ACKNOWLEDGMENTS

Financial support: None reported.

Potential conflicts of interest: All authors report no conflicts of interest relevant to this article.

Teena Chopra, MD, MPH;[1]
David Bavers, MS;[1]
Suganya Chandramohan, MD;[1]
Glenn Tillotson, PhD[2]

Affiliations: 1. Division of Infectious Diseases, Wayne State University, Detroit, Michigan; 2. GST Micro, Downingtown, Pennsylvania.

Address correspondence to Teena Chopra, MD, MPH, Division of Infectious Diseases, Wayne State University, 3990 John R St, Detroit, MI 48201 (tchopra@med.wayne.edu).

Infect Control Hosp Epidemiol 2016;37:620–622

 0899-823X/2016/3705-0025. DOI: 10.1017/ice.2016.25

REFERENCES

1. National Transitions of Care Coalition (NTOCC). Improving transitions of care. NTOCC website. http://www.ntocc.org/Portals/0/PDF/Resources/PolicyPaper.pdf. Published 2008. Accessed 2015.
2. Coleman EA. Falling through the cracks: challenges and opportunities for improving transitional care for persons with continuous complex care needs. *J Am Geriatr Soc* 2003;51:549–555.
3. Liu K, Baseggio C, Wissoker D, et al. Long-term care hospitals under Medicare: facility-level characteristics. *Health Care Financ Rev* 2001;23:1–18.
4. Stevens RD, Hart N, Herridge MS. eds. *Textbook of Post-ICU Medicine: The Legacy of Critical Care*. New York: Oxford University Press, 2014.
5. Kahn JM, Benson NM, Appleby D, et al. Long-term acute care hospital utilization after critical illness. *JAMA* 2010;303:2253–2259.
6. Gould CV, Rothenberg R, Steinberg JP. Antibiotic resistance in long-term acute care hospitals: the perfect storm. *Infect Control Hosp Epidemiol* 2006;27:920–925.
7. Austin DJ, Bonten MJ, Weinstein RA, et al. Vancomycin-resistant enterococci in intensive-care hospital settings: transmission dynamics, persistence, and the impact of infection control programs. *Proc Nat Acad Sci* 1999;96:6908–6913.
8. Furuno JP, Hebden JN, Standiford HC, et al. Prevalence of methicillin-resistant *Staphylococcus aureus* and *Acinetobacter baumannii* in a long-term acute care facility. *Am J Infect Control* 2008;36:468–471.
9. Goldstein EJ, Polonsky J, Touzani MH, Citron DM. *Clostridium difficile* infection (CDI) in a long-term acute care facility (LTAC). *Anaerobe* 2009;15:241–243.
10. Medicare Payment Advisory Commission (MEDPAC). Report to the Congress: Medicare payment policy. Pages 261–282. MEDPAC website. http://www.medpac.gov/documents/reports/mar2015_entirereport_revised.pdf?sfvrsn=0. Published 2015.
11. Harris-Kojetin L, Sengupta M, Park-Lee E, Valverde R. Long-term care services in the United States: 2013 overview. National Center for Health Statistics. Vital Health Stat 3. CDC website. http://www.cdc.gov/nchs/data/nsltcp/long_term_care_services_2013.pdf. Published 2013.
12. Long-term and post-acute care (LTPAC) health information technology (HIT) collaborative. http://ltpachealthit.org. Accessed December 2015.
13. Association of American Medical Colleges (AAMC). The 2012 physician specialty data book. AAMC website. https://www.aamc.org/download/313228/data/2012physicianspecialtydatabook.pdf. Accessed December 2015.

Benchtop Whole-Genome Sequencing for Identification of Nosocomial Outbreaks in Tanzania

To the Editor—Rapid and reliable identification, characterization, and comparison of microorganisms from clinical samples are essential means for guiding clinical treatment as well as for detecting and controlling disease outbreaks. Developments in benchtop whole-genome sequencing (WGS) hold great promise for enhancing microbial diagnostics and thus for improving public health.[1–6] The great value of WGS in studying bacterial evolution, disease outbreaks, and transmission has been demonstrated in recent studies,[5,6] and the technology is increasingly being implemented in routine clinical diagnostics in developed countries. There is huge potential for WGS to improve clinical diagnostics and infection control in developing countries where clinical laboratories do not have access to different routine typing methods and where the burden of infectious diseases is highest.

To test the feasibility of integrating WGS into the routine diagnostics workflow, in February 2015, a total of 18 bacterial genomes were sequenced on a benchtop sequencer (MiSeq; Illumina) at the Kilimanjaro Christian Medical Centre, the second largest referral hospital in northeastern Tanzania. Sequence data were immediately analyzed using open access web-based tools (http://cge.cbs.dtu.dk/services).

Two *Enterococcus faecalis* from different patients were identified, both having sequence type 415. A similar *E. faecalis* with sequence type 415 had been found in poultry and humans in Vietnam.[7] Single-nucleotide polymorphism analysis[6,8] revealed complete similarity between these isolates and both had resistance gene lsa(A) encoding lincosamide and streptogramin A resistance.[9]

Patient records revealed that the 2 patients were hospitalized in the same room and both were receiving ceftriaxone medication. Patient 1 had been hospitalized for 1 month when a swab sample was collected from a diabetic wound. Patient 2 had undergone emergency surgery for an abdominal gunshot wound, a week after which a swab sample was collected from the surgical wound. The exact match in sequence type strongly

suggests nosocomial transmission. Owing to limited resources, the current routine microbiology workflow at our setting—as is the case in most laboratories in developing countries—does not include bacterial typing to identify nosocomial infections. The hospital infection prevention strategies are generic and focus on hygienic procedures rather than identification of microorganisms.

Availability of robust and rapid WGS allowing simultaneous genotyping of different microorganisms within a relatively short time holds the potential of controlling nosocomial infections and improving care. The decreasing initial and recurrent costs of WGS give optimism that in the near future this technology will be applied more widely in resource-limited settings, which are struggling with a disproportionately high burden of infectious diseases with suboptimal infection control strategies.

ACKNOWLEDGEMENTS

Financial support. This study was supported by the Danish International Development Agency (project 12007DTU).

Potential conflicts of interest. All authors report no conflicts of interests relevant to this article.

Tolbert Sonda, MSc;[1,2]
Happiness Kumburu, MSc;[1,2]
Marco van Zwetselaar, MSc;[1]
Johanne Ahrenfeldt, MSc;[3]
Michael Alifrangis, PhD;[4,5]
Ole Lund, PhD;[3]
Gibson Kibiki, MD;[1,2]
Frank M. Aarestrup, PhD[6]

Affiliations: 1. Kilimanjaro Clinical Research Institute, Kilimanjaro Christian Medical Centre, Moshi, Tanzania; 2. Kilimanjaro Christian Medical University College, Moshi, Tanzania; 3. Centre for Biological Sequence Analysis, Technical University of Denmark, Copenhagen, Denmark; 4. Centre for Medical Parasitology, Institute of International Health, Immunology, and Microbiology, University of Copenhagen, Copenhagen, Denmark; 5. Department of Infectious Diseases, Copenhagen University Hospital, Copenhagen, Denmark; 6. Centre for Genomic Epidemiology, Technical University of Denmark, Copenhagen, Denmark.

Address correspondence to Frank Møller Aarestrup, Centre for Genomic Epidemiology, Technical University of Denmark, 2800 Lyngby, Denmark (fmaa@food.dtu.dk).

Infect Control Hosp Epidemiol 2016;37:622–623
 0899-823X/2016/3705-0026. DOI: 10.1017/ice.2016.28

REFERENCES

1. Koser CU, Fraser LJ, Ioannou A, et al. Rapid single-colony whole-genome sequencing of bacterial pathogens. *J Antimicrob Chemother* 2014;69:1275–1281.
2. Aarestrup FM, Brown EW, Detter C, et al. Integrating genome-based informatics to modernize global disease monitoring, information sharing, and response. *Emerg Infect Dis* 2012;18:e1.
3. Quiñones D, Kobayashi N, Nagashima S. Molecular epidemiologic analysis of *Enterococcus faecalis* isolates in Cuba by multilocus sequence typing. *Microb Drug Resist* 2009; 15:287–293.
4. Larsen MV, Cosentino S, Rasmussen S, et al. Multilocus sequence typing of total-genome-sequenced bacteria. *J Clin Microbiol* 2012;50:1355–1361.
5. Joensen KG, Scheutz F, Lund O, et al. Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic *Escherichia coli*. *J Clin Microbiol* 2014; 52:1501–1510.
6. Leekitcharoenphon P, Nielsen EM, Kaas RS, Lund O, Aarestrup FM. Evaluation of whole genome sequencing for outbreak detection of *Salmonella enterica*. *PLoS One* 2014;9:e87991.
7. Poulsen LL, Bisgaard M, Son NT, Trung NV, An HM. *Enterococcus faecalis* clones in poultry and in humans with urinary tract infections, Vietnam. *Emerg Infect Dis* 2012;18: 1096–1100.
8. Kaas RS, Leekitcharoenphon P, Aarestrup FM, Lund O. Solving the problem of comparing whole bacterial genomes across different sequencing platforms. *PLoS One* 2014;9:e104984.
9. Zankari E, Hasman H, Cosentino S, et al. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 2012;67:2640–2644.

Revised Risk Estimates for MRSA Infection in Patients with Intermittent Versus Persistent MRSA Nares Colonization

We thank Beyersmann and Schrade[1] for their comments, and we agree that the use of an estimator that accounts for death without prior infection is appropriate for our data. As they point out, the raw incidence proportions of methicillin-resistant *Staphylococcus aureus* (MRSA) we reported (16.33% for persistently colonized, 11.18% for intermittently colonized, and 0.51% for non-colonized) reflected observed infections, and did not account for infections that may have occurred after administrative censoring at the study end date. Thus, these data represent an underestimation of risk.

For this reason, we reported proportions based on Kaplan-Meier analysis: 21.26% for persistently colonized, 12.83% for intermittently colonized, and 0.55% for non-colonized. Beyersmann and Schrade aptly pointed out that this analysis does not account for death without prior infection and thus overestimates risk. They propose that the Aalen-Johansen method is a better estimator in this case because it accounts for competing causes. We agree, and we conducted an additional analysis. These new calculations produced results that fall between the other 2 estimates: 20.61% for persistently colonized, 12.16% for intermittently colonized, and 0.54% for non-colonized. The use of the Aalen-Johansen estimator increases the precision of the estimates without changing our overall conclusions.