Results. A total of 410 IPD cases were identified. The cumulative incidence of IPD (0-22 years of age) decreased from 99.2/100,000 admissions in 2017-2019 to 53.8/100,000 admissions in 2020 (risk ratio 0.54, CI: 0.40-0.72, p< 0.00001). Pneumococcal bacteremia and pneumonia decreased significantly in 2020 (p< 0.05), and although not statistically significant, there were fewer cases of meningitis and mastoiditis when compared to previous years (p=0.08) (Figure 1). Sex, race, age or presence of comorbidities were not significantly different between groups. Most common serotypes in 2020 were 35B, 3 and 15B/C (Figure 2).

Figure 1. Number of IPD cases per year according to site of infection

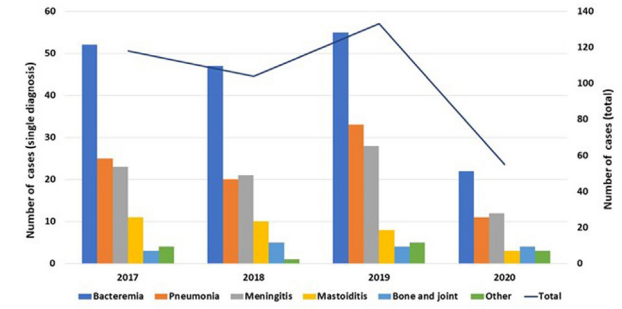
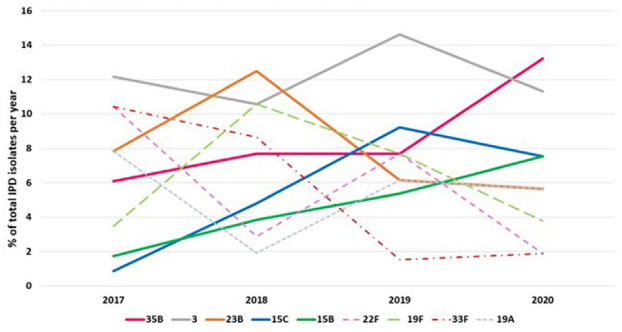


Figure 2. Most common *S. pneumoniae* IPD serotypes, 2017-2020



Conclusion. The observed decline in IPD cases during the first year of the SARS-CoV-2 pandemic is likely associated with mask use and physical distancing limiting transmission of *S. pneumoniae* via droplets and viral infections frequently preceding IPD. These precautions might be useful in the future to decrease IPD, especially in high-risk patients.

Disclosures. **Sheldon L. Kaplan, MD**, **Pfizer** (Research Grant or Support) **Tina Q. Tan, MD**, GSK (Individual(s) Involved: Self): Advisor or Review Panel member, Grant/Research Support; ILiAD (Individual(s) Involved: Self): Advisor or Review Panel member; Merck (Individual(s) Involved: Self): Advisor or Review Panel member, Grant/Research Support; Moderna (Individual(s) Involved: Self): Advisor or Review Panel member; Pfizer (Individual(s) Involved: Self): Advisor or Review Panel member **Pia S. Pannaraj, MD, MPH**, **Pfizer** (Grant/Research Support)**Sanofi-Pasteur** (Advisor or Review Panel member)**Seqirus** (Advisor or Review Panel member) **Larry Givner, MD**, **AstraZeneca** (Advisor or Review Panel member) **Kristina G. Hulten, PhD**, **Pfizer** (Research Grant or Support)

184. Inducible Clindamycin Resistance Testing on Pediatric *Streptococcus pneumoniae* Isolates

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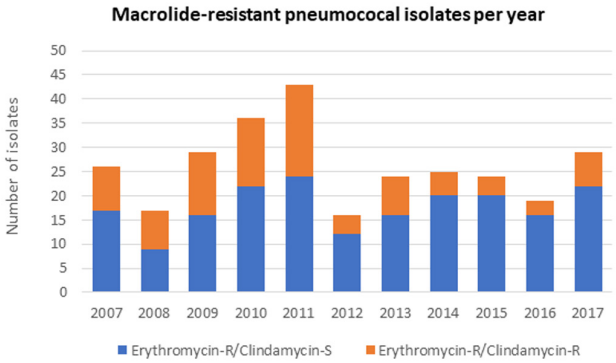
Session: O-36. Trends in Pediatric Bacterial Disease

Background. In 2013, the Clinical and Laboratory Standards Institute recommended inducible clindamycin resistance (ICR) testing on macrolide-resistant *Streptococcus pneumoniae* isolates, which arises due to the *erm*B gene. Ribosomal methylation by *erm*B confers resistance to macrolides (high-level resistance), lincosamides and streptogramin B. The goal of our study is to characterize the prevalence of ICR among pediatric pneumococcal isolates.

Methods. We identified erythromycin-resistant(R) (minimum inhibitory concentration [MIC] ≥ 1 µg/mL) and clindamycin-susceptible(S) (MIC ≤ 0.25 µg/mL) pneumococcal isolates from pediatric patients seen at Children's Mercy Hospital from 2007 to 2017. Determination of ICR was achieved via disk approximation (D-zone test) with standard erythromycin (15 µg) and clindamycin (2 µg) disks. Isolates with high-level erythromycin resistance (MIC ≥ 32µg/mL) were also tested for *erm*B gene by PCR. Positive and negative controls were used for D-zone test and *erm*B PCR.

Results. We identified 289 erythromycin-R pneumococcal isolates; of those 194 (67.1%) were clindamycin-S (**Figure 1**). One-hundred and sixty-nine isolates were available for ICR testing, 166 (98%) isolates represented non-invasive disease samples. Median age of patients with erythromycin-R and clindamycin-S isolates was 19 (range 0.1 – 180) months. None of the isolates expressed ICR based on the D-zone test. Thirteen of those isolates (7.7%) expressed high-level erythromycin-R (MIC range 32-128 µg/mL); all were negative for *erm*B. The most common serotypes/serogroups among erythromycin-R and clindamycin-S isolates were: 15 (n=22), 35B (n=19), 11 (n=16), 6 (n=16), 19A (n=14) and 33 (n=12).



Conclusion. Erythromycin-R and clindamycin-S pneumococcal isolates did not express ICR and isolates with high-level erythromycin-R did not carry *erm*B. Multicenter studies are needed to determine if ICR testing is required for macrolide-resistant pneumococcal isolates in the PCV13 era.

Disclosures. **Liset Olarte, MD, MSc**, **GSK** (Research Grant or Support)**Merck** (Research Grant or Support)**Pfizer** (Research Grant or Support)**Sanofi** (Research Grant or Support) **Douglas S. Swanson, MD**, **Merck** (Research Grant or Support)**Pfizer** (Research Grant or Support)**Sanofi** (Research Grant or Support)

185. Trends in Clinical Presentation and Antibiotic Resistance of Viridans Group Streptococci Bloodstream Infections in Immunocompromised Children

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Session: O-36. Trends in Pediatric Bacterial Disease

Background. Levofloxacin prophylaxis (LVXp) is recommended in children with severe neutropenia from underlying malignancy or hematopoietic cell transplantation (HCT). The impact of LVXp on the epidemiology of viridans group streptococcus bloodstream infections (VGS-BSI) is unknown. At our center, LVXp was prescribed to high-risk children with expected prolonged neutropenia (ANC < 100, > 7 days) as part of a clinical trial (2013-17) and routinely since November 2018. We aim to describe our local epidemiology, antibiotic susceptibilities, and clinical outcomes of VGS-BSI over time.

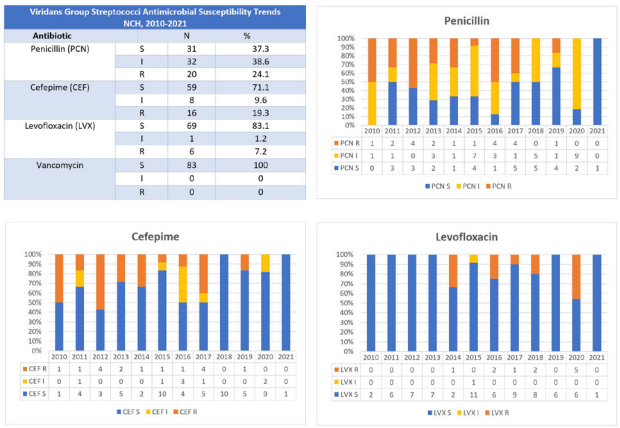
Methods. VGS-BSI from 1/1/10-1/31/21 were identified via the laboratory database. Clinical data of patients followed at NCH with underlying malignancy, severe neutropenia, or HCT were extracted from the electronic health record. Available VGS isolates were subcultured, species identification confirmed by MALDI-ToF or 16s rDNA sequencing and susceptibility to penicillin (PCN), cefepime (CEF), vancomycin (VAN), and LVX performed via Etest per CLSI M100 guidelines. Non-parametric descriptive statistics were applied.

Results. Over a 10-yr period, 111 VGS-BSI occurred in 93 patients (Table 1); 15 (16%) patients had ≥ 2 VGS-BSI. 80 (86%) patients had fever and neutropenia (F&N); 26 (28%) required ICU care for vasopressors (N=17, 18%) or mechanical ventilation (N=10, 11%). Most VGS isolates were *S. mitis/oralis* group. In total, 15 (16%) patients received LVXp ≤ 6 months before VGS-BSI; 9 (10%) had breakthrough VGS-BSI while receiving LVXp and all isolates were LVX resistant. Figure 1 shows susceptibilities: overall, 24% of isolates had frank resistance to PCN, 19% CEF, 13% LVX; all were VAN susceptible. When evaluating for changes in susceptibilities over time, there was a significant difference in the proportion of LVX-resistant isolates (p=0.009, Cochran-Armitage χ^2), but not CEF (p=0.08) or PCN (p=0.86).

Table 1. Demographic and Clinical Characteristics of Immunocompromised Children with Viridans Group Streptococci Bloodstream Infections (VGS-BSI)

Variable	N=93 patients
Age, in years (median, [IQR])	6.2 [0.8-13.9]
Male sex (N, %)	48 (51)
Underlying condition (N, %)	
Leukemia	43 (46)
Acute myelogenous leukemia (AML)	21 (22)
Acute Lymphoblastic Leukemia (ALL)	22 (24)
Hematopoietic cell transplantation (HCT)	21 (22)
Allogeneic (allo-HCT)	14 (15)
Autologous (auto-HCT)	7 (8)
Central Nervous System tumors	8 (9)
Sarcoma	7 (8)
Other	14 (15)
Absolute neutrophil count (ANC, in mm^3, median, [IQR])	0 cells [0-38]
Mucositis at time of VGS-BSI (N, %)	27 (29)
Time to bacteremia from hospital admission, in days (median, [IQR])	10 [1-16]
Time to blood culture positivity, in hours (median, [IQR])	15 [12-16.25]
Time to sterilization of blood culture, in days (median, [IQR])	1 [0-2]
Empirical antibiotic therapy in first 24 hours, N (%)	
β-lactam monotherapy	21 (22)
Combination therapy, including vancomycin	68 (73)
Other	4 (4)
Duration of total antibiotic therapy, in days (median, [IQR])	14 [10-15]
Duration of hospitalization, in days (median, [IQR])	23 [9.5-36]
Identification of VGS, N (%)	**N=83 isolates[1]**
S. mitis/oralis group	70 (84)
S. salivarius	7 (8)
S. parasanguinis	3 (4)
S. sanguinis	2 (2)
S. gordonii	1 (1)
[1]83/111 (75%) VGS-BSI were available for testing	

Figure 1. Antimicrobial Susceptibility Profile of Viridans Group Streptococci Bloodstream Isolates from Immunocompromised children, 2010-2021. Of 111 VGS-BSI reported during the study period from immunocompromised children, 83 (75%) were available for further testing. Antimicrobial susceptibility testing was performed by Etest and interpreted per CLSI M100. Susceptibility profiles to penicillin (PCN), cefepime (CEP) and, levofloxacin (LVX) are shown. Abbreviations: S—susceptible, I—intermediate, R—resistant.



Conclusion. Breakthrough, LVX-resistant VGS-BSI occurred in 10% of patients, most frequently in children with AML or HCT. Over time, there was a trend towards increased LVX resistance in the cohort. Routine antimicrobial testing and ongoing monitoring for emergence of resistance are warranted to inform local prophylaxis and empirical antibiotic strategies for high-risk children with F&N.

Disclosures. **Monica I. Ardura, DO, MSCS**, **Shire** (Grant/Research Support)

186. Characteristics of COVID-19 Vaccine Breakthrough Cases in Minnesota, 2021

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Session: O-37. Updates in COVID Epidemiology

Background. Over 600,000 COVID-19 cases, including >7000 deaths reported to MN Dept of Health (MDH) by June 1, 2021. Clinical trials demonstrated high effectiveness of COVID vaccines. We assessed COVID-19 cases among fully vaccinated residents [vaccine breakthrough (VB) cases].

Methods. COVID-19 VB cases were MN residents with completed COVID-19 vaccination series ≥14 days prior to symptom onset or positive for SARS-CoV-2 by nucleic acid amplification or antigen test. COVID-19 cases were reported to MDH and COVID-19 vaccinations reported to the MN Immunization Information Connection (MIIC). COVID-19 cases were matched to MIIC to identify VB and interviewed; medical records of hospitalized cases were reviewed. Available VB case specimens underwent whole genome sequencing (WGS) at MDH or collaborating lab.

Results. Jan 19 – June 1, 2021, 2765 VB cases were reported among >2.45 million fully vaccinated residents and 147,445 COVID-19 cases. VB case median (MED) age was 52 y (IQR 38, 68), 83% white, 65% female; MED age of fully vaccinated was 55 y (IQR 30, 68), 77% white, 54% female. Of VB cases, 273 (10%) were hospitalized and 32 (1%) died (MED age 74 y; IQR 66, 85). 2212 (80%) VB cases were interviewed; 60% reported symptoms; most common were fatigue (53%), rhinorrhea (49%), cough (42%), headache (41%). 35% reported a comorbidity.

Of hospitalized VB cases, 120 had completed record reviews. 64 were admitted for COVID-19 related illness (MED age 74 y, IQR:65, 83) including 27 admitted to ICU (MED age 71 y, IQR: 65, 83). 90% (108) reported a comorbidity, most common being chronic metabolic conditions (46%), obesity (45%), renal disease (31%) and chronic lung disease (26%); 27 were immunocompromised (not mutually exclusive), including immunosuppressive therapy (15), hematological malignancy (9), other cancer (11), and organ transplant recipients (8).

Of 604 VB case specimens, 79% were B.1.1.7, 9% B.1.427/429, 3% P.1, and 2% B.1.351; lineage distribution was similar to overall 24,157 MN SARS-CoV2 WGS data.

Conclusion. Identified VB cases were 0.1% of those vaccinated and < 2% of total cases reported in the time period. COVID-19 vaccines are an important tool in preventing COVID-19. Additional surveillance, including WGS and case characteristics will be useful to monitor VB.

Disclosures. **Ruth Lynfield, MD**, Nothing to disclose

187. Characterizing Household Clustering of COVID-19 Cases in Fulton County, Georgia, June 2020–April 2021

Carol Liu, MSc[1]; Sasha Smith, MPH[2]; Allison Chamberlain, PhD[2]; Neel Gandhi, MD[3]; Fazle N. Khan, MBBS, DPH. MPH[4]; Steve Williams, M Sc[5]; Sarita Shah, MD[1]; [1]Emory University, Atlanta, Georgia; [2]Fulton County Board of Health, Atlanta, Georgia; [3]Rollins School of Public Health, Atlanta, Georgia; [4]Georgia Depat. of Public Health, Atlanta, Georgia; [5]Fulton County, Atlanta, Georgia

Session: O-37. Updates in COVID Epidemiology

Background. Households are important for SARS-CoV-2 transmission due to close proximity in enclosed living spaces over long durations. Using contact tracing, the secondary attack rate in households is estimated at 18-20%, yet no studies have examined COVID-19 clustering within households, an important measure to inform testing and prevention. We sought to quantify and characterize household clustering of COVID-19 cases in Fulton County, Georgia.

Methods. We used state surveillance data to identify all PCR- or antigen-confirmed cases of COVID-19 in Fulton County. Clustered cases were defined as cases with matching street address, including unit number. Communal places (e.g., nursing homes, correctional facilities) were excluded, as were apartments missing unit number. Household clusters were defined as ≥2 COVID-19 cases at the same residential address with positive sample collection dates within 14 days of one another. We described proportion of COVID-19 cases that were clustered, stratified by age, sex, and race/ethnicity over time.

Results. There were 60,614 COVID-19 cases with available address reported in Fulton County during 6/1/20–4/30/21. Of these, 25,149 (41.6%) had an address that matched at least one other case; 20,793 (34.3%) were from 8,582 household clusters with positive sample collection dates within 14 days (Fig 1). Majority of clusters had 2 individuals (N=6119, 71%), though some had ≥6 individuals (N=79, 0.9%). Clustering increased through January 2021 (Fig 2). Children were more likely to be in household clusters (Fig 4) and 15% of clusters had a child as first diagnosed case with increases since January 2021 (Fig 3). Consistently higher clustering was observed among Hispanic persons, with rising clustering among Asian persons (Fig 5).

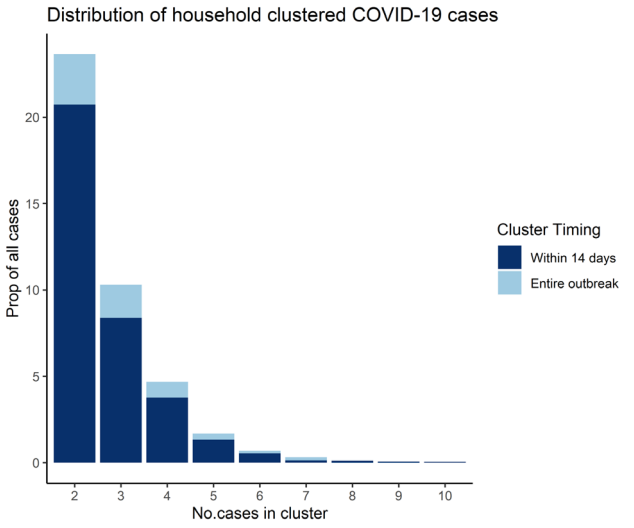

Figure 1. Distribution of household-clustered COVID-19 cases in Fulton county between June, 2020 and April 2021