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Epidemiology of Gram Negative Antimicrobial Resistance in a Multi-State Network of Long Term Care Facilities

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Abstract

We identified 1,805 gram-negative organisms in urine cultures from residents of 63 long-term care facilities (LTCFs) over 10 months. Fluoroquinolone resistance was 51% among *E. coli*, while 26% and 6% of Klebsiella were resistant to ceftazidime and imipenem, respectively. Resistance varied significantly by type of LTCF, LTCF size, and geographic region.

Keywords

Resistance; gram-negative; long-term care	

Introduction

Increasing attention has been focused on the importance of antimicrobial resistance in the long-term-care facility (LTCF) population [1-3]. Antimicrobial resistance in this rapidly growing segment of the population is important because these patients often have multiple comorbidities and functional impairments that increase susceptibility to infection [4,5]. Furthermore, LTCF residents are frequently treated empirically with broad-spectrum antibiotics, which increase selection pressure for resistance [6]. Curbing emergence of antibiotic-resistant pathogens in the LTCF has challenges that are unique to this setting including fewer nursing resources, less availability of diagnostic testing, and morbidity associated with isolation control practices [1, 3-5].

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The epidemiology of antimicrobial resistance in LTCFs remains poorly understood. Furthermore, most available data are derived from single centers. How resistance patterns differ across geographic regions, facility type (e.g., skilled nursing, assisted living), and facility bed size has not been well defined. Understanding the impact of these characteristics on resistance patterns would provide important insights to inform strategies to curb future emergence of resistance. The goals of this study were to identify the prevalence of antimicrobial resistance among urine isolates from a network of LTCFs, and to elucidate differences in resistance patterns across geographic regions, facility type, and facility size.

Methods

We conducted a cross sectional study in a network of 63 LTCFs located across three US states (New Jersey, Pennsylvania, and Delaware). All microbiologic analyses of urine cultures for these LTCFs are performed by a single laboratory (Silver Labs Inc., Cherry Hill, NJ). Species identification and antimicrobial susceptibilities were confirmed according to criteria of the Clinical and Laboratory Standards Institute (CLSI) using the Microscan Walkaway (Dade Behring Inc, West Sacramento, CA) automated susceptibility testing system [7]. All urine cultures obtained from January 15, 2008 through November 15, 2008 were included. No repeat isolates from the same patient were included.

Initially, we assessed overall susceptibilities of all gram-negative organisms to the tested antimicrobial agents. These agents were amikacin, amoxicillin/clavulanate, ampicillin/sulbactam, aztreonam, cefazolin, cefepime, ceftazidime, ceftriaxone, gentamicin, imipenem, levofloxacin, piperacillin-tazobactam, tetracycline, tobramycin, and trimethoprim-sulfamethoxazole (TMP-SMX).

Subsequently, we focused on the three most commonly isolated organisms: *Escherichia coli, Klebsiella* species, and *Proteus mirabilis*. For these organisms, we assessed differences in the prevalence of resistance by geographic region, institution size, and institution type (i.e., skilled nursing facility (SNF) vs. assisted living facility (ALF)). Geographic location of the LTCF was assigned to one of six pre-determined geographic regions. These regions were based on counties and were divided into the following regions: Northern New Jersey, Central New Jersey, Southern New Jersey, Coastal New Jersey, Southeastern Pennsylvania, and Delaware. LTCFs were grouped into different size categories as follows: 1) <100 beds; 2) 100-150 beds; 3) 151-200 beds; and >200 beds). In analyzing difference across geographic regions and bed size, we focused only on SNFs as the majority of clinical isolates came from SNFs rather than ALFs. Differences in prevalence were assessed using an overall chi-square test [8]. All statistical calculations were performed using STATA version 10.0 (Stata Corp, College Station TX).

Approval was obtained from the Institutional Review Board of the University of Pennsylvania.

Results

Among residents of the 63 included facilities, there were 1,805 gram-negative organisms identified during the study period, including 1,653 isolates from SNF residents and 152 isolates from ALF residents. The three most common gram-negative organisms were E. coli (n=874), Klebsiella species (n=323); and P. mirabilis (n=285). For all organisms, there was substantial resistance to various antibiotics tested. Notably, the prevalence of levofloxacin resistance was 51% among *E. coli* and 29% for *Klebsiella* species. The prevalence of ceftazidime resistance (often used as a marker for extended-spectrum beta-lactamase (ESBL)-mediated resistance) was 26% among *Klebsiella* species and 12% among *E. coli*. Finally, 6% of *Klebsiella* species and 37% of *Pseudomonas aeruginosa* were resistant to imipenem.

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Among the 63 included facilities, there were 44 skilled nursing facilities (SNFs) and 19 assisted living facilities (ALFs). There were many significant differences in antimicrobial susceptibilities when comparing ALFs and SNFs (Table 1).

Among the 44 SNFs, 12 facilities had <100 beds, 12 had 101-150 beds, 13 had 151-200 beds, and seven facilities had >200 beds. Among $E.\ coli$, there were significant differences in susceptibilities to the following agents (for bed sizes <100, 100-150, 151-200, and >200, respectively): aztreonam (79%, 90%, 87%, and 87%; p=0.005); cefepime (84%, 92%, 88%, and 88%; p=0.03); ceftazidime (81%, 92%, 88%, and 87%; p=0.003); and ceftriaxone (79%, 92%, 87%, and 87%; p=0.001). Among Klebsiella, there were no significant differences in susceptibilities across facilities of different sizes. Finally, among $P.\ mirabilis$, there were significant differences in susceptibilities to the following agents (for bed sizes <100, 100-150, 151-200, and >200, respectively): ampicillin-sulbactam (74%, 89%, 87%, and 92%; p=0.02); and cefazolin (74%, 91%, 88%, and 92%; p=0.02). Of note, the distribution of SNFs within a geographic region with regard to bed size was not substantively different across geographic regions.

The 44 SNFs represented six different geographic regions. The number of SNFs in each region ranged from four to 16 (median = 6.0) and the distribution by facility type and size were similar across the six regions. There were significant differences in antimicrobial susceptibilities across geographic regions (Table 2).

Discussion

Among a broad range of gram-negative organisms, there is was marked resistance to multiple antibiotics. Furthermore, resistance rates varied significantly by type of facility (i.e., SNF vs. ALF), LTCF size, and geographic region. This variability in resistance may be due to various differences across facilities including patient populations, antimicrobial use patterns and infection control practices. To elucidate the reasons for the variability in prevalence of resistance, studies specifically examining institutional and individual level risk factors for resistance should be pursued. Furthermore, given the marked differences across facilities, future studies should include multiple facilities to improve the generalizability of the results.

The high levels of resistance noted in this study have important implications for future therapeutic options. Fluoroquinolones are very commonly used in the LTCF setting but the very high rates of resistance will limit their future use. The prevalence of ceftazidime resistance (often used as a marker for ESBL-producing organisms) was also noted to be very high. Future studies should more clearly elucidate the epidemiology of ESBL-mediated resistance specifically in the LTCF setting [9]. Finally, we noted imipenem resistance among Klebsiella (~6%) which was greatest in the Northern New Jersey geographic region. Given recent increases in carbapenemase-producing Klebsiella noted in particular in the New York City region, trends in carbapenem resistance in LTCF patients must be monitored very closely [10].

There are several potential limitations to our study. First, we were unable to determine whether isolates represented infection versus colonization. Second, LTCFs might choose to transfer a patient with suspected infection to an acute care facility without obtaining cultures. As such patients would likely be at increased risk of a resistant infection, the result of such a practice would be to underestimate the prevalence of resistance.

We found marked resistance to multiple antibiotics among urine cultures from LTCF residents. Furthermore, resistance rates varied significantly by type of facility, facility size, and geographic region. These results show the continued decrease in antibiotic therapy options in

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LTCF residents and emphasize the critical need for rigorous, multi-facility, research focused on elucidating the epidemiology of resistance in the LTCF population.

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Table 1

Antimicrobial Susceptibilities by Type of Facility

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Organisms	Facilities	Test	AMK	A/C	AZT	CFZ	CPM	CTZ	CAX	LVX	P/T	TOB	S/L
E. Coli	ALF=19 SNF-44 P value	908	100 99 NS	84 76 0.09	91 87 NS	82 76 0.14	96 89 0.06	94 88 0.08	94 87 0.06	66 47 0.002	96 95 NS	84 79 <i>NS</i>	75 62 0.02
Klebsiella spp	ALF=19 SNF-44 P value	30 293	93 79 0.04	93 78 0.03	93 71 0.004	90 69 0.009	90 73 0.03	90 72 0.02	90 72 0.02	93 69 0.002	93 75 0.01	93 71 0.004	93 68 0.002
P. Mirabilis	ALF=19 SNF-44 P value	19 266	95 100 <i>NS</i>	100 94 NS	95 97 NS	89 87 NS	95 98 <i>NS</i>	95 97 NS	95 97 NS	68 52 0.12	100 100 <i>NS</i>	89 92 <i>NS</i>	84 77 NS

AMK: amikacin; A/C: amoxicillin/clavulanate; AZT: aztreonam; CFZ: cefazolin; CPM: cefepime; CTZ: ceftazidime; CAX: ceftriaxone; LVX: levofloxacin; P/T: piperacillin/tazobactam; TOB: tobramycin; T/S Trimethoprim-sulfamethoxazole

Only those p values ≤0.10 shown

Only those antibiotics shown for which at least one organism was statistically different when comparing SNF and ALFs

by Region
d Susceptibilities
Antimicrobia

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Organisms	Region-# Sites	TEST	A/C	AZT	CFZ	CPM	CTZ	CAX	GEN	IMP	LVX	P/T	TET	TOB	S/L
E. Coli	All SNF-44 North NJ-7 Central NJ-6 South NJ-16 Shore NJ-5 DE-4 PA-6	806 172 71 304 113 65 81	76 79 87 73 77 78 69	87 90 94 85 94 86 74 <.001	76 80 90 72 81 81 80 63 <.001	89 91 94 87 96 89 77 0.003	88 89 85 95 89 777 001	88 88 93 85 95 77 001	82 86 84 74 74 85 86 0.03	99 100 100 100 100 89 89	47 45 65 50 39 42 40 <.001	95 94 96 96 97 87 87	64 61 75 75 62 60 60 68	79 76 85 83 70 70 85 80 0.03	62 60 75 65 58 54 58 0.01
Klebsiella spp	All SNF-44 North NJ-7 Central NJ-6 South NJ-16 Shore NJ-5 DE-4 PA-6	293 71 26 110 29 29 28	78 69 58 84 86 97 71	71 69 54 75 75 86 62 71 0.07	69 65 54 75 75 83 62 64 0.04	73 70 58 78 86 62 71 0.04	72 69 54 76 86 62 71 0.07	72 69 54 76 86 62 71	86 85 69 86 93 97 82 0.009	94 85 85 98 97 100 89	63 63 75 75 86 86 64 0.04	75 70 50 81 81 86 83 71	84 69 85 83 89 90 0.09	71 69 54 78 90 59 57 60005	68 65 50 75 75 83 83 61 0.02
P. Mirabilis	All SNF-44 North NJ-7 Central NJ-6 South NJ-16 Shore NJ-5 DE-4 PA-6	266 51 37 37 25 25 34	94 96 93 93 100 96 97 87	97 100 97 98 98 98 88	84 84 86 88 88 92 79 70	98 100 99 99 86 98 87 87 87	97 100 97 98 96 96 91	97 100 99 96 96 97 87 87	88 98 97 80 80 80 96 85	100 100 100 100 100 100 NS	52 51 43 51 52 69 69 53	100 100 100 100 100 NS	NS 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	92 100 95 88 80 80 96 94 94	77 84 95 72 76 73 65

AMK: amikacin; A/C: amoxicillin/clavulanate; AZT: aztreonam; CFZ: cefazolin; CPM: cefepime; CTZ: ceftazidime; CAX: ceftriaxone; GEN: gentamicin; IMP: imipenem; LVX: levofloxacin; P/T: piperacillin/tazobactam; TET: tetracycline; TOB: tobramycin; T/S Trimethoprim-sulfamethoxazole

Only those p values ≤0.10 shown

Only those antibiotics shown for which at least one organism was statistically different when comparing SNF and ALFs