

Fluimucil®) frequently bought and remaining unreimbursed. Overall and across ATC3 groups, the correlation between NIDHI and IQVIA estimates was almost perfect across years and the Bland–Altman plots showed high agreement. **Conclusion:** Reimbursement data are reliable for outpatient AMC monitoring with slightly lower estimates than retail data across most categories. The 2018 quinolone reimbursement criteria change highlights the necessity of incorporating retail data for accurate assessments in this specific category. The synergistic use of reimbursement and retail datasets is crucial for a comprehensive understanding of consumption patterns, supporting effective AMR mitigation strategies in Belgium.

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Variability of MDRO Reporting Across Tennessee Microbiology Laboratories

Matthew Lokant, Vanderbilt University Medical Center; Christopher Wilson, Tennessee Department of Health; Tom Talbot, Vanderbilt University School of Medicine; Priscilla Pineda, Tennessee Department of Health; Erin Hitchingham, Tennessee Department of Health; Melphine Harriott, TN Department of Health HAI/AR Program; Raquel Villegas, state of TN; Kaleb Wolfe, Vanderbilt University Medical Center and Milner Owens Staub, Vanderbilt University Medical Center

Background: Identification and timely reporting of multi-drug resistant organisms (MDROs) drives efficacy of infection prevention efforts. Data on MDRO reporting timeliness and inter-facility variability are limited. Facility-dependent variability in MDRO reporting across Tennessee was examined to identify opportunities for MDRO surveillance improvement. **Methods:** Data for reported Tennessee MDROs including carbapenem-resistant Enterobacteriales (CRE), carbapenem-resistant Acinetobacter baumannii (CRAB), Carbapenem-resistant Pseudomonas aeruginosa (CRPA) and Candida auris, were obtained from the southeast regional Antibiotic Resistance Laboratory Network (ARLN) from 2018-2022,

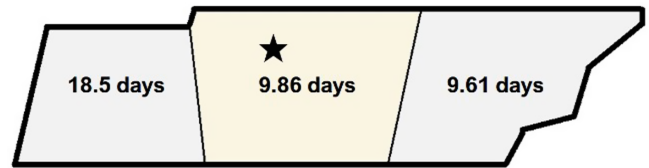


Figure. Three grand divisions of Tennessee (West, Middle, and East) with average time to report. ARLN site denoted by star.

excluding screening and colonization specimens. Variance in days accrued from specimen collection to ARLN receipt was analyzed using one-way analysis of variance (ANOVA) with Tukey’s test (SAS 9.4). Facilities were categorized as fast (1-10 days), slow (11-20 days), or delayed (21-100 days) reporters. **Results:** There were 9,569 MDRO isolates reported. CRPA was reported faster than other MDROs ($p < 0.001$), while specimens from West Tennessee compared to other regions ($p < 0.001$) (Figure) and blood cultures compared to other specimens were reported more slowly ($p < 0.001$) (Table). There was no difference in reporting times for facilities using on-site microbiology laboratories versus reference laboratories ($P = 0.062$). **Conclusion:** MDRO reporting times varied across Tennessee by region, specimen, and organism. Future work to elucidate drivers of variability will consist of surveys and focused interviews with laboratory personnel to identify shared and unique barriers and opportunities for improvement.

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Serratia marcescens Burden in a Neonatal Intensive Care Unit: Colonization Rate, Clinical Infections and Strain Relatedness

Halima Dabaja Younis, Sinai Health System- Toronto; Angelie Seguban, Sinai Health; Andrea Morillo, Sinai Health; Tony Mazzulli, Mount Sinai Hospital; Ming Lum, Mount Sinai Hospital and Jennie Johnstone, Mount Sinai Hospital

Background: Serratia marcescens (S. marcescens) is an environmentally associated organism known for causing healthcare associated infections and outbreaks in neonatal intensive care units (NICUs). The colonization or infection rates in NICU settings remain uncertain. This study aims to evaluate the rate of baseline colonization and clinical infection and relatedness of S. marcescens isolates. **Methods:** Prospective surveillance of rectal colonization and clinical infection of S. marcescens was conducted on patients admitted to the NICU at Mount Sinai Hospital in Toronto, Ontario, from March 1, 2023, to September 30, 2023. The NICU is a 57

Table. Reporting Times

	Fast (%)	Slow (%)	Delayed (%)	Average Time to Report in Days (SD)	ANOVA P-Value
MDRO Type					<.0001
CRAB	436 (67.39)	154 (23.8)	57 (8.81)	11.16 (10.23)	
CRE	4282 (67.39)	1671 (26.3)	1671 (26.3)	10.84 (9.09)	
CRPA	1933 (75.63)	568 (22.22)	55 (2.15)	8.82 (5.51)	
Candida auris	6 (50)	5 (41.66)	1 (8.3)	11.17 (5.10)	
Reporting Region					<.0001
East	2474 (70.2)	950 (26.96)	100 (2.84)	9.61 (5.52)	
Middle	3094 (74.48)	840 (20.22)	220 (5.3)	9.86 (9.02)	
No Identified Location	836 (65.36)	419 (32.76)	24 (1.88)	9.86 (3.57)	
West	253 (41.34)	189 (30.88)	170 (27.78)	18.50 (16.79)	
Specimen Type					<.0001
Abscess and Wound	861 (71.27)	297 (24.59)	50 (4.14)	9.76 (7.34)	
Blood	242 (65.94)	88 (23.98)	37 (10.08)	12.17 (12.31)	
Lower Respiratory	695 (71.87)	225 (23.27)	47 (4.86)	9.64 (7.04)	
Urine	3180 (68.79)	1259 (27.23)	184 (3.98)	10.08 (7.31)	
All other	1679 (69.84)	529 (22.00)	196 (8.15)	11.04 (10.38)	

Figure 1: Patients chronological age at S. marcescens detection in accordance to strain

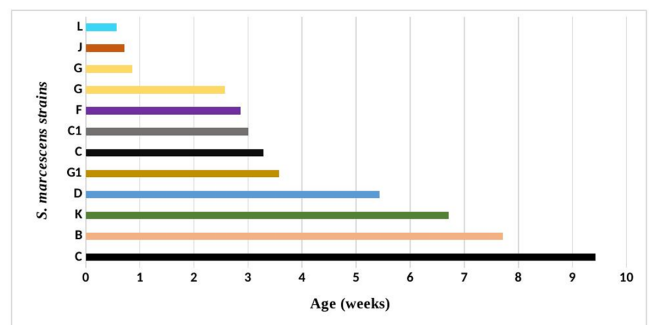


Figure 2: Patients with repeated screening for *S. marcescens* who were positive in at least one screening point

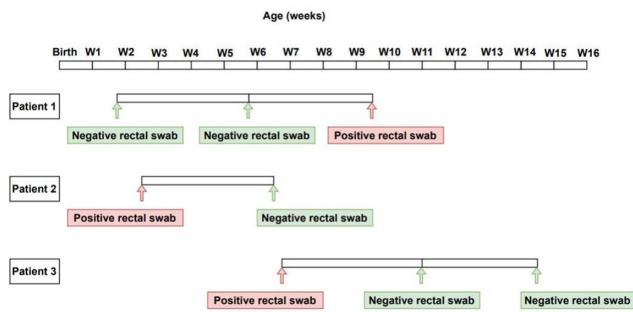
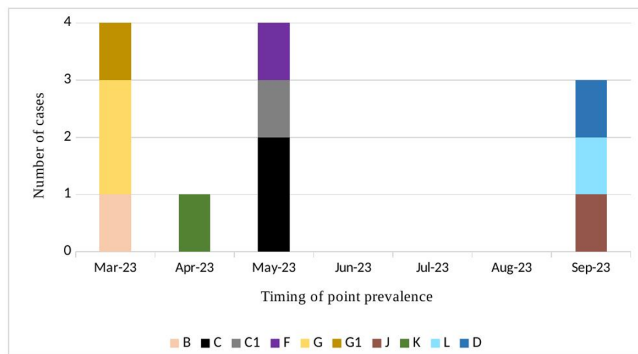


Figure 3: *S. marcescens* cases over 7 months of active surveillance



bed unit with all private rooms. Monthly point prevalence assessments by rectal screening were performed, alongside active surveillance for clinical infections associated with *S. marcescens*. Isolates from screening or clinical samples underwent assessment for relatedness using pulse field gel electrophoresis (PFGE). **Results:** Over the 7 month study period, 12 different patients (5.4%) were colonized/infected with *S. marcescens*. Among these, 10 patients (4.5%) were identified through rectal screening (316 rectal swabs were collected from 224 patients) and two patients (0.9%) exhibited positive clinical specimens (urine and endotracheal aspirate) in association with pyelonephritis and ventilator-associated pneumonia, respectively. Of the two clinical cases, one case showed a negative preceding rectal swab and the other detected through a clinical sample before the point prevalence date. The age at which a positive *S. marcescens* swab or positive clinical specimen was identified ranged from 4 to 66 days (median=18 days, IQR 5-38.8) (Figure 1). Sixty seven infants had repeated screening. Three out of 67 (4.5%) were colonized with *S. marcescens*, the timing and sequence of positive and negative testing are presented in Figure 2. Females demonstrated a higher positivity rate compared to males [9.1% (9/99) vs 2.4% (3/125), $p=0.04$, respectively]. PFGE analysis of all 12 (100%) isolates revealed a polyclonal pattern. Most cases were detected from March to May in 9/12 cases (75%). Ten different strains were identified. Notably, two strains demonstrated clusters of two cases each, one during March and the other during May (Figure 3). No mortality was reported among the cases. **Conclusions:** The study highlights the polyclonal nature of *S. marcescens* and raises questions about the utility of point prevalence in anticipating clinical cases or patient-to-patient transmission, especially in patients with clinical infection where there were no preceding positive screening tests.

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Comparative Analysis of Healthcare-associated Bloodstream Infections & CLABSI Surveillance in A Singaporean tertiary Hospital

Shalvi Arora, Singapore General Hospital; Sheena Jin Min Ong, Singapore General Hospital; Pinhong Jin, Singapore General Hospital; Aung Myat Oo, Singapore General Hospital; May Kyawt Aung, Singapore General Hospital; Yak Weng Darius Chan, Singapore General Hospital; Yang Yong, Singapore General Hospital; Ian Wee Liang En, Singapore General Hospital; Xiang Ying Jean Sim, Singhealth; Lai Chee Lee, Singapore General Hospital; Moi Lin Ling, Singapore General Hospital and Indumathi Venkatachalam, Singapore General Hospital

Background: Healthcare-associated central line associated bloodstream infection (HA-CLABSI) surveillance is important for monitoring healthcare-associated infections (HAIs) and evaluating effectiveness of infection prevention (IP) measures. However, implementing it is a laborious and time-consuming approach. Exclusive focus on central lines neglects HAI risk due to peripheral vascular catheters. This study aimed to assess whether HA-CLABSI incidence could be inferred from HA-bloodstream infection (BSI) trends and explore shift to HA-BSI surveillance. **Methods:** The study was performed in a Singaporean tertiary care hospital. Electronic medical records review was performed to determine whether positive blood cultures met Centers for Disease Control/National Health Safety Network (CDC/NHSN) definitions for HA-CLABSI and HA-BSI. Incident episodes of HA-BSI were included (excluding positive cultures repeated within 14 days). Incident organisms were explored to identify common causative pathogens (excluding same organisms isolated from

Figure: Incidence rate of HA-CLABSI from Jan 2022 to Oct 2023



cultures repeated within 14 days). CLABSI and BSI occurring ≥ 72 hrs after admission were considered healthcare-associated. Patients under oncology or hematology service were considered immunocompromised. Incidence rates (IR) per 10,000 patient-days, patient characteristics and causative pathogens were compared between both indicators. **Results:** From January 2022 to October 2023, mean IR for HA-CLABSI was 0.63 ($n=68$) and for HA-BSI was 10.06 ($n=1094$). Median age of patients with HA-CLABSI was 66 years and HA-BSI was 68 years. HA-CLABSI and HA-BSI were more common in males (60.86% & 58.68%). Median duration

Figure: Incidence rate of HA-BSI from Jan 2022 to Oct 2023

