594. A Multi-Centered Study of the Clinical and Molecular Epidemiology of AmpC Cephalosporinase-Producing (AmpC) Enterobacteriaceae (Ent) Infections in Children

Rachel L. Medenbach, MD1; T. Nicholas, Domitrovich, MS2; Karen C. Hayani, MD3; Andrea M. Hujer, BS4; Nadia K. Qureshi, MD2; Steven H. Marshall, MS5; David C. Nguyen, MD6; Susan D. Rudin, BS7; Jared R. Rispens, MD7; Xiaotian Zheng, MD, PhD7; Robert A. Weinstein, MD7; Robert A. Ronomo, MD8 and Latania K. Logan, MD, MSFPH9; Rush University Medical Center, Chicago, Illinois; 8VA Cleveland Medical Center, Cleveland, Ohio; 9University of Illinois at Chicago, Chicago, Illinois; 10Louis Stokes VA Medical Center, Cleveland, Ohio; 11Loyola University Medical Center, Maywood, Illinois; 12Case Western Reserve University/University Hospitals Cleveland Medical Center, Cleveland, Ohio; 13Northwestern University Feinberg School of Medicine; Ann and Robert H. Lurie Children's Hospital of Chicago, Chicago, Illinois; 14Rush University Medical Center; Cook County Hospital, Chicago, Illinois; 15Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio

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Background. AmpC producing Ent are an important cause of multidrug-resistant (MDR) infections in pediatrics. Since most AmpC Ent studies have been conducted in adults, we characterized the molecular epidemiology of AmpC Ent strains with transmissible resistance and identified factors associated with AmpC Ent infections in children.

Methods. A case–control study of children (0–18 years) at 4 Chicago hospitals during 2011–18 was performed. Cases were 44 children with infections due to Ent harboring an AmpC as detected by DNA microarray (Check-Points®). PCR, DNA sequencing, MLST, and phylogenetic analyses were performed. Controls (cths) were 132 children with expanded-spectrum cephalosporin-susceptible Ent infections matched by age and hospital. Demographics; residence; comorbidities; device, antibiotic, and healthcare exposures were evaluated. Predictors of AmpC Ent infection were assessed by logistic regression.

Results. The median age of AmpC Ent patients was 3.0 years; 50% were male. Of blaAmpC genes, 68% were blaCTX-M-15/18, and 25% blaCMY-2. Predominant organisms were Enterobacter cloacae (59%) and Escherichia coli (32%); 27% of AmpC Ent cloacae belonged to ST114 and 62% co-harbored a blaESBL gene, predominantly blaCTX-M (94%). Most AmpC E. coli strains were unrelated; 71% carried blaHTX-M, 64% belonged to phylogroups B2/D, and 50% co-harbored blaOXA-23. On bipartite analysis vs. cths, AmpC Ent infections were more likely to be respiratory (39% vs. 18%, P < 0.01) and less likely to be urinary tract (41% vs. 67%, P < 0.01) or community-acquired (14% vs. 33%, P < 0.02). By multivariable analysis, children with AmpC Ent infections were more likely to be nonwhite, non-black, non-Hispanic (OR 4.7, CI 1.4–16.1) and have infections due to Enterobacter (OR 7.7, CI 3.5–17). Differences in gender, healthcare location, residential neighborhood, antibiotic exposures, comorbidities, devices or outcomes were not found.

Conclusion. AmpC Ent infections often had healthcare onset, were due to Enterobacter, and occurred in nonwhite, non-black, non-Hispanic children. AmpC Ent commonly co-harbored blaOXA-23 and blaCTX-M ESBL genes which affects therapeutic options and suggests the need for contact precautions. Control of AmpC Ent infections in children will require validating sources and risk factors.

Disclosures. All authors: No reported disclosures.

596. Distinct, Segregated Daptomycin-Susceptible and Daptomycin-Nonsusceptible Staphylococcus aureus Populations Associated with Tricyspid-Valve Infective Endocarditis

Christopher R. Miller, RA, Biology1; Somrita Dey, PhD2; Paulina Smolenski, MS1; Pushkar S. Kulkarni, MS Engineering3; George Sakoulas, MD4; Jonathan M. Monk, PhD5; Richard Szubin6 and Andrew David. Berti, PharmD PhD6; Wayne State University College of Pharmacy, Detroit, Michigan; 7Wayne State University College of Engineering, Detroit, Michigan; 8University of California San Diego, San Diego, California; 9University of California at San Diego, La Jolla, California

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Background. Loss of daptomycin susceptibility in Staphylococcus aureus is often associated with sequestered foci of infection, driven by selection pressure from both administered antibiotics and host defense peptides. Susceptibility testing of the organism cultured from blood is assumed to parallel that of the infectious foci, such as heart valves. We studied a case of tricuspid valve endocarditis where one leaflet yielded exclusively daptomycin-nonsusceptible S. aureus and another leaflet yielded purely daptomycin-susceptible S. aureus. We examined the responses of the two populations to different anti-staphylococcal therapies to identify regimens effective against both isolates.

Methods. Both isolates were whole-genome-sequenced using Illumina technologies. The presence of heterogeneous daptomycin-resistant subpopulations was assessed by deletion plating and population analysis profiling. One compartment pharmacokinetic/pharmacodynamic modeling was used to simulate different potential antistaphylococcal pharmacotherapies against each isolate. Hemolysin activity was evaluated as a surrogate for accessory gene regulator function.

Results. The daptomycin-susceptible isolate did not demonstrate heterogeneous resistance while the daptomycin-resistant population was uniformly daptomycin-resistant.