1516. Early-Onset Neonatal Sepsis Due to Haemophilus influenzae Alyssa Varghese; Kent Korgenski, MS, MT(ASCP); Hillary Crandall, MD, PhD; Anne Bonkowski, MD/PhD; *University of Utah, Draper, Utah; †Intermountain Healthcare, Salt Lake City, Utah

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Background. Haemophilus influenzae causes serious invasive disease across all ages, but has not been widely described in neonatal early-onset sepsis (EOS). EOS, likely caused by organisms acquired from the mother, can lead to significant morbidity and mortality, particularly for preterm infants. There are reports of increasing ampicillin resistance in H. influenzae. We describe a case series of EOS due to H. influenzae at our institution.

Methods. Neonatal H. influenzae EOS was identified based on positive sterile site cultures at <72 hours of life in infants hospitalized at an Intermountain Healthcare (ICH) facility from 2007–2017. Demographics, clinical and microbiologic data were obtained through an IRB-approved electronic chart and microbiology review.

Results. Twelve neonates with H. influenzae EOS were identified over 11 years. Nine were preterm (<37 weeks); five were extremely preterm (<28 weeks). Eight had low birth weight (<2,500 g); five had very low birth weight (<1,500 g). Most (66%) mothers were primiparous; median maternal age was 24.5 years. Only four (33%) mothers had prolonged rupture of membranes (>24 hours).

All infants had signs and symptoms of sepsis within 24 hours of birth. The majority (10/12) had a blood culture positive for H. influenzae from the time of delivery. Two infants had negative blood cultures but a H. influenzae-positive placental culture. No infant had > 1 day of bacteremia. One H. influenzae isolate was serotype b, one serotype c and one non-typeable, but most isolates (9/12) were not serotyped. Only one isolate produced a β-lactamase. All infants were empirically started on ampicillin and gentamicin at delivery. Nine infants underwent lumbar puncture, two were suggestive of meningitis but cultures were negative. Five infants developed interventricular hemorrhage and six required vasoactive medications. No infant died.

Conclusion. H. influenzae is an infrequent but important cause of neonatal EOS. EOS involving H. influenzae is in infants with known risk factors, including prolonged rupture of membranes, prematurity, and low birth weight. Recognition of H. influenzae as a potential pathogen in EOS has implications for the use of empiric antibiotic therapy particularly ampicillin, in septic neonates.

Disclosures. All authors: No reported disclosures.

1517. Multidrug-Resistant Escherichia coli ST131 Late-Onset Neonatal Sepsis in Premature Twins Linked to Contaminated Maternal Frozen Breast Milk Bishara J. Freij, MD; Fozia Salem-Rasheed, MD; Scott A. Cunningham, MS, MT (ASCP) SM; Robin Patel, MD; Robin Patel, MD; Graham Krasan, MD; Barbara Robinson-Dunn, PhD, D(ABMM), FIDSA, FAAM; Beaufont Children’s Hospital, Royal Oak, Michigan; ‡Mayo Clinic, Rochester, Minnesota; §William Beaumont Hospital - Royal Oak, Royal Oak, Michigan; †Beaufont Health, Royal Oak, Michigan

Session: 160. Pediatric Bacterial Diseases: Epidemiology
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Background. Sequence type 131 (EC-ST131) is a prevalent cause of extraintestinal Escherichia coli infection, including in neonates, and accounts for a majority of multidrug-resistant strains. Rare reports of neonatal unit outbreaks have emerged, with one linking the source to freshly expressed breast milk (BM) sharing. We report a case series of early-onset neonatal sepsis in twin girls whose infection was linked to their mother’s contaminated BM.

Methods. Blood culture isolates were from twin girls born at 24–1/7 weeks’ gestation who developed severe sepsis caused by ampicillin- and gentamicin-resistant E. coli on days 11 (Baby A; died) and 8 (Baby B; survived) of life; both neonates had sterile blood cultures at birth, and received orogastric feeds using frozen BM provided by their mother. Five remaining frozen BM samples predateing onset of sepsis were thawed and cultured; E. coli resistant to ampicillin and gentamicin was recovered from 1 collected on day 5 of life. DNA was extracted from cultured isolates using the Zymo Research Quick-DNA™ Fungal/Bacterial Minprep kit, sequencing libraries prepared (Nextera® XT PE), and sequencing (Illumina MiSeq with V2 2 X 250 bp chemistry) completed for the 2 blood and 1 BM isolates. Multilocus Sequence Typing (MLST) and core genome MLST (cgMLST) analyses were performed using SeqSphere+, version 5.1.0 (Ridom, Munster, DE) software, with 2513 alleles analyzed for cgMLST.

Results. The 2 blood and 1 BM isolates were typed as ST131 by MLST and were indistinguishable by cgMLST. Of the 2513 alleles queried, only 263 (10.5%) differed were performed using SeqSphere+, version 5.1.0 (Ridom, Munster, DE) software, MiSeq® with V2 2 X 250 bp chemistry) completed for the 2 blood and 1 BM isolates.

Disclosures. Robin Patel, MD, ASM and IDSA: Other Financial or Material Support; Travel reimbursement, editor’s stipends; CD Diagnostics, Merck. Hutchinson Biofilm Medical Solutions, Accelerate Diagnostics, ContraFect, TenNor Therapeutics Limited, Shionogi: Grant/Research Support; Curetis, Specific Technologies, NextGen Diagnostics, PathoQuest, Quida: Consultant; NBME, Up-To-Date, the Infectious Diseases Board Review Course: Honorarium recipient, Other Financial or Material Support; Patent on Bordetella pertussis/parapertussis PCR issued, a patent on a device/method for sonication with royalties paid by Samsung to Mayo Clinic, and a patent on an anti-biofilm substance issued: Other Financial or Material Support, Patents.

1518. The Microbiology of Osteoarticular Infections in Patients with Sickle Hemoglobinopathies at Texas Children’s Hospital, 2011–2018 Saki Ikeda, MD; Julika Kaplan, MD; Jonathon C. McNeil, MD; Sheldon L. Kaplan, MD; Jesus G. Vallejo, MD; Baylor College of Medicine, Houston, Texas

Session: 160. Pediatric Bacterial Diseases: Epidemiology
Friday, October 4, 2019: 12:15 PM

Background. Osteoarticular infections (OAI) are common in patients with major sickle hemoglobinopathies (Hemoglobin [Hgb] SS, Hgb SC, and Hgb Sβ thalassemia). Although Salmonella spp. cause a substantial number of OAsIs in these patients, contemporary data regarding the most common etiology in the era of community-acquired methicillin-resistant Staphylococcus aureus (MRSA) is lacking. This introduces challenges for selecting empiric antimicrobial therapy. We evaluated the microbiology and management of OAI in children with sickle hemoglobinopathies.

Methods. Children with sickle hemoglobinopathies admitted to Texas Children’s Hospital with acute hematogenous OAI from 2011 to 2018 were identified based on ICD10 codes and the consult database of the pediatric infectious diseases service. Culture-negative cases were included if treated for OAI. Medical records were reviewed. Statistical analyses were conducted with STATA ver. 13.

Results. 36 patients met inclusion criteria; 53% were diagnosed with isolated osteomyelitis and 47% with osteomyelitis and septic arthritis. In 42% a microbial etiology was identified (Figure 1) with Salmonella spp. being the most common (n = 7, 47%) followed by S. aureus (n = 5, 33%). 11 (31%) patients had subperiosteal or intraosseous abscesses and 26 (72%) underwent diagnostic and/or therapeutic surgical procedures; 36% had positive blood cultures. Children with Salmonella spp. infections had a longer duration of fever (median-5, range: 4–9 days) compared with those caused by other pathogens (median-2, range: 0–6 days; P = 0.04). The median duration of IV therapy was longer in culture-positive than culture-negative cases (30 vs.10 days, P = 0.009); the total duration of therapy was similar for all cases (32 days, IQR: 28–42). No patients were readmitted due to OAI.

Conclusion. At our institution, Salmonella spp. were the most common cause of OAI among children with sickle hemoglobinopathies. Subperiosteal/intraosseous abscess formation and the need for surgical procedures were common. The role of oral antibiotics for the treatment of Salmonella OAI in patients with sickle hemoglobinopathies warrants further study.