Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Microbiology
In Vitro Antimicrobial Activity of Taurolidine against Isolates Associated with Catheter-Related Bloodstream Infections
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Background: Taurolidine exhibits broad antimicrobial activity and is a component of a recently FDA approved catheter lock solution (DefenCath®, taurolidine 13,500 µg/mL and heparin 1000 Units/mL) indicated for reducing the risk of catheter-related bloodstream infections (CRBSI) in adult patients receiving chronic hemodialysis through a central venous catheter (HD-CVC). FDA approval was based on a Phase 3 randomized trial (LOCK-IT-100) in which DefenCath showed a 71% reduction in CRBSI risk among HD-CVC patients as compared with heparin alone. Although individual isolates from the clinical program were not available for testing, this study evaluated the in vitro antimicrobial activity of taurolidine against a set of recent clinical isolates representative of those recovered from the LOCK-IT-100 trial and/or those commonly associated with CRBSI. **Methods:** 420 bacterial and 50 yeast isolates were selected from the SENTRY Antimicrobial Surveillance Program. All isolates were collected from the bloodstream of patients in the U.S. between 2018-2023. Isolates were tested for susceptibility to taurolidine and comparators using Clinical and Laboratory Standards Institute (CLSI) broth microdilution guidelines. JMI Laboratories produced susceptibility test panels for testing. CLSI-recommended quality control strains were also tested concurrently. MIC values were determined after 24 hours. **Results:** Taurolidine exhibited broad antimicrobial activity against all isolates tested (see table). Against gram-positive bacteria, taurolidine MIC50/90 values ranged from 256-512/512-1,024 µg/mL for S. aureus, Coagulase-negative Staphylococcus, Enterococcus species, and Viridans group streptococci. This activity was maintained regardless of methicillin susceptibility for Staphylococcal isolates or vancomycin resistance among Enterococcal species. Against gram-negative bacteria, taurolidine MIC50/90 values ranged from 256-1,024/512-2,048 µg/mL for Enterobacterales, P. aeruginosa, S. maltophilia, A. baumannii-calcoaceticus, and B. cepacia. This activity was maintained in both multidrug resistant Enterobacterales and P. aeruginosa isolates. Among Candida isolates, taurolidine MIC50/90 values ranged from 256-512/512 µg/mL for C. glabrata and C. parapsilosis while taurolidine MIC50/90 values of 4,096/4,096 µg/mL were observed for C. albicans. **Conclusions:** Taurolidine activity was very similar among a large collection of gram-positive, gram-negative, and yeast organisms. MIC90 values for all species/groups were ≤2,048 µg/mL, except C. albicans where an MIC90 of 4,096 µg/mL was observed. The activity of taurolidine was unaffected by resistance to antibiotics (i.e. methicillin, vancomycin, or multidrug resistance) among gram-positive or gram-negative organisms. Based on these data, catheter lock solutions containing the broad-spectrum antimicrobial taurolidine at 13,500 µg/mL have the potential to prevent CRBSI caused by a variety of species, including those observed in the recent LOCK-IT-100 clinical trial and other common bloodstream pathogens

Table Distributions of taurolidine MIC values against various species/groups

	No. of isolates inhibited at a taurolidine MIC (100% read, µg/mL) of:								Taurolidine	
Organism (No. isolates)	≤32	64	128	256	512	1,024	2,048	4,096	MIC_{50}	MIC_{90}
S. aureus (76)				1	75				512	512
MSSA (37)					37				512	512
MRSA (39)				1	38				512	512
CoNS (52) [a]				10	38	4			512	512
S. epidermidis (36)					32	4			512	1,024
MSCoNS (21)				7	14				512	512
MRCoNS (31)				3	24	4			512	1,024
E. faecalis (38)				1	48	2			512	512
E. faecium (10)				5	5				256	512
Viridans group streptococci (18) [b]		1	2	5	10				512	512
Enterobacterales (136)			1	22	105	8			512	512
MDR Enterobacterales (19)				1	16	2			512	1,024
E. coli (43)				1	42				512	512
K. pneumoniae (43)				2	38	3			512	512
P. mirabilis (10)				10					256	256
E. cloacae sc (10)					6	4			512	1,024
Citrobacter species (10)				9	1				256	256
S. marcescens (20)			1		18	1			512	512
P. aeruginosa (45)					20	23	2		1,024	1,024
MDR *P. aeruginosa* (10)					8	2			512	1,024
S. maltophilia (15)				12	2	1			256	512
A. baumannii-calcoaceticus sc (15)				2	13				512	512
B. cepacia sc (15)				10	1	2	2		256	2,048
C. albicans (17)							5	12	4,096	4,096
C. glabrata (17)				3	13	1			512	512
C. parapsilosis (16)			3	9	4				256	512

MSSA, Methicillin-susceptible *S. aureus*; MRSA, Methicillin-resistant *S. aureus*; CoNS, coagulase-negative *Staphylococcus*; sc, species complex; MDR, Multidrug resistant
[a] Species include: *Staphylococcus capitis* (2), *S. epidermidis* (36), *S. haemolyticus* (2), *S. lugdunensis* (10), and *S. saprophyticus* (2).
[b] Species include: *Streptococcus anginosus* group (2), *S. bovis* group (5), *S. gallolyticus* (2), *S. mitis* group (2), *S. salivarius* group (2), and *S. sanguinis* (5).

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Improving Consistency and Accuracy: A Novel C. auris Colonization Screening Strategy Using a Nares + Hands Composite Swab
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Background: Candida auris is often identified in healthcare settings through bilateral composite of axilla/groin skin swabs screening. Re-screening the same patient has demonstrated inconsistent results over time, complicating the understanding of longitudinal colonization and limiting confidence in negative **Results:** Previous studies have described identification of colonized patients using other anatomical sites. Here, we compare bilateral composite of nares/hands with bilateral composite of axilla/groin screenings in a cohort of hospitalized patients in Miami, Florida, to assess the use of screening other body sites for C. auris surveillance. **Methods:** This study took place in a 560-bed academic acute-care facility and included patients previously colonized with C. auris who were cohorted on a 30-bed unit. Bilateral composite samples from both the axilla/groin and nares/hands were obtained simultaneously. Swabs were collected at six different time points at biweekly intervals between March and May 2023 (Figure 1) and sent to the Centers for Disease Control and Prevention for testing with culture and Real-time PCR-based

Figure 1. Collection methods

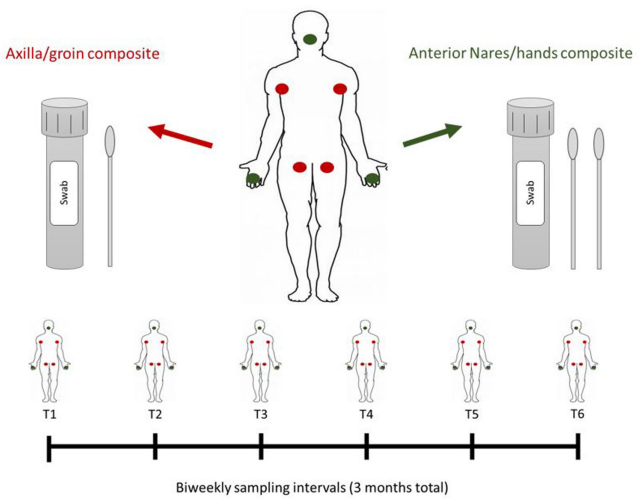
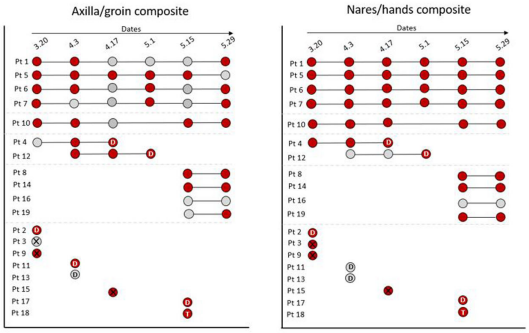


Figure 2. Results of bilateral axilla/groin composite and bilateral nares/hands composite swabs (n=102) using culture-based testing.



Red circles display positive results, and gray circles display negative results. Circles with "D" inside represent patients who were discharged, circles with an "X" inside represent patients who deceased during the study period, and circles with a "T" inside represent patients who were transferred out of the cohort unit.

Figure 3. Venn Diagram showing body site positivity for 48 samples positive using culture-based testing

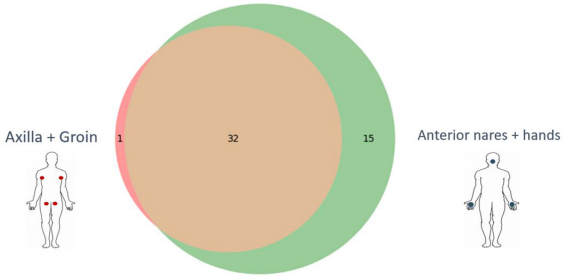
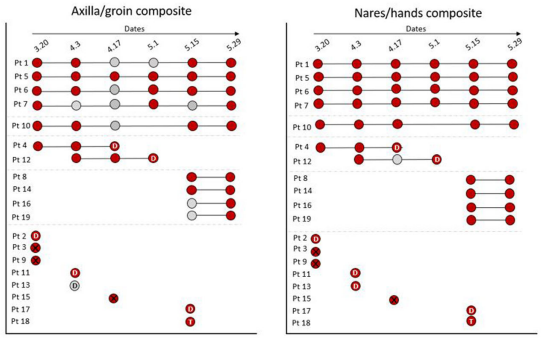


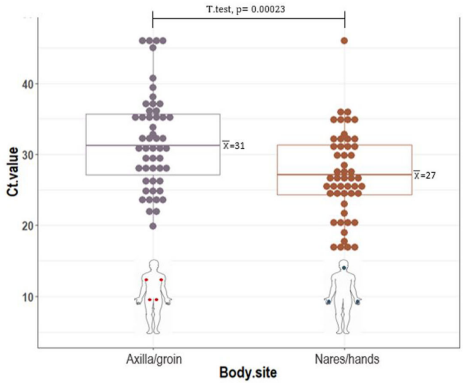
Figure 4. Results of bilateral axilla/groin composite and bilateral nares/hands composite swabs (n=102) using real-time PCR testing.



Red circles display positive results, and gray circles display negative results. Circles with "D" inside represent patients who were discharged, circles with an "X" inside represent patients who deceased, and circles with a "T" inside represent patients who were transferred out of the cohort unit.

methods. **Results:** A total of 102 swabs (51 from each swab type) were collected from 19 patients who were each sampled a median of twice (IQR: 1-5). Among the 102 swabs, 35 of 51 (69%) axilla/groin swabs were positive compared with 45 of 51 (88%) nares/hands swabs using culture (Figure 2). Furthermore, 48 of 51 (94%) swabs were positive by culture for both methods, with 15 positive from the nares/hands and one positive from the axilla/groin (Figure 3). Among 11 patients who were tested ≥2 times with nares/hands swabs, 9/11 (81%) tested positive on all sequential swabs via culture and 10/11 (90%) tested positive via PCR (Ct threshold < 3 6.9). Among the same 11 patients but using the axilla/groin swabs, 3/11 (27%) patients tested positive on all sequential swabs using culture, and 5/11 (45%) tested positive using PCR (Figures 2-4). On average, samples collected from

Figure 5. Ct values of bilateral axilla/groin composite and bilateral nares/hands composite swabs using real-time PCR testing.



nares/hands swabs had lower Ct values (mean=27) compared to axilla/groin swabs (mean=31) (p-value=< 0.001) (Figure 5). **Discussion:** Identifying the swab site with most consistent C. auris detection is important for surveillance purposes. In our study, there were more positives and consistent positivity for nares/hands by both culture and PCR-based methods, as well as lower Ct values, suggesting that these swabs provide more reliable detection of C. auris colonization. Alternative screening methods deserve consideration as CDC continues to explore whether swabbing of other body sites (e.g., nares, hands) would improve accuracy and consistency when identifying colonized patients.

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Real-time Whole Genome Sequencing Surveillance as an Effective Outbreak Detection and Mitigation Tool

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Background: Detection of outbreaks traditionally relies on passive surveillance, and often misidentify or miss outbreaks. Whole genome sequencing (WGS) surveillance has emerged as a proactive measure, enabling early detection of outbreaks and facilitating rapid intervention strategies. WGS surveillance has not been widely studied due to infrastructure, cost, and evidence barriers regarding its impact on reducing healthcare-associated infections (HAIs). This study represents findings from two years of a real-time WGS surveillance program called the Enhanced Detection System for Healthcare-associated Transmission (EDS-HAT). **Methods:** The study was conducted at UPMC Presbyterian hospital, a 694-bed tertiary care center. Patient isolates of select bacterial pathogens were collected and underwent WGS weekly from November 2021 to November 2023. Potential transmission was defined using single-nucleotide polymorphism thresholds (≤15 for all organisms except Clostridioides difficile). Genetically related clusters were reviewed weekly for epidemiological linkages (unit, personnel, or procedural commonalities) and appropriate interventions were initiated by the infection prevention and control team. We described the frequency of genetic relatedness and nature of epidemiological linkages. **Results:** Of 7,051 eligible unique patient organism isolates,