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Letters to the editor

First isolation of *Skermanella aerolata* from a human sample

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Sir,

Skermanella aerolata is a Gram-negative, strictly aerobic, motile, non-endospore-forming, bacteria, with a high G+C DNA content. This species has been isolated from the environment, but, so far, isolation in humans had never been reported. We describe the first case of *S. aerolata* isolation in a human sample and the susceptibility pattern of the isolate.

A 37-years-old Spanish woman, without previous medical records, gave birth in the General University Hospital Gregorio Marañon (Madrid) by an uncomplicated caesarean delivery. After one month, she volunteered for a study on the diagnosis of puerperal mastitis from breast milk samples carried out by the Microbiology Department of the Hospital. Since she did not develop mastitis at the time of collection of any sample, she was included as a control in the study. Two samples of breast milk were obtained on days 29 and 62 postpartum, carried out under optimal conditions, as indicated in national and international guidelines. After extraction, each sample was immediately refrigerated until processing. A direct Gram staining performed in all samples did not exhibited either polymorphonuclear leukocytes or bacteria. A quantitative culture of the samples was performed in aerobic atmosphere on MacConkey and Brucella agar (Becton Dickinson, Heidelberg, Germany), in an atmosphere containing 5-10% CO_2 on chocolate agar (Oxoid S.A, Thermo Fisher Scientific, Madrid, Spain) and in anaerobiosis on Brucella agar (Becton Dickinson, Heidelberg, Germany) for 5-7 days at 35-7°C. Culture of the 29-day sample showed the growth of *Staphylococcus aureus* (1,000 cfu/mL), *S. epidermidis* (30,600 cfu/mL), *Corynebacterium amycolatum* (800 cfu/mL) and *Propionibacterium granulosum* (2,000 cfu/mL). The 62-day postpartum sample culture showed

Figure 1 Aspect of the light-pink-coloured colonies with "bread crumbs" morphology of *Skermanella aerolata* in Brucella agar

20 cfu/mL of light-pink-coloured rough colonies with "bread crumbs" morphology, positive to the catalase and oxidase tests (figure 1). Although the isolate generated a sharp, specific protein fingerprint by MALDI-TOF MS using the Biotyper 3.1 software (Bruker Daltonik GmbH, Bremen, Germany) (figure 2), this microorganism was not identified since it is not included in the 6,903 MSP database. To identify the bacteria, PCR and sequencing of the entire *16S rRNA* gene was performed, using primers fD1 y rP2 previously described [1]. The sequence generated (1350 bp) was compared with those stored in GenBank using BIBI software (http://pbil.univ-lyon1.fr/bibi). Sequence

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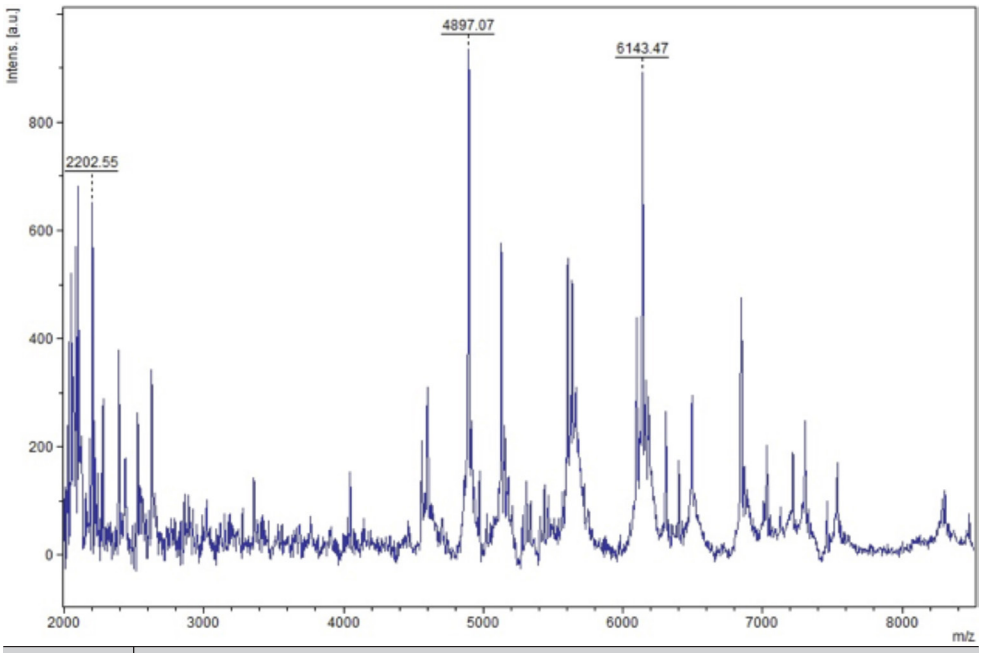

Figure 2 | **Protein spectrum from the *S. aerolata* isolate analyzed by MALDI-TOF MS. Intensity is represented in the y-axis as arbitrary units (a.u.) and the mass/charge ratio in the x-axis (m/z).**

similarity was interpreted following previously reported criteria [1] and bacteria was finally identified as *S. aerolata*. The remaining microorganisms isolated on the second sample were *C. amycolatum* (5,000 cfu/mL), *S. epidermidis* (14,000 cfu/mL) and *Facklamia hominis* (14,000 cfu/mL).

Antimicrobial susceptibility testing of *S. aerolata* against 22 antimicrobials was performed by E-test strips (all antimicrobials were obtained from bioMérieux, Marcy-l'Etoile, France; except for moxifloxacin and piperacillin/tazobactam that were obtained from Liofilchem Diagnostic, Roseto degli Abruzzi, Italy) using a 4 MacFarland bacterial suspension on Brucella agar. Plates were incubated for 96 hours at 35-37°C in aerobic condition. The ATCC® strains *E. coli* 25992 and *S. aureus* 29213 were included in the testing. The susceptibility profile (mg/L) was as it follows: penicillin G (0.25), amoxicillin (<0.016), amoxicillin/clavulanic (<0.016), piperacillin/tazobactam (1), cefoxitin (24), cefotaxime (1), ceftazidime (1), imipenem (0.012), fosfomycin (>1,024), clindamycin (12), erythromycin (2), clarithromycin (3), doxycycline (0.094), tigecycline (0.047), levofloxacin (0.047), moxifloxacin (0.032), rifampicin (16), metronidazole (>256), linezolid (>256), vancomycin (>256), teicoplanin (>256) and daptomycin (>256).

Species belonging to *Skermanella* genus are phylogenetically associated with that of *Azospirillum*, which represents the best characterized genus of plant growth-promoting rhizobacteria, within the *Alphaproteobacteria* class. While most of the species belonging to *Azospirillum* genus are nitrogen-fixing soil bacteria, *Skermanella* species are not. At present, seven *Skermanella* species from environment have been described: *S. aerolata*, first isolated from ambient air samples from a study of airborne particle transmission from Mongolia to Korea during violent sandstorms ('Hwangsa' in Korean) [2], *S. parooensis*, isolated from water [3], *S. stibiiresistens*, isolated from coal-mining soil [4], *S. xinjiangensis* and *S. rubra*, both isolated from sandy soil of China [5,6], and two *Skermanella* species from contaminated desert soil [7,8]. Despite recent studies showing the presence of *Skermanella aerolata* genome in the human gastrointestinal and skin microbioma [9,10], this microorganisms has never been isolated from a direct human specimen. This is the first report showing the isolation of *Skermanella aerolata* from a human sample and characterizing its sensitivity profile to different antibiotic classes. Because of the first natural step towards infection is colonization, laboratories should be aware of this microorganism in future clinical situations by means of several measures, as the use of techniques that quickly identify this species. Useful procedures, for example, could be the inclusion of this species in the database of mass spectrometry-based techniques such as MALDI-TOF MS or the knowledge of the susceptibility pattern of an enough number of *S. aerolata* isolates to guide empirical therapy. Although this last action is still pending to perform, results of the present study suggest beta-lactams, tetracyclines and quinolones as candidates to be empirically used for future infections.

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CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

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