between Xpert SA and the culture results. Methicillin resistance was determined using conventional methods (susceptibility testing or detection of altered penicillin binding protein).

Results. When compared with culture for the identification of SA ($n = 481$), there was an agreement of 95.0% with sensitivity and specificity being 95.6% and 94.8%, respectively. Among those culture-confirmed and Xpert SA positive samples ($n = 131$), concordance between Xpert SA and conventional methods for detection of methicillin resistance was 97.0% with sensitivity and specificity being 100% and 96.3%, respectively. Four culture-confirmed methicillin-susceptible SA (MSSA) were identified as MRSA by Xpert SA. Among 504 nasal specimens, 23 (4.6%) samples had invalid or instrument failure results. Nasal swabs collected from pediatric patients (≤21-year-old) had a higher invalid/instrument failure rate (5.0%) than those from adults (0%) ($P < 0.001$).

Conclusion. Xpert SA Nasal Complete assay provides a rapid and sensitive method to detect and differentiate between MSSA and MRSA colonization. The higher invalid rate in pediatric patients and misidentification of MSSA as MRSA by Xpert SA warrant the confirmation by bacterial culture and conventional susceptibility test.

Disclosures. **A. Leber**, Nationwide Children's Hospital: Research Contractor, Research support.

2005. T-SPOT®.TB Test for Latent Tuberculosis Infection Diagnosis and Treatment Guidance in Thai Healthcare Professionals

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Background. Data on efficacy of T-SPOT®.TB Test (T-SPOT) in diagnosing latent tuberculosis infection (LTBI) and guiding isoniazid preventive therapy (IPT) among healthcare professionals (HCP) in tuberculosis (TB)-endemic settings are limited.

Methods. A prospective study was conducted among Thai HCP undergoing T-SPOT in June 2016 (initial screening) and June 2017 (follow-up). Nine-month isoniazid preventive therapy (IPT) was offered among the HCP with positive T-SPOT. The incidence of TB and the rates of conversion and reversion of T-SPOT were evaluated during the 1-year follow-up period (June 2016 to June 2017).

Results. A total of 140 HCP underwent initial T-SPOT; the median age was 27 years (IQR 25–31 years), 89% were female and 23 (16%) were T-SPOT-positive. Eighty-nine HCP (64%) had both initial and follow-up T-SPOTs. Among the 89 HCP, the initial and follow-up rates of T-SPOT positivity were 19% ($N = 17$) and 24% ($N = 21$), respectively. The conversion and reversion rates were 10% ($N = 9$) and 6% ($N = 5$), respectively. All of the nine HCP (100%) with T-SPOT conversion reported significant contacts with patients who had active pulmonary TB without using appropriate personal protection equipment. During the 1-year follow-up period, incidence of TB were significantly higher among HCP with T-SPOT conversion compared with HCP with persistent positive T-SPOT, HCP with T-SPOT reversion and HCP with persistent negative T-SPOT [22 vs. 8 vs. 0 vs. 0 cases/100 person-years; $P < 0.001$]. Of the 17 HCP with positive initial T-SPOT, 8 (47%) completed IPT. The incidence of TB was significantly lower and the T-SPOT reversion rate was significantly higher among HCP completing IPT compared with HCP declining or not completing IPT (0 vs. 11 cases/100 person-years; $P < 0.001$ and 63% vs. 0%; $P = 0.009$, respectively).

Conclusion. T-SPOT could be used for diagnosing LTBI, guiding IPT and identifying HCP with subsequent risk for TB. The serial T-SPOT may be used for evaluating IPT efficacy.

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

2006. Implementation of the T2 Biosystems T2Bacteria Panel in a Level-One Trauma Center, Safety Net Hospital

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Background. Rapid detection and identification of sepsis causing pathogens are critical for optimizing antimicrobial therapy to improve patient survival and reduce healthcare costs. The T2Bacteria Panel RUO is a molecular diagnostic allowing detection of Gram-negative *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and Gram-positive *Staphylococcus aureus* and *Enterococcus faecium* within a few hours. The purpose

of our study was to determine the feasibility and efficacy of the T2Bacterial Panel RUO in an Emergency Medicine (ED) and Surgical Intensive Care Unit (SICU) setting.

Methods. An IRB-approved, prospective, observational study was implemented at a Safety-Net, Level One Trauma Center in Denver, Colorado. Patients were enrolled who received an order for a blood culture from the ED or SICU. Patients who had blood drawn for cultures had a concurrent draw for testing with a T2Bacteria Panel RUO.

Results. Sixty-six patients are included in the present interim analysis. Mean patient age was 51 years old (19–84), 36% were female, 86% Caucasian (34% Hispanic/Latino), and 74% of patients were enrolled upon presentation to the ED, 13% from the SICU, and 15% from the wards. 90% of blood sampling (culture and T2Bacteria) was done from peripheral stick while 7% were from the initial stick of a peripheral IV and 2% obtained from an indwelling catheter. 85% of blood cultures were negative. Of the 56 patients with negative blood culture, 53 had concordant negative T2Bacteria results, providing a specificity of 94.6%. 10 patients had positive blood cultures (15%) for T2Bacteria Panel RUO targets. Interestingly, only five of these (50%) had concordant positive T2Bacteria testing. Examining the discordant samples, all (5) blood culture positive, T2Bacteria negative were found to have clinically false-positive blood cultures. T2Bacteria positive samples were distributed as follows: two *E.coli*, one *S. aureus*, one *K. pneumoniae*, and one *P. aeruginosa*. No detections were made for *E. faecium* or *A. baumannii*.

Conclusion. In this interim analysis, T2Bacteria Panel RUO provides feasible rapid diagnostics for ED and surgical ICU settings with a high specificity and much shorter time to result when compared with gold standard blood cultures.

Disclosures. **C. Robinson**, T2 Biosystems: Research Coordinator for funded study from T2 Biosystems, Research support. **R. Jackson**, T2 Biosystems: Research Assistant for funded study from T2 Biosystems, Research support. **M. Cohen**, T2 Biosystems: PI on study being funded by T2 Biosystems, not paying for any part of salary, Research support.

2007. To Treat or Not to Treat: Does a More Sensitive and Specific Testing Methodology Make the Treatment Decision More Clear?

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Background. *Clostridium difficile* infection (CDI) is a leading cause of infectious diarrhea in healthcare settings in the United States. Accurate testing methodology provides guidance to clinicians as to when to treat. Our study was designed to determine whether more sensitive testing methodology implemented in 2013 reduced unnecessary treatment of hospital associated diarrhea (HAD).

Methods. In 2012, patients with HAD were tested with the less sensitive testing method of *C. difficile* Toxin Assay by EIA. In 2013, a three-step algorithm incorporated CDI glutamate dehydrogenase antigen (GDH) in combination with an enzyme-linked immunoassay for Toxin A and B was introduced. Those samples with discrepant results (positive on only one of the two) were considered indeterminate and subjected to the nucleic acid amplification test (NAAT) for CDI genes. In a retrospective chart review of HAD, we assessed the decision to treat based on the laboratory results available at the time in the pre-algorithmic and post-algorithmic periods. Multiple demographic factors and comorbid conditions were analyzed to provide clues to why the patient may have had continued treatment despite negative assays.

Results. The rate of treated patients despite negative CDI testing in the pre-algorithm period was 59% (118/444) and 41% (82/249) in the post-algorithm period ($P = 0.0765$). A multiple logistic regression analysis was done for all tested factors. The factors that led to treatment despite negative testing in both time periods included: organ transplantation ($P = 0.0003$), other immunosuppressive conditions ($P = 0.0447$), prior hx of CDI ($P = 0.0021$), longer length of stay ($P = 0.0105$), and hx of hypertension ($P = 0.0173$).

Conclusion. While there was a downward trend toward holding CDI treatment in those with negative CDI testing as the more sensitive and specific algorithm was introduced it did not reach statistical significance. The higher risk patients were statistically more likely to be treated even if the testing was negative. Further efforts should be made to educate clinicians as to the accuracy of the testing methods so that appropriate antibiotic de-escalation can be achieved even in high-risk patients with diarrhea.

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

2008. Effective and Early Diagnosis of Pneumonia in Patients With Acute Leukemia in a Comprehensive Cancer Center: How Can We Improve the Microbiological Diagnosis?

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Background. Pneumonia is one of the main causes of morbi-mortality in acute leukemia (AL) patients. The positive yield of microbiology diagnosis is still significantly low. The aim of the study was to evaluate the possible impact of use of diagnostic methods (within first 48 hours of diagnosis) in AL patients with pneumonia during chemotherapy.

Methods. Retrospective study (January 2017–December 2017) at MD Anderson Cancer Center. The medical records of adult patients with AML, MDS, or ALL who developed CT-confirmed pneumonia after induction or second-line chemotherapy were reviewed, including demographic, clinical, microbiology data, and outcomes.

Results. During 2017, 174 patients with AL developed pneumonia confirmed by CT chest. Fifty (29%) of them during induction/second-line chemotherapy: 42 (84%) AML, five (10%) MDS, and three (6%) ALL. Thirty-one (62%) showed consolidation in CT, 14 (28%) nodules, and five (10%) both findings. Mean age was 65 (SD: 11.5, range: 24–87) years with 46% males. Thirty-three (66%) patients had neutropenia (ANC<500) at the time of pneumonia. ID was consulted in 38 (76%) and pulmonary in 37 (74%) patients. Bronchoscopy/BAL (bronch) was performed in only 24 (48%) patients, still with the highest diagnostic yield (13/24, 54%) compared with other diagnostic methods (sputum and blood cultures; and galactomannan, β-glucan, and cryptococcal antigen in serum). Twelve of 24 (50%) patients had an early bronch (within 48 hours), with higher identification of bacteria (3/12, 25%), fungi (2/12, 16.7%), and virus (3/12, 25%) compared with those 12 performed later. A trend of more viral infection (6/12, 50%), including CMV, was found in late-performed bronch (>48 hours after diagnosis). The patients with early bronch were sicker, with higher rate of ICU admission (42% vs. 0% in late group) and in-hospital mortality (25% vs. 8% in late group). However, those patients who underwent bronch later had a higher rate of 30-day re-admission (33% vs. 22% in early group).

Conclusion. Bronchoscopy/BAL was the best diagnostic test in patients with AL and CT-confirmed pneumonia, even though it was only performed in 48% of patients. Early bronchoscopy (first 48 hs) has better diagnostic yield than late bronchoscopy (>48 hs), directing the antimicrobial therapy on these patients (based on the identification of bacteria, fungus or viruses), and decreasing the 30-day re-admission rate.

Timing of Bronchoscopy and Diagnostic Yield
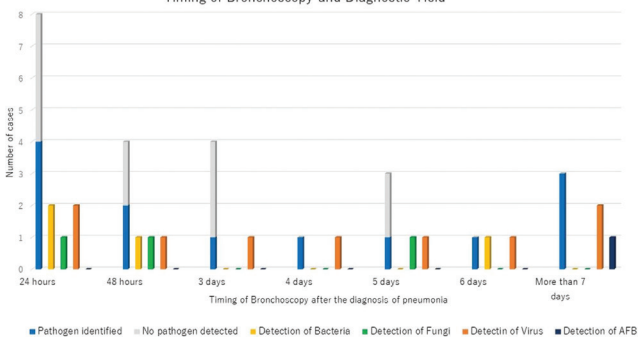
Disclosures. **J. Adachi**, Merck: Grant Investigator, Research grant.

2009. Misidentification Rate of *Acinetobacter baumannii* Isolated From Invasive Infections in Children

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Background. *Acinetobacter baumannii* (AB) invasive infections are known to have a worse clinical outcome than non-*baumannii Acinetobacter* infections. However, currently, phenotypic identification by semi-automated commercial identification systems struggle to distinguish *Acinetobacter* subspecies; especially the four closely related subspecies of the *Acinetobacter calcoaceticus–Acinetobacter baumannii* (ACB) complex. The purpose of this study was to examine the rate of misidentification of AB isolated from invasive infections in children.

Methods. From January 2001 to December 2017, patients 18 years old and below who were treated for invasive AB infections at Seoul National University Hospital and Chungnam National University Hospital were included. *Acinetobacter baumannii*, identified by commercial identification systems, cultured from sterile body fluids of the study participants were prospectively collected. The DNA from the stored bacteria were isolated, and subspecies identification was carried out by PCR and sequencing of the partial *gyr*B gene. Clinical data were retrospectively reviewed.

Results. During the 17-year study period, 113 AB isolates were obtained from patients treated for invasive infections. The median age of the patients was 2 (IQR 0–7) years old and 47 (49.5%) were male. Duplicate isolates were eliminated, and a total 95 isolates underwent further investigation. The isolates were retrieved from the blood (n = 82), peritoneal fluid (n = 8), pleural fluid (n = 2), cerebrospinal fluid (n = 2), and bronchoalveolar fluid (n = 1). Of the AB isolates identified by the commercial identification systems, 55 (57.9%) were AB. Of the non-AB isolates identified by partial *gyr*B sequencing, 22 (23.2%) were identified as *A. nosocomialis*, 8 (8.4%) as *A. pittii*, and 1 (1.1%) as *A. calcoaceticus*. Non-ACB complex subspecies included *A. soli* (n = 3), *A. seifertii* (n = 3), *A. iwoffii* (n = 1), *A. bereziniae* (n = 1), and *A. junnii* (n = 1).

Conclusion. There was a high rate of misidentification of the *Acinetobacter* subspecies causing invasive infections in children. Further studies are needed to analyze the burden that misidentification has on the treatment and outcome of patients with invasive infections.

Disclosures. H. Lee, Korean Society of Pediatric Infectious Diseases: Member, Research grant.

2010. Volatile Organic Compounds Patterns in Breath, Plasma, and Stool in Patients with *Clostridium difficile* Infection: A Cross-Sectional Proof of Concept Study

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Background. Volatile organic compounds (VOCs) are hydrocarbon compounds which are end product metabolites of physiological and pathophysiological processes. Many disease processes can be identified by examining metabolome patterns in clinical samples from patients. The purpose of this study was to identify *Clostridium difficile* infection (CDI) based on differences in VOCs in stool, blood and breath of patients with CDI and controls without.

Methods. Patients aged >18 years at Cleveland Clinic with *CDI* (> 3 watery stools in the preceding 24 hours and stool PCR positive for *C. difficile*), and matched controls (for age, sex, and date of PCR test) were included. Stool and plasma samples (within 24 hours of collection) and fresh breath samples were collected. Headspace gas from clinical samples was tested using selected ion flow tube mass spectrometry (SIFT-MS) on a VOICE200 instrument (*Syft Technologies Ltd., Christchurch, New Zealand*). The MS assay comprised of 22 common analytes: 2-propanol, acetaldehyde, acetone, acetonitrile, acrylonitrile, benzene, carbon disulfide, dimethyl sulfide, ethanol, isoprene, pentane, 1-decene, 1-heptene, 1-nonene, 1-octene, 3-methyl hexane, 2-nonene, ammonia, ethane, hydrogen sulfide, triethyl amine, and trimethyl amine. VOC analysis findings were classified as positive or negative using the K-nearest neighbors (KNN) method. Model accuracy was evaluated by *k*-fold cross-validation with 5-folds. Sensitivity and specificity were determined and receiver-operating characteristics curves generated for each sample type.

Results. Thirty-one patients with CDI and 31 controls were studied. The optimal KNN classifier model was achieved with *k* = 7, 5, and 9, for breath, plasma, and stool samples, respectively. The sensitivity/specificity for detection of CDI were 87.1%/77.4%, 66.7%/63.6%, and 61.3%/36.4%, for breath, stool, and plasma samples, respectively. Model accuracy was no better if positives were limited to those with *C. difficile* PCR CT <30 cycles.

Conclusion. VOC analysis of fresh breath, but not plasma or stool samples ≤24 hours old, by the method studied had good sensitivity and moderate specificity for identifying patients with CDI.

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