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Human Discovertebral Infection Caused by *Camelimonas* Species Bacteria, France, 2025

Appendix

Supplemental Materials and Methods

The patient has given his written informed consent following full and informed disclosure.

Antibiotic susceptibility was assessed using the agar diffusion method (Etest®) to measure the MICs (MICs) of the antibiotics tested. The results were interpreted according to the 2024 CA-SFM guidelines.

Initial bacterial identification was performed by 16S rDNA sequencing (*1*).

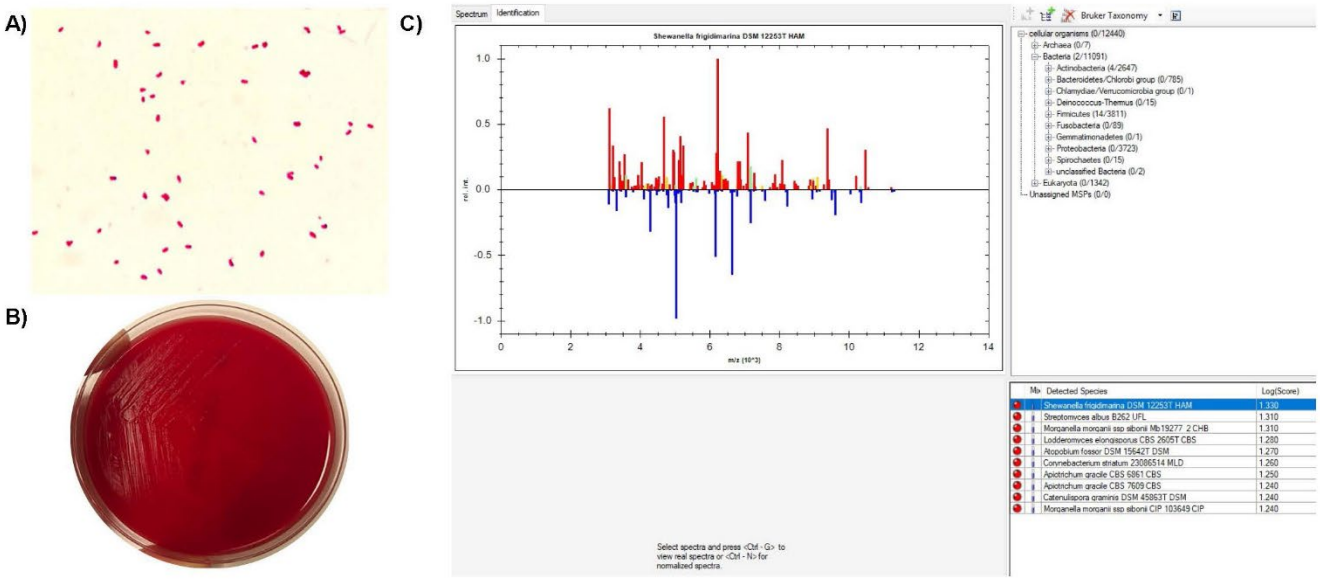
Whole-genome sequencing was performed on pure subcultures of each isolate at the Henri Mondor sequencing platform (Créteil, France). Paired-end sequencing was performed using an Illumina NovaSeq X. The raw sequencing data (.fastq) were cleaned using Sickle v1.33 (https://github.com/najoshi/sickle), and the genome was de novo assembled using SKESA v2.5.1 (*2*). The assembled genome was 4,292,006 bp of size, with 119 contigs, 3,471 coding sequences and a GC percentage of 63%. Pairwise average nucleotide identity analysis using FastANI v1.1 (*3*) and DNA-DNA hybridization analysis using GGDC online tool (http://ggdc.dsmz.de/ggdc.php) were performed to enable whole-genome comparison of FR25 isolate against the *Camelimonas* species strain ID_303_24, *Camelimonas lactis* strain M 2040^T, *Camelimonas fluminis* strain XZ2^T and *Camelimonas abortus* strain UK34/07–5^T.

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Appendix Figure. Microscopic morphology, colony appearance, and MALDI-TOF MS spectral analysis of the clinical isolate FR25DVI isolated from a human discovertebral infection, 2025. A) Gram stain highlighting short rod-shaped Gram-negative bacilli, 2025. B) Small gray, translucent and smooth colonies on agar plate after 72 hours of incubation, 2025. C) MALDI-TOF MS mass spectrum comparison fails to identify the novel clinical isolate FR25DVI, 2025. The Bruker MALDI Biotyper (Smart, Brüker Daltonics, Bremen, Germany) identification window displays a spectrum comparison (higher-left panel) and a ranked results list (lower-right panel). Left, mass spectrum displays the mass-to-charge ratio (m/z; x-axis, expressed as 103) of detected protein peaks on the horizontal axis and their relative intensity on the vertical axis. Positive red peaks above the baseline represent the sample spectrum, whereas negative

blue peaks below the baseline represent the reference spectrum used for comparison. Right, the panel displays the ranked database match list generated by the MALDI Biotyper software (version 4.1.1 database); the highest match achieved a log(score) of only 1.330 (Shewanella frigidimarina DSM 12253T HAM), which is below the 1.70 threshold for reliable identification. This lack of high-scoring matches indicates that the clinical isolate represents a novel species or one that is missing from the commercial database.