299. Shigellosis in Children: Antimicrobial Susceptibility Testing by Automated Instrument vs. Etest Reveals Disagreements
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Background. In April 2017, CDC recommended testing Shigella isolates at ciprofloxacin concentration down to 0.12 μg/mL to detect potential novel resistance in isolates with MICs > 0.12–1 μg/mL. The CLSI breakpoint for ciprofloxacin susceptibility (S) is 1 μg/mL and the Vitek® system currently tests only down to 0.25 μg/mL. Our objective was to perform S testing by Vitek® and Etest to assess frequency of ciprofloxacin MIC ≥ 0.12 μg/mL and antibiotic S discrepancies between tests in clinical Shigella isolates.

Methods. Retrospective query of microbiologic data was performed to identify Shigella isolates from 2010 to 2016 to trend epidemiology and antibiotic S by Vitek®. Shigella isolates recovered between June and October, 2016 were tested in parallel using Vitek® and Etest. MIC interpretation disagreements were defined as very major error (S by Vitek® but resistant [R] by Etest) and major error (R by Vitek® and S by Etest).

Results. There was marked increase in shigellosis in 2016 (Fig 1). S. sonnei accounted for 90% of sporadic and outbreak isolates. Ampicillin resistance increased over time (21% in 2010, 90% in 2016) (Fig 2). Parallel testing of 36 isolates revealed 7 instances of antimicrobial S discrepancy with 5 very major errors (S by Vitek® to ampicillin and TMP-SMX, R by Etest) and 2 major errors (R by Vitek® to TMP-SMX, S by Etest) (Table 1). All 36 isolates were inhibited at the lowest Vitek® concentration of ciprofloxacin (0.25 μg/mL); Etest confirmed that 34/36 had MIC ≤ 0.12 μg/mL, and 2 had MIC > 0.12 μg/mL (Fig S).

Conclusion. MIC of Vitek® and Etest had major discrepancies among 7/36 isolates, for antibiotics other than ciprofloxacin. Etest mirrored Vitek® for ciprofloxacin testing. Etest revealed that 2/36 isolates with Vitek® MICs of 0.25 μg/mL (i.e. lowest concentration tested) had MICs greater than 0.12 μg/mL. Vitek® system adjustments to test ciprofloxacin at lower concentrations would address the CDC advisory. Data are needed to determine clinical relevance of Shigella susceptibility test results.

Table 1. MIC Disagreements between Vitek® and Etest

| Antibiotic | Patient/Isolate Number | Vitek® 2 | Etest | Vitek® 2 | Etest |
|------------|------------------------|---------|-------|---------|-------|
| Ampicillin | 23                     | S ≤ 2   | R > 256 | S ≤ 2   | R > 256 |
|            | 25                     | S ≤ 2   | R > 256 | S ≤ 2   | R > 256 |
|            | 26                     | S ≤ 2   | R > 256 | S ≤ 2   | R > 256 |
|            | 5                      | S 1/10  | R 4/76  | S 1/10  | R 3/808 |
|            | 7                      | R 8/152 | S 2/38  | R 8/152 | S 1/19  |

Fig 1. Shigella Isolates 2010-2016

Fig 2. Antimicrobial Resistance among Shigella Isolates Tested by Vitek® 2010-2016

Disclosures. All authors: No reported disclosures.

2990. Genetic Structures of Streptococcus pneumoniae Invasive Isolates from Korean Children Obtained Between 1995 and 2013
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Background. Understanding the population genetics of pneumococci will allow detection of changes in the prevalence of circulating genotypes and evidence for capsular switching after the use of pneumococcal conjugate vaccines (PCVs). We aimed to analyze the genetic structures of invasive pneumococcal isolates obtained from children before and after the optional use of PCV7 and PCV10/13 in Korea.

Methods. A total of 285 invasive pneumococcal isolates obtained from children aged <18 years in multicenters during 1995–2013 were included. We classified the isolates by serotypes, multilocus sequence typing, and antimicrobial susceptibility testing.

Results. Between pre-PCV7 and post-PCV13 periods, PCV7 serotypes decreased significantly (from 67.1% to 9.6%, P < 0.001) whereas non-vaccine serotypes (NVTs) showed a significant increase (from 2.9% to 53.9%, P < 0.001). Of the 10 clonal complexes (CCs), antibiotic-resistant international clones, CC320 (31.6%), CC81 (14.7%), and CC166 (6.7%) were the main complexes. Serotype 19A was the main serotype of CC320 throughout the periods. Serotype of CC81 mainly comprised of 23F (53.3%) in pre-PCV7 period and replaced by non-vaccine types (NVTs: 66.10%, 13 [30%], 15A [40%], and 15B/C [20%]) in post-PCV13 period. The main serotype responsible for CC166 also changed from 9V (80%) in pre-PCV7 to NVT 11A (30%) in post-PCV13 periods. Non-susceptibility to penicillin (42.3%) was the highest in CC320, increasing from 0% to 76%.

Conclusion. Genetic structure of IPD isolates in Korean children has changed after the PCV7 and PCV10/13 implementations, and the genotypes of PCV7 types during pre-PCV7 period were mostly disappeared and re-occupied by genotypes of PCV13 types/NVTs in post-PCV13 period. Serotype 19A/ST320 were expected to decrease rapidly after the use of PCV13 in national immunization program.

Disclosures. All authors: No reported disclosures.

2997. Predictors of Persistence Community Acquired Staphylococcus aureus Bacteremia in Children. Cohort Study
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Background. Community acquired Staphylococcus aureus bacteremia (SAB) is a frequent cause of hospitalization in children. Persistent bacteremia (more than 7 days) is associated with higher mortality. The main objective of this study was to identify clinical predictors of persistent SAB.

Methods. Prospective cohort study. January 2010- December 2016. Inclusion criteria: age<30 days and ≤16 years, hospitalized in a pediatric referral hospital with community acquired infections, with development of SA in blood cultures. Exclusion criteria: history of recent hospitalization, attendance at a health care center, living in a closed community, or venous catheter. Microbiological, demographic and clinical characteristics were compared in children when SAB lasted > or < 7 days. Bivariate and multivariate analysis was performed. Stata13 was used.

Results. n = 250. One hundred and sixteen (64%) were male. Median age was 60 months (IQR 22–131). Methicillin-resistant Staphylococcus aureus(MRSA) was
identified in 163 patients (65%). Clindamycin resistance was identified in 21 cases (8%). Median length of SAB was 3 days (IQR 2–4). In twenty-six patients (11%) SAB lasted 7 or more days. In bivariate analysis, pneumonia (OR 4.6, 95% CI 2–10.6, P < 0.001), sepsis at admission (OR 3.8 95% CI 1.6–8.7, P = 0.002), intensive care unit admission (OR 2.9 95% CI 1.3–7.7, P < 0.01), delayed drainage (OR 4.7, 95% CI 1.4–16, P = 0.01) and MRSA (OR 7.4, 95% CI 1.7–31, P = 0.01) were associated with prolonged SAB. No association with age, sex, site of infection, Vancomycin or Clindamycin empiric treatment was found. In multivariate logistic model, MRSA (OR 5.9 95% CI 1.4–25.9 p = 0.02) and sepsis at admission day (OR 2.9, 95% CI 1.3–2.5, P = 0.01) were predictors of SAB duration more than 7 days.

Conclusion. In this study of Community Acquired SAB, MRSA was prevalent. Methicillin-resistance and sepsis at admission day were identified as predictors of SAB persistence (more than 7 days).

Disclosures. All authors: No reported disclosures.

2298. Association of Staphylococcus aureus Colonization with the Evolving Neonatal Nasal Microbiome and the Impact of Intranasal Mupirocin

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Background. Little is known about the bacterial communities in the noses of critically ill neonates. The objectives were to explore the evolving nasal microbiome in neonates who acquire Staphylococcus aureus (S. aureus) colonization and the impact of intranasal mupirocin on the nasal microbiome.

Methods. In the setting of a tertiary care neonatal intensive care unit S. aureus control program, nasal cultures are screened weekly using chromogenic agar cultures and treated with intranasal mupirocin if found to acquire S. aureus colonization. We identified 15 neonates who acquired S. aureus colonization (cases) and 7 who did not acquire S. aureus colonization (controls). Cases and controls were matched on chronologic age and systemic antibiotic exposure. DNA was extracted for amplification of the 16S rRNA gene (V3-V4 region), followed by next-generation sequencing using Illumina MiSeq. Sequences were merged into consensus fragments by FLASH and submitted for high-resolution taxonomic assignment using Resphea Insight.

Results. Compared with conventional bacterial culture results, sequencing identified S. aureus membership in residual culture samples of all neonates who acquired S. aureus colonization. Figure 1 illustrates statistically significant differences in abundant taxa comparing cases prior to S. aureus colonization and controls. Several species were more abundant in controls, including Corynebacterium propinquum and acorellus and Rothia mucilaginosa. C. propinquum and acorellus and Rothia mucilaginosa were also more abundant in neonates after treatment with intranasal mupirocin than before treatment.

Conclusion. These data suggest that there are differences in bacterial taxa abundance in the nasal microbiome in neonates who do and do not acquire S. aureus colonization and in neonates before and after treatment with intranasal mupirocin.

A single species may not provide sufficient resistance to a single species may not provide sufficient resistance to abundant in controls, including comparing cases prior to S. aureus nonparametric difference test with p-value correction using the False Discovery Rate.

Figure 1. Abundant Taxa by S. aureus Acquisition

Disclosures. J. White, Resphea Biosciences: Shareholder, Equity

2299. An Outbreak of Group A Streptococcus Invasive Infections among Pediatric Patients in Columbus, Ohio

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Background. A cluster of invasive disease caused by Group A Streptococcus (GAS) was identified among children admitted to Nationwide Children’s Hospital (NCH) in Columbus, Ohio. Clinical characteristics and molecular epidemiology of this cluster were studied to find out whether the observed cases were caused by closely related GAS strains.

Methods. Patient electronic medical records were reviewed for demographic, epidemiologic and clinical data. Cases were defined as patients with GAS isolated from a normally sterile site, or from a non-sterile site in combination with clinical signs of severe streptococcal illness. Susceptibility testing (E-test), analysis of the GAS envelope, multilocus sequence typing (MLST) and pulse field gel electrophoresis (PFGE) from isolates were performed.

Results. Ten children were admitted to NCH with invasive GAS disease between February 19 and March 23, 2017, from seven different Ohio counties (total population of approximately 1.8 million). The spectrum of illness was broad, including STSS (3 patients), GAS sepsis (3), orbital cellulitis with epidermal abscess (3), bacteremia and subdural empyema (2), peritonsillar abscess (1), and septic arthritis (1). One patient with STSS died. Only two patients had chronic illnesses. One patient was diagnosed with acute myeloid leukemia on admission. Median age was eight years (range 0.1–16 years). Of six patients with STSS and sepsis only one received clindamycin and four were given IVIG. Hypocalcemia (67%) was common. Isolates from 12 patients were available for emm gene analysis and belonged to nine different emm types: 1, 2, 3, 6, 12, 22, 89, 118, 227. Two emm 1 and one emm 227 isolates had the same PFGE pattern. All isolates were susceptible to macrolides.

Conclusion. In a population of 1.8 million, 13 pediatric patients with invasive GAS disease during a five-week period represented an apparent outbreak with polyclonal GAS isolates. There was no reported epidemiologic association among the patients and the outbreak was not preventable. A proposed 30-valent M-protein vaccine would have provided protection against 93% of outbreak isolates.

Disclosures. A. Leber, BioFire Diagnostics: Research Contractor and Scientific Advisor, Research support, Speaker honorarium and Travel expenses

2300. Staphylococcus aureus Bacteremia in Children: The Effect of Methicillin Resistance

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Background. Staphylococcus aureus bacteremia can occur in children in association with cutaneous, soft tissue, musculoskeletal, respiratory, and endovascular infections. The effect of methicillin resistance on clinical outcomes in children with S. aureus bacteremia has not been clearly described.

Methods. Single center retrospective cohort study over a 5-year period of children ≤18 years hospitalized with monomicrobial S. aureus bacteremia at a tertiary care children’s hospital. We compared baseline characteristics and clinical outcomes between those with methicillin-sensitive S. aureus (MSSA) and methicillin-resistant S. aureus (MRSA) bacteremia using chi-squared test for dichotomous and t-test for continuous variables. We built a multivariable linear regression model to determine the effect of methicillin resistance on duration of bacteremia.

Results. We identified 334 episodes of S. aureus bacteremia, 233 (70%) with MSSA and 101 (30%) with MRSA. Mean age was 5.4 years; 42.6% were hospitalized onset infections (49.8% MSSA vs. 25.7% MRSA; P = 0.001); 68.4% (73.3% vs. 55.7%; P = 0.003) occurred in children with chronic medical conditions; and 31.5% occurred in black children (25.9% vs. 44.6%; P = 0.001). Primary site of infection was catheter-related in 31.7% (37.9% vs. 18.7%), musculoskeletal in 28.1% (25.3% vs. 34.1%); skin/soft tissue in 14.2% (13.2% vs. 16.5%); pneumonia in 6.4% (3.2% vs. 13.2%); and no source identified in 11.4% (13.7% vs. 6.6%). Elevated creatine kinase levels (range 0.1–16 years). Of six patients with STSS and sepsis only one received clindamycin and four were given IVIG. Hypocalcemia (67%) was common. Isolates from 12 patients were available for emm gene analysis and belonged to nine different emm types: 1, 2, 3, 6, 12, 22, 89, 118, 227. Two emm 1 and one emm 227 isolates had the same PFGE pattern. All isolates were susceptible to macrolides.

Conclusion. In a population of 1.8 million, 13 pediatric patients with invasive GAS disease during a five-week period represented an apparent outbreak with polyclonal GAS isolates. There was no reported epidemiologic association among the patients and the outbreak was not preventable. A proposed 30-valent M-protein vaccine would have provided protection against 93% of outbreak isolates.

Disclosures. A. Leber, BioFire Diagnostics: Research Contractor and Scientific Advisor, Research support, Speaker honorarium and Travel expenses

2301. Osteoarticular Infections Following Open or Penetrating Trauma in Children in the Era of Community-Acquired MRSA

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