independently associated with anticarcinogenic drug use within 30 days (OR: 43.90; 95% CI: 4.69–411.08), older age (OR: 1.05; 95% CI: 1.02–1.09), and admission to the neonatology ward (OR 0.019; 95% CI: 0.005–0.076).

Conclusion. One-fourth of GNB BSI cases were MDR. Anticarcinogenic drug use and older age were risk factors for MDR GNB BSI in children's hospitals. MDR *P. aeruginosa* infections were associated with higher all-cause mortality.

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2335. *Acinetobacter baumannii* Infection—Clinical Profile, Drug Resistance, and Presence of Virulence Factor *AdeRS*: Experience From a Pediatric Tertiary Care Centre in North India

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Background. *Acinetobacter baumannii* has emerged as an important opportunistic pathogen. Its ability to develop resistance to multiple antibiotics leaves few treatment options. *AdeRS*, a two-component regulatory system, which controls expression of the adeABC efflux pump is involved in multidrug resistance. There is lack of data regarding presence of virulence factors leading to antimicrobial resistance and their correlation with the outcome of the patients. The study was done to evaluate the prevalence of virulence factors *AdeRS* gene responsible for the accentuation of drug resistance, and correlation with the clinical outcome of the patient.

Methods. Clinical details of 80 patients with labeled *A. baumannii* infection were collected and analyzed with the resistance patterns of the isolates and molecular detection of the *AdeRS* virulence gene.

Results. 80 patients with labeled *A. baumannii* infection were included in the study. Most common presentation among patients with *A. baumannii* was pneumonia (46.25%) followed by sepsis. 63.75% of patients were admitted in the ICU. Neonates were mostly affected. Of the total 37 neonates with *A. baumannii* infections, 26 were hospital acquired. Mean weight of neonates with infection was 2.1 kg. 45.9% neonates with *A. baumannii* infections had undergone surgery for congenital anomalies. Sepsis was the most common presentation among neonates. Overall, mortality was 41.25%. The maximum mortality was among neonates (57.6%). Children presenting with sepsis had a higher mortality. Mortality in ICU patients was 78.8% compared with 21% in the wards. Average length of stay in the hospital after acquisition of *A. baumannii* infection was 20.2 days. Of the total 80 isolates, 2.5% were MDR and 86.25% were XDR strains. *AdeRS* was present in 90% of the isolates. All the isolates with XDR pattern of drug resistance had *AdeRS* gene. 27.5% of the isolates were tigecycline resistant and *AdeRS* gene was present in all them. Thirty-three patients who died all possessed *AdesRS* gene and were XDR strains.

Conclusion. *A. baumannii* is responsible for a substantial percentage of nosocomial infections. Presence of *AdeRS* gene reduces the susceptibility to large number of drugs and thus selects out XDR *A. baumannii* with high mortality rates in the hospital settings, leaving efflux pump inhibitors as the therapy of choice.

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2336. Resistance Mechanisms and Factors Associated With CTX-M-9 Group Extended-Spectrum β-Lactamase (ESBL)-Producing *Enterobacteriaceae* Infections in Children

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Background. There is an increasing incidence of extended-spectrum β-lactamase (ESBL) producing *Enterobacteriaceae* infections in children. However, most studies focus only on CTX-M-1 group (CTX-M-15). We sought to define the epidemiology of the CTX-M-9 group (CTX-M-9) producing *Enterobacteriaceae* infections in children to devise more effective treatment and prevention strategies.

Methods. A case–control study of children (0–21 y), cared for by 3 Chicago area hospitals during 2011–16, was performed. Cases were 44 children diagnosed with third-generation cephalosporin (3GC) resistant and/or carbapenem-resistant (CR) *Enterobacteriaceae* infections who had CTX-M-9 genes accounting for β-lactam resistance. PCR amplification, DNA sequencing, and DNA microarray analysis (Check-Points®) assessed for *bla* genes. MLST, rep-PCR and phylogenetic analysis were also performed. Controls were 135 children with 3GC and carbapenem susceptible *Enterobacteriaceae* infections matched by age range and hospital. Demographics; comorbidities; device, antibiotic, and healthcare exposures; and the impact of location of patient residence were evaluated. Race categories were white, black, Hispanic, and other. Stratified analysis and multivariable logistic regression were used to explore associations between predictors and CTX-M-9 infection. Data were analyzed in SAS 9.4.

Results. The median age of cases was 4.1 years. The predominant organism (39/44, 89%) was *E. coli* of virulent phylogroups B2 (41%) and D (59%). MLST analysis revealed that this collection of strains was polyclonal.

On multivariable analysis, children with CTX-M-9 *Enterobacteriaceae* infections were more likely to be diagnosed in an outpatient clinic (OR 4.5), have *E. coli* infection (OR 7.0), and be of race "other" (OR 7.6) vs. controls. Residents of South Chicago were 6.7 times more likely to have a CTX-M-9 *Enterobacteriaceae* infection than controls; while residence in Northwest Chicago was associated with a 81% decreased risk. Significant differences in other demographics, comorbidities, invasive devices, antibiotic use, or recent healthcare were not found.

Conclusion. We observed striking regional differences in occurrence of CTX-M-9 producing *Enterobacteriaceae*, suggesting that environmental influences and plasmid transfer may contribute to acquisition. It is worrisome that a large number of ESBL *Enterobacteriaceae* strains bearing CTX-M ESBLs circulate in the community among children.

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2337. Clinical Characteristics of Children Infected With Macrolide-Resistant Mycoplasma Pneumonia in Central Ohio—Preliminary Data

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Background. Macrolide-resistant *Mycoplasma pneumoniae* (MRMp) has emerged in the last 2 decades, with rates as high as 93% in Asia. Rates in the United Stated vary from 3.5 to 13.2%. By sequencing we identified our local resistance rate of 1.8% (9/477) in isolates collected from October 2015 to December 2017. Previous reports described increased morbidity in patients with MRMp. We evaluated the clinical characteristics of children infected with MRMp in Central Ohio.

Methods. Of the 9 MRMp isolates identified, clinical data were available in 7 cases. We performed a case–control (1:3) analysis, where Mp patients were matched by month and year of presentation. Retrospective analysis of electronic health records (HER) was performed to identify clinical and treatment characteristics. Continuous variables are shown as medians and inter-quartile ranges (IQR), and categorical variables as percentages. For comparisons T, Mann–Whitney U, and Fisher's exact tests were used as appropriate.

Results. Both groups had similar demographics with no differences in age and gender. Median age (IQR) was 8.5 years (6–17) for the MRMp and 8 (IQR 3.5–11.5) for the Macrolide-susceptible Mp (MSMp). Duration of symptoms at presentation was similar, median (IQR) of 11 (4–14) days for MRMp, and 8 (6.25–13.25) days for MSMp ($P = 0.7$). All patients with MRMp had fever compared with 17 (81%) of the MSMp ($P = 0.07$). Tmax was similar in both groups ($P = 0.11$). All patients (100%) had cough. There were no differences in the frequency of oxygen requirement, fatigue, shortness of breath, sore throat, nasal congestion, rash, headache and chest radiographic findings. There were similar rates of hospitalization with 4 (57%) in the MRMp and 8 (38%) in the MSMp ($P = 0.42$). Among hospitalized children, there were no differences in duration hospitalization, median (IQR) 6 (1.25–21.25) days for MRMp and 2 (1–2.75) for MSMp ($P = 0.31$). None required invasive ventilation. One MRMp patient had encephalitis; this was the only patient requiring intensive care compared with none MSMp ($P = 0.25$). All patients were initially treated with azithromycin, but 2 (12%) of the MRMp were switched to levofloxacin ($P = 0.06$).

Conclusion. We did not identify significant differences in clinical characteristics between patients with MRMp and MSMp. This could be related to our low local rate of MRMp.

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2338. Change in Genetic Structure of *Streptococcus pneumoniae* Isolates From Invasive Diseases After National Immunization Program of Extended-Valency Pneumococcal Conjugate Vaccines in Korea

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