

Outbreaks and Clusters

160. Cluster of *Pseudomonas aeruginosa* infections in a Neonatal Intensive Care Unit

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Background: *Pseudomonas aeruginosa* infections are relatively uncommon at the level 3 neonatal intensive care unit (NICU) in our medical center. An increase in cases during 2006 prompted this investigation.

Objective: To identify the source(s) of the cluster and implement strategies to prevent future infections.

Methods: The study period was Oct-05 to Jun-07. The NICU has about 300 admissions per year. An epidemic curve revealed a cluster of 9 cases during Apr-06 to Jun-06. Clinical and demographic data were obtained through review of medical records. Subsequently, extensive environmental surveys including cultures were done. To examine risk factors for infection with *P. aeruginosa* during the cluster, patients with *P. aeruginosa* infection (cases; n=9) were compared to patients without *P. aeruginosa* admitted within 2 days of a case patient (controls; n=9). Pulsed-field gel electrophoresis (PFGE) was performed on available clinical and environmental isolates to determine strain identity. Control measures included practice changes for warming breast milk, reinforcement of hand hygiene, barrier precautions, environmental cleaning and disinfection.

Results: Overall, twenty-three patients developed infection with *P. aeruginosa* during Oct-05 to Jun-07. The median gestational age was 29 weeks; median birth weight 1200 grams. Eighteen (65%) were male. Median time from admission to date of first positive culture was 19 days (range 0 - 158). *P. aeruginosa* was identified from multiple clinical sites: respiratory (14), exudate (4), blood (5), eye (4), and other (4). Antibiotic resistance was absent in 20 (87%) patients; unknown in one. Resistance to piperacillin was present in two, one of whom was intermediately resistant to cefepime as well. Median length of stay in NICU was 69 days. Sixteen patients (70%) were discharged home or transferred, while 7 (30%) expired.

The nine patients who developed *P. aeruginosa* infections during the cluster period were more likely to be male (8 vs. 3; P=0.02), and tended to receive mechanical ventilation (9 vs. 6; P=0.06). Other patient characteristics as well as outcomes were not significantly different between cases and controls. Cultures from water in cups used to thaw breastmilk were positive for multiple gram negative bacteria including *P. aeruginosa*. PFGE analysis of 7 available isolates identified two predominant clones among 2 patients each. Remaining two clinical isolates and one environmental isolate were unrelated to the clonal strains or to each other. The number of *P. aeruginosa* infections reduced to 0-2 per month after institution of control measures.

Conclusions: *P. aeruginosa* infections in our NICU during a cluster tended to occur in male patients receiving mechanical ventilation. Clonal transmission is suggested, although no common source was identified. Control measures were successful in containing the cluster.

161. Nosocomial Outbreak of *Listeria monocytogenes* Infection: Unexpected Infections Affecting Empirical Antimicrobial Therapy

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Background: The incidence of *Listeria monocytogenes* infections in Brazil is unknown. The present study was designed to investigate the emergence of nosocomial infections caused by this agent in patients admitted to Hospital Universitário Clementino Fraga Filho of Universidade Federal do Rio de Janeiro (HUCFF)/UFRJ, in the city of Rio de Janeiro, Brazil. Objective: to describe the cases of infections caused by *Listeria monocytogenes* occurred in patients admitted to HUCFF/UFRJ.

Methods: a retrospective study from January 2002 to June 2007 was performed. All patients presenting symptoms or signs of infection and isolation of *L. monocytogenes* from a normally sterile site were defined as cases. Healthcare associated infections were defined as proposed by the Centers for Disease Control and Prevention. Data were collected by medical charts and laboratory records review. Microbiological procedures were performed according to the Manual of Clinical Microbiology (American Society for Microbiology) recommendations.

Results: during the study period, six cases of listeriosis clustered from August 2006 to June 2007 (Cumulative incidence: 0.53/1,000 admissions). Four patients had bloodstream infections (two with hematologic malignancies and other patients with heart failure) and two had peritonitis (both of them with liver cirrhosis Child's class C and B). The median length of stay from admission to infection was 8.1 days (Range: 5-14 days) among hospitalized patients (n: 5). One patient admitted with ambulatory diagnosis of infection was being submitted to chemotherapy at the day clinic. The median age was 81 years (Range: 62-99 years). Five patients were empirically treated with cephalosporin and one with ampicillin. Five patients died, including the one correctly treated with ampicillin. Three patients died within the first week of diagnosis.

Conclusions: the epidemic curve included patients with more than three days of admission or followed up at the day clinic, suggesting an outbreak of health-care associated infections by *L. monocytogenes*. This is a rare epidemiological situation where unexpected cases were followed by inadequate empirical therapy with cephalosporin in most of the infected patients. These data highlight how changing in an epidemiological situation could affect empirical treatment and patient prognosis. During the outbreak investigation that was carried out by infection control team, measures focusing improvement in food storage and manipulation were adopted. Since July 2007, there were not new cases.

162. An Outbreak of Catheter related infection due to *Chlorhexidine* Contaminated with *Burkholderia cepacia*

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Background: Burkholderia cepacia has emerged as human pathogen causing numerous outbreaks, particularly among cystic fibrosis patients.

Objective: We investigated a hospital outbreak of B. cepacia probably associated with a contaminated chlorhexidine disinfectant.

Methods: This study was investigated a hospital outbreak of infection in 11 patients with blood culture positive for *B. cepacia*. The characteristics of 11 patients with *B. cepacia* bacteremia occurring from 22nd September to 15th October 2007 were analyzed retrospectively. Environmental and surveillance cultures were conducted about 160 samples including disinfectants (chlorhexidine, povidone, alcohol), sterile saline etc. The Pulsed Field Gel Electrophoresis (PFGE) for the blood culture specimens and for the culture specimen of chlorhexidine was done.

Results: Eleven patients had hematologic malignancy (5 acute lymphoblastic leukemia, 6 acute myelogenous leukemia) and they admitted to the same station of cancer center with permanent central venous catheterization and neutropenic state. We identified that 0.5% chlorhexidine gluconate, used for disinfecting catheter cap (opening site) was found to be contaminated with B. cepacia.

Conclusions: This report summarizes an outbreak of B. cepacia bacteremia that occurred predominantly among patients with hematologic malignancy, during the period August-October 2007.

163. Outbreak/pseudo-outbreak of *Pseudomonas aeruginosa* Associated With Contamination of a Flexible Bronchoscope

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Background: a cluster of ICU patients with positive respiratory cultures for *Pseudomonas aeruginosa* (PA) with a unique antibiogram was observed during July 2007. These PA isolates had the same antimicrobial susceptibility pattern and were recovered from bronchoscopically obtained specimens.

Methods: A cross-sectional study was performed to test the hypothesis that the cluster was associated with exposure to a particular bronchoscope (B1); cultures from bronchoscopes and the environment were obtained, and molecular typing of PA isolates was performed using pulsed-field gel electrophoresis (PFGE). Cases were defined as patients with a bronchoscopically obtained culture that yielded PA with a unique susceptibility pattern (intermediate susceptibility to ceftazidime, resistant to ticarcillin-clavulanate, susceptible to aminoglycosides, quinolones, piperacillin-tazobactam and imipenem). Medical records of all patients exposed to B1 during the cluster period (June-July 2007) were reviewed.

Results: Twelve patients with a positive culture for PA with the unique susceptibility pattern were identified between June 1 and July 23, 2007 ("cases"). No cases were documented between March 1 and May 31, 2007. Cultures obtained from B1 before and after high-level disinfection revealed PA which prompted its immediate removal from service on July 23, 2007. Since then, no further cases occurred. Eleven (55%) of 20 patients exposed to B1 during the cluster period had a positive culture for PA and met the case definition compared to 1 (1.8%) of 53 patients exposed to other bronchoscopes ($p < 0.001$). PFGE patterns for PA isolates obtained from case patients and from B1 were identical but differed from PFGE patterns of PA isolates recovered from the environment and from patients not meeting the case definition. B1 was sent to the manufacturer for engineering evaluation. Despite a negative pressure leak, multiple defects were found: kinked forceps channel tube; damaged bending section sheath cover; pinched insertion tube; peeling of light-guide tube coating. Of the 20 patients exposed to B1 during the cluster period, the first case that had PA recovered was considered the index case and likely had PA pneumonia at the time of bronchoscopy. Two (10.5%) of the remaining 19 cases may have developed a PA pneumonia following exposure to B1.

Conclusions: An outbreak/pseudo-outbreak of PA occurred due to a damaged bronchoscope. Bronchoscope contamination resistant to high-level disinfection may occur despite a negative air-leak test. Periodic engineering maintenance may be needed to prevent these events.

164. A Cluster of *Aspergillus flavus* Wound Infections in a Burn Unit

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Background: *Aspergillus flavus* is the most frequently isolated species associated with outbreaks of cutaneous aspergillosis, and is a common cause of *Aspergillus* wound infections. During a 3-day period, 3 patients admitted to adjacent rooms in the burn unit at our university hospital had operative specimens from burn wounds that grew *A. flavus*.

Objective: To determine if there was a common source for this cluster of *A. flavus* burn wound infections, and to prevent further colonization and infection.

Methods: Infection control staff initially walked through the burn unit to identify possible reservoirs or practices that might have been associated with the cases. Staff also: 1) assessed the air handling system and measures used to prevent dust dissemination from the concurrent construction project in the hospital's Emergency Treatment Center (ETC); 2) obtained air cultures and particle counts from the case patients' rooms, the hydrotherapy room, the nursing station, and an outside air sample in the week following the reported cases; 3) obtained cultures from the ceiling tiles that lay below reels storing retractable hoses used to bathe patients in their own rooms; 4) reviewed patients' medical records to determine whether patients had shared community space on the ward or space in the operating room; 5) reviewed data from the clinical microbiology laboratory to identify additional cases; and 6) typed isolates from patients and the environment by random amplification of polymorphic DNA (RAPD; 3 different primers).

Results: The total body surface area burned for the 3 affected patients ranged from 32% to 68%. Retrospective case finding revealed no other *A. flavus* infections on this unit during the prior 18 months. The 3 affected patients did not have known contact with each other and did not share rooms while hospitalized. We did not identify an air leak from the ETC construction site to the burn unit, and air samples throughout the ward did not detect growth of *A. flavus*. However, *A. flavus* was isolated from the inner surface of a ceiling tile below the water hose reel in one case-patient's room. RAPD testing determined that 2 of 3 patients' *A. flavus* isolates were identical to the environmental isolate, and differed from *A. flavus* isolates from epidemiologically unrelated sources. The involved burn unit area was temporarily closed, and bathing practices in this pod were altered such that the retractable water hoses were no longer used. No further cases of *A. flavus* infection occurred in the burn unit over the subsequent year.

Conclusions: We linked 2 cases of *A. flavus* wound infection in our burn unit to contamination of the ceiling surrounding a water hose used for in-room patient bathing. We hypothesize that *A. flavus* mold spores above the ceiling may have been dislodged when the water hoses were extended or retracted during patients' baths. Equipment used for patient care must be designed such that it does not mobilize mold spores.

165. Vancomycin Resistant Enterococci Outbreak Caused by Patient Transfer in Two Separated ICUs

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Background: On April 2007, Infection Control Unit was reported that there were unusually increased vancomycin resistant enterococci (VRE) isolates in intensive care units (ICUs). The outbreak occurred in a 16-bed neurosurgical intensive care unit (NSICU) and in a 16-bed medical intensive care unit (MICU) of Gachon University, Gil Medical Center, 1200-bed tertiary care teaching hospital in Incheon, Korea.

Objective: The purpose of this study is to determine cause of VRE outbreak in MICU and NSICU.

Methods: We undertook a medical record review and performed a case-control study to determine risk factor. Case patients were defined as all patients in MICU and NSICU who had positive for VRE from April to July 2007. Control was matched to cases in a 3:1 ratio by presence on the same ICU as the case and no evidence of having VRE. We conducted 36 environmental cultures in MICU and NSICU. We performed pulsed field gel electrophoresis (PFGE) with SmaI and analyzed the dendrogram by using Fingerprinting software (Bio-Rad).

Results: We identified 30 VRE colonized patients (15 patients in MICU and 15 in NSICU) for 4 months which exceed the 3 SD on statistical process control chart. PFGE of isolates showed there were 4 main outbreak strains (2 strains in MICU and 2 in NSICU) and some sporadic cases. Index patient of one main outbreak in MICU was transferred from NSICU.

Among 12 environmental samples from MICU, 4 were positive for VRE, identical PFGE pattern to that of transferred index patient. Multivariate analysis showed that combined infection was significant risk factor (OR, 3.1; CI95, 1.2 to 7.9; P = .018).

Conclusion: Multiple factors contributed this VRE outbreak. Transfer of colonized patient was one of the causes of VRE outbreak in separated two ICUs.

166. Outbreak of Late-Onset Group B Streptococcus in a Neonatal Intensive Care Unit - Tennessee, 2007

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Background: Late-onset Group B Streptococcus (GBS) disease is the most common cause of meningitis among newborns aged 7-90 days and is spread from person to person. On September 10, the Tennessee Department of Health was notified of an outbreak of late-onset GBS sepsis in a neonatal intensive care unit (NICU). We investigated to determine the source of infection and prevent additional cases.

Objective: To investigate and describe the outbreak, identify the outbreak source, implement control measures, and cease transmission.

Methods: We defined a case as a culture-confirmed late-onset GBS infection, during August 15-September 15, 2007, in a neonate aged ≥ 7 days. A retrospective review of patients' and mothers' charts was performed. We examined all 2007 NICU microbiology reports for GBS and performed serotyping, pulsed-field gel electrophoresis (PFGE), and multi locus sequence typing (MLST) on isolates. We reviewed maternal GBS screening and prophylaxis protocols and infection control protocols, observed staff practices, and performed a point-prevalence survey for colonization.

Results: We identified five cases (including three deaths) occurring during August 23-September 6; only one had occurred during the preceding 10 months. Among isolates from these cases, two serotypes, two PFGE patterns, and two distinct MLST patterns were identified. Three case isolates were indistinguishable on PFGE and MLST subtyping. The point-prevalence survey identified four additional GBS-colonized neonates. Multiple potential pathways of transmission were identified, including one neonate with early onset GBS whose isolate was indistinguishable from the three identical isolates on subtyping.

Conclusions: This outbreak likely resulted from multiple factors; three cases probably had a common source. Novel molecular subtyping (PFGE and MLST), not previously used to characterize this type of outbreak, enabled us to identify this GBS outbreak as multiclonal. Rapid epidemiologic investigation and molecular subtyping resulted in identification of multiple transmission pathways, and implementation of control measures.

167. A City Outbreak of Nosocomial Blood Stream Infection: Investigation Using Case-Crossover Design.

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Background: in March 2006, primary bloodstream infections (BSI) caused by *Burkholderia cepacia* complex (BCC) isolates (BCC-BSI) emerged in patients admitted to several hospitals in Rio de Janeiro (RJ). Although case-crossover has been used as an alternative to case-control design for studying risk of acute events, it was rarely applied to nosocomial infections.

Objective: to investigate an outbreak of BCC-BSI by using a case-crossover study design.

Methods: retrospective study, from March 2006 to May 2006, in three hospitals in RJ, Brazil. A case-patient with nosocomial BCC-BSI was defined as a patient who had at least one blood culture positive for BCC and symptoms and signs of BSI starting more than 72 hours after hospital admission. Primary BSI was diagnosed according to Center for Disease Control and Prevention definitions. After determining the date BSI symptoms started for each case-patient, three types of 3-day period were defined: case-period, starting just before the BSI onset; control-period, starting 6 days before that date; and wash-out period, the 3 days between control-period and case-period. One control-period was included for each case-period. Patients admitted for less than 9 days until BSI symptoms started were excluded from statistical analysis. Variables evaluated were use of intravascular solutions, invasive devices and procedures. To identify risk factors, variables with $p < 0.25$ by bivariate analysis were included in a multiple logistic regression model. Molecular typing was performed by PFGE with *SpeI*. Banding patterns were interpreted by visual inspection and with the GelCompar II program.

Results: twenty-three cases of BCC-BSI were detected. Two of them were excluded from statistical analysis. Use of bromopride (OR: 14.89; 95%CI: 2.68-82.57 $p < 0.002$) and dipyrone (OR: 6.76; 95%CI: 1.18-38.43; $p < 0.03$) were independently associated with BCC-BSI. Bromopride and dipyrone from unopened vials were cultured. Two BCC isolates were recovered from one bromopride vial. BCC isolates from case-patients and bromopride were genotyped. Six genotypes were detected: A, B, C, D, E, F. Most of the BCC strains from case-patients belonged to genotype A. Only the both BCC strains from bromopride belonged to genotype F. The outbreak stopped immediately after the collection of all bromopride vials of the contaminated manufacturer.

Conclusions: the use of case-crossover design seems to be an important epidemiological tool to investigate nosocomial primary bacteremia outbreaks where contaminated solutions are suspected as the source. The case-crossover design brings advantage over classical case-control studies because several critical issues

involved in selecting control-patients. Moreover, the time and effort required for data collection are minimized. In the present investigation, the source of a polyclonal BCC-BSI was determined, leading to the prompt control of the outbreak.

168. Nosocomial Food-borne Related Outbreak by Enteric Toxin Producing *B. cereus*

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Background: Food-borne-related gastroenteritis outbreaks may occur by enterotoxin or emetic toxin producing *B. cereus*. Gastroenteritis outbreaks by *B. cereus* are infrequently reported in health-care settings.

Objective: To diagnose and describe a health-care-associated outbreak with an enterotoxin positive *B. cereus* strain.

Setting: Long-term health-care facility with elderly, disabled persons and children groups comprising 600 inhabitants and 350 employees. A central kitchen prepares 950 meals per day. Rice and chicken and a pudding for the desert were offered for lunch at the day of the onset of the outbreak.

Methods: Persons with either diarrhea or vomitus were recorded. Stool, vomitus and lunch samples were cultured for pathogenic bacteria. Adeno-, Rota-, Norovirus and *C. difficile* toxin antigen tests were performed additionally. *B. cereus* was tested for the emetic and enterotoxins by PCR.

Results: Health-care authorities were involved and started the epidemiologic and microbiological investigation 4 hours after lunch in the long-term health facility. 104 persons developed vomiting or diarrhea 2 to 4 hours after lunch. One patient required infusion therapy and was admitted to a hospital. One vegetarian who eat only rice developed diarrhea as well. From the lunch meal (chicken with rice) *B. cereus* was cultured and genes for enterotoxin were detected. The isolated *B. cereus* strain had no gene for the emetic toxin although most patients developed vomiting. Stool and vomitus of 5 patients were negative for all tested pathogens. The charge of rice was stopped by health-care authorities.

Conclusions: Nosocomial gastroenteritis outbreaks may occur by enterotoxin producing *B. cereus*. *B. cereus* is known as a current contamination in rice. As spores of *B. cereus* are heat-resistant and may survive steam cooking the storage of rice-containing prepared meals should be put safe at temperatures >70°C to avoid germination and thus potentially toxin producing forms of the bacterium. Preferably, food should be served immediately after cooking.

169. An Outbreak of *Bacillus* Pseudobacteremia Implicating Blood Culture Bottle Tops

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Background: In 8/07, we detected a 4-fold increase in *Bacillus* spp.-positive blood cultures at CCH. Pseudobacteremia was suspected based on single positive cultures at hospital admission in some patients.

Objective: To determine the source of a *Bacillus* spp. outbreak.

Methods: We calculated the incidence of *Bacillus* spp. from 8/07-12/07 and compared it to the incidence from the same period 1 year prior. A case was defined as any patient at CCH with a single blood culture positive for *Bacillus* spp. from 8/07-12/07. To analyze hospital location of blood draw as a risk factor for a positive blood culture, we performed a case-control study: for each case, 2 controls were selected from the 10th preceding and subsequent blood culture specimens received by the lab. We examined blood culture collection procedures and audited blood culture bottle storage. We interviewed a sample of staff that had performed phlebotomy leading to cases. We cultured equipment used for skin disinfection/phlebotomy and blood culture bottles. We applied pulsed field gel electrophoresis (PFGE) to *Bacillus* spp. recovered from environmental sources and blood isolates.

Results: In 8-11/07, 34 patients met the case definition; none appeared to have a clinical *Bacillus* spp. infection. 4 patients had repeated *Bacillus*-positive blood cultures (>3) likely representing true infection and were excluded from analysis. The per-bottle blood culture positivity rate was 0.30% versus 0.09% from the same period one year prior (P<0.001). By 12/07, *Bacillus* rates returned to baseline. A case-control study showed no relation between hospital location of blood draw and *Bacillus* positivity. Among available *Bacillus* blood isolates from case patients (N=29), 17 PFGE patterns were noted, with 2 predominant PFGE types. Of 322 blood culture rubber septa (stored with protective cap intact), 2 were positive for *Bacillus* spp.; one's PFGE pattern matched that of a clinical blood specimen (predominant PFGE type). Review of phlebotomy practice showed that 4 of 9 respondents did not sterilize the blood culture bottle rubber septum before inoculation. After enforcing universal alcohol wiping of blood culture rubber septa, removal of uncapped blood culture bottles, and disposal of remaining bottles from lots implicated by cultures or cases, the pseudobacteremia outbreak ended.

Conclusions: Blood culture bottle rubber septa, although covered by a flip-top cap, are not guaranteed sterile by manufacturers and require mechanical cleansing and disinfection (e.g., with alcohol swab). Our pseudobacteremia outbreak possibly was caused by *Bacillus* spores contaminating rubber septa and entering blood culture media during inoculation. Further investigation into the cause of *Bacillus* on rubber septa -- by manufacturing processes or local environmental contamination -- and the relation of contamination to apparent real infection (i.e., patients with multiple positive cultures) is warranted.

170. Active Tuberculosis In A Healthcare Worker: Are You Ready?

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Background: The proportion of foreign born healthcare workers (HCW) is increasing. Although the incidence of *Mycobacterium tuberculosis* infection (TB) continues to decline in the U. S., foreign born individuals have been recognized to have TB rates 9.5 times higher than that of U.S. born persons. This equates to a higher prevalence of latent tuberculosis (LTBI) and a higher risk for active tuberculosis among foreign born HCWs. The Cleveland Clinic, a 1,200 bed referral center, is deemed a medium risk facility for TB transmission based on an average of 4 yearly admissions for active TB. All HCWs undergo TB assessment at time of hire to include a tuberculin skin test (TST). Those with a positive TST or documented past positive receive a chest x-ray (CXR). Those negative for LTBI receive a TST annually, those positive complete a questionnaire as a screen for active TB. HCWs with positive TSTs are offered referral for LTBI therapy.

Objective: To describe an investigation of a HCW with active tuberculosis with emphasis on the use of (1) a multidisciplinary team in an incident command system model and (2) an electronic health record (EHR) to assist in contact tracing.

Methods: HCW X, a 29 year old intern, native of Ethiopia, was diagnosed with active TB 12/1/06. She had a history of a positive TST and a normal CXR 18 months prior. At time of diagnosis HCW X was rotating on the hematology-oncology inpatient service and had a weekly ambulatory clinic. Upon notification of the diagnosis, a team was assembled using an incident command system model with representatives from Infection Control, Occupational Health, Risk Management, Ombudsman, and Media Relations. Contact tracing was based on interview of HCW X, review of work schedules, and a query of the EHR to further define patient contacts. 280 contacts were identified and assigned to priority groups using a concentric ring approach as follows: I household contacts, IIa hematology-oncology patients, IIb HCWs, IIc ambulatory patients, III other inpatient contacts.

Results: Results of contact tracing are shown in the Table. There were no converters among household contacts, exposed inpatients, or healthcare workers as compared with 3 converters identified among ambulatory clinic contacts ($p=0.008$ for the comparison of groups I, IIa, IIb with group IIc) . None of the contacts developed active TB.

Results of Contact Tracing					
Group	n	Baseline + TST n	Post-Exposure TST done n(%)	Converters n	INH Prophylaxis n
I	2	1	1	0	1
IIa	12	1	9(82%)	0	6
IIb	122	11	99(89%)	0	0
IIc	19	-	10(53%)	3	0
III	125	-	4(3%)	0	0

Conclusions: A successful contact investigation of a HCW with active TB is facilitated by a multidisciplinary incident command system model. The EHR provides a novel and rapid tool to enhance contact tracing. Our experience suggests that the prevalence of LTBI among HCWs should be part of a TB control plan risk assessment.

171. Nosocomial Transmission of US Military Related Multidrug-Resistant *Acinetobacter baumannii-calcoaceticus* (MDR-ABC) in a Canadian Civilian Hospital

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Background: A MDR-ABC outbreak has recently been identified and characterized by the US military. It remains an ongoing infection control problem at military hospitals amongst injured American military personnel. The Canadian Armed forces have served in Afghanistan since 2002 as part of the International Security Assistance Force. Critically injured soldiers are transferred through Landstuhl Regional Medical center (LRMC), before returning to Canadian civilian hospitals. MDR-ABC has been documented in returning Canadian soldiers, including a small number of infections. Unlike the US military hospitals, no documented nosocomial MDR-ABC outbreaks have occurred in Canadian civilian hospitals from returning soldiers. We describe the first Canadian outbreak in an academic hospital burn trauma/intensive care unit after the arrival of a MDR-ABC colonized Canadian soldier from LRMC.

Objective: To verify an outbreak of military related MDR-ABC.

Methods: Surveillance of routine patient care cultures, point prevalence and standard infection control colonization swabs were performed to define the outbreak period. Identification and susceptibility testing using Vitek 1 were performed, with confirmatory susceptibility testing done by disc diffusion. One strain from each patient underwent *Sma*I digest and pulse field gel electrophoresis (PFGE), then analyzed by Bionumerics gel software.

Results: The index patient was recovering from necrotizing fasciitis when a post operative wound swab was positive for MDR-ABC. This was felt to be linked to a soldier transferred to our center (via a Toronto academic hospital and LRMC) given the rarity of nosocomially acquired ABC at our hospital. The soldier was colonized rectally and at the site of his tracheostomy. Eighty one cultures for MDR-ABC were found on eight patients between July 2006 and August 2007. All patients were male and were colonized from at least one site. Three burn patients had clinical infections (skin grafts, bacteremias, ventilator-associated pneumonias) requiring treatment. One death occurred but was not related to MDR-ABC colonization. Amikacin was the only antibiotic with reliable susceptibility, but resistance increased as the outbreak progressed. Only 2/81 strains had carbapenem susceptibility, and all other standard antibiotics were resistant. PFGE demonstrated at least 82% clonal relatedness to the soldier's isolate.

Conclusions: Our cluster of patients represents the first nosocomial spread of war-related MDR-ABC in a Canadian civilian hospital. A delay in recognizing the risk and screening for MDR-ABC in our soldier likely resulted in the outbreak. Therefore all injured soldiers should be screen for MDR-ABC upon entering any civilian hospital.

172. Multiple Interventions Succeed In Containing An Outbreak Of Vancomycin Resistant Enterococcus (VRE) In A Pediatric Oncology (ONCO) Unit

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Background: In June 2006, routine surveillance identified an increase in the number of VRE bloodstream infections (BSI) in a 42 bed pediatric ONCO unit over a 4 month period. A prevalence survey demonstrated that ~10% of ONCO inpatients had previously unrecognized VRE colonization. Over the following year, the outbreak was controlled through enhanced infection control interventions and knowledge gained from an outbreak investigation.

Objective: To control an outbreak of VRE in a pediatric ONCO unit and to determine potential risk factors for new-onset VRE.

Methods: Upon recognition of the outbreak, multiple interventions were implemented: 1) VRE screening upon hospitalization and weekly thereafter; 2) enhanced infection control (IC) interventions; 3) enhanced environmental cleaning; 4) development of a VRE IC team; 5) focused education for staff and families; and 6) antimicrobial management. A matched case control study was conducted to identify risk factors for new-onset VRE. Cases were defined as ONCO patients with new-onset VRE, no prior history of VRE, with at least one negative VRE screen before their positive screen. Controls were defined as ONCO patients who had no prior history of VRE and 2 consecutive negative screens. An exposure window was defined as the number of days between 2 screens. Cases and controls were matched based on the exposure window.

Results: Enhanced IC precautions were initiated sequentially over the first 4 months of the outbreak. Despite the initiation of empiric contact precautions (CP) for all ONCO inpatients, 26/629 subsequent screens were positive (4.1%), consistent with ongoing transmission of VRE. All ONCO inpatients were then maintained on CP for their entire hospitalization regardless of VRE status. Over the following 8 months, the proportion of positive VRE screens decreased to 1.2% (15/1,270). Observations when VRE patients left the ONCO unit found that CP were not always followed. Further investigation revealed that a mechanism to identify these patients was not readily available to staff in other areas of the hospital. Upon multivariate analysis, presence of a gastrointestinal device (OR=4.03, p=0.04) and lack of empiric CP (OR=17.16, p=0.02) were identified as independent risk factors for VRE. Over the past six months, VRE transmission among ONCO inpatients has remained infrequent

(13/1,119; 1.2%) despite the gradual removal of specific enhanced IC practices.

Conclusions: Initial interventions to reduce new acquisition of VRE were only partially successful. The institution of CP for all ONCO inpatients for the duration of their stay was successful in reducing the frequency of new-onset VRE to an acceptable level. In an outbreak situation, use of CP in ancillary hospital settings are necessary. Patients with a GI device in place may be more likely to become colonized with VRE.

173. Strange Bedfellows: MSSA and PVL Team Up to Cause an Outbreak of Severe Skin Infections in a College Football Team

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Background: There have been several recent reports of outbreaks of severe skin infections due to community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) in sports teams. The pathogenicity of CA-MRSA is strongly linked to the presence of genes encoding for Panton-Valentine leukocidin (PVL). Although PVL-encoding genes are present in some strains of methicillin-sensitive *Staphylococcus aureus* (MSSA), reports of sports-associated outbreaks due to any strains of MSSA are extremely rare. We investigated an outbreak of severe skin infections due to multidrug-resistant MSSA in a college football team. The outbreak strain was identified because of a unique susceptibility pattern: resistant to penicillin, erythromycin and ciprofloxacin, but sensitive to oxacillin, cephalosporins, tetracycline and trimethoprim-sulfamethoxazole.

Objective: To determine whether the outbreak strain carried PVL-encoding genes, and to assess the association of the outbreak strain with nasal colonization.

Methods: A case was defined as a college X football player with culture-confirmed, ciprofloxacin-resistant MSSA skin infection occurring anytime from pre-season training to the end of the 2007 season. Isolates were characterized by antibiotic susceptibility patterns, pulsed field gel electrophoresis (PFGE), and polymerase chain reaction (PCR) for presence of the genes encoding for the specific protein sub-units of PVL (LukS-PV and LukF-PV). Nasopharyngeal swab cultures were also obtained mid-season from all the football players and athletic trainers to determine SA colonization rates and to identify those colonized with the outbreak strain.

Results: Eight cases were identified in 110 players (attack rate= 7%). Isolates were indistinguishable by PFGE and all were positive for PVL genes by PCR. Of the 118 players and athletic trainers screened, 62 (53%) were colonized with MSSA and 5 (4%) were colonized with MRSA. Despite this high colonization rate, none of the athletes or trainers was colonized with the outbreak strain.

Conclusions: To our knowledge, this is the first reported outbreak of PVL-positive MSSA skin infection in a sports team. In addition, the susceptibility pattern of the outbreak MSSA strain was more similar to CA-MRSA strains than to typical CA-MSSA strains. These features may reflect important events in the ongoing evolution of these organisms. As in previous studies of MRSA outbreaks in athletic teams, infection did not appear to be associated with nasal carriage: the reason for this is not well-understood. Finally, the teaming up of MSSA with PVL to cause this outbreak should prompt broadening of the scope of community infection prevention beyond MRSA- targeted strategies.

174. An Outbreak of Nosocomial Legionnaire's Disease Linked to a Contaminated Hospital Water Feature

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Background: Nosocomial outbreaks of *Legionella* spp. have been linked to contaminated water in hospitals. Immunocompromised patients are particularly vulnerable to Legionnaire's disease and, when infected, have a high mortality rate. In November 2007, an outbreak of nosocomial pneumonia due to *L. pneumophila* serogroup 1 occurred in patients hospitalized on our stem cell transplantation unit. Two patients who had therapy-induced profound neutropenia developed clinical *Legionella* pneumonia.

Objective: To investigate the source of nosocomial *Legionella* exposure.

Methods: We conducted a record review to identify common points of potential exposure. Once such sources were ascertained, we conducted environmental and water sampling for *Legionella* spp. from those sources. We used an air sampler loaded with buffered charcoal yeast extract agar plates in an attempt to detect aerosolized *Legionella*. We used pulsed-field gel electrophoresis (PFGE) to compare all clinical and environmental *Legionella* isolates.

Results: The most likely potential common sources identified were the water supply in the patients' rooms (they were housed two doors apart) and a decorative water feature in the radiation oncology suite (both patients received radiation during eight visits each to the suite). Samples of water and environmental cultures from the patients' rooms did not grow *Legionella* spp. However, *L. pneumophila* serogroup 1 was recovered from samples of water from the fountain. Fountain cultures also yielded prolific growth of several other microorganisms, including potential pathogens. The isolates from both patients and the fountain were identical by PFGE. Both patients developed clinical pneumonia within 10 days of completing radiation therapy, and, on subsequent interview, each reported observing the fountain at close range on at least two occasions. Efforts at additional case finding failed to reveal other patients who had undiagnosed pneumonias. We are reasonably confident none were missed, because every bronchoalveolar lavage specimen in our institution is tested for *Legionella* by culture and PCR. Both patients' infections were identified early and treated promptly, and both recovered.

Conclusions: This outbreak was caused by contamination of a hospital water feature and was likely facilitated by restarting the feature after it was shut off for five months. Despite a bromide filter and ozone generator, numerous potential pathogens, including *L. pneumophila*, were isolated from water in the fountain. PFGE is useful for tracing the environmental source of a *Legionella* outbreak. Indoor water features are a potential source of nosocomial Legionnaire's disease despite standard maintenance and sanitizing measures. Water features present unacceptable risk in hospitals serving compromised patients. The fountain has been drained and will be removed.

175. Pseudo-outbreak of *Mycobacterium mucogenicum* Infection Associated with Contaminated Water Supply

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Background: *M. mucogenicum* is a nontuberculous mycobacterium that can cause invasive disease including pneumonia and outbreaks of catheter-related bacteremias. *M. mucogenicum* can contaminate medical devices and water supplies and cause a variety of infections and outbreaks.

Objective: To describe a pseudo-outbreak of *M. mucogenicum* infection affecting cancer pts who underwent pulmonary procedures in the cardiopulmonary center (CPC).

Methods: We reviewed medical records of pts from whom *M. mucogenicum* was recovered from either pleural fluid, pleural biopsy or broncho-alveolar lavage (BAL) between 1/1/07 and 4/30/07. We collected environmental samples from various sites and evaluated specimen processing procedures from collection and transportation and the procedures in the microbiology laboratory. Seventeen environmental cultures (water from sinks, ice from ice machines) were obtained; most collected from 2 rooms in the CPC where all pts had their procedures done. Organisms were identified as *M. mucogenicum* by 16S rRNA gene sequencing analysis.

Results: Eight pts were reported positive for *M. mucogenicum* (6 pleural fluid, 1 pleural biopsy, and 1 BAL) during the 4-month period. None of the 8 pts had signs or symptoms of infection, and the indication for thoracentesis or bronchoscopy was to relieve symptoms from malignant effusion or for diagnosis of a suspicious lung lesion. All environmental cultures were negative for *M. mucogenicum* except for 1 taken from sink water in 1 of the rooms suggesting water contamination. Water superheat for the area was performed, including flushing distal sites for > 15 minutes at temperature $\geq 140^{\circ}$ C, although this sink had not been used for patient care or for handling patient specimens. Instead, our investigation determined that placing specimen tubes directly inside a cup of ice (i.e. without placing them inside a plastic bag) prior to transporting them to the laboratory was the most commonly

identified factor. Although the specimens collected from the ice machine showed no growth, this particular ice machine had been cleaned and disinfected as per routine maintenance just few days prior to our investigation.

Conclusion: Although the exact source was never confirmed, our investigation suggests that this was a pseudo-outbreak of *M. mucogenicum* that likely resulted from contamination of collected specimens during transport on ice to the laboratory. By changing specimen transportation practices, which included sealing tubes inside double plastic bags prior to immersion in ice, as well as superheating water supply, the pseudo-outbreak was interrupted, with only 1 additional case identified five months later (under investigation).

176. Characterization of a Cluster of Filamentous Fungal Infections in a Pediatric Population

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Background: In October 2006, the pediatric hematology/oncology service in a university hospital moved to Hospital-X. During April -August 2007 (study period), 6 patients acquired infections caused by 4 different opportunistic filamentous fungi. There were no previous reports of this type of infection on this service in the preceding months.

Objectives: to (i) identify risk factors associated with acquisition of infection; (ii) institute recommendations.

Methods: Our investigation had four components: (i) two case control studies; (ii) observational studies and assessment of practices and procedures; (iii) assessment of building, walls, ventilation systems, ceilings, bathrooms and fixtures; and (iv) epidemiologically-directed cultures of rooms and control areas inside and outside the building using settle plates; of surfaces (e.g., ventilators, sills, beds); and of clinical items (e.g., tape). A case was defined as any pediatric patient admitted to Hospital-X's 5th floor during the study period and acquired a filamentous fungal infection. We ascertained cases through medical records, microbiology line listings, and personnel interviews. We used two control groups: (i) persons without infection and (ii) immunosuppressed persons without infection. Odds ratios and confidence intervals were calculated; Fisher's exact test was used, where appropriate.

Results: Six patients met the case definition; 14 controls were selected for each study. Case characteristics: median age=12 (range: 2-18) years; 5/6 were male. Pathogens: *Fusarium* sp., *Mucor* sp., *Rhizopus* sp., and *Aspergillus* sp. Infections occurred in skin or oral mucosa. Cases and controls were similar for age, platelet counts, blood glucose, or having an underlying malignancy. In contrast, cases were more likely to have a lower median blood count (200 vs. 750, $p < 0.1$); to be on tobramycin ($p < 0.001$), vancomycin ($p < 0.05$), or chemotherapy ($p < 0.05$) at admission; to have received high-dose steroids in the pre-chemotherapy induction

phase ($p < 0.001$), or to report a history of allergies to food/fruit ($p = 0.07$). Five hospital rooms were linked to cases ($p < 0.01$); however, no fungi linked to cases were isolated from walls, ceilings, ventilation systems, bathrooms, or fixtures. Observational studies revealed areas where infection control practices could be improved: e.g., fruits and food were observed in rooms. At various times during neutropenia, all cases had contact with persons outside their rooms or at home, where adherence to infection control practices might not have been optimal.

Conclusions: The nature of the pathogens and our findings suggest that infections were likely acquired through exposure to food/fruit sources. Patients with an inherent susceptibility to infections, who are profoundly immunosuppressed and continue unrestricted diets and movements during chemotherapy, are at risk of acquiring infections caused by filamentous fungi.

177. Outbreak Investigation and Control of Candidemia in Neonatal intensive Care Unit

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Background: The yeast *Candida* is the fourth most common cause of hospital-associated bloodstream infections. Also BSIs with candidemia account for 8% to 15% of hospital-associated sepsis in the United States. A few periods, we experienced an outbreak of hospital associated BSIs caused by *Candida parapsilosis* in neonatal intensive care unit and we investigated the cause of BSIs.

Objective: The aim of this study was to identified and control of the outbreak

Methods: We collected data from clinical records and observed the current methods of care of central catheter in the NICU. During the outbreak, we investigated the current procedures and maintenance care of central catheter insertion and educated the staff on the correct methods of the catheter insertion and care. Also we performed surveillance culture and hand hygiene monitor.

Results: Between June 2007 and August 2007, *Candida parapsilosis* was isolated from blood of 4 patients hospitalized in the NICU. All infections were attributed to the care of central catheter insertion. We identified that central catheter insertion procedure and hand hygiene have been done incorrectly during the outbreak period. So we served the correctly guideline - like a aseptic technique, maximum barrier precaution, a proper choice of site - and educated and monitored the insertion procedure including hand hygiene monitoring with real name. There was no specific result from the surveillance cultures.

Conclusions: According to contact precaution and central catheter insertion guideline, we enforced cohort isolation and emphasized strict hand hygiene and aseptic technique and maximum barrier precaution to health care workers. During the three months later, there was no more outbreak of hospital-associated BSIs due to *Candida parapsilosis*.

178. Transmission of USA-300 Methicillin-Resistant *Staphylococcus aureus* in a Newborn Nursery Also Affecting Post-partum Women

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Background: USA-300 has been increasingly detected as a healthcare-associated pathogen and has been associated with vaginal carriage in pre-partum women.

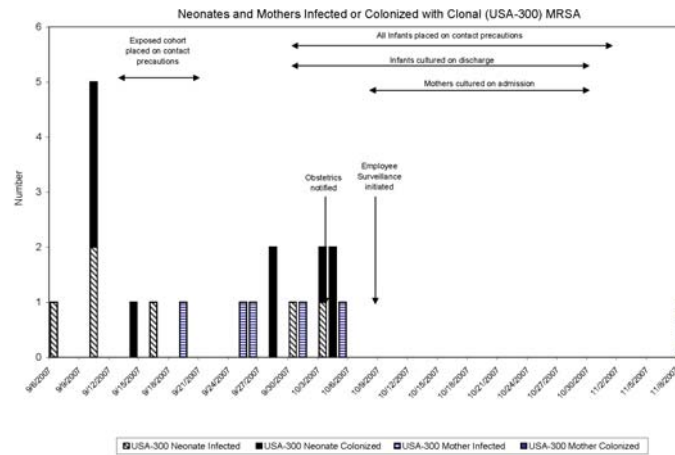
Objective: We describe an outbreak of USA-300 affecting newborns, their mothers, and healthcare workers (HCW).

Methods: When an infant in our Newborn nursery was diagnosed with MRSA pustulosis on day of life (DOL) 5, potentially exposed infants were cohorted, hand hygiene was reinforced, and enhanced environmental cleaning was initiated. Another infant was diagnosed with MRSA pustulosis at hospital discharge on DOL 5. Surveillance cultures (anterior nares, axilla, umbilicus, groin) of all infants in the nursery were performed. The cohort was disbanded when the last exposed infant was discharged. Ten days after the cohort was disbanded an infant (not from initial cohort) was admitted for MRSA pustulosis and 2 mothers presented with MRSA breast infections. Surveillance cultures were performed on all newborns at discharge, on anterior nares of mothers at admission, and on staff. Colonized HCWs were furloughed and decolonized with intranasal mupirocin and 3% hexachlorophene showers. All infants were placed on Contact Isolation, circumcisions were suspended, Triple Dye was applied to infants' umbilical stumps, the hand-washing agent was changed to a PCMX antimicrobial product, non single-patient use equipment (e.g., blood pressure cuffs) were eliminated and "infection control monitors" observed staff and intervened when needed. Education about MRSA and the outbreak was provided to families and staff.

Results: In all, 31 patients were colonized/infected with MRSA (68% USA-300, 16% unavailable, 16% other). 12 newborns were colonized (2.4%; mean 2 days, range 0-4) and 9 had skin and soft tissue infection (1.8%; mean 5 days, range 0-29). Ten mothers (2%) had infections after discharge (mean 25 days, range 8-69) and included skin (10%), breast abscesses (20%), mastitis (20%), and cesarean section wounds (50%). Eight (1.8%) of 450 HCWs had anterior nares colonization with MRSA, two of whom carried USA-300.

Conclusions: We report an outbreak of USA-300 skin and soft tissue infections in mothers and infants. The epidemiology of this outbreak suggests unique characteristics of USA-300 including rapid onset in the index case suggestive of vertical transmission, ongoing transmission in the nursery despite very short hospital stays, and delayed presentations of skin and soft tissue infections. A delay in notification to OB attendings may have led to inappropriate initial treatment of infected mothers. MRSA must be considered in all infants and post-partum women

with skin and soft tissue infections and obtaining cultures should be strongly



considered.

179. Intensive Care Unit Outbreak Due to Carbapenem Resistant *Klebsiella Pneumoniae* (crkp) in a Non-endemic Setting

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Background: Carbapenem resistant *Klebsiella pneumoniae* (CRKP) isolates are now endemic in many hospitals in New York City. Infections due to CRKP have high mortality, especially in high-risk patients and very few treatment options are available.

Objective: Investigate an outbreak of blood stream infections due to CRKP in the Intensive care unit (ICU) of a large tertiary care cancer center.

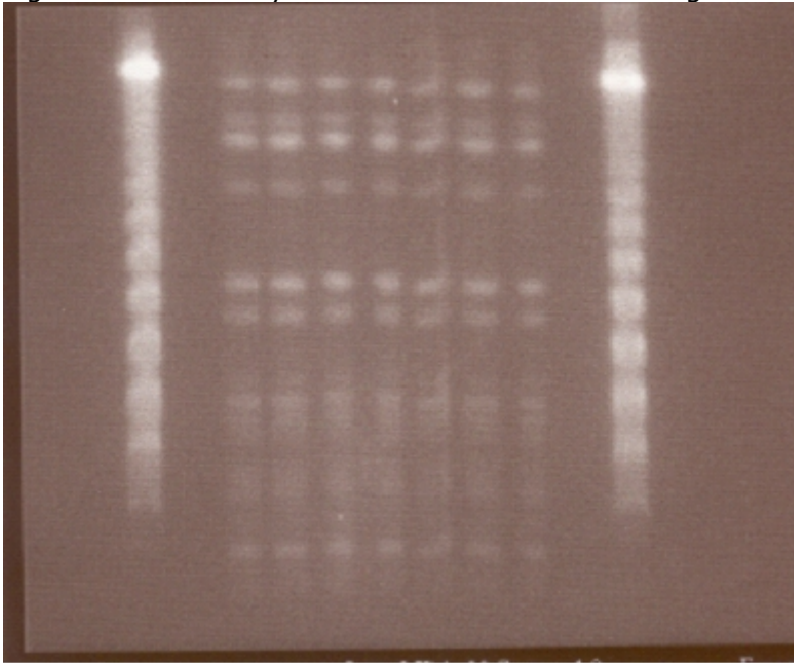
Methods: Healthcare-associated infection (HAI) with CRKP was defined by acquisition of infection 72 hours after admission to the hospital. Prior to outbreak, ICU patients were not routinely placed into isolation. MicroScan and disk diffusion was used to determine antimicrobial susceptibility. Screening with an ertapenem disk was used as a marker for carbapenem resistance. Pulse field gel electrophoresis (PFGE) was studied for genetic relatedness.

Results: From October -December 2007, nine cases of CRKP colonization and infection were detected in a 15 bed ICU. Six had bacteremia and eight episodes were healthcare-associated. The index case was a patient with extensive skin lesions from cutaneous T- cell lymphoma who had a brief stay in the ICU. Two subsequent cases included one patient who was admitted to the same ICU room as the index case, and

another patient who upon the index patient's transfer to the floor shared the room. Five more cases occurred over the next one month. In all, 5 of 6 patients with bacteremia died. PFGE analysis showed that the *Klebsiella* isolates belonged to the same clone (Figure 1). Interventions included: (a) contact precautions for entire unit; (b) cohorting CRKP infected and colonized patients, health care workers, respiratory therapist and house-keeping personnel; (c) increased environmental cleaning to twice daily; (d) assigning one nurse for each ICU patient (e) screening of all gram negative isolates from the ICU for sensitivity to ertapenem; (f) surveillance cultures on respiratory samples from all intubated ICU patients; (g) PFGE analysis of isolates from infected and colonized patients; (h) multi-disciplinary meetings with ICU, infection control, microbiology, pharmacy, hospital administration, respiratory therapy, and patient representative staff; (i) education of staff and families by ICP. No additional cases have been seen since these interventions.

Conclusions: Infection due to CRKP is associated with high mortality among critically ill cancer patients. Standard ICU interventions including isolation, cleaning, education, and staff cohorting were effective in stopping the outbreak.

Figure1 : PFGE analysis of outbreak strains showing clonal relatedness



180. A Cluster of Invasive Group B Streptococcal Disease: Changing Epidemiology or Transient Phenomenon

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Background: Invasive disease due to group B Streptococcus (GBS) has generally been associated with significant medical debility, pregnancy and the extremes of age. Although reported with increased frequency in the 1980s and 1990s, community

acquired group B Streptococcal sepsis and meningitis remain distinctly unusual. In the spring of 2007, the Adult Infectious Diseases Service noticed an increase in the incidence and severity of GBS sepsis.

Objective: To confirm and characterize a cluster of severe infections due to GBS and to investigate possible changes in the epidemiology of this pathogen.

Methods: The microbiology laboratory at our 500-bed university medical center identified cases of GBS bacteremia admitted in 2005, 2006 and 2007. For patients admitted between May 1 and July 31, 2007, demographic and clinical data were abstracted from medical records and isolates were submitted to the CDC for serotyping and for genetic analysis using pulse-field gel electrophoresis (PFGE) at the Public Health Research Institute Center at the University of Medicine and Dentistry of New Jersey.

Results: There were 5 cases of GBS bacteremia in 2005, 15 in 2006 and 21 in 2007, only one of which was a neonate. Nine of these 21 cases were admitted in the 3-month period beginning May 1, 2007. Patients were from 23 - 87 (mean 64.2) years old. All infections were community acquired with isolation of GBS from blood within 24 hours of admission. Seven patients had one or more known risk factors for invasive GBS infection: DM (6), Hepatitis C (1), Colon Cancer (1), Stroke (1). Two patients had no underlying medical condition. These two patients had severe and unusual presentations: one with rapidly fatal meningitis and one with recurrent deep neck infection. The remaining seven patients had primary septicemia (2), pneumonia (2), osteomyelitis (2) and septic arthritis. Laboratory analysis showed no predominant serotype: Ia (1), Ib (1), II (1), III (1), IV (2), V (1), VIII (1), NT (1) and PFGE likewise failed to indicate any genetic clustering.

Conclusions: Our experience does indeed suggest an increase in the incidence and severity of infection due to GBS in nonpregnant adults. The identification of nine cases of invasive group B Streptococcal infection in a three-month period in our hospital is an incidence that is approximately 10-fold greater than has been previously reported in hospitalized patients. Moreover, in prior studies, approximately 2% of patients with invasive GBS infection have been otherwise healthy, nonpregnant adults. The occurrence of severe GBS infection in two otherwise healthy nonpregnant adults - 22% of our patients - is also distinctly unusual. Serologic and molecular analysis does not, however, suggest a common source for these infections. Further study is needed to assess whether these findings represented a sustained change in the epidemiology and virulence of GBS.

181. Pseudo-outbreak of *Mycobacterium paraffinicum* in a Tertiary Care Medical Center

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Background: Pseudo-outbreaks of nontuberculous mycobacteria species have been reported in healthcare institutions. We describe the first *Mycobacterium*

paraffinicum" pseudo-outbreak in a tertiary care medical center.

Methods: During a 1-month period, mycobacteria recovered from 8 respiratory specimens and 1 stool specimen from 5 patients were initially identified as *Mycobacterium scrofulaceum*. Specimens from 5 additional patients taken 2-12 months later contained the same organism. Epidemiological and environmental investigations were conducted along with additional strain identification, typing and molecular analysis.

Results: During a one year period, a total of 15 specimens, (14 respiratory and 1 stool), from 10 patients admitted to the same patient care unit were initially identified as *Mycobacterium scrofulaceum*. The 10 patients submitted a total of 62 specimens for mycobacterial cultures: 44 respiratory, 2 stool, 5 pleural fluids, 2 cerebral spinal fluid, 6 surgical pathology tissue samples, and 3 blood cultures. All specimens were acid- fast bacilli smear negative. All of the patients were discharged with an alternative diagnosis prior to the identification or growth of *M. scrofulaceum* and none of the patients were subsequently treated for this NTM. Standard biochemical tests and high performance liquid chromatography initially identified the isolates to be *M. scrofulaceum*. Molecular analysis by 16S RNA gene sequencing and polymerase chain reaction restriction pattern analysis, however, identified the nontuberculous mycobacteria species as "*M. paraffinicum*". Pulsed-field gel electrophoresis revealed two main patterns among the isolates. The latter was also confirmed by repetitive-sequence based polymerase chain reaction typing. Environmental investigation of multiple water sources identified the ice machine on the patient care unit as the source of contamination.

Conclusions: "*M. paraffinicum*" was shown by molecular analysis to be associated with this pseudo-outbreak. The clinical significance of "*M. paraffinicum*" is unknown, as this species has not been previously associated with clinical disease or pseudo-outbreaks. An epidemiological investigation with molecular analysis was needed to confirm the suspicion of a pseudo-outbreak. Molecular methods are necessary to efficiently and accurately identify "*M. paraffinicum*" isolates.