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 exclusive 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 septicaemia 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.

### References

1. Leisner JJ, Laursen BG, Prévost H, Drider D, Dalgaard P. *Carnobacterium*: positive and negative effects in the environment and in foods. FEMS Microbiol Rev. 2007;31:592–613. http://dx.doi.org/10.1111/j.1574-6976.2007.00080.x
2. Afzal MI, Jacquet T, Delaunay S, Borges F, Millière JB, Revol-Junelles AM, et al. *Carnobacterium maltaromaticum*: identification, isolation tools, ecology and technological aspects in dairy products. Food Microbiol. 2010;27:573–9. http://dx.doi.org/10.1016/j.fm.2010.03.019
3. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. 1987;4:406–25.
4. Hoenigl M, Grisoll T, Leisner J, Zarfel G, Renner H, et al. Isolation of *Carnobacterium* sp. from a human blood culture. J Med Microbiol. 2010;59:493–5. http://dx.doi.org/10.1099/jmm.0.016808-0
5. Chmelar D, Matusek A, Korner J, Durnová E, Steffen M, Chmelarová E. Isolation of *Carnobacterium piscicola* from human pus—case report. Folia Microbiol (Praha). 2002;47:455–7. http://dx.doi.org/10.1007/BF02882606
6. Xu J, Yang H, Lai X, Fu X, Wu J, Huang L, et al. Etiological study for a case of multi-bacterial synergistic gangrene. Chin Sci Bull. 1997;42:511–7. http://dx.doi.org/10.1007/BF02818708
7. Cannon JP, Lee TA, Bolanos JT, Danziger LH. Pathogenic relevance of *Lactobacillus*: a retrospective review of over 200 cases. Eur J Clin Microbiol Infect Dis. 2005;24:31–40. http://dx.doi.org/10.1007/s10096-004-1253-y

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

O. Martin Williams, Thomas Abeel, Nicola Casali, Keira Cohen, Alex S. Pym, Sarah B. Mungall, Christopher A. Desjardins, Anindo Banerjee, Francis Drobniewski, Ashlee M. Earl, Graham S. Cooke

Author affiliations: Bristol Royal Infirmary, Bristol, UK (O.M. Williams); Delft University of Technology, Delft, the Netherlands (T. Abeel); Broad Institute, Cambridge, Massachusetts, USA (T. Abeel, C.A. Desjardins, A.M. Earl); Queen Mary University of London, London, UK (N. Casali); Imperial College London, London (N. Casali, F. Drobniewski, G.S. Cooke); K-Research Institute for TB/HIV, Durban, South Africa (K. Cohen, A.S. Pym); University Hospitals Bristol NHS Foundation Trust, Bristol (S.B. Mungall); University Hospital Southampton NHS Trust, Southampton, UK (A. Banerjee)

Address for correspondence: Christia Palacios, Avicenne Hospital, 125 Rue de Stalingrad, 93000 Bobigny, France;
email: christia.palacios@avc.aphp.fr

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 ≈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 ≈100× 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

| Isolate | Patient 1 | Patient 2 | KZN605 | Patient 3 | Patient 4 | H37Rv |
|---------|-----------|-----------|--------|-----------|-----------|-------|
| Patient 1 | 0         | 0         | KZN605 | 0         | 0         | 0     |
| Patient 2 | 4         | 0         | 21     | 24        | 0         | 0     |
| KZN605 | 21         | 24        | 0      | 0         | 0         | 0     |
| Patient 3 | 84        | 80        | 87     | 90        | 2         | 0     |
| Patient 4 | 87        | 83        | 90     | 2         | 0         | 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 Nikolayevsky, 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.

References
1. Brown TJ, Nikolayevsky VN, Drobniewski FA. Typing Mycobacterium tuberculosis using variable number tandem repeat analysis. Methods Mol Biol. 2009;465:371–94. http://dx.doi.org/10.1007/978-1-59745-207-6_25
2. Gandhi NR, Moll A, Sturm AW, Pawiński R, Govender T, Laloo U, et al. Extensively drug-resistant tuberculosis as a cause of death in patients co-infected with tuberculosis and HIV in a rural area of South Africa. Lancet. 2006;368:1575–80. http://dx.doi.org/10.1016/S0140-6736(06)69573-1
3. Cooke GS, Beaton RK, Lessells RJ, John L, Ashworth S, Kon OM, et al. International spread of MDR TB from Tugela Ferry, South Africa. Emerg Infect Dis. 2011;17:2035–7. http://dx.doi.org/10.3201/eid1711.110291
4. Ioerger TR, Koo S, No EG, Chen X, Larsen MH, Jacobs WR Jr, et al. Genome analysis of multi- and extensively-drug-resistant tuberculosis from KwaZulu-Natal, South Africa. PLoS ONE. 2009;4:e7778. http://dx.doi.org/10.1371/journal.pone.0007778
5. Li H, Darbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics. 2009;25:1754–60. http://dx.doi.org/10.1093/bioinformatics/btp324
6. Stamatakis A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics. 2006;22:2688–90. http://dx.doi.org/10.1093/bioinformatics/btl446
7. Walker TM, Ip CL, Harrell RH, Evans JT, Kapatai G, Dedicot MJ, et al. Whole-genome sequencing to delineate Mycobacterium tuberculosis outbreaks: a retrospective observational study. Lancet Infect Dis. 2013;13:137–46. http://dx.doi.org/10.1016/S1473-3099(12)70277-3
8. Köser CU, Holden MT, Ellington MJ, Cartwright EJ, Brown NM, Ogilvy-Stuart AL, et al. Rapid whole-genome sequencing for investigation of a neonatal MRSA outbreak. N Engl J Med. 2012;366:2267–75. http://dx.doi.org/10.1056/NEJMoa1109910
9. Anderson LF, Tamne S, Brown T, Watson JP, Mullarkey C, Zenner D, et al. Transmission of multidrug-resistant tuberculosis in the UK: a cross-sectional molecular and epidemiological study of clustering and contact tracing. Lancet Infect Dis. 2014;14:406–15. http://dx.doi.org/10.1016/S1473-3099(14)70022-2
10. Abdool Karim SS, Churchyard GJ, Karim QA, Lawn SD. HIV infection and tuberculosis in South Africa: an urgent need to escalate the public health response. Lancet. 2009;374:921–33. http://dx.doi.org/10.1016/S0140-6736(09)60916-8

Address for correspondence: Graham S. Cooke, Imperial College, Jefferiss Laboratories, St. Mary’s Campus, Praed St, London W21NY, UK; email: g.cooke@imperial.ac.uk

Fatal Bacteremia Caused by Campylobacter gracilis, United States

Takashi Shinha

Author affiliation: Vanderbilt University Medical Center, Nashville, Tennessee, USA

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

Technical Appendix

| Patient | MIRU-VNTR | RIF | rpoB | rpoB | INH | katG | mabA† | PZA | pncA | EMB | embB | STR | gidB‡ | gidB‡ |
|---------|-----------|-----|------|------|-----|------|-------|-----|------|-----|------|-----|-------|-------|
| 1       | 22431432615324 | R   | L452P§ | H1028R | R   | S315T | –8(t>a) | R   | ins‡ | R   | M306V | S   | 130 bp del | R     |
| 2       | 22431432615324 | R   | L452P§ | H1028R | R   | S315T | –8(t>a) | R   | ins‡ | R   | M306V | –   | 130 bp del | R     |
| 3       | 22431432615324 | S   | –     | –     | R   | S315T | –     | S   | –    | S   | –     | R   | –     | L26S  |
| 4       | 22431432615324 | 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