number of indeterminate IGRA results coincide with prevalent splenomegaly, we advise caution in attributing such results solely to splenomegaly without investigating other potential causes, such as mishandling specimens or errors in processing. This study underscores the prudence of a repeat IGRA after arrival in the United States for any refugee with an indeterminate or borderline IGRA result (*1*).

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We conducted this activity consistent with applicable federal law and CDC policy. The CDC reviewed the activity prior to its undertaking, deeming it not research. The findings and conclusions of this report are those of the authors and do not represent the official position of the Centers for Disease Control and Prevention or the institutions with which the authors are affiliated.

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Two Cases of Posttraumatic *Kosakonia* Infection, Argentina, 2023

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We describe 2 plant-associated posttraumatic *Kosakonia* infections in Argentina. Facing biochemical and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry limitations, we used whole-genome sequencing to successfully identify *K. cowanii* and *K. oryzae* as the causative agents. Our data highlight the crucial role of genomics in correctly identifying these underestimated emerging pathogens.

Medical literature recognized the genus *Kosakonia* in 2013, after the systematic reorganization of *Enterobacter* genus (*1*). Largely known as plant growth–promoting bacteria, or phytopathogens (*2*), the species included in this genus are rapidly gaining relevance as opportunistic human pathogens. However, because of the bacteria's phenotypic similarities with *Enterobacter* and *Pantoea*, clinicians frequently misidentify *Kosakonia* infections, leading to an underestimation of their true clinical incidence (*3*–*5*). We describe 2 cases of osteomyelitis in Argentina caused by *Kosakonia* species associated with environmental trauma.

Case 1 involved a 12-year-old girl with an open supracondylar elbow fracture sustained falling from a horse and involving soil contamination. Despite surgical fixation and cephalosporin prophylaxis, she sought treatment 10 days later for purulent discharge. Cultures yielded a gram-negative rod (isolate CMVA41). We treated the suspected osteomyelitis with intravenous piperacillin/tazobactam and clindamycin, followed by oral ciprofloxacin and clindamycin for 6 weeks, resulting in complete resolution.

Case 2 involved a 20-year-old man with chronic posttraumatic knee osteomyelitis following a puncture with a tree thorn. We cultured a gram-negative rod (isolate CMVA47) from surgical samples. We administered vancomycin and piperacillin/tazobactam, followed by a course of oral amoxicillin and ciprofloxacin for 6 weeks, achieving clinical cure.

We performed a polyphasic identification approach for both cases. Colonies were yellow and lactose-fermenting on eosin methylene blue (Levine) agar. Initial phenotypic identification using conventional biochemical tests failed to provide reliable genus-level identification (Appendix Table, https://wwwnc.cdc.gov/EID/article/32/3/25-1714-App1.pdf). We subsequently performed matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry (Bruker Biotyper, library v13.0; https://www.bruker.com). We identified isolate CMVA47 as *Kosakonia cowanii* with a secure species-level score (2.052). In contrast, we initially misidentified isolate CMVA41 as *K. radicincitans* with a low confidence score (1.717), indicating probable genus-level identification but species uncertainty. This result highlighted a limitation: the spectral library lacked a reference profile for *K. oryzae*, leading to potential misclassification (*6*).

To resolve those uncertainties, we performed whole-genome sequencing (WGS) using the Illumina NovaSeq6000 platform (https://www.illumina.com). For strain CMVA41, the 16S rRNA gene sequence showed 100% identity with the reference

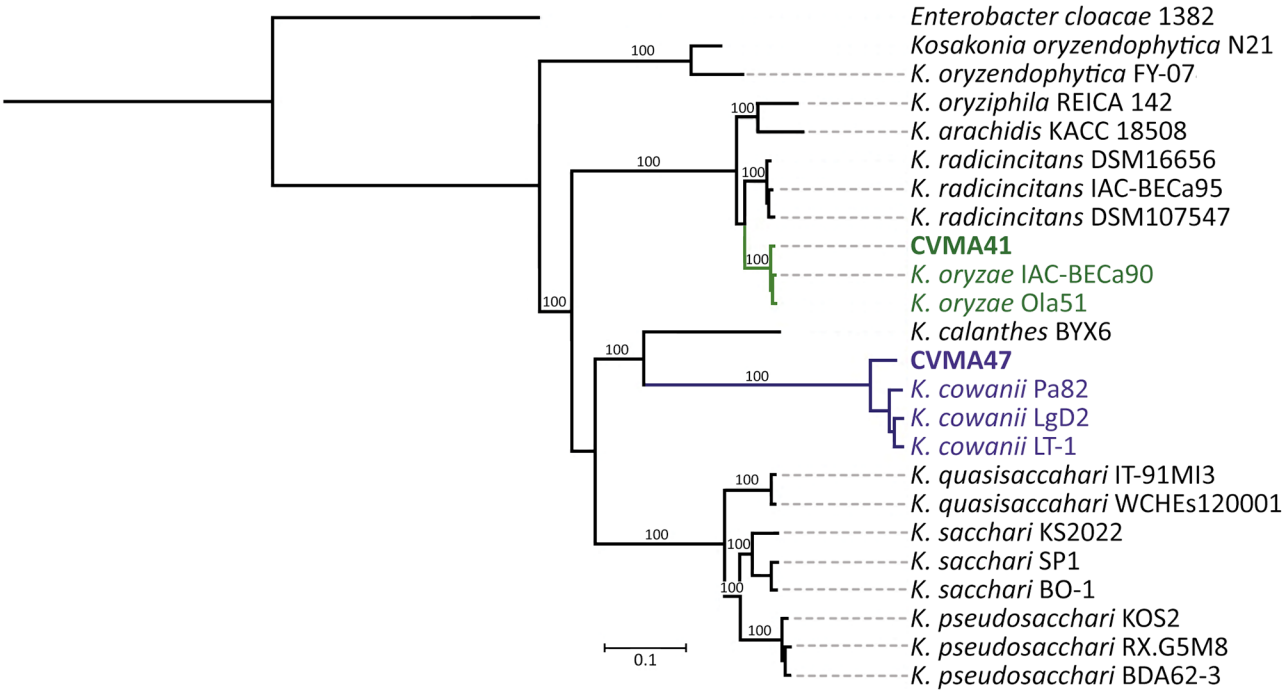

Figure. Data from a study of 2 cases of posttraumatic *Kosakonia* infection, Argentina, 2023. Maximum-likelihood phylogeny calculated using 1,214,977 single-nucleotide variants from a core-gene alignment of 3,232 genes from genomes of *Kosakonia*-described species with 1,000 bootstraps. Green indicates CVMA41 clusters, violet indicates CVMA47 clusters. Tree rooted in an *Enterobacter cloacae* genome included as an outgroup. Scale bar indicates substitutions per site.

K. oryzae sequence Ola 51. Relative to the same reference, we noted an average nucleotide identity value of 98.83% and a digital DNA-DNA hybridization value of 91.6%, with ribosomal multilocus sequence typing identifying the strain as the same species with 94% support. Those results differed from MALDI-TOF mass spectrometry identification and indicated *K. oryzae* as a clinically relevant human pathogen. For strain CMVA47, although the 16S rRNA gene (99.77% identity) and average nucleotide identity (95.94%) supported identification as *K. cowanii*, the digital DNA-DNA hybridization value (65.1%) fell below the 70% threshold typically used for species delineation.

We produced a core genome phylogeny analysis based on concatenated sequences of 3,232 core genes that shared ≥50% sequence identity and were present in ≥80% of the included genomes (1 reference genome of each *Kosakonia* species, if present, downloaded from the National Center for Biotechnology Information RefSeq database [https://www.ncbi.nlm.nih.gov/refseq]). CVMA41 clustered with *K. oryzae* and CVMA47 clustered with *K. cowanii*, with 100% bootstrap support (Figure). The genomic divergence observed in CMVA47 suggested that revisiting genomic thresholds within the *Kosakonia* genus might be necessary, as seen in other genera (*7*).

Antimicrobial susceptibility testing revealed that both isolates were susceptible to aminoglycosides, fluoroquinolones, trimethoprim/sulfamethoxazole, extended-spectrum cephalosporins, and carbapenems. Of note, although CMVA41 was susceptible to all tested agents, CVMA47 exhibited resistance to ampicillin and intermediate susceptibility to cefazolin. This phenotypic profile serves as a marker distinguishing *Kosakonia* spp. from *Enterobacter cloacae* complex. *Enterobacter cloacae* complex typically exhibits intrinsic resistance to ampicillin/sulbactam and carries an inducible chromosomal *ampC* β-lactamase that can lead to third-generation cephalosporin resistance upon derepression, but both *Kosakonia* isolates remained susceptible to these agents. Genomic analysis confirmed the absence of *ampC* and its regulator *ampR* in both strains. This distinction is clinically relevant, supporting the use of ampicillin/sulbactam or cephalosporins as therapeutic options, sparing carbapenems. Consequently, we theorized that the ampicillin resistance in CVMA47 was likely attributable to the putative chromosomic β-lactamase KSA-1, which was identified in *Kosakonia sacchari*, showing 78.6% similarity to this class A extended-spectrum β-lactamase, rather than an AmpC-type enzyme (*8*). Our results further support that genomic divergence in CVMA47 is biologically meaningful. Researchers noted similar findings regarding *Kluyvera* spp., where the presence of intrinsic β-lactamases were linked to species differentiation and the proposal of refined taxonomic thresholds (*9*).

Identifying *Kosakonia* isolates in this study illustrates the challenges that clinical laboratories face with emerging pathogens. The cases we describe contribute to the growing evidence that *Kosakonia* infections are strongly associated with traumatic inoculation of plant material, although reports have described endogenous infections (*3*,*10*). The identification of *K. oryzae* as a human pathogen expands the spectrum of *Kosakonia* species with clinical relevance. MALDI-TOF mass spectrometry represents a considerable improvement over biochemical tests, but the reliability of such analysis is contingent on updated databases (*6*). WGS thus stands as the standard for accurate identification of such environmental pathogens, essential for defining their epidemiology and guiding antimicrobial stewardship.

Short reads for both sequenced isolates have been submitted to the National Center for Biotechnology Information Short Read Archive (accession no. PRJNA1389793).

This study was conducted in accordance with the Ethics Committee of Hospital de Clínicas José de San Martín, Buenos Aires, Argentina, and the Declaration of Helsinki (2024 version), the National Ministry of Health Resolution 1480/11, and the National Law on Personal Data Protection No. 25.326

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Dr. Barberis is an adjunct professor at the University of Buenos Aires and serves at the "Hospital de Clínicas José de San Martín", Buenos Aires, Argentina, as a biochemist and bacteriologist. Her areas of clinical interest include microbiology teaching, identification and taxonomy of emerging pathogens, and the challenges in clinical diagnostics, including proteomics and antimicrobial resistance.

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nov. as *Kosakonia cowanii* comb. nov., *Kosakonia radicincitans* comb. nov., *Kosakonia oryzae* comb. nov. and *Kosakonia arachidis* comb. nov., respectively, and *E. turicensis*, *E. helveticus* and *E. pulveris* into *Cronobacter* as *Cronobacter zurichensis* nom. nov., *Cronobacter helveticus* comb. nov. and *Cronobacter pulveris* comb. nov., respectively, and emended description of the genera *Enterobacter* and *Cronobacter*. Syst Appl Microbiol. 2013;36:309–19. https://doi.org/10.1016/j.syapm.2013.03.005

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Mycobacterium riyadhense Pulmonary Disease after Relocation from Saudi Arabia, Japan

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We report a case of *Mycobacterium riyadhense* pulmonary disease in a patient who relocated from Saudi Arabia to Japan. Epidemiologic data and whole-genome analyses of the isolated strains suggested that the infection might have been acquired in Saudi Arabia and persisted, rather than a recent local acquisition in Japan.

Mycobacterium riyadhense, first isolated in Saudi Arabia, has been reported mainly in the Middle East (*1*) and sporadically elsewhere (*2*,*3*). We describe a patient who experienced slowly progressive pulmonary deterioration caused by *M. riyadhense* infection after she relocated from Saudi Arabia to Japan. Because *M. riyadhense* has not been reported in Japan, genomic analysis of the patient's isolates was more consistent with within-host persistence of a preexisting infection than recent local acquisition from environmental exposure in Japan.

A 47-year-old woman was referred to Kitasato University Kitasato Institute Hospital (Tokyo, Japan) after granular opacities were detected in the right lung on screening. She had lived in Saudi Arabia for 2 years, where she had chronic exposure to sand and dust. A visibly contaminated, uncleaned air-conditioning unit at her home housed a bird's nest for 7 months and remained in use. She took only showers and rarely cleaned the shower room. She also gardened regularly. Shortly before her initial visit for care, she returned to Japan, bringing back only clothing and no other household belongings. She resumed tub bathing; the showerhead was replaced 4 years after her return, while her illness was being monitored.

Computed tomography (CT) revealed multiple small nodular opacities in the right upper and middle