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Implementation of daily chlorhexidine bathing to reduce colonization by multidrug-resistant organisms in a critical care unit

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Abstract

Background: Colonized patients are a reservoir for transmission of multidrug-resistant organisms (MDROs). Not many studies have examined the effectiveness of daily chlorhexidine gluconate (CHG) bathing under routine care conditions. We present a descriptive analysis of the trends of MDRO colonization following implementation of daily CHG bathing under routine clinical conditions in an intensive care unit (ICU).

Methods: From May 2010-January 2011, we screened patients admitted to a 24-bed ICU for and methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), and fluoroquinolone-resistant gram-negative bacilli (FQRGNB). We calculated and plotted monthly incidence and prevalence of colonization of these MDROs.

Results: Prevalence decreased in the immediate aftermath of daily CHG bathing implementation and generally remained at that level throughout the observation period. We observed low rates of incidence of MDRO colonization with VRE>FQRGNB>MRSA. Monthly prevalence of colonization and incidence for the composite of MRSA, VRE, and/or FQRGNB was 1.9%–27.9% and 0–1.1/100 patient-days, respectively.

Conclusions: Following the implementation of daily CHG bathing, the incidence of MDROs remained low and constant over time, whereas the prevalence decreased immediately after the implementation.

Keywords

Bacterial colonization; Antiseptics; Infection prevention; Sustainability of intervention

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Health care-associated infections are very costly to the health care system and they cause much morbidity and mortality.^{1–3} There are numerous interventions for the prevention of health care-associated infections.⁴ An efficacious intervention is daily bathing with chlorhexidine gluconate (CHG). This has been shown to reduce health care-associated bloodstream infections, particularly among intensive care unit (ICU) patients.^{5–7} CHG acts by reducing the density of skin colonization by pathogens (skin asepsis). CHG accomplishes this by binding to the negatively charged bacterial cell walls, which changes the bacteria's osmotic equilibrium.⁸ CHG is a broad-spectrum antiseptic active against gram-positive organisms such as vancomycin-resistant enterococci (VRE) and methicillin-resistant *Staphylococcus aureus* (MRSA). It is also active against gram-negative organisms such as fluoroquinolone-resistant gram-negative bacilli (FQRGNB).

Given this evidence about the efficacy of daily CHG bathing, we implemented this intervention as a quality improvement project in the adult ICU at our facility and focused our evaluation on VRE, MRSA, and FQRGNB. Gram-positive MRSA and VRE are both highly resistant to multiple antibiotics, cause the majority of bloodstream and surgical site infections, and are transmitted with ease in a hospital environment.^{9,10} We also examined FQRGNB primarily because not much evidence has been generated for this group of organisms as relates to CHG bathing. Although recent Food and Drug Administration guidance recommends use of fluoroquinolones for specific uncomplicated infections due to increased risk of adverse side effects, fluoroquinolones remain an important class of antibiotics due to their high bioavailability, relatively easy dosing, and the fact that they can be an alternative in patients with penicillin allergies.^{11,12}

In this article, we provide a descriptive analysis of multidrug-resistant organism (MDRO) colonization following implementation of daily CHG bathing under routine clinical care. Our objective is not to assess the influence of daily CHG bathing, but rather to describe the trend of MDRO colonization over time after the implementation of daily CHG bathing.

METHODS

Study design

Between May 2010 and January 2011, a quasiexperimental, pretest–posttest study was carried out as a quality improvement project. On June 14, 2010, our hospital began daily CHG bathing of all patients in the critical care unit. We collected samples for microbiologic testing (nasal, skin, oral, and stool) pre- and postimplementation of daily CHG bathing. During both the pre- and post-implementation periods, we collected admission and discharge surveillance samples, stored them, and later (April 2016) tested them for colonization by MRSA, VRE, and FQRGNB.

Setting and intervention

The project was conducted in a 24-bed critical care inpatient unit of a large academic medical center (566 beds) in Wisconsin. This unit primarily serves adult medical, surgical, and trauma patient populations. The intervention involved daily CHG bathing using no-rinse

prepackaged 2% chlorhexidine-impregnated washcloths (Sage 2% CHG Cloths; Sage Products LLC, Cary, IL).

Mostly certified nursing assistants carried out daily CHG bathing; very rarely registered nurses also carried out the CHG baths. Nursing staff members received training about CHG bathing from nurse managers during weekly staff meetings where they were informed about the steps involved in the process and special situations. For example, when CHG is contraindicated due to previous allergic reactions and the need to use specific CHG-compatible lotions after the bath.

The CHG bathing process involved gathering the necessary supplies, including the CHG cloths and CHG-compatible lotions. The next step was providing education and rationale for CHG bathing to the patients or caretakers and taking a quick history about allergic reactions to CHG. Nursing staff members then washed each body part with a new CHG cloth and applied a CHG-compatible lotion at the end. Compliance with CHG bathing was monitored by having nursing staff record in the patient's electronic medical record (EMR) whether or not a CHG bath was given.

Data sources

Surveillance specimens were collected for each patient upon admission (before first bath) and before transfer or discharge from the Trauma and Life Support Center, an ICU. All patients were eligible for surveillance cultures. Specimen data included the following variables: date of sample collection, date of admission, date of discharge, sample type, and the results of screening for the bacteria. We extracted data on patient demographic characteristics (ie, sex, age, and race) from the EMRs en masse and linked data to the specimen data using a unique identifier. We conducted individual chart reviews for a few patients whose data were not complete following the en masse EMR extraction.

Sample collection and testing

We used standard sample collection procedures to collect all samples.¹³ We collected samples from the following anatomic sites: the nares, the skin (axilla and groin using a paintbrush technique on bilateral 5×5 cm² areas of the axilla and groin with 1 swab), the mouth (gums and insides of both cheeks with 1 swab), and stool sample. When available, the stool sample was collected within 48 hours of unit admission or transfer. If the stool sample was not available, we only collected samples from the other anatomic sites. We screened samples for MRSA, VRE, and FQRGNB through subculture on blood agar plates (Thermo Fisher Scientific Remel, Lenexa, KS) and incubated at 37°C for 24 hours before testing for the bacteria. Resistance to ciprofloxacin, determined using the Kirby Bauer disk diffusion method,¹⁴ was used as the indicator of resistance to fluoroquinolone antibiotics. All results were interpreted using Clinical and Laboratory Standards Institute guidelines.¹⁵ We did not collect samples from patients who refused cultures or those who refused CHG bathing. Our institutional review board deemed our study exempt from full review because it was a quality improvement project.

Data analysis

We conducted bivariate analyses to make an overall comparison of age, race, and sex between the pre- and postimplementation periods. We used the χ^2 test for the comparison of categorical variables and the Wilcoxon-Mann-Whitney test for the comparison of the nonnormally distributed continuous variables. We calculated the prevalence at admission. We defined this as the total number of positive isolates at the first admission to the critical care unit.

We calculated the monthly incidence rate of colonization for each organism (MRSA, VRE, and FQRGNB) and for a composite of MRSA, VRE, and/or FQRGNB colonization by dividing the total number of isolates that were positive at the time of discharge from the critical care unit but were negative at admission by the patient-days at risk during a given month. For patients with multiple admissions, we excluded prevalent cases of colonization from previous visits when calculating new cases of colonization. We calculated the monthly prevalence of colonization by dividing the number of patients colonized by MDROs in given month by the total number of patients during that month. We treated readmitted patients as positive or negative depending on their laboratory test result during a given admission.

We assumed that patients were at risk of MDRO colonization throughout their ICU stay. Therefore, we estimated total length of ICU stay for each patient and summed it up across each month. For patients with multiple admissions, each admission experience contributed to the total length of stay. Patients included in the analysis needed to have an admission and discharge sample.

We considered statistical significance as a *P* value $\leq .05$ and conducted all statistical analyses using Stata version 14 (StataCorp, College Station, TX).

RESULTS

Of the 619 patients in this study, 463 (74.8%) were admitted during the postintervention period and contributed 5,608 patient days compared with 882 for the preintervention period. The median age, median length of stay, and race did not differ between the pre- and postimplementation periods, but there were more men in the postimplementation period (Table 1).

The prevalence of VRE, FQRGNB, and that of a composite outcome (MRSA, VRE, and/or FQRGNB) at the first admission to the ICU was higher during the preimplementation period compared with the postimplementation period (Table 1). With the exception of MRSA, all these differences in prevalence were statistically significant.

Figure 1 shows the monthly distribution of prevalence and incidence of MDRO colonization.

With the exception of MRSA, we noted an initial decrease in trend of the prevalence and incidence of MDROs immediately following implementation of daily CHG bathing. However, the incidence of MDROs was rare during both the pre- and the postimplementation periods.

Over the course of time, the prevalence was higher than the incidence for all MDROs. The prevalence and incidence followed an undulating pattern, with the prevalence increasing as the incidence increased, but this was not consistent throughout the entire study period.

The monthly prevalence of colonization ranged from 1.6%–10.3% for MRSA; 1.6%–15.8% for VRE; 5.8%–10.1% for FQRGNB; and 1.9%–27.9% for the composite of MRSA, VRE, and/or FQRGNB.

Monthly total patient-days ranged from 32–1,327 days. The monthly incidence density of colonization ranged from 0–0.5 new cases of colonization per 100 patient-days for MRSA; 0–1.1/100 patient-days for VRE; 0–0.4/100 patient-days for FQRGNB; and 0–1.1/100 patient-days for the composite of MRSA, VRE, and/or FQRGNB.

DISCUSSION

Here, we provide a descriptive analysis of MDRO colonization following real-world application of daily CHG bathing.

With the exception of MRSA, we observed an initial decrease in the trend of the prevalence and incidence of MDROs immediately following implementation of daily CHG bathing. The prevalence was higher than the incidence during most months after the intervention, but this was not consistent throughout the entire postimplementation period.

The initial decrease in the incidence and prevalence of MDRO colonization after daily CHG bathing is consistent with the many studies that have demonstrated the efficacy of CHG bathing.^{5,6} The immediate decrease in the prevalence and incidence of MDRO colonization may represent the initial momentum new interventions receive when they are newly implemented. In a previous study, we observed that nursing staff had a very good perspective of the daily CHG bathing intervention when it was newly implemented, but not later on.¹⁶ We also observed this in the project we describe here. Initially, the nursing staff members were very engaged in the new intervention and possibly conducted CHG baths with a high level of fidelity to the bathing protocol. However, this enthusiasm waned over time.

Another finding in this project was that the prevalence of VRE and FQRGNB colonization at admission to the ICU was significantly higher during the preimplementation period compared with the postimplementation period. However, our data show that generally the prevalence increased and decreased with the incidence. This suggests that the higher VRE and FQRGNB prevalence was not influenced by factors such as higher colonization pressure during the preimplementation period.

A strength of our study is that we describe the trend of both gram-positive MDROs and gram-negative MDROs (eg, FQRGNB) over time following implementation of daily CHG bathing. Much work regarding CHG bathing has been done with regard to gram-positive bacteria but not so much for gram-negative bacteria. Moreover, we carried out this work as a quality improvement project, which is more representative of what happens under routine clinical care.

Readers should interpret findings from this work in the context of certain limitations. First, absence of a concurrent control group was a limitation to this project. Without such a control group, it challenges the attribution of the observed findings to CHG bathing. However, the intention of this work was to show a descriptive analysis of MDRO colonization following implementation of daily CHG bathing but not to assess causality.

Secondly, although nursing staff members were trained on the CHG bathing protocol, we did not systematically audit or assess fidelity to the CHG bathing protocol intervention. Without monitoring fidelity, it is difficult to know whether the bathing procedure was optimal.^{17,18} Issues such as whether the entire body area was covered and whether CHG-compatible lotions were used could have influenced the effect of CHG bathing on colonization. This may be a true representation of what happens in clinical practice where fidelity to CHG bathing may not be regularly monitored. Another limitation is that we did not have data on certain risk factors for MDRO colonization. Examples of these factors include immunosuppression, underlying disease such as renal failure, presence of invasive devices like central lines and endotracheal tubes, prior antimicrobial therapy, and history of MDRO colonization. Patients with these factors are at a greater risk for colonization.^{19–21} Exclusion of patients without both admission and discharge samples might have led to underestimation of the prevalence if these patients happened to be colonized with MDROs.

CONCLUSIONS

Prevalence of MDROs decreased during the immediate after-math, but generally remained at that level throughout the postimplementation period. The incidence of MDROs remained low and constant over the observation period. Health care facilities need to identify and address factors that might influence the long-term sustainability of the effects of daily CHG bathing. Moreover, in light of the recent Food and Drug Administration warning about rare but serious allergic reactions to CHG,²² health care facilities need to carefully assess for occurrence and elicit any history of previous allergic reactions to CHG among patients receiving CHG baths.

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Fig 1.

Incidence rate and prevalence of colonization. (A) Monthly distribution of methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* (VRE), and/or fluoroquinolone-resistant gram negative bacilli (FRQGNB). (B) Monthly distribution of MRSA. (C) Monthly distribution of VRE. (D) Monthly distribution of FQRGNB.

Table 1

Characteristics of patients in this project

Characteristic	Preimplementation period n = 156(25.2%)	Postimplementation period n = 463(74.8%)	P value *
Age	61 (20.5)	60 (22)	.232
Length of stay	10 (15.5)	10 (12)	.667
Male sex	82 (52.6)	286 (61.8)	.043
Race			
White	146 (93.6)	429 (92.7)	.695
Other	10 (6.4)	34 (7.3)	
Prevalence of MRSA colonization	14 (9.2)	26 (5.6)	.119
Prevalence of VRE colonization	22 (14.5)	39 (8.4)	.030
Prevalence of FQRGNB colonization	13 (8.5)	17 (3.7)	.015
Prevalence of MRSA, VRE, and FQRGNB colonization	40 (26.3)	73 (15.8)	.004

NOTE. Values are presented as median (interquartile range) or n (%).

FQRGNB, fluoroquinolone-resistant gram-negative bacilli; *IQR*, interquartile range; *MRSA*, methicillin-resistant *Staphylococcus aureus*; *VRE*, vancomycin-resistant *Enterococcus*.

* The *P* value is comparing pre- and postintervention characteristics. Prevalence calculations for the preimplementation period are based on n = 152 because 4 out of 156 patients did not have samples tested during the preimplementation period.