

was listeriosis. Empirically prescribed antimicrobial therapy (ceftazidime, colistin, amikacin, and metronidazole) was given for 96 hours and then replaced by gentamicin for 48 hours and amoxicillin for 3 weeks; clinical results were favorable.

The isolate strain was analyzed by the Division of Bacterial Identification (Pasteur Institute, Paris, France). The 16S rRNA gene was completely sequenced. A phylogenetic tree was generated by using the neighbor-joining algorithm (3). The isolate was found to be *C. divergens*. Microbiological cultures and 16S rRNA testing results for another sample of enteral nutrition solution and a surgical specimen of the necrotic esophagus were negative.

Three reports of isolation of *Carnobacterium* sp. from humans have been published. The first report described isolation of *Carnobacterium* sp. from 1 set of blood cultures from a man who had prepared fish before onset of fever (4). The imputability of this diagnosis could not be clearly established because only 1 set of blood cultures had positive results. The second report described isolation of *C. piscicola* from pus after traumatic amputation of a hand by an industrial water sawmill (5). The third report described isolation from a child's hand with multibacterial synergistic gangrene (6).

For the case described here, the presence of *C. divergens* in blood cultures cannot be considered contamination because it was isolated from 4 sets of blood cultures collected over 5 days. We hypothesize that bacterial translocation was caused by low mesenteric flow after 2 episodes of cardiac arrest. Because the patient was receiving exclusively enteral nutrition, we presume that the origin of the infection was bacterial contamination of the solution or colonization of the feeding tube. Carnobacteria and lactobacilli (which are used as probiotic bacteria or fermented food products) are similar in that each is found in food, can be used as a biopreservative, and is considered nonpathogenic. The pathogenic relevance of lactobacilli is uncommon, but some clinical infections have been reported, including septicemia and meningitis (7). Because *C. divergens* seems to be able to cause life-threatening infection in immunocompromised patients, its safe use in such patients and in the food industry should be monitored.

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Fatal Nosocomial MDR TB Identified through Routine Genetic Analysis and Whole-Genome Sequencing

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DOI: <http://dx.doi.org/10.3201/eid2106.141903>

To the Editor: In November 2012, a 44-year-old HIV-negative white man (patient 1) with fever, fatigue, and breathlessness sought care at a hospital in the United Kingdom. He had never traveled abroad but had biopsy-proven alcoholic cirrhosis. No acid-fast bacilli were seen on multiple samples, including ascitic fluid, and he received treatment for presumptive abdominal tuberculosis (TB). *Mycobacterium tuberculosis* was subsequently cultured after 12 days. His clinical condition deteriorated, and he died of multiorgan failure 44 days after admission. The cultured *M. tuberculosis* was subsequently

confirmed as multidrug resistant (online Technical Appendix Table, <http://wwwnc.cdc.gov/EID/article/21/6/14-1903-Techapp1.pdf>).

Routine mycobacterial interspersed repetitive unit–variable-number tandem-repeat (MIRU–VNTR) testing was performed (1) (online Technical Appendix Table). A matching MIRU–VNTR profile was identified from a 42-year-old South African–born, HIV-positive health care worker (patient 2) who had died in 2008 after admission to the same hospital. She has been described previously in detail because she had worked at Tugela Ferry hospital in KwaZulu-Natal, South Africa, which was associated with a 2005 outbreak of multidrug-resistant TB (MDR TB) and extensively drug-resistant TB (2,3) (online Technical Appendix Figure 1). To ascertain whether these isolates could have matching MIRU–VNTR patterns by chance alone, we compared the MIRU–VNTR results with a national database of $\approx 11,745$ isolates typed since the UK typing service began in 2010. Only 2 other isolates matched (from patients 3 and 4), originating from a UK hospital ≈ 100 miles away. Although both patients were HIV-positive health care workers from sub-Saharan Africa, no history of contact could be established with patients 1 or 2.

A review of admission records established that patients 1 and 2 were admitted to the same medical ward in 2008 for 8 days, suggesting a high probability of nosocomial transmission. The ward had a traditional “Nightingale” configuration with beds for male and female patients arranged dormitory-style. In 2009, patient 1 had been identified as a contact of patient 2 and was offered screening for latent infection but had failed to attend appointments and was not under regular medical follow-up. No other common contact was identified. The estimated time from known contact between patients 1 and 2 until the clinical presentation of patient 1 was 49 months.

Sequencing libraries from genomic DNA extracted from the 4 UK *M. tuberculosis* isolates that had matching MIRU–VNTR profiles were paired-end sequenced by using Illumina MiSeq (Illumina, San Diego, CA, USA). To investigate the origins of the infections, they were compared with 36 South Africa strains (including 1 from the Tugela Ferry outbreak [4]) sequenced by using Illumina HiSeq 2000 platforms.

For each sequenced strain, a random subset of reads was aligned at $\approx 100\times$ coverage to the *M. tuberculosis* H37Rv reference genome by using BWA version 0.5.9-r16 (5). Pilon v1.5 (<http://www.broadinstitute.org/software/pilon/>) was run in variant discovery to generate a list of single-nucleotide polymorphisms (SNPs) and insertions and deletions. We estimated a phylogeny using RAxML v7.7.8 (6) using a general time reversible + gamma substitution model with 1,000 bootstrap replicates.

Pairwise comparison of whole-genome sequences from *M. tuberculosis* isolated from patients 1 and 2 found that the 2 sequences differed at only 4 SNPs (Table). Based on previous estimates of background mutations rates of 0.5 SNP/year (7), the pairwise distance between isolates from patient 1 and 2 increases confidence in the epidemiologic data implicating transmission >4 years earlier, although uncertainties exist around such estimates. Comparison between samples from patient pairs (1+2 vs. 3+4) found differences of 69–72 SNPs, which strongly argues against transmission between them.

In comparison with isolates sampled from KwaZulu-Natal (online Technical Appendix Figure 1), isolates from patients 1 and 2 were closely related to a strain associated with the Tugela Ferry outbreak (KZN605; online Technical Appendix Figure 2). Isolates from patients 3 and 4 were less closely related to isolates from the Tugela Ferry outbreak but were closely related to other isolates circulating within the region, consistent with the hypothesis that both infections originally occurred within South Africa.

This investigation illustrates the power of current technology to inform our understanding of the links in MDR TB transmission between low- and high-incidence areas. Whole-genome sequencing of pathogens is becoming part of routine practice for establishing transmission and resistance patterns (8). The greater certainty it brings to transmission data can provide evidence to justify more active policies of screening and isolation as part of infection control. The nosocomial transmission described here is consistent with the fact that a person with pulmonary TB (patient 2) was managed on an open ward before being put into respiratory isolation and had not been previously screened by occupational health services.

Recent data reviewing MDR TB transmission in the United Kingdom before 2007 did not identify cases of

Table. Pairwise distances between 2 pairs of *Mycobacterium tuberculosis* isolates from patients in the United Kingdom, an isolate from the 2005 Tugela Ferry outbreak in KwaZulu-Natal, South Africa (KZN605), and reference strain H37Rv

Isolate	Patient 1	Patient 2	KZN605	Patient 3	Patient 4	H37Rv
Patient 1	0					
Patient 2	4	0				
KZN605	21	24	0			
Patient 3	84	80	87	0		
Patient 4	87	83	90	2	0	
H37Rv	862	862	887	849	830	0

nosocomial transmission during that period (9). However, the emergence of MDR TB in regions of high HIV prevalence is relatively recent (10), and the cases described here suggest that increased vigilance for TB and MDR TB among migrating health care workers might be required.

Acknowledgments

We thank the families of patients who gave permission for this study and all those involved in data collection. We also thank Tim Brown, Vladyslav Nikolayevskyy, and Madeline Stone for the VNTR analysis and helpful comments and the staff of Public Health England National Mycobacterium Reference Laboratory for their assistance.

This study was supported in part by the Imperial College NHS Trust Biomedical Research Centre, National Institute for Health Research Health Protection Research Units (NIHR HPRU) in Healthcare Associated Infection and Antimicrobial Resistance and the NIHR HPRU in Respiratory Infections, both at Imperial College London in partnership with Public Health England. We received funding from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, US Department of Health and Human Services, under contract no. HHSN272200900018C and grant no. U19AI110818. T.A. is a postdoctoral fellow of the Research Foundation–Flanders.

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Fatal Bacteremia Caused by *Campylobacter gracilis*, United States

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DOI: <http://dx.doi.org/10.3201/eid2106.142043>

To the Editor: *Campylobacter* species are well known to cause gastrointestinal infections in humans. However, extraintestinal illnesses caused by *Campylobacter* spp., including bacteremia, can also occur, primarily in immunocompromised persons (1). *Campylobacter gracilis* is a newly recognized species (2) that is commonly found in the oral flora and that has been associated with periodontal diseases and pleuropulmonary infections (3–6). Furthermore, a wide range of infectious etiologies caused by *C. gracilis* at different anatomic sites have been reported in the literature, suggesting its highly pathogenic potential (7,8). We describe a case of bacteremia due to *C. gracilis* complicated by pneumonia.

An 80-year-old man with a history of hypertension, hypertensive nephropathy, and chronic obstructive pulmonary disease (COPD) was in his usual health status when he began having worsening productive cough, fevers, and malaise; he sought health care 5 days later at Long Island College Hospital (Brooklyn, NY, USA). A heavy smoker who was noncompliant with his COPD treatment, he had frequent episodes of COPD exacerbation necessitating chronic maintenance with oral steroid therapy.

At physical examination, the patient appeared chronically ill and had mild respiratory distress. His temperature was 100.8°F, blood pressure 124/67 mm Hg, pulse 106 beats/min, respiration 22 breaths/min, and oxygen saturation 94% on room air. His heart sounds revealed tachycardia without murmurs, and his lung sounds disclosed scattered wheezing and rhonchi.

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Technical Appendix

Technical Appendix Table. Characteristics of 4 clinical isolates from patients with multidrug-resistant tuberculosis*

Patient	MIRU-VNTR	RIF	rpoB	rpoB	INH	katG	mabA†	PZA	pncA	EMB	embB	STR	gidB‡	gidB‡
1	224331432615324 33241328	R	L452P§	H1028R	R	S315T	-8(t>a)	R	ins¶	R	M306V	S	130 bp del	R
2	224331432615324	R	L452P§	H1028R	R	S315T	-8(t>a)	R	ins¶	R	M306V	-	130 bp del	R
3	22433143261532- 3324132-	S	-	-	R	S315T	-	S	-	S	-	R	-	L26S
4	22433143261532- 33241328	S	-	-	R	S315T	-	S	-	S	-	R	-	L26S

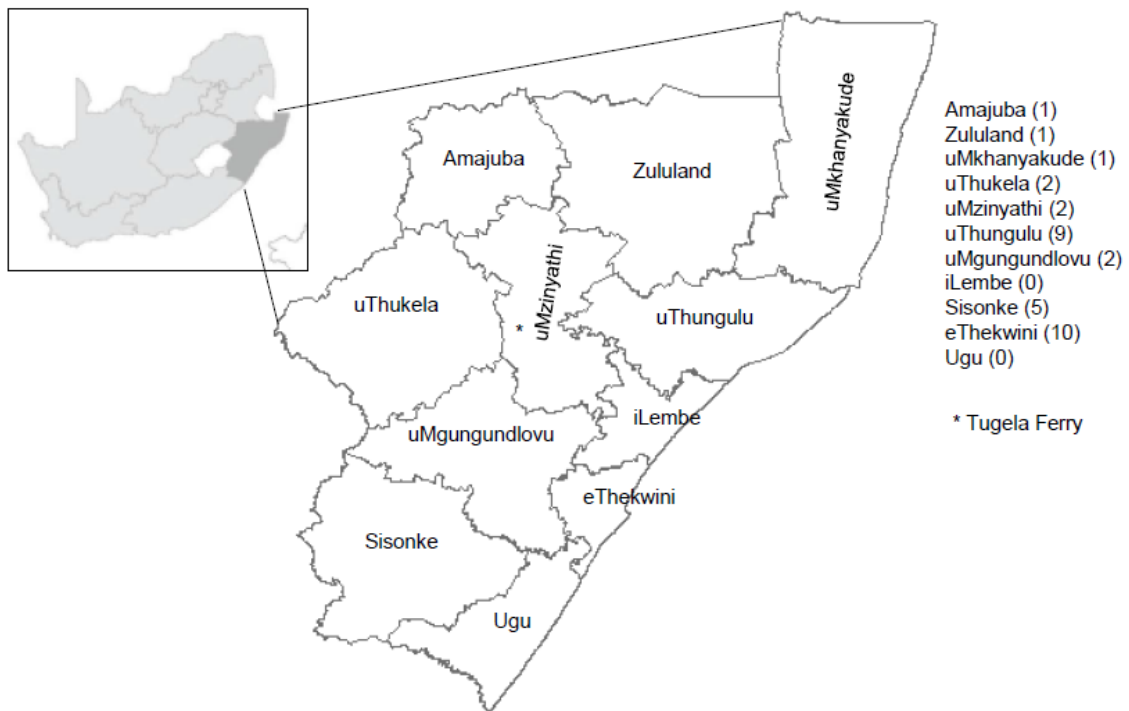
*EMB, ethambutol; INH, isoniazid; MIRU-VNTR, mycobacterial interspersed repetitive units-variable-number tandem-repeat; PZA, pyrazinamide; R, resistant; RIF, rifampin; S, sensitive; STR, streptomycin.

†Promoter mutation, cross-resistance to thioamides.

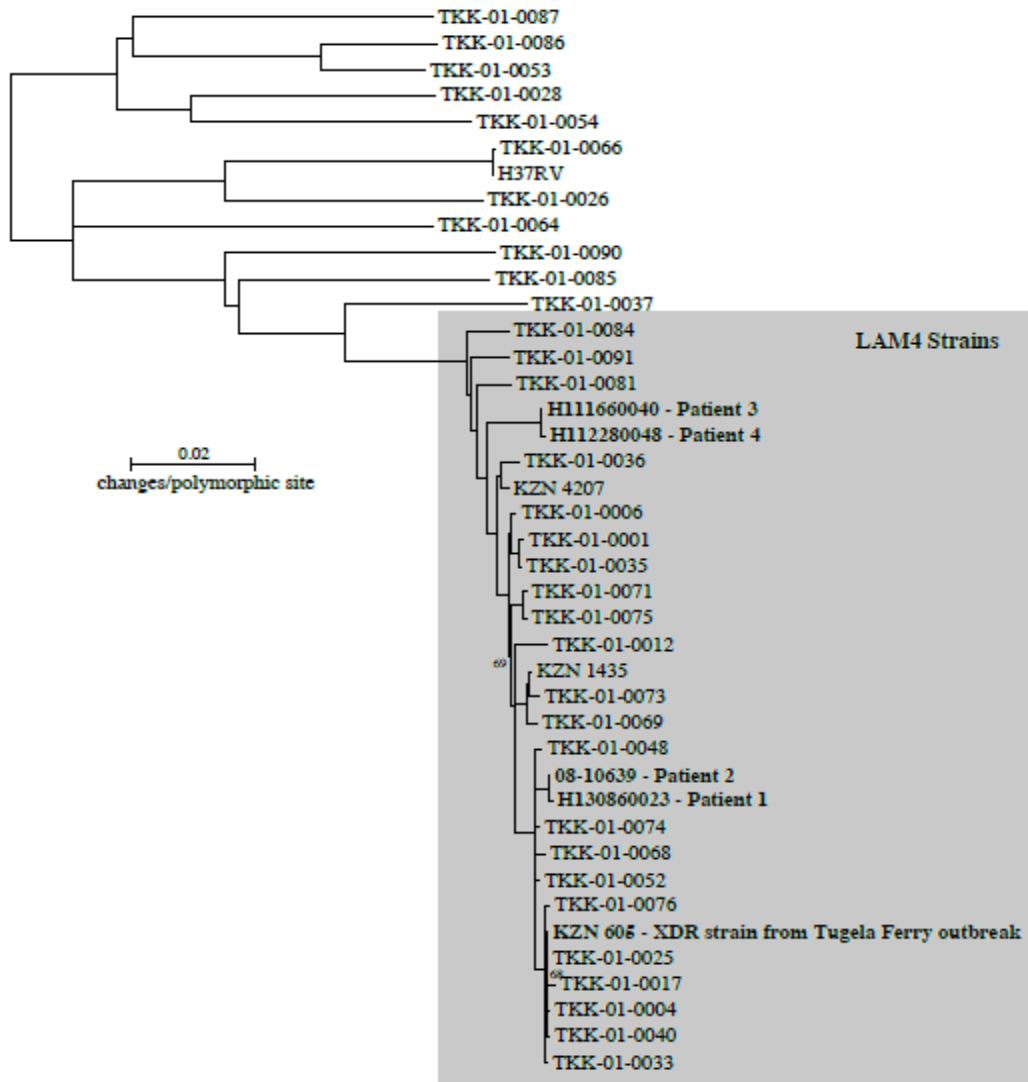
§*Escherichia coli* L533P

‡No resistance single-nucleotide polymorphisms in rpsL or rrs.

¶1 bp insertion in codon 153.



Technical Appendix Figure 1. Isolates sequenced from KwaZulu-Natal (KZN), South Africa, with number from each district sampled as part of KZNSUR project. Inset: Map of South Africa with KZN shaded



Technical Appendix Figure 2. Phylogenetic representation of isolates collected from the United Kingdom (patients 1–4) and KZN (33) Nodes with bootstrap values <80 are indicated. Sequencing data were submitted to the Sequence Read Archive with identifiers: PRJNA198182, PRJNA198181, PRJNA198148, PRJNA198149, PRJNA198124, PRJNA198185, PRJNA198180, PRJNA198186, PRJNA198176, PRJNA198108, PRJNA198103, PRJNA198130, PRJNA183521, PRJNA198168, PRJNA227150, PRJNA198163, PRJNA198172, PRJNA198106, PRJNA183515, PRJNA198122, PRJNA227148, PRJNA198135, PRJNA198128, PRJNA198147, PRJNA198169, PRJNA198143, PRJNA198113, PRJNA198167, PRJNA198170, PRJNA198131, PRJNA227149, PRJNA198179, PRJNA198132, PRJNA183519, PRJNA198161, PRJNA198159 ERS568284, ERS568285, ERS568286, ERS 568287