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Letters to the Editor

Water-borne infections and warming the sterile water for washing high-risk infants on neonatal intensive care units

Sir,

Further to Dr Weinbren's informative article, 'The handwash station: friend or fiend?' [1] we would like to mention our previous letter regarding washing high-risk infants on neonatal intensive care units (NICUs) [2]. Washing such infants with tap water runs the risk of colonizing them with water-borne organisms. Furthermore, the use of small water collection pots for these infants can sample the initial tap water with the highest bacterial contamination [1]. Following an outbreak with an antibiotic-resistant Gram-negative organism (which was also found in sink taps), high-risk infants on an NICU were washed with sterile water from single-use bottles [3]. (This is in accordance with the Department of Health advice that sterile or filtered water can be used for 'top and tailing' neonates [4].) Infection control actions regarding the water supply and hand hygiene were taken together with use of sterile water for washing and there were no further cases for several years. Then two more infants developed serious infections with this organism [2].

It was subsequently found that staff had noticed that infants in the warm atmosphere of an incubator could react badly to the cold sterile water, even if it was kept at room temperature. They had therefore changed back to using warm water directly from the sink taps to wash the infants. The problem was resolved by keeping the single-use bottles of sterile water in a warming cabinet so that they were always warm before use. This is a small change but one which may have helped prevent further outbreaks with such water-borne organisms.

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Hospital surface contamination with antimicrobial-resistant Gram-negative organisms in Tanzanian regional and tertiary hospitals: the need to improve environmental cleaning

Sir,

The upsurge of healthcare-associated infections (HCAIs) caused by multi-drug-resistant Gram-negative bacteria (MDR-GNB) has become a serious global threat, especially in resource-limited countries [1]. GNB, such as *Escherichia coli*, *Klebsiella* spp., *Acinetobacter* spp. and *Pseudomonas aeruginosa*, can survive on inanimate surfaces for months, thus serving as a transmission source to healthcare workers and susceptible patients [2]. It is now well established that room occupancy by a patient shedding nosocomial pathogens enhances the risk of acquisition in subsequent patients cared for in the same room [3].

A cross-sectional study was conducted from June to August 2015 at Bugando Medical Centre (BMC) and Sekou Toure Hospital (STH) in Mwanza City, Tanzania to determine the presence

of MDR-GNB on inanimate surfaces and objects. The protocol to conduct this study was approved by the Joint CUHAS/BMC Research Ethics and Review Committee (Clearance Number CREC/019/2014).

In total, 164 non-repetitive swabs (138 from BMC and 26 from STH) were collected. Extended-spectrum beta lactamase (ESBL) screening was performed using MacConkey agar supplemented with cefotaxime (2 μg/mL), followed by Vitek 2 and was confirmed using the double disk synergy method. Of the 164 samples collected, 55 (33.5%) had growth of GNB: *Acinetobacter baumannii* (*N*=17, 30.9%), *Enterobacter cloacae* (*N*=19, 34.5%), *E. coli* (*N*=5, 9.1%) and *Klebsiella pneumoniae* (*N*=14, 25.5%) (Table I). ESBL production was detected in 33 (20.1%) samples, and amongst these, resistance to ciprofloxacin, trimethoprim-sulfamethoxazole, gentamicin and tigecycline was detected in 31 (93.9%), 31 (93.9%), 29 (87.8%) and 11 (33.3%) isolates, respectively. None of the isolates were resistant to ertapenem and meropenem. Of the 17 *A. baumannii* isolates, two were resistant to meropenem (minimum inhibitory concentration ≥8 μg/mL).

ESBL genes (CTX-M Group I) were detected by polymerase chain reaction and DNA sequencing using primers and conditions as described previously [4]. $bla_{\text{CTX-M-15}}$ was the dominant ESBL allele among *E. coli* and *K. pneumoniae* isolates (*N*=15/19, 78.9%); this finding was similar to isolates from several interfaces in Mwanza City [5]. To determine the genetic relatedness of the MDR-GNB, 31 isolates were subjected to multi-locus sequence typing (MLST), including all 19 ESBL-producing *E. coli* and *K. pneumoniae* (these being the predominant Enterobacteriaceae causing infections at BMC), the two carbapenemase-producing *A. baumannii* and 10 selected *E. cloacae* isolates (one isolate per ward/unit).

The two carbapenem-resistant *A. baumannii* isolates were found to harbour *OXA-23* and *NDM-1* genes, respectively. MLST assigned them as sequence type (ST) 1325 and a new ST1334, respectively. Carbapenem-resistant *A. baumannii* have been implicated in causing HCAIs in other hospital settings in Africa [1], posing a threat of untreatable infections in most African countries.

Four ESBL-producing *E. coli* isolated from surgical wards carried $bla_{\text{CTX-M-55}}$ and were typed as ST405. Presence of *E. coli* ST405 in various wards indicated the possibility of a common source of contamination. Genetic variants of this ST carrying $bla_{\text{CTX-M-15}}$ had been implicated as the second most common *E. coli* genotype causing various infections in the same hospital in 2011 [6]. The remaining ESBL-producing *E. coli* isolate from a resuscitation bed of the premature unit carried $bla_{\text{CTX-M-15}}$ and was typed as ST410. This finding emphasizes the need to implement stringent surface disinfection protocols, especially in a hospital that experiences a high prevalence of colonization among neonates taken care of at the unit [7].

All three ESBL-producing *K. pneumoniae* isolates from STH carried $bla_{\text{CTX-M-15}}$ and were typed as ST607, whereas more than half of the BMC *K. pneumoniae* isolates were assigned to ST1962 and ST280; these genotypes were recently found to colonize surgical patients at BMC [8], indicating their potential contribution in surgical site infections.

E. cloacae ST84 was predominant in general wards, whereas *E. cloacae* ST513 was isolated from intensive care units (ICUs). Although the reason for different genotypes in general wards and ICUs is unclear, similarity of genotypes in ICUs can be explained, in part, by the close proximity (approximately 4 m apart) that allows frequent movement of staff and/or instruments. Therefore, these findings strongly support the need to revise ICU cleaning and disinfection protocols.

The high frequency of MDR-GNB on various hospital surfaces highlights the need for staff to take precautions to avoid hand and clothing contamination during clinical practices. Routine surface decontamination practices need to be evaluated in the light of MDR-GNB, but also regarding vancomycin-resistant enterococci, which are at least as robust as GNB and also shed via faeces. Surface contamination in the setting of a high colonization rate among patients calls for further studies using whole-genome sequencing to unravel transmission pathways. On a practical level, we advocate good hygiene, antibiotic stewardship and continuous infection surveillance according to World Health Organization recommendations.

Table I
Gram-negative bacteria (*N*=55) isolated from 164 hospital surfaces

Species	No. of isolates (%)	No. of ESBL producers	Hospital (no. of isolates)	MLST typed	β-lactamase gene	Sequence type (no. of isolates, ward)
Klebsiella pneumoniae	14 (25.5)	14	BMC (11)	11	*bla*CTX-M-15	ST1962 (6, GW)
						ST280 (3, GW)
						ST403 (2, GW)
			STH (3)	3	*bla*CTX-M-15	ST607 (4, GW)
Escherichia coli	5 (9.1)	5	BMC (5)	5	*bla*CTX-M-55	ST405 (4, GW)
					*bla*CTX-M-15	ST410 (1, PREM)
Enterobacter cloacae	19 (34.5)	14	BMC (19)	10	n.d.	ST84 (5, GW)
						ST513 (2, ICU)
						ST109 (1, GW)
						ST825[a] (1, GW)
						ST827[a] (1, GW)
Acinetobacter baumannii	17 (30.9)	–	BMC (13)	1	OXA-23	ST1325
			STH (4)	1	NDM-1	ST1334[a]

ESBL, extended-spectrum beta-lactamase; MLST, multi-locus sequence typing; BMC, Bugando Medical Centre; STH, Sekou Toure Hospital; GW, general wards; ICU, intensive care unit; PREM, pre-term babies' unit; n.d., not done.
[a] New sequence type.

Conflict of interest statement
None declared.

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