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1317. Prevalence of *Pseudomonas aeruginosa* as the Causative Organism for Community Acquired Pneumonia

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Session: P-73. Respiratory Infections - Bacterial

Background. IDSA/ATS guidelines regarding pneumonia diagnosis and treatment changed in 2019. Guidelines recommend determining local prevalence of MRSA and *P. aeruginosa* to help guide empiric antibiotic coverage. The aim of our study was to determine the prevalence of *P. aeruginosa* as the causative organism for adult patients admitted to a large urban academic medical center with community acquired pneumonia (CAP).

Methods. A report of urine streptococcus antigen tests collected January 1st-December 31st in 2019 was generated. Six hundred charts were reviewed and two hundred subjects met inclusion criteria (figure 1). Inclusion criteria were age >18, hospital admission, and documented suspicion of pneumonia by a physician.

Results. The average age was 70 and half of the cases were women. The causative organism was identified in 60/200 cases (table 1). No cases of *P. aeruginosa* were identified. The most commonly isolated organisms were Influenza A and pneumococcus. 66% of cases had age >65yo, 25% were from long term care facilities, 34% had structural lung disease, 20% had dementia, 15% were hospitalized in the prior 90 days and received IV antibiotics, and 30% of cases met severe CAP criteria (table 2).
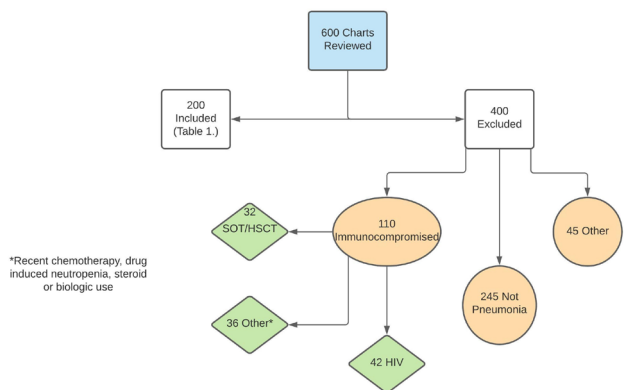

Figure 1. Workflow

Table 1. Organisms Identified

Organism	Frequency n=60
Influenza A	13
Pneumococcus	11
RSV	6
hMPV	5
MSSA	5
MRSA	3
Other GNB (*Klebsiella, E. coli*)	4
Legionella	3
Other Virus (Coronavirus, Rhinovirus, Parainfluenza)	5
Co-Infection (i.e. Influenza A + Pneumococcus)	5

Table 2. Risk Factors

Risk Factor	Frequency (%) n=200
Age >65yo	132 (66)
Hx of Smoking	96 (48)
Presence of Enteric Feeding Tube	12 (6)
Hx of Dementia	41 (20.5)
Hemodialysis	4 (2)
Structural Lung Disease (COPD, Cavitations, IPF, Bronchiectasis)	68 (34)
Hospitalization within prior 90 days with IV abx	31 (15.5)
From Long Term Care Facility	50 (25)
Severe CAP Criteria Met (IDSA 2007)	59 (29.5)
Pseudomonas in Respiratory or Blood Culture within One Year	1 (.05)

Conclusion. Limitations include a low prevalence of renal failure in the study population, and lack of a standardized respiratory infection evaluation. Our results suggest that empiric coverage for *P. aeruginosa* may not be needed at our center in this cohort of older patients with clinical characteristics sometimes thought to be risk factors for *P. aeruginosa*.

1318. Clinical and Molecular Characteristics of Hypermucoviscous *Klebsiella pneumoniae* Causing Pneumonia in Korea

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Session: P-73. Respiratory Infections - Bacterial

Background. Invasive *Klebsiella pneumoniae (K. pneumoniae)* was emerged in Asia, well-known for community-onset liver abscess. Healthcare-associated pneumonia caused by hypervirulent *K. pneumoniae* has been reported in recent studies. The purpose of this study was to evaluate the clinical and molecular characteristics of hypervirulent *K. pneumoniae* compared with classic *K. pneumoniae* in respiratory infection.

Methods. The study was performed on 163 *K. pneumoniae* isolates of respiratory infections collected from Keimyung University of Dongsan Medical Center from November 2013 to November 2015; group A, as classic *K. pneumoniae* and group B, as hypervirulent *K. pneumoniae*. Hypermucoviscous phenotype was confirmed with string test. Capsular serotypes, *rmpA, magA, allS, mrkD, entB, kfu,* and *iutA* were identified using specific primers by polymerase chain reaction. The biofilm mass was determined using the microtiter plate assay measured by optical density (OD, 570nm).

Results. A total 163 patients were analyzed, 100 (61.3%) of group A and 68 (38.7%) of group B. Community-acquired pneumonia was observed in 49.2% of group B and 18.0% of group A (*p*=0.001). Underlying diseases except chronic lung disease were more associated with group A. Mean age (72.6±11.7 vs. 68.8±12.5 years,

p=0.051) and antimicrobial resistant rates were higher in group A. Mechanical ventilators (21.0% vs. 36.5%, p=0.030) was more associated with group B. Concordances of initial antibiotics (57.5% vs. 92.1%, p=0.001) were more observed in group B. Biofilm formation and infection related 30-day mortality showed no differences between the two groups.

Conclusion. Contrary to our expectations, hypervirulent *K. pneumoniae* was more associated with community-acquired pneumonia in this study. Compared to classic *K. pneumoniae*, hypervirulent *K. pneumoniae* showed more association with severe pneumonia and less association with underlying diseases. In respiratory infection, biofilm formation was not different according to hypermucoviscosity.

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### 1319. Assessment of Spectrum Score-Based Antibiotic De-Escalation in Patients with Nosocomial Pneumonia

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Session: P-73. Respiratory Infections - Bacterial

Background. Hospital-acquired and ventilator-associated pneumonia (HAP/VAP) cause significant morbidity and mortality. Guidelines recommend broad-spectrum empiric antibiotic therapy, including treatment for *Pseudomonas aeruginosa* (PSAR) and methicillin-resistant *Staphylococcus aureus* (MRSA), followed by de-escalation (DE). This study sought to assess the impact of DE on treatment failure.

Methods. This single-center retrospective cohort study screened all adult patients with a discharge diagnosis code for pneumonia from 2016–2019. Patients were enrolled if they met pre-defined criteria for HAP/VAP ≥48 hours after admission. Date of pneumonia diagnosis was defined as day 0. Spectrum scores were calculated, and DE was defined as a score reduction on day 3 versus day 1. Patients with DE were compared to patients with no de-escalation (NDE). Data were compared using chi-square, Mann-Whitney U, or T-tests. The primary outcome was composite treatment failure, defined as all-cause mortality or re-admission for pneumonia within 30 days of diagnosis, analyzed using a Cox proportional hazards analysis to control for confounding variables.

Figure 1. Study Schematic
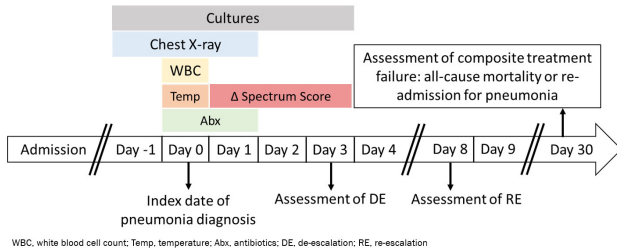
WBC, white blood cell count; Temp, temperature; Abx, antibiotics; DE, de-escalation; RE, re-escalation

Table 1. Spectrum Score Assignment

Agent	Score	Agent	Score	Agent	Score
Oxacillin	1	Sulfamethoxazole-trimethoprim	4	Cefepime	7
Dicloxacillin	1	Telavancin	5	Ciprofloxacin	7
Amoxicillin	1.5	Gentamicin	5	Ceftaroline	7
Ampicillin	1.5	Ceftriaxone	5	Ceftolozane-tazobactam	8
Cephalexin	2	Vancomycin	5	Ceftazidime-avibactam	8
Metronidazole	2	Minocycline	6	Piperacillin-tazobactam	8
Penicillin	2	Colistin	6	Levofloxacin	9
Aztreonam	3	Doxycycline	6	Ertapenem	9
Cefazolin	3	Amikacin	6	Moxifloxacin	9
Cefdinir	3	Tobramycin	6	Meropenem	10
Azithromycin	3	Amoxicillin-clavulanate	6	Meropenem-vaborbactam	11
Clindamycin	4	Ampicillin-sulbactam	6	Imipenem	11
Ceftazidime	4	Linezolid	6	Tigecycline	13

Results. Of 11860 admissions screened, 1812 unique patient-admissions were included (1102 HAP, 710 VAP). Fewer patients received DE (876 DE vs. 1026 NDE). Groups were well-matched at baseline, although more patients receiving DE had respiratory cultures ordered (56.6% vs. 50.6%, P=0.011). Patients receiving DE experienced a 65% and 44% reduction in anti-MRSA and anti-PSAR therapies by day 3, respectively. There was no difference in composite treatment failure (35.0% DE vs. 33.8% NDE, P=0.604). DE was not associated with treatment failure on Cox multivariate regression analysis (HR 1.13, 95% CI 0.97-1.33, P=0.149). Patients receiving DE had fewer antimicrobial days (median 9 vs. 11, P< 0.0001), episodes of *Clostridioides difficile* (2.2% vs. 3.8%, P=0.046), and days of hospitalization (median 20 vs. 22 days, P=0.006).
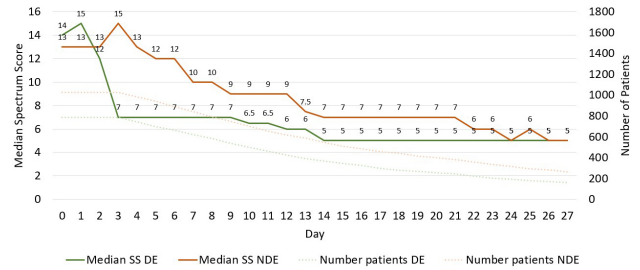
Figure 2: Median Spectrum Scores (SS) Days 0 to 28

Table 2: Cox Regression Analysis

Factors Associated with 30-Day Composite Treatment Failure			
Variable	Hazard Ratio	95% Confidence Interval	p-value
De-escalation	1.13	0.96-1.33	0.155
Modified APACHE II score	1.02	1.01-1.04	0.009
Charlson Comorbidity Index	1.14	1.11-1.17	<0.001
Ventilated HAP	1.34	1.07-1.67	0.011
Septic Shock	1.67	1.39-2.01	<0.001
Leukemia	1.50	1.18-1.90	0.001
Co-infection	0.77	0.65-0.91	0.002
Ventilated			
Day 0	1.80	1.32-2.45	<0.001
Day 1	0.87	0.60-1.27	0.474
Day 2	1.17	0.78-1.77	0.450
Day 3	0.62	0.44-0.86	0.004
Number of vasopressors			
Day 0	0.98	0.84-1.15	0.808
Day 1	0.94	0.77-1.15	0.537
Day 2	1.15	0.93-1.43	0.194
Day 3	1.18	0.98-1.41	0.083
Positive respiratory culture for likely pathogen	1.23	1.02-1.48	0.027
Immunosuppressive medications	0.83	0.65-1.06	0.140
Anti-MRSA antibiotics on day 1	0.97	0.79-1.21	0.822
Anti-PSAR antibiotics on day 1	1.39	1.00-1.95	0.054

Conclusion. DE and NDE resulted in similar rates of composite treatment failure at 30 days; however, DE was associated with fewer antimicrobial days, episodes of *C. difficile*, and days of hospitalization. Spectrum scores can objectively identify DE, but further studies are needed to fully understand their utility in this context.

1320. In Vitro Activity of Lefamulin against *Staphylococcus aureus* Isolated from the Lower Respiratory Tract of Children with Cystic Fibrosis

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Session: P-73. Respiratory Infections - Bacterial

Background. Lefamulin is a first-in-class, oral and IV pleuromutilin antibiotic approved in the US, EU, and Canada for the treatment of community-acquired bacterial pneumonia (CABP) in adults. Lefamulin inhibits bacterial protein synthesis via a unique mechanism of action and its potency against *S. aureus* has been well established. We evaluated the *in vitro* activity of lefamulin against *S. aureus* from patients with cystic fibrosis (CF).

Methods. Unique isolates (n=224) were collected from the lower respiratory tract (LRT) of children (≤17 years old) with CF and LRT infection. Organisms were from qualified respiratory specimens and determined to be the probable cause of infection by the participant center. The isolates were collected in 2018-2020 from 22 medical centers in 11 countries and tested by broth microdilution methods at JMI Laboratories. Most isolates were from the US (43.3%), Spain (24.1%), France (20.5%), and Costa Rica (7.1%).

Results. Lefamulin was highly active against the CF *S. aureus* collection ($MIC_{50/90}$, 0.06/0.12 mg/L), with 99.6% of isolates inhibited at ≤0.25 mg/L, consistent with the susceptible [S] breakpoint published by the US FDA, CLSI, and EUCAST. Only 1 lefamulin-non-S (MIC, 1 mg/L) isolate was observed, a methicillin-susceptible (MSSA) collected in Costa Rica in 2018 and carrying a *vga*(A) gene. Lefamulin retained potent activity against methicillin-resistant (R) *S. aureus* (MRSA, n=52; $MIC_{50/90}$, 0.06/0.12 mg/L), azithromycin-R (n=115; $MIC_{50/90}$, 0.06/0.12 mg/L), levofloxacin-R (n=23; $MIC_{50/90}$, 0.06/0.12 mg/L), clindamycin-R (n=11; $MIC_{50/90}$, 0.06/0.12 mg/L), and gentamicin-R (n=9; MIC range of 0.03-0.12 mg/L) isolates as well as those isolates with multiple resistance phenotypes. Against MRSA, susceptibility to azithromycin was 23.5% and to levofloxacin 64.7%. All isolates were susceptible to vancomycin, linezolid and ceftaroline (Table). Among isolates from the US (n=97), the MRSA rate was 30.9% and all isolates were Lefamulin-S ($MIC_{50/90}$, 0.06/0.12 mg/L).