on objective clinical criteria (i.e., presence of systemic and local signs of infection and use of antifungals for ≥10 days) or non-IFI wounds if they failed to meet clinical criteria.

Results. Of 1932 subjects, 246 (12.7%) had labortory evidence of fungal infection. There were a total of 143 IFI wounds (n = 94), 157 non-IFI wounds (n = 96), and 113 high suspicion wounds (n = 56). IFI subjects had significantly higher injury severity scores (ISS median: 39.5 vs. 33), Sequential Organ Failure Assessment (SOFA) scores (7 vs. 2) and were more likely to require mechanical ventilation (66 vs. 28%). IFI patients also had higher ISS (93 vs. 84% with ISS >25) and SOFA scores (7 vs. 4) compared with the subjects with high suspicion wounds. IFI wounds often grew molds belonging to the order *Mucorales* compared with high suspicion (19 vs. 10%, P = 0.04) and non-IFI wounds (19 vs. 7%, P = 0.02). About half of the IF wounds grew fungi of the order *Mucorales* either isolated alone or in conjunction with other fungi, in comparison, 25% of the high suspicion wounds and 11% of the non-IFI wounds grew fungi of the order *Mucorales*. Three groups of fungi belonging to the order *Mucorales*, genus *Aspergillus* and *Fusarium* accounted for 83% of the IFI wounds and 74% of the high suspicion wounds.

Conclusion. Labortory evidence of fungal infection is common among combat casualties. Clinical characteristics and wound microbiology allows us to group subjects into groups at low and high risk of IFI. Fungi of the order Mucorales, genus *Aspergillus* and *Fusarium* should not be considered contaminants. The presence of these fungi should obligate close clinical follow-up and debridement as needed.

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90. Increasing *Kingella* Identification in Bone and Joint Infections in Young Children

Rachel Quick, RN, MSN, CNS[1]; John Williams, MD[2,3]; Peter Cosgrove, MBBChBAO[4]; Kyle Kahlden, MD[5]; Marisol Fernandez, MD[1]; Lynn Thoreson, DO[6]; Sarmistha Hauger, MD[1]; [1]Pediatric Infectious Diseases, Seton Healthcare Family, Austin, Texas; [2]University of Texas at Austin, Dell Medical School, Austin, Texas; [3]Pediatric Orthopedics, Seton Healthcare Family, Austin, Texas; [4]Department of Pediatrics, Seton Healthcare Family, Austin, Texas; [5]Pediatrics, Seton Healthcare Family, Austin, Texas; [6]Pediatrcs, Seton Healthcare Family, Austin, Texas

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Background. *Kingella kingae* is an increasingly recognized pathogen among young children with bone and joint infections. Antibiotics given to cover methicillin-resistant *Staphylococcus aureus* are not effective against *Kingella,* and necessitate additional empiric antibiotics in this age group. Improving *Kingella* identification can narrow antibiotic choices and improve efficacy for long-term oral therapy.

Methods. We implemented a bone and joint infection guideline at a free standing children's hospital that called for early imaging, focal sampling, and polymerase chain reaction (PCR) testing for culture-negative specimens. The goal was to increase identification of *Kingella* and other pathogens to improve targeted antimicrobial therapy. Children 6 to ≤ 60 months of age with uncomplicated acute hematogenous osteomyelitis or septic arthritis between January 1, 2009–December 31, 2016, were included in this study. Outcomes of bacterial identification were measured.

Results. Charts for 49 cases that met criteria were reviewed. Prior to the algorithm, we identified *Kingella* in 4% (1/25) of cases. Following routine use of updated sampling and testing techniques, including PCR testing, *Kingella kingae* identification increased to 29% of cases (7/24; P = 0.02) and, in fact, was the predominant pathogen identified in this age group.

Conclusion. Identification of *Kingella* was enhanced as a result of changes to sampling and testing, including PCR testing (Figure 1). Post-implementation, *Kingella* was more commonly identified than *Staphylococcus aureus.* Widespread availability of PCR testing in the future may allow for the use of narrowed antibiotic therapy and targeted transition to oral antibiotics in young children with bone or joint infection.

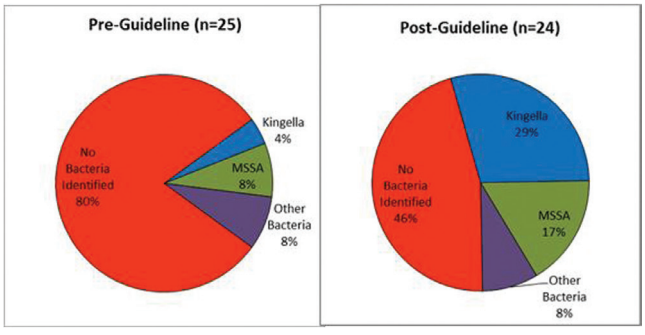

Figure 1. Bacterial identification pre and post guideline among children aged 6–60 months.

Disclosures. **All authors:** No reported disclosures.

91. Microbiology of Vertebral Osteomyelitis and Implications on Empiric Therapy

Abbye Clark, BS; Neha Sharma, BS; Sharon Weissman, MD; Majdi N. Al-Hasan, MBBS; Caroline Derrick, PharmD, BCPS and Kamla Sanasi-Bhola, MD; University of South Carolina School of Medicine, Columbia, South Carolina

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Background. The management of vertebral osteomyelitis (VO) includes empiric antibiotic therapy while clinical cultures are being processed. Optimal antimicrobial therapy for VO, particularly when Gram-negative (GN) organisms are involved, is an area of ongoing debate. Narrow spectrum and oral antimicrobial therapy are preferred. The objective of this study was to identify characteristics of local pathogens and to formulate an institution-specific antibiotic protocol for empiric treatment of VO.

Methods. We conducted a retrospective case series study of adults diagnosed with VO from August 1, 2010 to August 31, 2015 at Palmetto Health Hospitals in Columbia, South Carolina. Cases identified by ICD-9 codes were included in the analysis if they met clinical, imaging and microbiology, criteria.

Results. Analysis is based on 150 cases of VO with a mean age of 61 years, a male predominance (91; 61%), and an average body mass index of 29 kg/m^2. Comorbidities included diabetes mellitus (69; 46%), tobacco use (33; 22%), and hemodialysis (20; 13%). Thirty-seven (25%) cases had recent related injury or vertebral surgery, and 14 (9%) had prior hardware. Bone, disc, or adjacent tissue cultures were obtained in 129 (86%) of cases; 60 (40%) of these had >1 sample taken. The remaining 14% had blood cultures alone. Thirty-six cases (24%) had culture negative VO. In the remaining 114 cases, 132 organisms were isolated. A total of 111 (84%) organisms were Gram-positive cocci (GPC). Of those, the majority was *Staphylococcus aureus.* (66; 59%) (26/66 were methicillin-resistant), coagulase-negative staphylococci (20; 18%) and *Streptococcus* spp. (17; 15%). *Enterobacteriaceae* accounted for 13/17 Gram-negative bacilli (GNB), with only one isolate of *Pseudomonas aeruginosa.* Of the GNB, 11/17 were susceptible to either ceftriaxone or ciprofloxacin.

Conclusion. There was a predominance of VO due to GPC suggesting that intravenous vancomycin monotherapy may be reasonable for empiric therapy in noncritically ill patients while awaiting Gram stain and clinical culture results. Addition of either ceftriaxone or ciprofloxacin to vancomycin would increase cumulative antimicrobial coverage from 84 to 92%.

Disclosures. **All authors:** No reported disclosures.

92. Concordance of Results of Blood and Tissue Cultures from Patients with Pyogenic Spondylitis

Ji Yun Bae, MD[1]; Chung-Jong Kim, MD[1]; Uh Jin Kim, MD[2]; Kyoung-Ho Song, MD[1]; Eu Suk Kim, MD[1]; Seung Ji Kang, MD[3]; Myoung-Don Oh, MD, PhD[1]; Kyung-Hwa Park, MD[2]; Nam Joong Kim, MD, PhD[1]; [1]Department of Internal Medicine, Seoul National University College of Medicine, Seoul, Korea, Republic of South; [2]Chonnam National University Medical School and Hospital, Gwangju, Korea, Republic of South; [3]Department of Infectious Diseases, Chonnam National University Medical School, Gwang-ju, Korea, Republic of South

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Background. The aim of this study was to investigate the concordance of results of blood and tissue cultures in patients with pyogenic spondylitis.

Methods. We searched the patients with pyogenic spondylitis in whom micro-organisms were isolated from both blood and tissue cultures by retrospective review of medical records in three tertiary university-affiliated hospitals between January 2005 and December 2015. The species and antimicrobial susceptibility patterns of isolates from blood and tissue cultures were compared with each other.

Results. Among 141 patients with pyogenic spondylitis in whom micro-organisms were isolated from both blood and tissue cultures, the species of blood and tissue isolates were identical in 135 patients (95.7%, 135/141). Excluding the four anaerobic isolates, we investigated antimicrobial susceptibility patterns of 131 isolates of same species from blood and tissue cultures. Antibiotic susceptibility patterns were identical in 128 patients (97.7%, 128/131). The most common isolates were *Staphylococcus aureus* (86 patients; 85 concordant and 1 discordant), followed by streptococcus (24 patients; 22 concordant and 2 discordant), and *Escherichia coli* (8 patients; all concordant).

Conclusion. We suggest that a positive blood culture from patients with pyogenic spondylitis could preclude the need for additional tissue cultures, especially when *S. aureus* and streptococcus grew in blood cultures.

Table 1. Micro-organisms isolated from blood and tissues in 135 patients with pyogenic spondylitis

Concordant (n = 135)	
Staphylococcus aureus	85
Viridans streptococci	11
Streptococcus agalactiae	8
Escherichia coli	8
Enterococcus fecalis	4
Klebsiella pneumonia	2
Others	17
Discordant (n = 6)	
Blood	Tissue
Propionibacterium avidum	Coagulase-negative staphylococcus
Streptococcus constellatus, Actinomyces meyeri	*Streptococcus constellatus, Porphyromonas asaccharolytica*
Staphylococcus epidermidis, viridans streptococcus	*Staphylococcus epidermidis*
Staphylococcus aureus	*Staphylococcus aureus,* Nontuberculous mycobacteria

Table 1. Continued

Concordant (n = 135)	
Klebsiella pneumoniae, Acinetobacter baumannii	*Klebsiella pneumoniae*
Coagulase-negative staphylococcus	*Staphylococcus lugdunensis, Candida parapsilosis, Pediococcus species*

Disclosures. **All authors:** No reported disclosures.

93. Home Environmental Contamination Is Associated with Community-associated Methicillin-resistant *Staphylococcus aureus* Re-colonization in Treated Patients

Meghan Davis, PhD, DVM, MPH[1]; Daniel Morris, DVM, MPH, DACVD[2]; Valerie Cluzet, MD[3]; Warren Bilker, PhD[4]; Pam Tolomeo, MPH[4]; Kathleen G. Julian, MD[5]; Patrick Baron, PhD MSPH[6]; Amy Brazil, VMD MPH[7]; Jacqueline Ferguson, MHS[7]; Sally Ann Iverson, DVM, MPH[7]; Jonathan Shahbazian, BS, MPH[7]; Shanna Ludwig, PhD[7]; Baofeng Hu, MD[8,9]; Shelley Rankin, PhD[2]; Irving Nachamkin, DrPH, MPH, FIDSA[10]; Ebbing Lautenbach, MD, MPH, MSCE[11]; CDC Prevention Epicenters Network; [1]Environmental Health and Engineering, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland; [2]University of Pennsylvania School of Veterinary Medicine, Philadelphia, Pennsylvania; [3]Infectious Diseases, Hospital of University of Pennsylvania, Philadelphia, Pennsylvania; [4]Center for Clinical Epidemiology and Biostatistics, University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania; [5]Penn State Hershey Medical Center, Hershey, Pennsylvania; [6]Davidson College, Davidson, North Carolina; [7]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD; [8]University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania; [9]Pathobiology, University of Pennsylvania School of Veterinary Medicine, Philadelphia, Pennsylvania; [10]Department of Pathology and Laboratory Medicine, University of Pennsylvania, Perelman School of Medicine, Philadelphia, Pennsylvania; [11]Division of Infectious Diseases, Hospital of University of Pennsylvania, Philadelphia, Pennsylvania

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Background. Strategies to interrupt household transmission of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) that target human colonization show mixed results. Our aim was to determine whether home environmental contamination and pet carriage with MRSA were associated with re-colonization or persistent colonization of index patients diagnosed with CA-MRSA skin or soft-tissue infection (SSTI).

Methods. Index patients from a randomized controlled trial (NCT00966446) that tested household-wide decolonization of people were eligible to participate in this substudy. Before randomization, eight environmental sites and all pets were sampled in the home. Patients were treated by their physician for the initial SSTI between diagnosis (visit 0) and the home visit (visit 1). They provided swabs every 2 weeks for 3 months (7 visits). After broth-enrichment culture, MRSA isolates were PCR-confirmed and *spa*-typed.

Results. Of 88 index patients recruited from the main trial, 64 (73%) provided swabs for ≥3 visits and were included in this analysis. At visit 1, 41 (64%) households were MRSA contaminated and 6 (9%) had MRSA-positive pet(s). All MRSA-positive pets lived in homes with MRSA environmental contamination. After visit 1, 42 (66%) index patients and their household members were block-randomized to nasal mupirocin and chlorhexidine body wash decolonization. Thirty-seven (58%) index patients had two consecutive negative swabs (de-colonized); 13 (35%) of these later were MRSA-positive (re-colonized). Patients with home contamination had higher rates of re-colonization than those without (Cox proportional hazard ratio 6.0 [95% CI: 1.2, 30.6], $P < 0.03$). Persistent colonization (all or all but one swab positive) was identified in 6 (9%) of index patients and was associated with identification of matching *spa*-types in environmental and subsequent human MRSA isolates ($P < 0.05$).

Conclusion. In patients with MRSA SSTI, MRSA-contaminated homes, and potentially MRSA-positive pets, are associated with re-colonization and persistent colonization. Future studies are needed to determine whether environmental decontamination can improve the success of household decolonization interventions.

Disclosures. **All authors:** No reported disclosures.

124. Current Epidemiology of Serogroup W Meningococcal Disease—United States, 2010–2015

Heidi Soeters, PhD, MPH; Amy Blain, MPH; How-Yi Chang, PhD; Melissa Whaley, MS, MPH and Jessica Macneil, MPH; National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia

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Background. Serogroup W (NmW) meningococcal disease is a rare but severe infection. Following an NmW outbreak after the Hajj in 2000, NmW disease, predominantly caused by sequence type (ST)-11 clonal complex (cc), rapidly increased in South Africa, South America, and the UK. We describe NmW meningococcal disease epidemiology in the USA during 2010–2015.

Methods. Data were collected from the National Notifiable Diseases Surveillance System, Active Bacterial Core surveillance, and state health departments. Isolates were serogrouped via slide agglutination and real-time polymerase chain reaction. For cases lacking a serogroup result at CDC, the state result was used. Case-fatality ratios (CFR) were calculated using the proportion of cases with known outcomes as the denominator. cc and ST were determined using multilocus sequence typing (MLST).

Results. From 2010 to 2015, 3,504 meningococcal disease cases were reported to CDC; 2,976 (85%) had a serogroup result, of which 290 (10%) were NmW. Although the number of NmW cases reported annually remained fairly stable (range: 40–57), the total number of reported meningococcal disease cases decreased by 60%, and the proportion of cases due to NmW increased from 6% (42/830) in 2010 to 12% (40/332) in 2015. The majority of NmW cases were reported from five states: Florida (n = 106), California (n = 31), New York (n = 25), Georgia (n = 19), and Oregon (n = 11). Half of people with NmW disease were male, 185 (64%) were white, and 84 (29%) were Hispanic. The median age was 51 years (interquartile range: 26–70). Overall, 20% (52/259) of NmW cases were fatal, compared with CFRs for serogroups B (15%), Y (18%), or C (24%). NmW CFR was highest among adults aged 50–59 years (38%). MLST results were available for 119 (41%) of NmW cases: 76 (64%) were cc11, 40 (34%) were cc22, and 1 each were cc23, cc32, and an unassigned cc. cc appeared to be geographically associated: cc11 was concentrated in Florida and Georgia, while cc22 predominated on the West coast. Within cc11, the majority of isolates (86%) were ST-11, and within cc22 the majority (73%) were ST-22.

Conclusion. A rapid increase in NmW disease has not been observed in the USA. Most NmW cases were reported in a limited number of states, with geographic differences in clonal complex.

Disclosures. **All authors:** No reported disclosures.

125. Increased Risk of Invasive Meningococcal Disease Associated with Primary and Secondary Immunodeficiency

Lene Fogt Lundbo, MD, PhD[1]; Zitta Barrella Harboe, MD PhD[2]; Lars Smith-Hansen, BA Techn. Soc.[3]; Thomas Benfield, MD, DMSc[4]; [1]Department of Infectious Diseases, Hvidovre Hospital, University of Copenhagen, Hvidovre, Denmark; [2]Department of Infectious Diseases, Rigshospitalet, Copenhagen University Hospital, Copenhagen Ø, Denmark; [3]Clinical Research Centre, Hvidovre Hospital, University of Copenhagen, Hvidovre, Denmark; [4]Department of Infectious Disease, Hvidovre University Hospital, Hvidovre, Denmark

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Background. Risk of invasive meningococcal disease (IMD) is increased for persistent complement deficiency and HIV infection. However, risk associated with other primary and secondary immunodeficiency is unknown.

Methods. Nationwide case–control study of adults aged >18 years. Cases and matched controls were identified by registry linkage. Primary and secondary immunodeficiencies diagnosed prior to IMD were based on International Classification of Disease (ICD), eight or tenth revision. Odds ratios (OR) with 95% confidence intervals (CI) were estimated by conditional logistic regression after adjustment for sex, age, and the year of IMD.

Results. We identified 2,179 IMD cases (46% male) with a median age of 44 years (interquartile range: 24–63 years). Increased risk of IMD was associated with HIV infection (OR 10.03 [95% confidence interval (CI), 2.91–34.66]), splenectomy/splenic resection (OR 6.88 [95% CI, 3.9–14.82]), solid organ transplantation (SOT) (OR 20.00 [95% CI, 5.00–79.96]), hemolytic anemia (OR 7.78 [95% CI, 2.90–20.90]), antibody deficiency (OR 6.67 [1.11–39.90]) and autoimmune diseases (OR 1.80 [95% CI, 1.44–2.14]). Primary immunodeficiency overall was not associated with an increased risk (OR 1.43 (95% CI, 0.61–3.36)).

Conclusion. This large study of Danish adults with IMD over four decades showed an increased risk of IMD associated with HIV infection, SOT, asplenia, hemolytic anemia, antibody deficiency, and autoimmune disease ranging from 2- to a 20-fold increased risk. Vaccination may be warranted in these populations.

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126. Use of Adjunctive Steroids and Incidence of Delayed Cerebral Venous Thrombosis in Adults with Bacterial Meningitis

Cinthia Gallegos, MD[1]; Lucrecia Salazar, MD[2]; Farrell Tobolowsky, DO[3]; Masayuki Nigo, MD[4]; Rodrigo Hasbun, MD, MPH[5]; [1]Infectious Disease, University of Texas Medical School at Houston, Houston, Texas; [2]Division of Infectious Diseases, University of Texas McGovern Medical School at Houston, Houston, Texas; [3]Internal Medicine, University of Texas Medical School at Houston, Houston, Texas; [4]Division of Infectious Disease, Department of Internal Medicine, University of Texas Health Science Center at Houston, McGovern Medical School, Houston, Texas; [5]Division of Infectious Diseases, University of Texas Health Science Center at Houston, McGovern Medical School, Houston, Texas

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Background. Bacterial meningitis is associated with significant morbidity and mortality. Adjunctive steroids decrease mortality in adults with meningitis due to *Streptococcus pneumoniae*but its use has been recently linked to the development of delayed cerebral thrombosis (DCT). The purpose of our study was to determine the utilization of adjunctive steroids and its incidence.