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Original Article

Optimizing facility-specific urinary weighted-incidence syndromic antibiograms for nursing homes

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Abstract

Objective: To develop an approach for creating facility-specific urinary antibiograms accounting for the low number of isolates recovered in nursing homes (NHs).

Design: Retrospective analysis of urine culture data collected in NHs in five states.

Setting: Data on 5097 urine culture isolates collected across 59 study NHs from January 1, 2020 to December 31, 2021. Four consulting microbiology laboratories served the study homes.

Methods: We compared a Clinical and Laboratory Standards Institute (CLSI) standard antibiogram model to four weighted-incidence syndromic antibiogram (WISCA) models utilizing alternate formatting rules. Ability to produce a facility-specific antibiogram with at least 30 isolates and the impact on susceptibility predictions were compared.

Results: Only one facility could generate a CLSI standard antibiogram for the three most commonly recovered Gram-negative isolates over a one-year period. Ability to generate an antibiogram increased with each of the four WISCA models trialed (36%, 54%, 85%, 85%) with the most successful models combining all Gram-negative isolates over a two-year period. Shortening the definition of duplicate isolates from 12 to 3 months did not improve performance. Using all Gram-negative isolates, rather than the three most recovered pathogens, resulted in meaningful changes in the predicted activity of ampicillin-sulbactam, cefazolin, ceftriaxone, and trimethoprim-sulfamethoxazole in several study NHs.

Conclusions: These results suggest that WISCAs using 2-years of urinary culture data including all gram-negative isolates and excluding duplicate isolates within twelve months maximizes the number of NHs able to create a valid antibiogram.

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Introduction

Antibiograms are tools that summarize the antibiotic susceptibilities of bacterial isolates recovered from cultures collected in healthcare settings over a specific time frame. Antibiograms are mostly utilized in hospitals for tracking and trending antimicrobial resistance patterns over time and may also be used to support empiric antibiotic decision-making. Guidelines established by the Clinical Laboratory Standards Institute (CLSI) recommend that facility antibiograms compile the susceptibilities of clinically-relevant bacteria species collected over a one-year period.[1] These reports are typically displayed in a matrix format, with bacterial species of interest listed in rows and selected antimicrobial agents in columns, indicating the proportion of isolates susceptible to each agent (Figure 1A). To promote reliability, CLSI recommends that antibiograms exclude bacterial species with fewer than 30 isolates. Centers for Medicare and Medicaid Services (CMS) regulations require nursing homes (NHs) to develop systems to monitor outcomes of antibiotic use that may include patterns of antibiotic resistance.[2] Antibiograms could help NHs meet this regulatory requirement but the numbers of isolates recovered from cultures collected in most facilities are insufficient to produce a tool that complies with the CLSI standard employed in hospitals.[3,4]

The weighted incidence syndromic combined antibiogram (WISCA) is an alternative method for summarizing culture results that may address some of the barriers associated with producing

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(A) Example Nursing Home CLSI-standard Urinary Antibiogram

Species	N	% sensitivity to antibiotics						
		Amoxicillin	Amoxicillin-clavulanate	Cephalexin	Ceftriaxone	Nitrofurantoin	Ciprofloxacin	TMP-sulfa
E. coli	31	63	74	78	89	82	60	87
Klebsiella spp.	10	50	70	60	80	50	80	90
Proteus spp.	2	50	100	100	100	0	100	100

(B) Example Nursing Home WISCA
43 urinary isolates

Empiric antibiotic	% S
Amoxicillin	60
Amoxicillin-clavulanate	74
Cephalexin	75
Ceftriaxone	87
Nitrofurantoin	71
Ciprofloxacin	67
TMP-sulfa	88

Figure 1. Examples of urinary (A) CLSI-standard antibiograms and (B) WISCAs. Example A is of a NH CLSI-standard Urinary Antibiogram containing the three most commonly isolated Gram negative uropathogens and their cumulative susceptibilities to commonly used antibiotics for UTIs. Example B is a Weighted-incidence syndromic antibiogram (WISCA), which uses the same population of Gram negative uropathogens as example A, however, collapses them into a single population instead of by species.

NH antibiograms using CLSI standards.[5] In contrast to CLSI-standard antibiograms, which present antibiotic susceptibilities for individual bacterial species or genera, a WISCA aggregates susceptibility data across all eligible pathogens isolated from a specific body site (e.g., urine) to generate a single, composite susceptibility estimate for each antibiotic (Figure 1B). This approach may enhance empiric antibiotic decision-making prior to return of the cultured organism.[6] We previously demonstrated the feasibility of using the WISCA approach to generate facility-specific antibiogram tools for a group of NH served by a common reference laboratory located in geographically limited region.[7] Whether the WISCA approach can be applied to a more heterogeneous population of NHs served by other microbiology laboratories and how different isolate inclusion/exclusion criteria employed during facility-specific tool development impact reported susceptibility estimates remain poorly understood.

In this study, we first compared the number of NHs capable of producing a facility-specific urinary antibiogram using a CLSI-standard versus a WISCA approach. We then evaluated the influence of three variations on specimen inclusion on facility-specific antibiograms that could be developed by study NHs using a WISCA approach: types of species eligible for inclusion, timeframe over which cultures were collected, and timeframe over which duplicate isolates recovered from the same individual were excluded. Finally, we examined how these variations impacted susceptibility estimates for each facility-specific WISCA.

Methods

A limited dataset containing the results of urine cultures collected in 59 NHs in Indiana, Missouri, Nevada, Pennsylvania, Ohio, and Oregon in 2020 and 2021 were obtained from 3 contracted microbiology laboratories. These microbiology labs were chosen as they serve multiple NHs with existing relationships with the study team. The datasets included NH name, zip code, NH resident identifier, urine culture specimen identifier, organism name, amount growth, antibiotics tested, and results of antibiotic test (MIC and interpretation). These data were linked to NH demographics, including bed size, CMS star rating, profit status, state, and urban location. Urban was defined using the metropolitan statistical area urban classification from the 2020 United States Census Data. An honest broker removed NH resident identifiers. The de-identified dataset was cleaned using Open Refine 3.7.2 (Google) to standardize data elements that varied across reference laboratories (e.g. "cipro" versus "ciprofloxacin"). CLSI breakpoints were used to assess for potential differences in susceptibility interpretations across reference laboratories when minimum inhibitory concentration (MIC) data were available.

Only potentially pathogenic gram-negative bacteria were included in the sample. Cultures with recovery of more than three isolates were considered contaminated and removed from further analyses. Isolates that grew only yeast or bacteria isolates at less than 10,000 cfu/ml were also excluded although second isolates from the same culture that grew above this threshold were included in the final analytical dataset.[8] Duplicate isolates, defined as the same bacterial species obtained from the same nursing home resident within a specified timeframe, were excluded. Two timeframes – 3 versus 12 months within the same calendar year – for identifying the presence of a duplicate isolate were compared in this study and when identified, using either time threshold, only the earliest recovered isolate was retained for analyses. Intrinsic resistance for specific drug-bug pairs (e.g. *Proteus* spp. and nitrofurantoin) and inferred interpretations of unreported results (e.g. and *Escherichia coli* susceptible to amoxicillin was also susceptible to amoxicillin-clavulanate) were created based on guidance from CLSI, the European Committee on Antimicrobial Susceptibility Testing (EUCAST), and infectious disease experts

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Table 1. Characteristics of CLSI standard antibiogram and WISCA models

	Isolates included	Time period for culture inclusion	Time to exclude duplicates
CLSI Standard Antibiogram	*E coli*, *Klebsiella* spp, *Proteus* spp	12 months	Same isolate within 12 months
Base WISCA Model			
Alternate WISCA Model 1	All gram negative uropathogens		
Alternate WISCA Model 2		24 months	
Alternate WISCA Model 3			Same isolate within 3 months

Table 2. Nursing home characteristics

	Total ($n = 59$)
Average bed size (mean, SD)	112.7 (41.9)
Number of Beds (can refine these cut points)	
≤75 beds	11 (18.6%)
76–150 beds	37 (62.7%)
>150 beds	11 (18.6%)
Profit status (%)	
For-Profit	46 (78.0%)
Non-Profit	13 (22.0%)
2020 CMS Star Rating	
1 Star	7 (11.9%)
2 Star	14 (23.7%)
3 Star	12 (20.3%)
4 Star	7 (11.9%)
5 Star	16 (27.1%)
Missing	3 (5.1%)
Location	
Rural	23 (39.0%)
Urban	36 (61.0%)
State	
Indiana	12 (22.0%)
Missouri	2 (3.4%)
Nevada	1 (1.7%)
Ohio	30 (50.8%)
Oregon	5 (8.5%)
Pennsylvania	8 (13.6%)

(Supplemental Table 1) when actual susceptibility results were not available. Gram negative species were grouped by genus. We restricted our analyses to antibiotics commonly used to treat urinary tract infections in NHs for which susceptibility results are commonly available, including amoxicillin (ampicillin as surrogate), amoxicillin-clavulanate (ampicillin-sulbactam as surrogate), first generation cephalosporins, third generation cephalosporins, ciprofloxacin, nitrofurantoin, and trimethoprim-sulfamethoxazole.

We first assessed the capacity to create a facility-specific urinary antibiogram from each study NH's culture data using both a CLSI-standard approach (Figure 1A) and WISCA approach (Figure 1B). For these analyses, data used to create each antibiogram tool were restricted to cultures obtained in study NHs in 2020, and to the three most frequently recovered uropathogens (i.e. *E. coli*, *Klebsiella* spp., and *Proteus* spp.)[7] *Klebsiella aerogenes* was not included in the *Klebsiella* spp. group given its intrinsic resistance patterns. A susceptibility estimate was only generated if the number of isolates available for analysis exceeded 30, as per existing CLSI recommendations.[1]

We then used data from 2020 through 2021 to examine how different inclusion criteria impacted generation of facility-specific WISCA with 30 or more isolates for study NHs. A series of WISCAs with varying included isolates, specimen collection time period, duplicate isolate exclusion criteria were considered, with each WISCA model's key characteristics summarized in Table 1. A WISCA using the three most common uropathogens using one year of culture data was considered the base model. Three alternate WISCA models were developed to examine different methodological approaches that would increase the number of isolates. Alternate model 1 included all Gram-negative uropathogens. Alternate model 2 included all uropathogens and extended the time period over which isolates were collected from one to two years. Alternate model 3 modified alternate 2 to reduce the time interval for excluding duplicate isolates from twelve month to three months. With each stepwise comparison between models, the approach that optimized the number of NHs able to create a tool with greater than or equal to 30 isolates (as defined as number of isolates with testing to ceftriaxone) was adopted for the subsequent comparison. Differences in number of NHs able to create a tool with greater than or equal to 30 isolates were assessed via a Chi-squared test.

We also examined the influence of the methodological approach on change in the percentage of isolates reported as susceptible to the tested antibiotic. For individual study NHs, the susceptibility estimates for each antibiotic were categorized into three mutually exclusive categories: (1) ≥90% susceptible; (2) 80–89% susceptible; and (3) <80% susceptible.[9] For this analysis, a change in a WISCA parameter (included isolates, specimen collection time period, duplicate isolate exclusion criteria) that resulted in a shift from one susceptibility category to another (e.g. ≥90% to 80–89%) among the base or alternate WISCA models was deemed clinically meaningful. The number of NHs with clinically meaningful susceptibility changes for each of the tested antibiotics were enumerated for each WISCA model.

Results

Characteristics of the 59 study NHs are shown in Table 2. Most were for profit and located in Ohio. The mean number of beds was 112.7 (SD 41.9). Between 2020 and 2021, these 59 NHs had 5,398 cultures representing 6,485 isolates. After excluding likely contaminated cultures, isolates with too little growth, yeast, and

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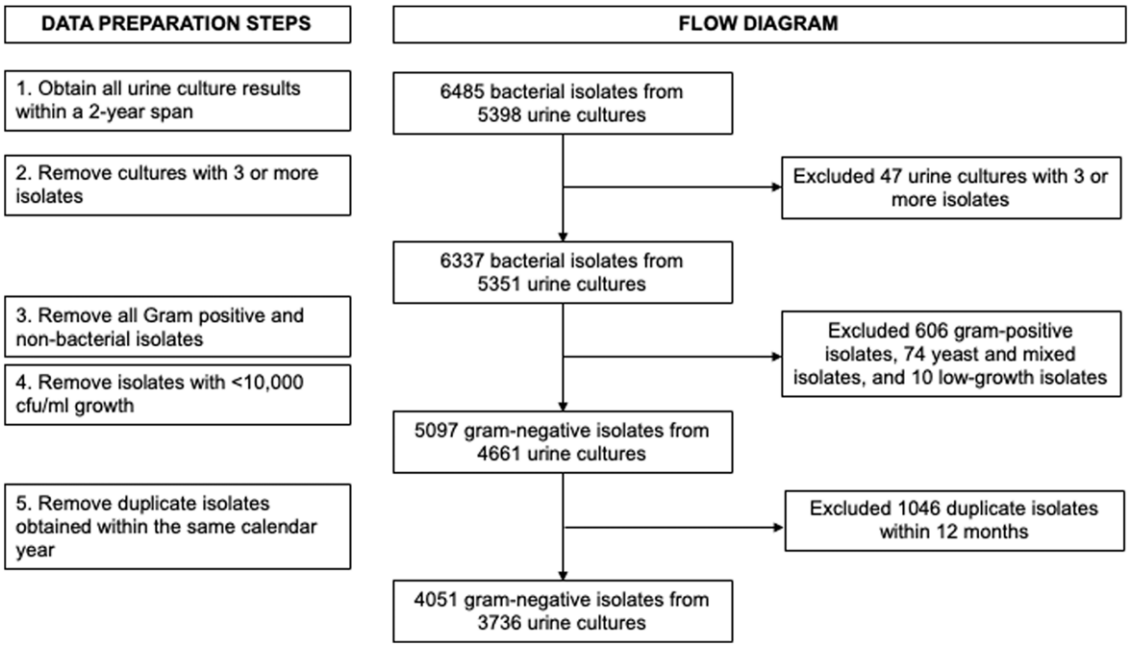


Figure 2. Data preparation steps and flow diagram of inclusion of only potentially pathogenic gram-negative urinary isolates.

Gram-positive isolates, there were 5,097 isolates from 4,661 urine cultures. Excluding duplicate isolates from the same individual within a 12-month period resulted in 4,051 isolates from 3,736 cultures (Figure 2). The median number of Gram-negative uropathogens after excluding duplicate isolates per NH in 2020 was 34 (IQR 23–52) and the median number of isolates per NH average across 2020–2021 was 58 (IQR 40–83). Testing these isolates against the 7 antibiotics commonly used to treat UTIs in NHs resulted in a total of 56,840 drug-bug pairs. Data to generate drug-bug susceptibility estimates were missing in 12,790 (22.5%) instances. Application of intrinsic susceptibility and inferred susceptibility patterns allowed for imputations of results for 2,970 and 3,221 of the drug-bug susceptibility pairs, respectively, reducing the number of missing values to 6,599 (11.6%).

Comparison of CLSI-recommended antibiogram versus WISCA

Using the CLSI-standard approach to generate an antibiogram, 7% of NHs (12/59) had enough isolates ($n \geq 30$) to produce a susceptibility estimate for *E. coli* to ceftriaxone (Table 3). Notably, only one of the 59 NHs had enough *Proteus* and *Klebsiella* isolates to produce susceptibility estimates for all three pathogens. In comparison, applying a WISCA format (one year of culture data restricted to the three most frequently recovered uropathogens) yielded a facility-specific antibiogram for 36% of NHs (21/59). Given the inability of all study NHs, except one, to produce a CLSI-standard antibiogram, subsequent analyses focused on how different isolate inclusion criteria impacted antibiogram production and susceptibility estimates using a WISCA format.

Impact of isolate inclusion criteria on ability to produce a facility-specific WISCA

Compared to the base WISCA model (one year of culture data for the three most recovered gram-negative pathogens), alternate model 1, which includes all gram-negative isolates, increased the proportion of NHs that could generate a facility-specific WISCA from 36% to 54% ($\chi^2 = 9.5$, P-value = .002; Figure 3). Alternate model 2, which combined two years of culture data, led to further increases in the proportion of NHs that could generate a facility-specific WISCA to 85% ($\chi^2 = 5.5$, P-value = .02 compared to alternate model 1). Alternate model 3 compressed the timeframe of excluding duplicate isolates from the same individual from a 12-month to a 3-month window, reducing the number of excluded isolates from 21% (1,046 of 5,097 isolates excluded) to 13% (647 of 5,097 isolates excluded). This change did not result in a significant increase in the number of NHs capable of producing a facility-specific WISCA compared to alternate model 2 ($\chi^2 = 0.09$, P-value = .95).

Impact of isolate inclusion criteria on WISCA susceptibility estimates

Comparing alternate model 1 to the base WISCA model revealed a clinically meaningful change in the reported ampicillin-sulbactam susceptibility at one study NH. Clinically meaningful decreased susceptibility to cefazolin and trimethoprim-sulfamethoxazole occurred for nine and four study NHs, respectively. Four NHs saw a clinically meaningful increase in susceptibility to ceftriaxone (Figure 4). The stepwise comparison of alternate models 2 and 3 were not associated with any additional clinically meaningful shifts in the reported antibiotic susceptibilities in any of the study NHs (Supplemental Figures 1 and 2).

Discussion

Our results underscore that few NHs can use the CLSI-standard approach to generate a facility-specific antibiogram. Even a WISCA approach, when restricted to one year of culture data and the three most frequently recovered pathogens, allowed only a third of participating NHs to generate a facility-specific instrument. To maximize the proportion of NHs using a facility-specific urinary antibiogram, we recommend a WISCA approach that includes all gram-negative isolates recovered from urine cultures

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Table 3. Number and percent of NHs able to create a tool with n>= 30 isolates

	Ampicillin	Ampicillin-sulbactam	Cefazolin	Ceftriaxone	Ciprofloxacin	Nitrofurantoin	TMP-Sulfa
CLSI-Standard Antibiogram	1 (2%)	1 (2%)	0	1 (2%)	1 (2%)	1 (2%)	1 (2%)
E coli	7 (12%)	7 (12%)	5 (8%)	7 (12%)	7 (12%)	7 (12%)	8 (14%)
Klebsiella spp.	1 (2%)	1 (2%)	0	1 (2%)	1 (2%)	1 (2%)	1 (2%)
Proteus spp.	1 (2%)	1 (2%)	1 (2%)	1 (2%)	1 (2%)	1 (2%)	1 (2%)
WISCA Base Model	21 (36%)	21 (36%)	20 (34%)	21 (36%)	19 (32%)	21 (36%)	21 (36%)

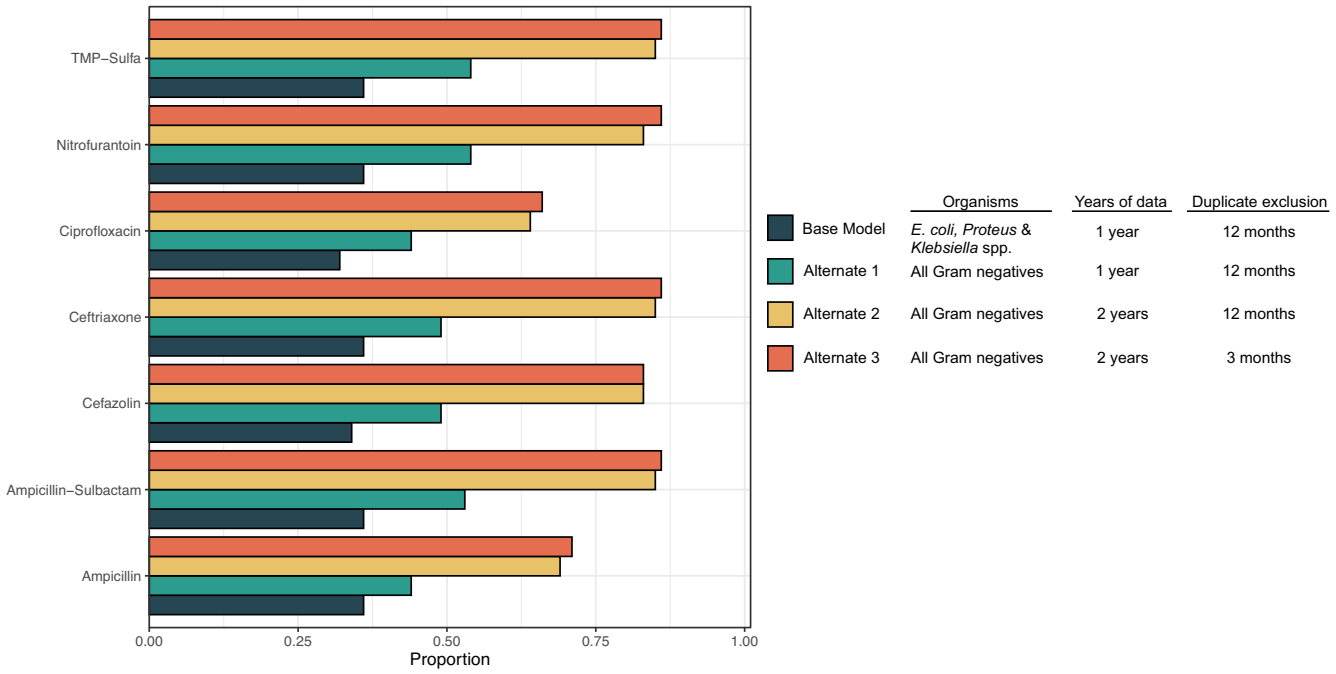


Figure 3. Proportion of NHs able to create a facility-specific WISCA, comparing 4 models.

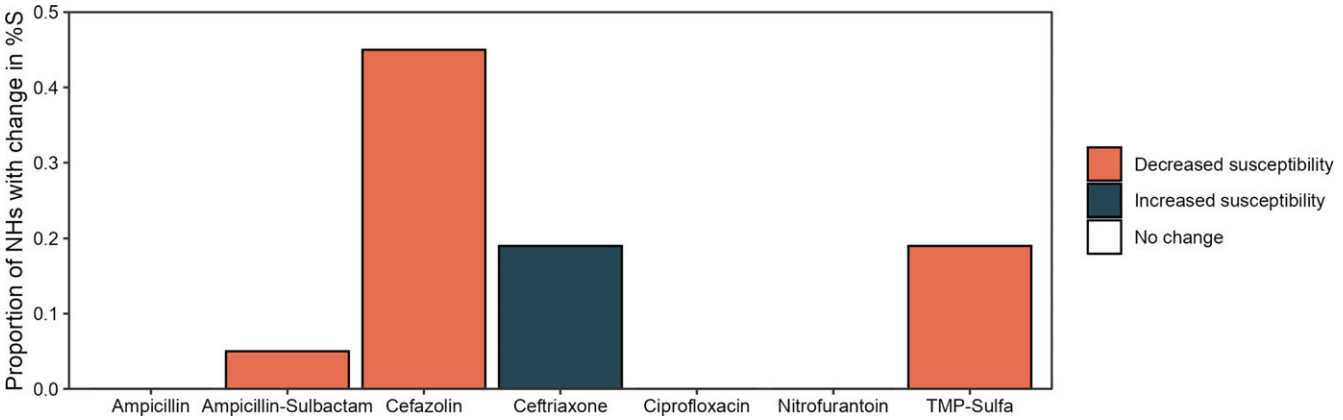


Figure 4. Proportion of NHs with categorical change in susceptibility when expanding inclusion criteria from the base model to alternate 1, considering 21 NHs able to create the base model. WISCA base model used the three most common uropathogens, 1 year of culture data, and a 12-month duplicate isolate threshold. Alternate 1 included all Gram-negative uropathogens, 1 year of culture data, and excluded duplicate isolates within a 12-month timeframe. There were no categorical changes in ampicillin, ciprofloxacin, or nitrofurantoin.

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over a two-year period while excluding duplicate isolates obtained within the same calendar year. With this approach, a facility-specific WISCA tool was able to be generated for 85% of the NHs in the current study.

WISCAs have previously been reported to be a viable approach for overcoming the problem of too few isolates in NHs.[7] The approach Davenport et al. employed in generating a WISCA for NHs in their study was identical to the base model employed in the current study (i.e., the three most recovered uropathogens from urine cultures collected during a single year). The NHs included in the current study are smaller and more rural than the facilities represented in the Davenport *et al.* study. The methodological modifications we propose should allow most NHs of all sizes and geography to produce a facility-specific WISCA.

The current study clearly demonstrates it may be difficult to generate a facility-specific CLSI standard urinary antibiogram for most NHs given the typically low number of isolates recovered annually. Less than half of the NHs in our study recovered enough *E. coli* isolates from urine cultures collected over one year to generate viable susceptibilities against tested antibiotics. Only one study NH recovered enough isolates from cultures to produce susceptibility estimates for the three most common gram-negative genus categories associated with UTI in NH residents. This is similar to reported limitations of creating facility-specific antibiograms in Australian residential aged care facilities.[10] Pooling cultures from multiple NHs within a region may result in enough isolates to create a traditional antibiogram and has been suggested.[10,11] However, while a recent study failed to identify a significant facility effect on pooled-facility antibiogram susceptibility estimates for a large cohort of NHs in Georgia, susceptibility estimates in VA NHs diverged significantly from those in affiliated VA hospitals.[12] It, therefore, remains unclear if pooled-facility antibiograms should be used to support empiric antibiotic decision-making in most NHs.

The WISCA was initially developed as a tool to enhance the probability of empirically selecting a microbiological active antibiotic in critically ill hospitalized patients.[6,12,13] Randhawa *et al.* found that use of WISCAs more than doubled the likelihood of microbiologically active empiric antibiotic therapy among intensive care unit patients with ventilator-associated pneumonia and catheter-associated bloodstream infection.[13] However, real-world implementation of WISCAs is limited, with a single study integrating WISCAs into a hospital's antimicrobial stewardship prospective audit and feedback noting no differences in hospital length of stay or mortality.[14]

Collapsing Gram-negative urinary isolates into a single category can affect reported resistance. This is due to the intrinsic resistance patterns of less commonly isolated Gram-negative uropathogens. For example, although nitrofurantoin might be active against 90% or more of the *E. coli* isolated at a NH, the overall activity of nitrofurantoin will be adversely impacted by the higher prevalence of intrinsically-resistant uropathogens (e.g. *Proteus* spp. or *Pseudomonas aeruginosa*) in the NH setting. Including all gram-negative uropathogens in the WISCA was associated with clinically meaningful decrease in the reported susceptibilities to first-generation cephalosporins and TMP-sulfamethoxazole in nine and four study NHs, respectively. In contrast, the reported susceptibility to ceftriaxone improved in four study NHs. In our sample, these less commonly isolated uropathogens were more likely to be intrinsically resistant to first-generation cephalosporins (i.e. *Pseudomonas*) or harbor narrow-spectrum beta-lactamases (i.e. *Enterobacter* spp. or *Klebsiella aerogenes*). Interestingly, the increase in ceftriaxone susceptibility suggests that the less commonly isolated Enterobacteriaceae had less ESBL activity. How these changes in reported susceptibilities might impact NH clinician prescribing patterns remains unclear although a recently published simulation study did demonstrate making these results available to clinicians is likely to have some effect.[6] Avoiding empiric use of oral cephalosporins in facilities with low cefazolin activity seems prudent. Future studies should explore the if urinary WISCA use is associated with increased and unnecessary broad-spectrum empiric antibiotic use.

Although existing regulations require NHs to track and report antibiotic susceptibility patterns,[15,16] incorporation of antibiograms into NH antibiotic stewardship programs has been limited, and when used, they are infrequently facility-specific.[3,17] Other barriers to development and use of antibiograms are likely to include high rates of staff turnover, competing demands of the infection preventionist, and need for infectious disease or microbiology expertise, which limits opportunities for developing in-house antibiograms. Our study obtained the necessary data elements from consulting microbiology laboratories, suggesting that it would be feasible for laboratories to provide this as a service.

This study has several limitations. We only had access to culture results and were unable to assess if sending a urine culture was clinically appropriate. Over-diagnosis of UTI is a common problem encountered in NHs.[18] Consequently, the uropathogens represented in this study likely represent a mixture of organisms from NH residents with UTI as well as asymptomatic bacteriuria. We were also unable to assess or control for the quality of urine specimen collection in study NHs. Antibiogram results from facilities with lower quality urine specimen collection technique may be inordinately influenced by the recovery of organisms residing on skin and/or mucosal surfaces rather than those involving the urinary tract. How variation in the threshold for ordering a urine culture as well as differences in technique of urine specimen collection may impact antibiotic susceptibility patterns reported in a given facility-specific antibiogram remains poorly understood. Although NHs in our sample did not see significant changes in %S when expanding to 2 years of urine culture data, it is possible that a 2-year interval may dilute clinically relevant changes in resistance patterns in certain settings.

Our described approach provides guidance on creation of facility-specific urinary WISCAs for NHs by including up to 2 years of all gram-negative urinary isolates and exclusion of duplicate isolates obtained within 1-year. Although this method allows for the vast majority of NHs to make a facility-specific tool, 15% of NHs in our study still could not create a facility-specific urinary WISCA with this approach. Perhaps regional pooling of cultures from facilities like these would be a reasonable alternative, however, whether the percent susceptibility of facility-specific antibiograms deviate substantially from regionally pooled tools is not clear. Future studies should assess whether regional antibiograms adequately reflect facility-specific resistance patterns to ensure accurate guidance for empiric therapy and antimicrobial stewardship.

Supplementary material. To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2025.10391

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Competing interests. All authors report no conflicts of interest relevant to this article.

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