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Major Article

High-risk *Staphylococcus aureus* transmission in the operating room: A call for widespread improvements in perioperative hand hygiene and patient decolonization practices

Randy W. Loftus MD *, Franklin Dexter MD, PhD, FASA, Alysha D.M. Robinson BS

Department of Anesthesiology, University of Iowa Hospitals and Clinics, Iowa City, IA

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Background: Increased awareness of the epidemiology of transmission of pathogenic bacterial strain characteristics may help to improve compliance with intraoperative infection control measures. Our aim was to characterize the epidemiology of intraoperative transmission of high-risk *Staphylococcus aureus* sequence types (STs).

Methods: *S aureus* isolates collected from 3 academic medical centers underwent whole cell genome analysis, analytical profile indexing, and biofilm absorbance. Transmission dynamics for hypertransmissible, strong biofilm-forming, antibiotic-resistant, and virulent STs were assessed.

Results: *S aureus* ST 5 was associated with increased risk of transmission (adjusted incidence risk ratio, 6.67; 95% confidence interval [CI], 1.82-24.41; $P = .0008$), greater biofilm absorbance (ST 5 median absorbance ± SD, 3.08 ± 0.642 vs other ST median absorbance ± SD, 2.38 ± 1.01; corrected $P = .021$), multidrug resistance (odds ratio, 7.82; 95% CI, 2.19-27.95; $P = .002$), and infection (6/38 ST 5 vs 6/140 STs; relative risk, 3.68; 95% CI, 1.26-10.78; $P = .022$). Provider hands (n = 3) and patients (n = 4) were confirmed sources of ST 5 transmission. Transmission locations included provider hands (n = 3), patient skin sites (n = 4), and environmental surfaces (n = 2). All observed transmission stories involved the within-case mode of transmission. Two of the ST 5 transmission events were directly linked to infection.

Conclusions: Intraoperative *S aureus* ST 5 isolates are hypertransmissible and pathogenic. Improved compliance with hand hygiene and patient decolonization may help to control the spread of these dangerous pathogens.

Staphylococcus aureus pathogens have evolved to acquire genetic traits that are associated with increased antibiotic resistance, virulence, and transmissibility.[1] As a result, there has been an alarming increase in the spread of these invasive pathogens from acute care settings to healthy members of the community.[2]

The operating room patient care arena is contributing to this problem. Perioperative *S aureus* nasal carriage occurs frequently,[3,4] is associated with intraoperative transmission in up to 39% of cases,[4] and has been directly linked to postoperative bacteremia in patients undergoing orthopedic surgery.[3]

There are evidence-based solutions that can address this alarming patient safety issue. Preoperative *S aureus* decolonization has been shown to reduce the incidence of surgical site infections.[5,6] Novel hand hygiene improvement measures,[7] disinfectable needleless closed catheter devices,[8] and catheter hub disinfection prior to injection have been shown to reduce intraoperative transmission and subsequent postoperative infection development.[9] However, despite this solid foundation of evidence, intraoperative adherence to these evidence-based, basic preventive measures is abysmal.[7-10]

As a result of suboptimal compliance with these basic preventative measures, at least 7% of patients undergoing surgery will acquire ≥1 health care–associated infections (HAIs),[11,12] with *S aureus* as a leading cause.[2-6] The Centers for Disease Control and Prevention,

* Address correspondence to Randy W. Loftus, MD, University of Iowa Hospitals and Clinics, 200 Hawkins Rd, Iowa City, IA 52240.
E-mail address: randy-loftus@uiowa.edu (R.W. Loftus).

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the World Health Organization, and the White House consider HAIs to be a devastating and persistent issue linked to antibiotic resistance, and they have urged health care providers to tighten compliance with basic preventive measures to prevent infections and unnecessary antibiotic use.[13-15]

We think a heightened awareness of the overall incidence and implications of the intraoperative spread of more pathogenic *S aureus* strain characteristics can help to augment intraoperative compliance with infection control measures. In this study, our aim was to characterize the epidemiology of particularly pathogenic *S aureus* sequence types (STs) in the operating room environment.

MATERIALS AND METHODS

Background and general description

A computer-generated list was used to randomly select 274 case pairs (first and second case of the day in each of 274 operating room environments) from 3 academic medical centers in the United States. The randomized unit study design was intended to include a wide variety of surgical procedures, patient comorbidities, infection control measures, and health care providers. More than 8,184 bacterial pathogens were collected over a 1-year period to capture seasonal variation.[4,10] Because the activity was limited to analysis of de-identified data from a previous institutional review board–approved project (no. 201507774, Assessment of Routine Intraoperative Horizontal Transmission of Potentially Pathogenic Bacterial Organisms II), the University of Iowa waived the need for institutional review board review.

A total of 178 *S aureus* isolates were collected. One hundred and seventy-three isolates were implicated in possible transmission, defined as at least 2 *S aureus* isolates identified from 2 distinct reservoirs within or between cases in an intraoperative case pair. An additional 5 isolates were identified in postoperative patient infection cultures without a possible intraoperative link.[4,10]

Institutional infection control policies were tracked and recorded during the study period. At all centers, usual infection control practices included routine and terminal environmental cleaning involving quaternary ammonium compounds with or without surface disinfection wipes. All providers had access to alcohol dispensers located on the wall or anesthesia carts, and gloves were immediately available for use. There were no changes in these usual procedures during the study period.[4,10]

S aureus *reservoir collection process and analysis of transmission*

The study unit was a case pair which involved the first and second case of the day in a given operating room environment. Bacterial reservoirs were systematically sampled over time to use the platform of temporal association.[4,10,16,17] Temporal association was defined as organisms collected from ≥2 distinct reservoirs in the same operating room on the same day at the same time.[4,10,16,17]

The conceptual framework for the utilization of temporal association in the model was considered as follows. First, prior to phenotypic or genomic testing to examine relatedness, 2 isolates obtained from ≥2 distinct reservoirs within a study unit were considered more likely to be related than independent, given that the probability of *S aureus* isolation from any one tested site ranged from 3% (hand and environmental samples) to 16% (patient nasopharynx and axilla).[10] Second, the probability of isolating *S aureus* from 2 distinct reservoirs within the platform of temporal association (probability of A × B) was considered to range from 0.09% to 3%, whereas the probability of being related to a common reservoir was considered to range from 97%-99.91%. Third, the reservoirs sampled included anesthesia provider (attending and resident physicians and Certified Registered Nurse Anesthetists) hands before, during, and after patient care; environmental sites proven to reliably represent the magnitude of contamination of the anesthesia work environment[16]; patient skin sites strongly correlated with surgical site infections[16]; and the internal lumen of open lumen intravascular stopcock sets.[4,10,16,17] Air was considered a continuous medium in the model that could impact all reservoirs in parallel through settling of aerosolized particles. Finally, temporal association of reservoirs in a given study unit was applied according to the following sequence of events. Environmental sites (adjustable pressure-limiting valve and agent dial of the anesthesia machine) were decontaminated and subsequently cultured to establish a baseline (time 0). Anesthesia provider hands were then sampled on operating room entry (time 1). After induction of anesthesia and patient stabilization, the patient's nasopharynx and axilla were sampled (time 2). Provider hands (any provider that entered the anesthesia workspace outside of the sterile field including but not limited to anesthesia providers and technologists) were sampled during care (time 3). The same environmental sites were sampled at case end (time 4), along with the internal lumen of the patient intravenous stopcock set (time 5). Provider hands were again sampled at case end (time 6). The internal lumen of the patient intravenous stopcock set was then sampled (time 7). This process was repeated for the second case in an observational unit, except that environmental sites were not decontaminated so residual contamination after routine cleaning procedures between cases could be assessed. The specific methods of culture acquisition and handling for this process are previously described.[4,10,16,17]

Temporal association was then strengthened by a systematic phenotypic and genomic approach. First, temporally associated isolates from at least 2 distinct reservoirs in a study unit underwent phenotypic testing and molecular typing to identify epidemiologically related isolates (steps 1 and 2, Fig 1). Simple rapid tests, analytical profile indexing, antibiotic susceptibility testing, and multilocus sequence typing were conducted as previously described.[17] Epidemiologically related isolates then underwent whole cell genome analysis and single nucleotide polymorphism analysis (step 3, Fig 1).

Clonally related isolates were aligned according to the timing of culture acquisition (step 4, Fig 1). Provider origin of within-case transmission was confirmed if the transmitted isolate was clonally related to an isolate from the hands of ≥1 anesthesia providers sampled on room entry before patient care. Provider origin of between-case transmission was confirmed if ≥1 isolates from provider hands in case 1 were clonally related to ≥1 isolates in case 2 without potential alternative sources of transmission from case 2 reservoirs. Environmental origin of within-case contamination was confirmed if the transmitted isolate was clonally related to an isolate from the environment sampled at baseline or at case end but not isolated either from the hands of providers or from the patient at case start. Environmental origin of between-case transmission was confirmed if ≥1 environmental isolates from case 1 were clonally related to ≥1 isolates in case 2 without potential alternative sources of transmission from case 2 reservoirs. Patient origin of within-case contamination was confirmed if the transmitted isolate was clonally related to an isolate from the patient sampled at case start but was not isolated either from the hands of providers at case start (because patient samples were obtained after induction of anesthesia) or from baseline environmental samples. Patient origin of between-case transmission was confirmed if ≥1 patient isolates from case 1 were clonally related to ≥1 isolates in case 2 without potential alternative sources of transmission from case 2 reservoirs. The within-case mode of transmission was confirmed if the origin and transmission location(s) for a clonal series were confined to a single