Determinants for Antibiogram Development for use by Skilled Nursing Facilities in a Large Geographic Region, 2016-2017

Scott K Fridkin, MD (1), Ziduo Zheng, MSc (2), Jacob S. Pack, ASc (3), Sam Sefton, MPH (1), Renee Moore, PhD (2), Steve Price (3), Mayfield Camp Jr., M.S. (3)
(1) Department of Medicine, Emory University School of Medicine, (2) Department of Biostatistics, Emory Rollins School of Public Health, and
(3) Clinical Laboratory Services, Inc., Winder, GA

Background

- Skilled nursing facilities (SNFs) are an important and growing component of the U.S. healthcare system and recognized as settings in which resistant pathogens and inappropriate antimicrobial use are prevalent (1-2).
- As of January 2018 all SNFs are required to have an antibiotic stewardship program (ASP) (3-4), including access to cumulative susceptibility data (antibiograms) from isolates recovered from infections among residents (5).
- However, most SNFs submit so few specimens in a given year that constructing SNF-specific antibiograms for a single year cannot be performed consistent with CLSI Guideline M39-A4 (30>= isolates per organism recommended (6,7,8).
- Sharing data across SNFs within a given year is one method to overcome this limitation of data and provide more robust antibiograms for each SNF in a region.

Objectives

This analysis explores best methods to combine data across SNFs in order to enable clinical laboratory staff producing antibiograms to assess:

1. Are there significant regional differences in AR (antibiotic resistance) patterns?
2. Should groups of SNFs be combined to produce an antibiogram based on SNF characteristics?

Methods

- Retrospective observational cohort study of SNF residents in 2016-2017 with urine culture processed by Clinical Laboratory Services (CLS) in Winder, GA.
- Testing results in study population were limited to:
  - CMS (Centers for Medicare and Medicaid Services) designated skilled nursing facilities in the GA
  - *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*
  - Patients aged 65-75 years.
- Susceptibility testing was performed using a MicroScan Walkway96 Plus, select results were suppressed consistent with standards (2nd gen suppressed if gram negative fermenters test susceptible to cefazolin)
- Linkage by National Provider Number to a CMS Certification Number (CMS CCN) allowed abstracting facility characteristics from 2016 Nursing Home Compare
- Log-Binomial Regression was performed at the isolate level to identify critical facility or encounter characteristics predictive of testing susceptible.
- Spider plots of estimated % susceptible were plotted by characteristic to evaluate consistent differences in % susceptible across antibiotic-pathogen pairs.
- Acronyms: CEF3 = non-susceptible to any 3rd generation cephalosporin tested, FQ = non-susceptive to either ciprofloxacin or levofloxacin.

Results

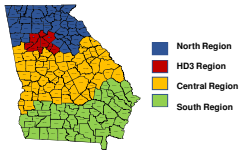
Table 1. **No. of facilities submitting isolates, and no. of isolates per facility, by pathogen.**

Organism	All Facilities		No. of Isolates per Per Facility					
	No. of facilities	% submitting >1 isolate	Mean	Min	25%	50%	75%	Max
E.coli	195	74	6.25	1	2	4	8	35
K. pneumoniae	145	55	3.14	1	1	2	4	14
P. aeruginosa	73	59	2.34	1	1	2	3	16
Proteus mirabilis	154	28	3.25	1	1	2	4	17
E. faecium	50	19	1.40	1	1	1	1	7

- Crude values will be heavily weighted by facilities reporting more pathogens

Table 2. **Estimated Percent Susceptible for Select Urinary Pathogens, by geographic region**.

- Yellow boxes illustrate statistically significant differences in %S between two regions, orang boxes are of borderline statistical significance. Overall only 18 of 144 comparisons were statistically significant (10 of these 18 involved the northern region). HD3 = Health District 3.

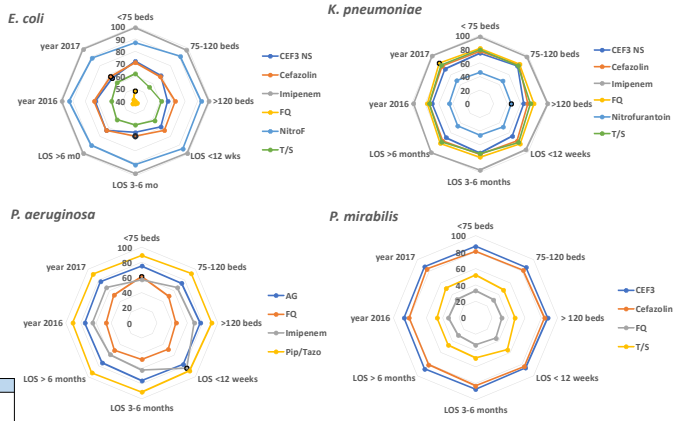


		% Susceptible, by Region				Mean difference in percentage points comparing two regions (P-value)					
Pathogen	Antibiotic	Central	HD3	North	South	Central to Atlanta HD3	Central to Southern	Atlanta HD3 to Southern	Northern to Central	Northern to Atlanta HD3	Northern to Southern
E.Coli	CEF3	73.1	63.6	62.1	73.8	9.5 (0.01)	-0.7 (0.88)	-10.1(0.03)	11 (0.01)	1.5 (0.74)	-12 (0.02)
	Cefazolin	71.8	69.7	65.5	73.5	2.1 (0.58)	-1.7 (0.70)	-3.8 (0.41)	6.4 (0.14)	4.3 (0.35)	-8.0 (0.11)
	FQ	42.9	41.7	32.9	46.5	1.3 (0.74)	-3.7 (0.40)	-4.9 (0.29)	10 (0.02)	8.8 (0.05)	-14 (0.01)
	Imipenem	99.2	99.0	97.3	98.3	0.3 (0.95)	0.9 (0.83)	0.7 (0.88)	2.0 (0.65)	1.7 (0.71)	-1.0 (0.84)
	Nitrofurantoin	91.0	92.1	89.0	89.7	-1.1 (0.77)	1.2 (0.77)	2.4 (0.61	2.0 (0.64)	3.1 (0.50)	-0.7 (0.88)
	Trimeth/Sulfa	59.4	62.6	53.7	62.2	-3.2 (0.40)	-2.8 (0.51)	0.4 (0.93)	5.7 (0.18)	8.9 (0.05)	-8.5 (0.09)
K. pneumoniae	CEF3	64.5	65.7	82.7	78.7	-1.2 (0.82)	-14 (0.02)	-13 (0.04)	-18 (0.01)	-17 (0.01)	4.0 (0.56)
	Cefazolin	71.1	72.9	86.2	78.6	-1.7 (0.74)	-7.5 (0.21)	-5.8 (0.35)	-15 (0.01)	-13 (0.03)	7.6 (0.27)
	FQ	76.3	77.0	87.6	86.3	-0.6 (0.91)	-10 (0.10)	-9.4 (0.13)	-11 (0.07)	-10 (0.09)	1.2 (0.86)
	Imipenem	98.9	97.4	97.8	97.0	1.4 (0 .79)	1.9 (0.75)	0.5 (0.94)	1.1 (0.86)	-0.4 (0.95)	0.8 (0.91)
	Nitrofurantoin	46.5	45.6	53.7	40.7	0.8 (0.87)	5.8 (0.34)	4.9 (0.43)	-7.2 (0.24)	-8.1 (0.20	13 (0.06)
	Trimeth/Sulfa	73.6	73.0	84.0	81.0	0.6 (0.90)	-7.3 (0.22)	-8.0 (0.19)	-10 (0.09)	-11 (0.08)	3.0 (0.66)
P. aeruginosa	AG	78.2	72.2	84.0	73.4	6.0 (0.44)	4.8 (0.60)	-1.2 (0.90)	-5.8 (0.58)	-11 (0.24)	10 (0.34)
	FQ	46.7	42.5	63.6	57.5	4.2 (0.58)	-10 (0.24)	-15 (0.09)	-16 (0.11)	-21 (0.03)	6.1 (0.59)
	Imipenem	62.3	67.6	66.5	65.4	-5.3 (0.49)	-3.1 (0.74)	2.2 (0.80)	-4.2 (0.69)	1.1 (0.91)	1.1 (0.92)
	Pip/Tazo	93.5	89.0	92.3	90.3	4.4 (0.56)	3.2 (0.73)	-1.3 (0.88)	1.1 (0.91)	-3.3 (0.74)	2.1 (0.85)
P. mirabilis	CEF3	87.1	87.3	88.7	85.7	-0.2 (0.98)	1.5 (0.80)	1.6 (0.79)	-1.6 (0.78)	-1.4 (0.81)	3.0 (0.65)
	Cefazolin	83.0	84.9	86.1	76.0	-1.9 (0.70)	7.0 (0.23)	8.9 (0.14)	-3.1 (0.59)	-1.2 (0.85)	10 (0.13)
	FQ	25.1	33.6	30.5	44.7	-8.5 (0.09)	-19 (0.00)	-11 (0.07)	-5.4 (0.35)	3.2 (0.60)	-14 (0.03)
	Trimeth/Sulfa	50.5	46.4	43.8	55.4	4.1 (0.41)	-4.8 (0.41)	-8.9 (0.14)	6.8 (0.24)	2.7 (0.65)	-11 (0.08)
No. of comparisons (%) with significant/borderline differences						2 (9%)	2 (9%)	3 (13%)	8 (33%)	9 (38%)	7 (29%)

- Significant differences in %S by geographic region was rare, occurring in only 18 of 144 possible comparisons; however, the majority of differences involved the northern region (Table 2)

Figure 1. **Spider plots illustrating the percent of isolates (one pathogen per figure) testing susceptible to each drug (designated by different colors).**

- The vertical axis is estimated % susceptible by the statistical model adjusting for characteristic on an axis of "spider."
- Black circles indicate significantly higher or lower %S.
- No differences would result in a **symmetrical octagon**.



- Any single SNF characteristics were not consistently associated with different % susceptibility rates; although average LOS (Length of Stay), bed size, or year affected some drug-bug combination rates (Figure 1).
- These data are limited in age and time, the observed differences may become significant with addition data added to the analysis.

Conclusions

- SNFs submit too few specimens to produce a SNF-specific antibiograms;
- Combining test results across SNFs is an attractive solution to produce viable reports. There appears to be little statistical justification to producing distinct antibiograms for a SNF by grouping "similar" SNFs based on a SNF characteristic (e.g., beds). Likewise, in GA, a regional antibiogram could be produced for northern vs. other areas, but the observed differences were still of little clinical relevance.

Contact

Scott K. Fridkin, Emory University Department of Medicine – sfridki@emory.edu

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