- characterization of peste des petits ruminants virus, Sierra Leone. Emerg Infect Dis. 2012;18:193–5. http://dx.doi.org/10.3201/eid1801.111304
- Libeau G, Diallo A, Parida S. Evolutionary genetics underlying the spread of peste des petits ruminants virus. Anim Front. 2014;4:14–20. http://dx.doi.org/10.2527/ af.2014-0003
- Baron MD, Parida S, Oura CA. Peste des petits ruminants: a suitable candidate for eradication? Vet Rec. 2011;169:16–21. http://dx.doi.org/10.1136/vr.d3947
- Banyard AC, Parida S, Batten C, Oura C, Kwiatek O, Libeau G. Global distribution of peste des petits ruminants virus and prospects for improved diagnosis and control. J Gen Virol. 2010;91:2885–97. http://dx.doi.org/10.1099/vir.0.025841-0
- De Nardi M, Lamin Saleh SM, Batten C, Oura C, Di Nardo A, Rossi D. First evidence of peste des petits ruminants (PPR) virus circulation in Algeria (Sahrawi territories): outbreak investigation and virus lineage identification. Transbound Emerg Dis. 2012;59:214–22. http://dx.doi. org/10.1111/j.1865-1682.2011.01260.x
- Kwiatek O, Ali YH, Saeed IK, Khalafalla AI, Mohamed OI, Obeida AA, et al. Asian lineage of peste des petits ruminants virus, Africa. Emerg Infect Dis. 2011;17:1223–31. http://dx.doi.org/10.3201/eid1707.101216
- Wang Z, Bao J, Wu X, Liu Y, Li L, Liu C, et al. Peste des petits ruminants virus in Tibet, China. Emerg Infect Dis. 2009;15:299–301. http://dx.doi.org/10.3201/ eid1502.080817
- ProMedMail. Peste des petits ruminants— China (11): Sheep, goat, spread, OIE, request for information. ProMed 2014 May 5. http://www.promedmail.org, archive no. 20140511.2465094.

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Possible Exiguobacterium sibiricum Skin Infection in Human

To the Editor: The genus Exiguobacterium was first described in 1983 by Collins et al., who characterized the species E. aurantiacum (1). Since then, 9 new species have been added: E. acetylicum, E. antarcticum, E. undae, E. oxidotolerans, E. aestuarii, E. marinum, E. mexicanum, E. artemiae, and E. sibiricum (2,3). The genus Exiguobacterium belongs to the group of coryneform bacteria, which encompasses aerobically growing, non-spore-forming, irregularly shaped, gram-positive rods (2). Exiguobacterium spp. have been isolated from a wide range of habitats, including cold and hot environments (3). Although strains of Exiguobacterium spp. have been isolated from human clinical specimens (e.g., skin, wounds, and cerebrospinal fluid), the clinical significance of these bacteria is poorly understood (4). We present a case of cutaneous infection possibly caused by *E. sibiricum*.

In January 2014, a previously healthy 66-year-old farmer was admitted to the Health Center of Molina de Aragón (Guadalajara, Spain) with a 7-day history of an ulcer on the dorsal surface of the second finger on his right hand with a painful black eschar surrounded by edema, greenish exudate, erythema, and a broken blister. The lesion had progressively increased in size. The patient was a hunter who had handled the skin of a deer and a wild boar 4 days before. He had no history of trauma or receipt of antimicrobial drugs. At admission, he was afebrile with no systemic symptoms. Cutaneous anthrax was suspected on the basis of the clinical appearance of the lesion and the patient's contact with animals. An exudate sample was obtained for culture, and treatment with oral ciprofloxacin (500 mg/12 hour) was initiated. The Gramstained sample showed leukocytes

without organisms. Culture was performed according to standard practice.

Colonies observed after 24 hours of incubation on blood agar in pure culture were gray but turned orange after 48 hours. The colonies appeared mucoid and were nonhemolytic. Gram staining revealed wide, short, nonspore-forming, gram-positive rods. The isolate was motile, catalase positive, oxidase negative, and it fermented glucose and lactose. Reactions for indole, urea, and bile esculin were negative. The strain did not grow on Mc-Conkey agar and was facultatively anaerobic. The strain was initially identified as *Bacillus* spp. and was sent to the National Reference Laboratory of Majadahonda (Madrid, Spain) for species identification. There, the isolate was identified as E. sibiricum by means of 16S rRNA sequence analysis according to a previously reported method (5). The fragment of 16S RNA gene obtained from this isolate was 1,413 bp, and similarity with GenBank sequences was 99.6% (GenBank accession nos. CP00122, GQ869573, and others).

After the organism was identified, we found that it was able to grow on blood agar at 4°C after 6 days of incubation. Antimicrobial drug susceptibility testing was performed by using the Etest method (AB Biodisk, Solna, Sweden) on Mueller-Hinton agar plates incubated at 37°C for 24 hours. The isolate was susceptible to penicillin (MIC 0.023 mg/L), cefotaxime (0.5 mg/L), imipenem (0.047 mg/L), levofloxacin (0.19 mg/L), vancomycin (0.5 mg/L), clindamycin (0.125 mg/L), erythromycin (0.047 mg/L)mg/L), gentamicin (0.094 mg/L), doxycycline (0.032 mg/L), linezolid (0.5 mg/L), and daptomycin (0.5 mg/L). The patient's clinical outcome was good, and the lesion resolved after 10 days of continuous ciprofloxacin therapy.

This patient's cutaneous infection and the morphologic appearance of the lesion resembled cutaneous anthrax. Initially, the Gram-stained appearance and culture were compatible with those of Bacillus species other than B. anthracis. In this sense, cutaneous infections caused by Bacillus species other than B. anthracis have been reported and are clinically similar to cutaneous anthrax (6). Isolation of coryneform bacteria from the ulcer may represent colonization rather than true infection, and the absence of the organism on the initial Gram-stained slides may support contamination. However, the evidence points to E. sibiricum as a pathogen and not a contaminant because it was the only organism isolated, and Gram staining of the exudate revealed leukocytes. In addition, the patient had not previously received any antimicrobial drug that could change the result of the culture. Moreover, the isolate was susceptible to ciprofloxacin, and clinical response to this drug was good. However, we cannot absolutely rule out another organism as the cause of the infection or co-infection with some uncultured bacterium.

Identification of Exiguobacterium spp. based on conventional methods is difficult and should be confirmed with molecular assays. Bacteria in this genus can be misidentified as Oerskovia xanthineolytica when the API Coryne kit (bio-Mérieux, Marcy l'Étoile, France) is used (7); 16S rRNA gene sequencing seems to be useful for identification of E. sibiricum (8). Consequently, the frequency of this infection can be underdiagnosed. In patients with lesions suspected of being cutaneous anthrax, E. sibiricum should be considered as a potential cause and should be differentiated from B. anthracis (Table) (9,10).

This case of human infection was most likely caused by *E. sibiricum*. Identification of this organism is difficult, and it can be confused with *Bacillus* spp. *E. sibiricum* should be considered as a possible cause of lesions suspected of being cutaneous anthrax.

Table. Microbiological and clinical characteristics of *Exiguobacterium sibiricum* and *Bacillus anthracis**

Characteristic	E. sibiricum	B. anthracis
Colony on blood agar	Mucoid and orange	Gray-white to white
Spore production	_	+ (central)
Motility	+	_
Hemolysis on blood agar	_	_
Penicillin susceptibility	+	+
Catalase production	+	+
Indole production	_	_
Growth at 4°C	+	_
Anaerobic growth	+	+
Cutaneous infection	Ulcer, black eschar, blister	Eschar, malignant pustule
Other infections	None reported	Intestinal anthrax, pulmonary anthrax, meningitis
*+ present - absent		

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References

- Collins MD, Lund BM, Farrow JAE, Schleifer KH. Chemotaxonomic study of an alkalophilic bacterium, *Exiguobacterium aurantiacum* gen. nov. J Gen Microbiol. 1983;129:2037–42.
- Farrow JAE, Wallbanks S, Collins MD. Phylogenetic interrelationships of roundspore-forming bacilli containing cell walls based on lysine and the non-spore-forming genera Caryophanon, Exiguobacterium, Kurthia, and Planococcus. Int J Syst Bacteriol. 1994;44:74–82.
- Vishnivetskaya TA, Kathariou S, Tiedje JM. The Exiguobacterium genus: biodiversity and biogeography. Extremophiles. 2009;13:541–55. http://dx.doi.org/10.1007/s00792-009-0243-5
- Hollis DG, Weaver RE. Gram-positive organisms: a guide to identification. Special Bacteriology Section. Atlanta Centers for Disease Control; 1981.
- Drancourt M, Bollet C, Carliotz A, Martelin R, Gayralt JP, Raoult D. 16S

- ribosomal DNA sequence analysis of a large collection of environmental and clinical identified bacterial isolates. J Clin Microbiol. 2000;38:3623–30.
- Tena D, Martínez-Torres JA, Pérez-Pomata MT, Sáez-Nieto JA, Rubio V, Bisquert J. Cutaneous infection due to *Bacillus pumilus*: report of 3 cases. Clin Infect Dis. 2007;44:e40–2. http:// dx.doi.org/10.1086/511077
- Kenny F, Xu J, Millar BC, McClurg RB, Moore JE. Potential misidentification of a new *Exiguobacterium* sp. as *Oerskovia* xanthineolytica isolated from blood culture. Br J Biomed Sci. 2006;63:86.
- Murayama M, Kakinuma Y, Maeda Y, Rao JR, Matsuda M, Xu J, et al. Molecular identification of airborne bacteria associated with aerial spraying of bovine slurry waste employing 16S rRNA gene PCR and gene sequencing techniques. Ecotoxicol Environ Saf. 2010;73:443-7. http://dx.doi. org/10.1016/j.ecoenv.2009.10.003
- Rodrigues DF, Ivanova N, He Z, Huebner M, Zhou J, Tiedje JM. Architecture of thermal adaptation in an *Exiguobacterium sibiricum* strain isolated from 3 million year old permafrost: a genome and transcriptome approach. BMC Genomics. 2008;9:547–64. http://dx.doi.org/10.1186/1471-2164-9-547
- Logan NA, Popovic T, Hoffmaster A. Bacillus and other aerobic endosporeforming bacteria. In: Murray PR, Baron EJ, Jorgensen JH, Landry ML, Pfaller MA, editors. Manual of clinical microbiology. 9th ed. Washington (DC): ASM Press;2007. p. 455–73.

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