| 31798–35526 | Gram_pos_anchor(F) Plasmid | + | + | – | – | – | – | – | – |

HGT, horizontal gene transfer; MSCRAMM, microbial surface component recognizing adhesive matrix molecules; PSM, phenol-soluble modulin; SCIN, staphylococcal complement inhibitor; PIA, polysaccharide intercellular adhesion; D, domain; R, repeat; F, family; M, motif.
the type strain *S. condimenti* DSM 11674, it seems likely that the virulence potential of our clinical strain may also apply to strains associated with food and food production.

In conclusion, we present a case of severe soft tissue infection caused by the CoNS *S. condimenti*, which has usually been considered nonpathogenic. Whole genome sequencing showed that the genome is highly conserved between the clinical strain and the type strain isolated from food. The genome contains several putative virulence factors, including leucocidin toxin—like proteins. Although uncommon, *S. condimenti* may cause severe infections in previously healthy persons.

**Conflict of Interest**

None declared.

**References**

[1] Becker K, Heilmann C, Peters G. Coagulase-negative staphylococci. Clin Microbiol Rev 2014;27(4):870–926.
[2] Zell C, Resch M, Rosenstein R, Albrecht T, Hertel C, Gotz F. Characterization of toxin production of coagulase-negative staphylococci isolated from food and starter cultures. Int J Food Microbiol 2008;127(3):246–51.
[3] Probst AJ, Hertel C, Richter L, Wassill L, Ludwig W, Hammes WP. Staphylococcus condimenti sp. nov., from soy sauce mash, and Staphylococcus camurus (Schleifer and Fischer 1982) subsp. subsp. nov. Int J Syst Bacteriol 1998;48(Pt 3):651–8.
[4] 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.
[5] Loman NJ, Quinlan AR. Poretools: a toolkit for analyzing nanopore single-cell sequencing. J Comput Biol 2012;19(5):455–77.
[6] Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, et al. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res 2014;42(Database issue):D206–14.
[7] Alikhan NF, Petty NK, Ben Zakour NL, Beattson SA. BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. BMC Genomics 2011;12:402.
[8] Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, et al. Clustal W and Clustal X version 2.0. Bioinformatics 2007;23(21):2947–8.
[9] Vernikos GS, Parkhill J. Interpolated variable order motifs for identification of horizontally acquired DNA: revisiting the Salmonella pathogenicity islands. Bioinformatics 2006;22(18):2196–203.
[10] Payart C, Quesne G, Bommals C, Trieu-Cuot P. Rapid and accurate identification of coagulase-negative staphylococci by using the sodA gene as a target. J Clin Microbiol 2001;39(12):4296–301.
[11] Chen Hj, Tzai JC, Hung WC, Tseng SP, Hseuh PR, Teng LJ. Identification of fusB-mediated fusidic acid resistance islands in *Staphylococcus epidermidis* isolates. Antimicrob Agents Chemother 2015;59(12):5842–9.
[12] Shore AC, Brennan OM, Deasy EC, Rossney AS, Kinnevey PM, Ehricht R, et al. DNA microarray profiling of a diverse collection of nosocomial methicillin-resistant staphylococcus aureus isolates assigns the majority to the correct sequence type and staphylococcal cassette chromosome mec (SCCmec) type and results in the subsequent identification and characterization of novel SCCmec-SCCM1 composite islands. Antimicrob Agents Chemother 2012;56(10):5340–55.
[13] Kwan T, Liu J, DuBow M, Glos P, Pelletier J. The complete genomes and proteomes of 27 *Staphylococcus aureus* bacteriophages. Proc Natl Acad Sci U S A 2005;102(14):5174–9.
[14] Heilmann C, Schweitzer O, Gerke C, Varitansakom N, Mack D, Gotz F. Molecular basis of intercellular adhesion in the biofilm-forming *Staphylococcus epidermidis*. Mol Microbiol 1996;20(5):1083–91.
[15] Thanhamronga V, Kim HK, Misiasak D, Schneewind O. Staphylococcal manipulation of host immune responses. Nat Rev Microbiol 2015;13(9):529–43.
[16] Foster TJ, Geoghegan JA, Ganesh VK, Hook M. Adhesion and evasion: the many functions of the surface proteins of *Staphylococcus aureus*. Nat Rev Microbiol 2014;12(1):49–62.
[17] Otto M. Phenol-soluble modulins. Int J Med Microbiol 2014;304(2):164–9.
[18] Argemi X, Riegel P, Lavigne T, Lefebvre N, Grandpre N, Hansmann Y, 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(7):2030–6.
[19] Misawa Y, Kim HW, Takemoto K, Matsui K, Takahashi K, Nakamura S, et al. DNA microarray analysis of *Staphylococcus epi-

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