

Foot Infection by *Clostridium sordellii*: Case Report and Review of 15 Cases in France

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We report a case of foot infection by *Clostridium sordellii* and review 15 human infections registered at a Reference Center in France during the period 1998 to 2011. All strains were found nontoxigenic, lacking the lethal toxin gene coding for TcsL. Like *Clostridium septicum*, several *C. sordellii* infections were associated with intestinal neoplasms.

CASE REPORT

A 78-year-old patient living alone under bad cognitive and hygienic conditions in a rural village of South of France was hospitalized for 4 days in August 2008 for confusion, major asthenia, and fever (38.2°C). Dehydration was marked, and diabetes mellitus and dyslipemia were discovered that necessitated insulin therapy. A burn on the foot (caused by exposure to boiling water) was colonized with a methicillin-resistant *Staphylococcus aureus* strain that necessitated only local treatment. Previous history was unremarkable, with treated arterial hypertension, episodes of painful constipation in 2005, acute epigastralgia 2 years before in 2006 with ultrasound echographic and nuclear magnetic resonance imaging (MRI), as well as endoscopic gastroscopy and *Helicobacter pylori* investigation all negative. Fifteen days later, the patient was admitted to the emergency ward with confusion, vertigo, fever (39°C), and abdominal pain beginning at the right hypochondrium and later at the epigastrium. There was neither shock (arterial tension of 17/7.2), nor were there pulmonary, urologic, clinical, or biological signs. Computed tomography scan examination revealed neither angiocholitis nor appendicitis. At the time of admission, there were 18,300 leukocytes/mm³, including 16,300 polymorphonuclear leukocytes (PMNs). The C-reactive protein level was slightly elevated (42 mg/liter, increasing 2 days later to 160 mg/liter). Coagulation was normal (prothrombin index, partial prothrombin time [PTT], and fibrinogen). Biochemistry was unremarkable (ionogram, glycemia, troponin, and pancreatic, muscular, and hepatic enzymes). Only renal clearance was slightly disturbed (60 ml/min/1.73 m², as estimated by the Modification of Diet in Renal Disease [MDRD] Study equation), although in the same range as before, and more remarkably, the bilirubin level was elevated (24 μmol/liter; normal, 2 to 22 μmol/liter): all bilirubin was constituted of free indirect bilirubin, meaning hemolysis. Bilirubinemia was normal (14 μmol/liter) at the preceding hospitalization 3 weeks before. The patient had hemoglobin concentration (hemoglobin, 153 g/liter [usually 12 to 13 g/liter before and at late controls]; total proteins, 80 g/liter [usually around 65 g/liter]). Blood cultures were rapidly drawn, but the malleolar lesion, still present and now painful, was not sampled, and antibiotherapy started less than 3 h after admission, with metronidazole given at 500 mg three times a day (t.i.d.) and ceftriaxone given at 1 g/day. A Gram-positive spore-forming (subterminal or terminal spores) rod-shaped bacterium was evidenced within 11 h from anaerobic blood cultures (BacT/Alert FN; bio-

Mérieux, Durham, NC). Colonies on Columbia sheep blood agar (bioMérieux, Marcy l'Etoile, France) plates were nonhemolytic and grayish with an irregular margin. Strain was kept frozen in 15% glycerolyzed brain heart infusion (BHI) broth at −75°C after only two subcultures and shipped at that time to the reference laboratory.

Identification based on reference methods (1), as well as using commercial kits (rapid ID 32A; BioMérieux, Marcy l'Etoile, France), or analysis of metabolic end products (volatile and non-volatile fatty acids) by gas-liquid chromatography (2) gave typical urease- and indole-positive *Clostridium sordellii*. Virulence factor (neuraminidase or sialidase) and toxin (lethal toxin [TcsL]) genes were determined by PCR according to the method described by Popoff (3). The isolate was found negative for the TcsL gene and positive for the neuraminidase gene. To further characterize the *C. sordellii* isolate, termed CS166.08, whole-genome sequencing was performed as previously described (4), as well as for the reference *C. sordellii* strains IP82 and VPI 9048 (5, 6). While this study was in progress, VPI 9048 sequences were made available in GenBank, and the gene sequence of TcsH was described (7–9). The DNA sequences of the 16S rRNA genes were 99% identical in CS166.08 and the type strain of the species, further supporting that this isolate belongs to the species *C. sordellii* (Table 1). CS166.08 also retains conserved *C. sordellii* phospholipase C and neuraminidase gene sequences (Table 1). Phospholipase C activity was not detected on egg yolk agar after a 4-day incubation period in an anaerobic atmosphere with strains VPI 9048 and CS166.08. Compared to a phospholipase C-positive strain, such as strain IP82, which has a run of 6 G bases at positions 66 to 71 in its nucleotide sequence (KM657127) that leads to a predicted native protein of 399 residues, strains VPI 9048 (KM657126) and CS166.08

Received 4 December 2014 Returned for modification 6 January 2015

Accepted 13 January 2015

Accepted manuscript posted online 21 January 2015

Citation Bouvet P, Sautereau J, Le Coustumier A, Mory F, Bouchier C, Popoff M-R. 2015. Foot infection by *Clostridium sordellii*: case report and review of 15 cases in France. *J Clin Microbiol* 53:1423–1427. doi:10.1128/JCM.03414-14.

Editor: A. B. Onderdonk

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doi:10.1128/JCM.03414-14

TABLE 1 Analysis of virulence factor genes and genes coding for proteins involved in DNA mobility in the genomes of *C. sordellii* VPI 9048, IP82, and CS166.08^a

Gene product, gene no. ^b (GenBank accession no.)	% nucleotide identity (GenBank accession no.) ^c		
	VPI 9048	IP82	CS166.08
16S rRNA (AB075771) ^d	98.8 (KM657123)	99.0 (KM657124)	99.0 (KM657125)
Phospholipase C, H476_3275	100.0 (KM657126)	98.9 (KM657127)	97.8 (KM657128)
Sialidase, H476_2657	100.0 (KM657129)	99.5 (KM657130)	97.6 (KM657131)
TcsL, H476_0269	100.0 (KF726110)	97.9 (KF726114)	—
TcsH, H476_0271, 7,794 bp ^e	99.2 (KF726111 [7,857 bp])	95.1 (KF726115; pseudogene [1,186 bp])	—
TcsH (KC814176 [7,857 bp]) ^e	100.0 (KF726111 [7,857 bp])	95.2 (KF726115 [1,186 bp])	—
TcsR sigma factor, H476_0272	100.0 (KF726113)	96.2 (KF726117)	—
TcsE holin, H476_0270	100.0 (KF726112)	99.8 (KF726116)	—
Recombinase RecA-like family, H476_0278	100.0	96.2	86.3
Plasmid replication protein, H476_0274	100.0	98.8	—
Replication protein Rep_3 superfamily, H477_0270	99.0	99.6	—
Type IV secretion system conjugative DNA protein, HA476_0297	100.0	97.9	—
Type IV secretion system coupling DNA, H476_0302	100.0	96.5	—
Type IV secretion system VirD4 component, H477_0297	98.7	100.0	—
Type IV secretion system VirD4 component, H477_0298	97.2	99.8	—
RecA recombinase, H477_0275	96.2	100.0	—
Transposase, H476_0286	100.0	—	—
Transposase, H476_0321	100.0	—	—
TraB family protein, H476_0319	100.0	—	—

^a Whole-genome sequencing of the three strains was performed as previously described (4). DNA homology between target genes from GenBank, including sequences from VPI 9048 (NZ_AQJ000000000.1) and ATCC 9714 (NZ_APWR000000000.1), and the whole-genome sequences obtained in this study was investigated by BLAST. The results are expressed as percentages of nucleotide identity.

^b H476_xxxx genes are from VPI 9048 genome contigs (NZ_AQJ000000000.1), and H477_xxxx genes are from ATCC 9714^T genome contigs (NZ_APWR000000000.1).

^c —, the gene is lacking.

^d Sequence from strain ATCC 9714^T.

^e Gene H476_0271 lacks 63 nucleotides compared to the sequences of accession no. KC814176 or KF726111 (7,857 bp [positions 7098 to 7161]).

(KM657128) have runs of 5 G bases and 7 G bases, respectively, that lead to reading frame shifts and subsequent truncated proteins. Strain CS166.08 lacks the toxin genes coding for TcsL and TcsH, as well as the genes associated with the *C. sordellii* toxin gene locus, including TcsR and TcsE (7). Evidence for genes encoding proteins involved in DNA mobilization, such as type IV secretion system conjugative DNA transfer and coupling DNA-binding domain proteins, plasmid replication protein, transposases, and DNA transfer protein from the TraB family (Table 1), has been found in the *C. sordellii* toxin gene locus (7). All of these DNA mobilization genes are missing in CS166.08 (Table 1). IP82 produces only TcsL not TcsH type IV secretion system transfer genes, but it lacks transposase genes. This strongly suggests that *C. sordellii* toxin genes are localized in a mobile element, possibly a plasmid, and that nontoxic strains derive from toxigenic strains by loss of such a mobile DNA element. The case report associated with CS166.08 could result from a nontoxic strain, or CS166.08 is a nontoxic derivative after subculture of an initial toxic strain by loss of the plasmid or mobile element carrying toxin genes. A nontoxic *C. sordellii* strain has been reported to be associated with a polymicrobial cholangitis (10). However, the severity of the case presented in this study rather suggests the involvement of a toxigenic strain. In our hands, *C. sordellii* isolates often lacked the TcsL gene, although TcsL was evidenced in clinical samples, such as intestinal contents from animals who died of enterotoxemia. This observation suggests that the toxin-negative isolates probably derived from toxigenic strains. The toxin genes might have gone lost in the course of subculturing. From 1998 to January 2011, 16 *C. sordellii* isolates of human origin were sent to

the National Reference Center (NRC) (Table 2). The strains showed the standard properties of *C. sordellii*. However all strains (16/16) were found PCR negative for the TcsL gene, probably supporting the instability of the toxin gene. In contrast, the neuraminidase gene was detected in all of the tested strains (10/10). The mean age of the patients was 61.1 years (minimum, 38 years; maximum, 85 years). The male/female sex ratio of patients was 1.0. Sample origins were known for 15 out of 16 cases: 7 from blood culture, 2 from skin, and 1 each from synovial fragment, stool culture, intra-abdominal sample, ascitic fluid, peritoneal fluid, and finger necrosis (Table 2). Most *C. sordellii* strains isolated from infected wounds were associated with myonecrosis or cellulitis. One *C. sordellii* strain was isolated from stool in a context of pseudomembranous colitis, and 5 strains were obtained from blood cultures of patients with underlying neoplasms (2 intestinal neoplasms, 1 hepatic neoplasm, 1 pulmonary neoplasm, and 1 endometrium neoplasm).

Clostridium sordellii, is a Gram-positive, spore-forming bacterium and an obligatory anaerobe. This bacterium is an environmental rod found in soil and occasionally in animal and human intestine. It is one of the *Clostridium* species responsible for myonecrosis and gangrene in humans and animals. Up to 4% of cases of *Clostridium* myonecrosis were reported to be caused by *C. sordellii* (11). Cases of *Clostridium* gangrene are now infrequent in humans, but *C. sordellii* is responsible for sporadic cases of gas gangrene subsequent to trauma or surgery, and it is a more com-

TABLE 2 Cases of *C. sordellii* infections reported to the NRC from 1998 to 2011^a

Yr	Age (yr)/sex	Presenting illness or condition	Sample origin
2011	83/F	Hepatic adenocarcinoma (originated from the gallbladder)	Blood culture
2010	73/F	Perforated acute appendicitis	Peritoneal fluid
2010	50/F	Lawn mower accident: D2 D3 amputation followed by an important necrosis	Finger necrosis
2009	62/M	Ascites	Ascitic fluid
2008	38/M	Polytraumatism (motorbike fall): cellulitis, myonecrosis	Blood culture (2/6 positive)
2008	78/M	Superinfected foot wound	Blood culture ^b
2007	Unknown/F	Colonic surgery	Unknown
2006	65/M	Intestinal obstruction (underlying disease, cancer)	Blood culture (1/4 positive)
2004	85/F	Pseudomembranous colitis	Stool culture
2004	55/F	Necrotizing fasciitis	Blood culture (3/6 positive): mixed culture with a group G <i>Streptococcus</i> strain
2002	68/M	Pulmonary neoplasm with metastasis	Blood culture
2000	45/M	Intestinal neoplasm	Intra-abdominal sample
2000	65/F	Endometrium neoplasm: peritoneum carcinosis	Blood culture
1999	>21/M	Finger wound after a cut (pork butcher)	Skin
1999	Unknown/M	Skin ulcer	Skin
1998	66/F	Bone infection	Synovial fragment

^a All of the *C. sordellii* strains were PCR negative for the TcsL gene and PCR positive for the neuraminidase gene where tested (11/11). No toxicity was evidenced in the culture supernatant from all strains by the mouse bioassay.

^b This case is more completely described above.

mon cause of myonecrosis in injection drug users (12–14). Infection by this bacterium is characterized by a marked local edema and variable production of gas, followed by extensive tissue necrosis and total absence of leukocyte infiltration and tissue inflammatory response, severe hypotension, shock, and absence of hemolysis, (14). Sporadic cases of *C. sordellii* infections are commonly encountered in women after a postpartum wound, endometritis, or postabortion disease. Although rare, these cases are all dramatic. A fulminant toxic shock syndrome (irreversible hypotension, apyrexia, hemoconcentration with hyperproteinemia, leukocytosis, and high hematocrit) accompanies the local infection of uterus or perineum. Pleural effusions and serosanguineous ascites have been reported in almost all of the cases (15–23). In the recent period, several cases of fatal toxic shock syndrome due to *C. sordellii* were reported following medical abortion (15, 24–33). From a series of 45 cases of *C. sordellii* infections, 8 (18%) were associated with normal childbirth, 5 (11%) with medical abortion, 2 (0.4%) with spontaneous abortion, 10 (22%) with drug injection, and 19 (43%) occurred after trauma or surgery. The issue was fatal in 31 of 45 patients (68%) within 2 to 6 days after the initial infection (34). In addition, *C. sordellii* is responsible for bacteremia and arthritis, resulting in a high rate of mortality (35, 36). A few cases of *C. sordellii* pericarditis and pleuropneumonia have been reported, which probably result from aspiration of oropharyngeal flora associated with pulmonary embolism and valvular heart disease (37, 38). *C. sordellii* bacteremia without myonecrosis of skeletal muscle are rare but often fatal (mortality of >50%). The portal of entry is presumed to be mainly the gastrointestinal tract, and trauma to the anus through manual self evacuation is a possible cause. A few cases were consecutive to a transcutaneous biopsy, such as liver biopsy or transrectal prostatic biopsy. These infections can be found in all ages. Underlying malignancy and being immunocompromised are aggravating risk factors (11, 35, 39, 40). More rarely, *C. sordellii* infections can occur as small pseudo-outbreaks (41).

In contrast, *C. sordellii* diseases are more common in animals.

C. sordellii induces large outbreaks of enterotoxemia in animals, mainly in sheep and lambs (42–47), sporadic cases of necrotic and hemorrhagic enteritis in cattle (42, 43), and equine myopathy (48). *C. sordellii* toxic infections in sheep and lambs most often result in sudden death, in which no characteristic postmortem abnormalities are observed. However, some animals show a marked edema and emphysema of the abomasum wall. Moreover, *C. sordellii* is associated with sudden death in periparturient sheep (49). The most relevant feature of *C. sordellii* pathologies in humans and animals, whatever the initial site of infection, consists of a rapid and fatal toxic shock syndrome, indicating a major role of toxin(s) in the onset of the disease. However, the cause of the death has not been yet deciphered.

C. sordellii lethal toxin (TcsL) is the major virulence factor. TcsL disrupts the actin cytoskeleton through inactivation of Rho- and Ras-GTPases, such as Rac, Ras, Rap, and Ral, by glucosylation at the conserved Thr35/37 (50). This leads to a disorganization of the intercellular junctions, mainly basolateral junctions by redistribution of the whole E-cadherin–catenin complex from the cell membrane to the cytosol, and to an increase in epithelial and endothelial barrier permeability (51–53). Thereby, TcsL is a potent edematogenous toxin. Locally, TcsL induces a degeneration of skeletal neuromuscular tissues (54), and when injected intravenously into mice, TcsL causes an increase in lung endothelial vascular permeability that results in massive extravasation of blood fluid in the thoracic cage, profound dehydration, hypoxia, and finally cardiorespiratory failure (55). In addition, TcsL represses glucocorticoid receptor transactivation, thus impairing the anti-inflammatory response, and this effect is amplified in the presence of the glucocorticoid antagonist RU486 (56). This could explain, at least partially, the association of TcsL-dependent toxic shock with RU486. It is noteworthy that the gene encoding TcsL is unstable, and most of the strains lose their toxin gene after isolation from clinical specimen, compromising their identification.

Clostridium septicum is well known to be associated with malignancy (57, 58). In addition to its involvement in gangrene, *C.*

sordellii could be an occasional agent of superinfection of certain neoplasms. Although *C. sordellii* toxin-infections are rare in humans, they are always severe and dramatic. For this reason, an attentive survey of these infections is required.

Nucleotide sequence accession numbers. The nucleotide gene sequences obtained from whole-genome sequencing of the strains VPI 9048, AIP82, and CS166.08 done in this study have been deposited in the GenBank database under the following accession numbers: 16S rRNA, [KM657123](#) to [KM657125](#); phospholipase C, [KM657126](#) to [KM657128](#); and sialidase (neuraminidase), [KM657129](#) to [KM657131](#), respectively.

ACKNOWLEDGMENTS

We thank French private and hospital laboratories for sending *Clostridium sordellii* isolates to the NRC. Maria Manich, Marie Bedora-Faure, and Guylène K'Ouas from the NRC are warmly thanked for excellent technical assistance.

The authors of this article have no conflicts of interest to disclose.

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