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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.

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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.