Determinants for Antibiotic Development for use by Skilled Nursing Facilities in a Large Geographic Region, 2016-2017
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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 consistently with CLSI Guideline M39-A4 (30x=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:
  o CMS (Centers for Medicare and Medicaid Services) designated skilled nursing facilities in the GA
  o E. coli, K. pneumoniae, P. aeruginosa, P. mirabilis
  o 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, FO = non-susceptive to either ciprofloxacin or levofloxacin.

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

<table>
<thead>
<tr>
<th>Organism</th>
<th>All Facilities</th>
<th>No. of Facilities</th>
<th>% submitting iso isolate</th>
<th>Mean</th>
<th>Min</th>
<th>25%</th>
<th>50%</th>
<th>75%</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>145</td>
<td>74</td>
<td>3.34</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>8</td>
</tr>
<tr>
<td>P. aeruginosa</td>
<td>73</td>
<td>59</td>
<td>2.34</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>16</td>
</tr>
<tr>
<td>Proteus mirabilis</td>
<td>154</td>
<td>28</td>
<td>3.25</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>4</td>
<td>17</td>
</tr>
<tr>
<td>P. falcium</td>
<td>60</td>
<td>19</td>
<td>1.40</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>7</td>
</tr>
</tbody>
</table>

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

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 %
  • No differences would result in a symmetrical octagon.

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

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>North Region</th>
<th>HHD Region</th>
<th>Central Region</th>
<th>South Region</th>
<th>All Regions</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td></td>
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<td></td>
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<tr>
<td>P. aeruginosa</td>
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<tr>
<td>Proteus mirabilis</td>
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<td></td>
</tr>
<tr>
<td>P. falcium</td>
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</tbody>
</table>

- 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.

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References