Methods. Between September 15-20 of 2019, 160 patients with gastroenteric symptoms resulting from the ingestion of a common food, arrived at Fundación Valle del Lilí. *Salmonella* spp were cultured from stool specimens of patients and 15 isolates were sent to the Genomic Unit of Agrosavia for whole-genome sequencing. Genomic DNA was sequenced using an Illumina®MiSeqX10 platform. Genome assembly was performed with standardized bioinformatics pipelines and in-silico serotyping with SISTR. Genomic comparisons included newly-sequenced isolates of Infantis(n=6) from a Colombian poultry farms as well as datasets from Patric(n=441) and EnteroBase(n=54).

Results. The 15 outbreak isolates were identified by in silico serotyping as *S. Infantis,* these isolates showed phenotypic sensitivity to all tested antibiotics except by tetracycline. Antimicrobial resistance plasmids IncFIBKpn3, IncX4 and the host-environment persistence plasmid pSL483 were only detected in 2 outbreak-related and 1 in poultry isolates. Out of a total of 511 high-quality sequences, ST32 was the most prevalent and were phylogenetically grouped into a single non-host specific clade. Outbreak-isolates were included in a monophyletic group with some genomes from the US and Chile, suggesting that the parent strain could have originated in those countries.

Conclusion. The magnitude of the outbreak(288 informed-cases) evidenced a high-virulent potential of outbreak-isolates. Routine sequencing of S.enterica and availability of genomes in Colombia can improve outbreak detection and resolution in the future. The presence of plasmids, although with low frequency, suggests a risk of the appearance of resistant clones.

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1297. Azithromycin vs Beta Lactams in Acute Exacerbations of COPD

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Session: P-73. Respiratory Infections - Bacterial

Background. Bacterial infections cause approximately 50% of Acute Exacerbations of COPD (AECOPD). Current guidelines recommend a wide range of antibiotics, but evidence comparing agents is limited. The purpose of this study is to compare the effectiveness of azithromycin to beta lactams in the treatment of hospitalized patients with AECOPD.

Methods. A multicenter, retrospective, observational study of adult patients admitted with AECOPD who received at least two consecutive days of either a beta lactam or azithromycin were included. The primary endpoint was treatment failure which is a composite endpoint defined as in-hospital mortality, admission to intensive care, initiation of invasive mechanical ventilation, requirement of a new antibiotic, steroid therapy escalation, or readmission due to AECOPD within 30 days. Secondary endpoints included each individual component of the composite endpoint and length of stay.

Results. Of 11,395 patients screened, 595 met the inclusion criteria (428 were treated with azithromycin and 167 patients were treated with a beta lactam). The most common reason for exclusion was the receipt of both azithromycin and beta-lactam in 9857 patients. The patients were similar except the azithromycin group was more likely to be African-American and less likely to have failed an outpatient antibiotic. Treatment failure rate was 19.6% in the azithromycin group and 32.3% in the beta lactam group (P=0.001). Patients in the beta lactam group were more likely to experience in-hospital mortality (P=0.023), require a new antibiotic during admission (P< 0.001), and were more likely to be readmitted within 30 days of discharge due to AECOPD (P=0.032). Length of stay was significantly shorter in the azithromycin group compared to the beta lactam group. There were no statistically significant differences in the rates of adverse events among both groups.

Conclusion. Treatment failure rate and length of stay were significantly higher in the beta lactam group compared to the azithromycin group. However, there were no differences in the side effect profile among both groups. Further studies should be performed to confirm these findings.

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1298. Validation of Local *Pseudomonas aeruginosa* Risk Factors in Patients with Community-Onset Bacterial Pneumonia

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Session: P-73. Respiratory Infections - Bacterial

Background. Clinical guidelines for community-acquired pneumonia (CAP) encourage validation of local risk factors for multidrug-resistant organisms. This study aimed to validate previously derived, local risk factors for *Pseudomonas aeruginosa* in patients with community-onset bacterial pneumonia at Prisma Health-Midlands' hospitals.

Methods. In this retrospective, observational cohort study, adult patients hospitalized with pneumonia MS-DRG codes from January 1, 2017 to March 31, 2020 were randomly screened. Enrolled subjects were admitted to 1 of 3 Prisma Health-Midlands' hospitals with: diagnosis of pneumonia; receipt of inpatient antibiotics within 48 hours of symptom onset; receipt of over 48 hours of antibiotic therapy; and a causative bacterial pathogen identified via respiratory or blood culture, urinary antigen, or respiratory multiplex PCR panel. Performance of the locally derived score was compared to the Drug Resistance in Pneumonia (DRIP) Score, IDSA 2019 CAP guideline risk factors, and healthcare-associated pneumonia (HCAP) risk factors. Endpoints included sensitivity, specificity, positive and negative predictive value, overall accuracy, and over- and undertreatment rates. Overall accuracy was defined as a case in which the gram-negative antibiotic coverage recommended by the scoring schema would have been appropriate for the identified organism, i.e. neither overtreatment (overly broad-spectrum) nor undertreatment (inadequate spectrum).

Results. Of 713 patients screened, 36 patients met criteria and were enrolled. The most common bacterial pathogens identified were *Pseudomonas aeruginosa* (n = 10, 27.8%) and *Streptococcus pneumoniae* (n = 10, 27.8%). Performance characteristics for each scoring schema are summarized in Table 1.

Table 1. Performance characteristics of risk scores predicting for Pseudomonas aeruginosa community-onset bacterial pneumonia.

Scoring Schema	Minimum Cutoff Value Predictive of MDRO	Overall Accuracy (N=36), n (%)	Overtreatment (N=36), n (%)	Undertreatment (N=36), n (%)	Sensitivity	Specificity	Positive Predictive Value	Negative Predictive Value
Local	1	29 (80.6%)	2 (5.6%)	5 (13.9%)	54.5%	92.0%	75.0%	82.1%
DRIP	4	30 (83.3%)	3 (8.3%)	3 (8.3%)	72.7%	88.0%	72.7%	88.0%
IDSA	1	28 (77.8%)	4 (11.1%)	4 (11.1%)	63.6%	84.0%	63.6%	84.0%
HCAP	1	24 (66.7%)	7 (19.4%)	5 (13.9%)	54.5%	72.0%	46.2%	78.3%

MDRO=multidrug-resistant organism; DRIP=Drug Resistance in Pneumonia Score; IDSA=Infectious Diseases Society of America 2019 Community-Acquired Pneumonia Guideline risk factors ; HCAP=healthcare-associated pneumonia risk factors

Conclusion. Compared to DRIP or IDSA 2019 CAP risk scores, the local risk score performed well at ruling out resistant gram-negatives given its higher specificity and lower overtreatment rate; yet, it did not perform as well at ruling in resistant gram-negatives given a lower sensitivity and undertreatment rate. All scores performed better than HCAP risk factors. Data from this study will be utilized to further refine the local risk score algorithm.

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1299. Epidemiology of Invasive Pneumococcal Disease (IPD) in the United States 2011-2019

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Session: P-73. Respiratory Infections - Bacterial

Background. Thirteen-valent pneumococcal conjugate vaccine (PCV13) was recommended for U.S. children aged < 5 years in February 2010 and recommended in series with 23-valent pneumococcal polysaccharide vaccine (PPSV23) for adults aged ≥ 65 years in 2014. PCV13 has led to dramatic reductions in invasive pneumococcal disease (IPD) burden. New, higher valency PCVs (PCV15, PCV20) are expected to be licensed for adults in late 2021. We examined remaining PCV13-type IPD among children and adults and assessed IPD burden potentially preventable through PCV15 and PCV20 use.

Methods. IPD cases (isolation of pneumococcus from sterile sites) were identified through CDC's Active Bacterial Core surveillance during 1998–2019. Isolates were serotyped by Quellung or whole genome sequencing. Incidence rates (cases/100,000) were calculated using U.S. Census Bureau population denominators.

Results. After introduction of PCV13 in children, by 2013–2014, PCV13-type IPD declined 89% (from 15 to 2 cases/100,000) in children age < 5 years and 67% (from 19 to 7 cases/100,000) in adults age ≥ 65 years. During 2014–2019, rates of PCV13-type IPD in children and adults remained stable. In 2018–2019, among children age < 5 years, serotypes 3, 19F, 19A, and 6C accounted for most of the remaining