Navaneeth Narayanan, Pharm D, BCPS[4] and Thomas Kirn, MD, PhD[3]; [1]Rutgers-RWJMS, New Brunswick, New Jersey, [2]Rutgers Robert Wood Johnson Medical School, New Brunswick, New Jersey, [3]Medicine and Pathology, Rutgers Robert Wood Johnson Medical School, New Brunswick, New Jersey, [4]Department of Pharmacy Practice and Administration, Rutgers Ernest Mario School of Pharmacy, Piscataway, New Jersey

Session: 236. Diagnostics - Mycology
Saturday, October 7, 2017: 12:30 PM

Background. *Candida* species are the fourth leading cause of nosocomial bloodstream infections in the United States, however incidence is low and most patients who receive empiric treatment do not actually have candidemia. Unfortunately, detection, identification and susceptibility testing using standard instrumented blood culture systems and routine microbiological techniques takes 4–10 days. Astute clinicians may empirically treat patients with antifungal therapy (AFT) prior to having any results, often leading to unnecessary coverage for candida infection for up to 10 days. The T2 Candida Panel is an FDA-approved assay that rapidly detects the presence of 5 *Candida* species directly from whole blood in 3–5 hours. We determined whether AFT decisions were altered based on negative (neg) results of a T2 assay.

Methods. We performed a retrospective chart review of the first 50 patients at our institution from March 1, 2016 to March 1, 2017 with a neg T2 *Candida* assay result (data collection is ongoing). If a patient had multiple valid T2 assays, only the first result was used for analysis. The patients' medical records were reviewed for use and duration of empiric AFT, results of blood cultures, treatment modification, underlying illness, risk factors for candida infection, length of stay, and 14-day mortality from the time of the T2 assay.

Results. Twenty-four patients were never started on AFT. Of the 26 who received AFT, it was stopped in 15 (57%) following T2 results (median time to stop empiric AFT = 2 days (1–16)). The reasons for continuing AFT in the cases of neg T2 assays included hematologic malignancy patients who were on long-term prophylaxis with antifungals (6 patients), empiric use in a case of severe sepsis (1 patient), and positive culture results despite neg T2 assay in 4 patients: 1 patient with *C. lusitaniae* in blood culture, 1 patient with *C. parapsilosis* from positive culture of medical device, 1 patient with neg T2 but positive blood cultures from 2 days prior for *C. albicans* (was on antifungal therapy at time of test), 1 patient with *C. guilliermondii* in blood culture.

Conclusion. We conclude that a neg T2 Candida assay affects empirical use of AFT in certain patient populations and may be useful in controlling the overuse of antifungal agents.

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

2082. Rapid Detection of Pediatric Bacteriuria Using Narrow Angle Forward Laser Scattering Technology (NAFLST) with Bacterioscan

Adriana Cline, MD[1]; Ravi Jhaveri, MD, FIDSA, FPIDS[2]; Kara Levinson, PhD, MPH[3] and Melissa Miller, PhD[4]; [1]Pediatrics, University of North Carolina Healthcare, Chapel Hill, North Carolina, [2]Pediatrics, University of North Carolina, Chapel Hill, North Carolina, [3]Microbiology and Immunology, UNC Health Care Chapel Hill, Chapel Hill, North Carolina, [4]Pathology and Laboratory Medicine, University of North Carolina, Chapel Hill, North Carolina

Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Pediatric urinary tract infections (UTI) are common, but culture-based diagnosis can take up to 48 hours. This time delay means patients are exposed to potentially unnecessary antibiotics. The sensitivity of screening urinalysis can vary, so rapid detection of UTI by another means would be beneficial. Narrow Angle Forward Laser Scattering Technology (NAFLST) with Bacterioscan can rapidly detect bacteriuria by shining a laser continuously through a liquid sample containing replicating bacteria, and graphing the degree of light refraction over time. Higher degrees of light refraction represent higher initial bacterial load and continued bacterial growth. After 3 hours, the optical scatter classifies a sample as either *Likely Positive* or *Likely Negative*. We compared Bacterioscan results to culture data in pediatric patients to assess the ability to diagnose UTI and avoid unnecessary urine culture.

Methods. This protocol was approved by the UNC Biomedical Institutional Review Board. Over one month, 169 pediatric (<18 yo) urine cultures were collected as part of routine patient care. An individual urine sample and 2.5mL of Sterile Tryptic Soy Broth were pipetted into a Bacterioscan micro-curette. Bacterioscan labeled the specimen as *Likely Positive* or *Likely Negative* after a 3 hour period. Results were then compared with urine culture results obtained by routine microbiologic methods.

Results. Of the 169 urine cultures, 96 were positive, but only 27 were positive for uropathogens. Bacterioscan was 100% sensitive and 58.4% specific in predicting clinically relevant/pathogenic bacterial growth in culture (PPV 31.3%, NPV 100%), and 70.8% sensitive and 75.3% specific in predicting any bacterial growth (PPV 79.0%, NPV 66.2%). If a "Likely Positive" Bacterioscan result had been used in our study population to screen urine samples for culture, then 58% (83/142) of negative urine cultures would have been eliminated with no UTIs missed.

Conclusion. By rapidly identifying urine cultures likely to be positive, NAFLST with Bacterioscan can safely obviate the plating of every urine sample and reduce empiric antibiotic use while waiting for culture results. Larger studies are required to confirm these results.

Disclosures. **A. Cline**, Bacterioscan: Equipment necessary to perform this study was provided by Manufacturer, Equipment necessary to perform this study; **R. Jhaveri**, Gilead: Investigator, Research support; Abbvie: Investigator, Research support; Merck: Grant Investigator, Research grant

2083. Direct Detection and Quantification of Bacterial Cell-free DNA in Patients with Bloodstream Infection (BSI) Using the Karius Plasma Next Generation Sequencing (NGS) Test

Lisa Wanda, BS, BA[1]; Felicia Ruffin, MSN, RN[1]; Jonathan Hill-Rorie, BA[1]; Desiree Hollemon, MSN, MPH[2]; Hon Seng, BS[2]; David Hong, MD[2]; Tim Blauwkamp, PhD[2]; Mickey Kertesz, PhD[2] and Vance Fowler Jr., MD, MHS[3]; [1]Division of Infectious Diseases, Duke University Medical Center, Durham, North Carolina, [2]Karius, Inc., Redwood City, California, [3]Medicine, Duke University Medical Center, Durham, North Carolina

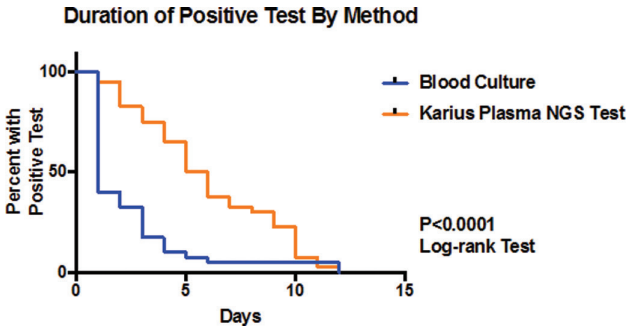
Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Blood cultures can have low sensitivity if a patient is pretreated with antibiotics. A molecular diagnostic for bloodstream infection (BSI) that can also quantitate pathogen DNA could be a useful tool in detecting and monitoring culture-negative infections.

Methods. We prospectively enrolled 75 patients (50 with culture confirmed BSI due to *Staphylococcus aureus* [n = 21] or Gram-negative bacilli [n = 29] at baseline, and 25 with negative blood cultures) to evaluate the Karius plasma next generation sequencing (NGS) test to detect BSI. Blood samples from patients with confirmed BSI were collected for the study within one day of positive blood culture and then every 2–3 days. Cell-free DNA (cfDNA) was extracted from plasma and underwent NGS in the Karius CLIA/CAP laboratory (Redwood City, CA). After removal of human sequences, remaining reads were aligned against a curated pathogen database. Organisms present at a significance-level above a predefined threshold were reported. Quantity of cfDNA for each reported pathogen was expressed as molecules per microliter (MPM).

Results. When compared with baseline blood culture, the plasma NGS test had a positive agreement of 80% (40/50) and negative agreement of 84% (21/25). Overall, serially collected samples were positive by plasma NGS testing significantly longer than blood culture (mean 6.0 days vs. 2.4 days, respectively; $P < 0.0001$. Figure). Patients with BSI were positive longer by NGS testing than blood culture for both *S. aureus* (mean 6.9 days vs. 4.0 days, respectively; $P < 0.005$) and gram-negative bacilli (mean 5.4 days vs. 1.3 days, respectively; $P < 0.001$). Pathogen cfDNA in BSI patients, quantified as MPM, declined over time during treatment. *S. aureus* MPM declined more slowly than gram-negative MPM and was significantly higher than gram-negative MPM at day 6 ($P < 0.001$).

Conclusion. The Karius plasma NGS test can directly detect pathogens in patients with BSI. Pathogen cfDNA signal in plasma remains positive longer than blood culture and combined with quantification of pathogen cfDNA, could be a useful biomarker to aid in diagnosis and monitoring of infections, particularly in those with sterile blood cultures.



Disclosures. **L. Wanda**, Karius, Inc: Collaborator and Employee, Salary; **F. Ruffin**, Karius, Inc.: Collaborator and Research Contractor, Salary; **J. Hill-Rorie**, Karius, Inc: Collaborator, Research support and Salary; **D. Hollemon**, Karius, Inc: Employee, Salary; **H. Seng**, Karius, Inc: Employee, Salary; **D. Hong**, Karius, Inc.: Employee, Salary; **T. Blauwkamp**, Karius, Inc: Employee, Salary; **M. Kertesz**, Karius, Inc: Employee, Salary; **V. Fowler Jr.**, Karius, Inc: Grant Investigator, Grant recipient Pfizer, Novartis, Galderma, Novadigm, Durata, Debiopharm, Genentech, Achaogen, Affinium, Medicines Co., Cerexa, Tetraphase, Trius, MedImmune, Bayer, Theravance, Cubist, Basilea, Affinergy, Janssen, xBiotech, Contrafect: Consultant, Consulting fee NIH, MedImmune, Cerexa/Forest/Actavis/Allergan, Pfizer, Advanced Liquid Logics, Theravance, Novartis, Cubist/Merck; Medical Biosurfaces; Locus; Affinergy; Basilea; Contrafect; Karius: Grant Investigator, Grant recipient Green Cross, Cubist, Cerexa, Durata, Theravance; Debiopharm: Consultant, Consulting fee UpToDate: Royalties, Royalties

2084. Performance of the Karius Plasma Next Generation Sequencing Test in Determining the Etiologic Diagnosis of Febrile Neutropenia: Results from a Pilot Study

Esther Benamu, MD[1]; Kiran Gajurel, MD[2]; Jill N. Anderson, BA[3]; Hon Seng, BS[4]; Desiree Hollemon, MSN, MPH[4]; David Hong, MD[4]; Timothy A. Blawkamp, PhD[5]; Mickey Kertesz, PhD[4]; Heather Ishak, MS[3]; Paul L. Bollyky, MD, PhD[3]; Bruno C. Medeiros, MD[6]; Steven Coutre, MD[6]; Jose G. Montoya, MD, FIDSA[7] and Stan Deresinski, MD, FIDSA[7]; [1]Division of Infectious Diseases and Geographic Medicine,Department of Medicine, Stanford University School of Medicine, Stanford, California, [2]Division of Infectious Diseases, Department of Medicine, University of Iowa Carver College of Medicine, Iowa City, Iowa, [3]Division of Infectious Diseases

and Geographic Medicine, Department of Infectious Diseases, Stanford University School of Medicine, Stanford, California, [4]Karius, Inc., Redwood City, California, [5]Karius Inc., Redwood City, California, [6]Division of Hematology, Department of Medicine, Stanford University School of Medicine, Stanford, California, [7]Division of Infectious Diseases and Geographic Medicine, Department of Medicine, Stanford University School of Medicine, Stanford, California

Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Blood cultures (BC) fail to detect a pathogen in most patients with neutropenic fever (NF). We examined the performance of the Karius next generation sequencing plasma test (plasma NGS) compared with that of BC in chemotherapy-induced NF.

Methods. Patients 18 years or older with absolute neutrophil count <500 cells/mm^3 anticipated for > 7 days were enrolled at the time of BC collection (T0) due to fever. Plasma samples were collected at T0 and twice weekly until neutrophil recovery or discharge. Samples were shipped to the Karius CLIA/CAP laboratory (Redwood City, CA) where cell-free plasma was prepared, DNA extracted, and NGS performed. After removing human reads, remaining sequences were aligned to a curated pathogen database. Organisms present at a significance- level above a predefined threshold were reported. T0 BC and plasma NGS results were compared, excluding organisms (eg, viruses) not recoverable by BC. Positive agreement was defined as plasma NGS identification of at least one isolate seen on BC. Plasma NGS+/BC- results underwent adjudication by 3 infectious diseases specialists. Diagnosis was Definite if microbiology confirmed NGS result within 7 days of enrollment; Probable if clinical, radiologic, and laboratory data were compatible with plasma NGS test result; and otherwise Indeterminate.

Results. The first 18 patients were evaluated. At the time of enrollment, 6 patients were on antibiotics and 3 were on antifungals. There were 4 positive BC (each monomicrobial) at T0 and all were concordant with plasma NGS. The plasma NGS test identified additional organisms in 2 of the BC+ patients with surgical abdomen. Compared with BC, plasma NGS positive agreement was 100% (4/4) with lack of agreement in 43% (6/14). All 8 NGS+/BC- cases were deemed Probable by adjudication. These included patients with single or mixed organisms in patients with enterocolitis or severe mucositis. In one sample, *Aspergillus fumigatus* was detected in a patient with new lung nodules.

Conclusion. The etiologic diagnosis of NF is frequently unknown, leading to broad antibiotics and sometimes delay of targeted treatment. Plasma NGS may provide useful data for managing NF given its ability to detect a breadth of pathogens even when patients are pretreated with antibiotics.

Disclosures. **H. Seng**, Karius, Inc: Employee, Salary; **D. Hollemon**, Karius, Inc: Employee, Salary; **D. Hong**, Karius, Inc.: Collaborator, Research support and Salary; **T. A. Blawkamp**, Karius Inc.: Board Member and Employee, Salary; **M. Kertesz**, Karius Inc.: Board Member and Employee, Salary

2085. Metagenomic Analysis reveals Importance of Anaerobes in Development and Clinical Outcome of Necrotizing Soft-tissue infections

Hannah Zhao-Fleming, BS[1]; Jeremy Wilkinson, PhD[2] and Kendra Rumbaugh, PhD[1]
[1]Department of Surgery and Burn Center of Research Excellence, Texas Tech University Health Sciences Center, Lubbock, Texas, [2]Research and Testing Laboratory, Lubbock, Texas

Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Skin and soft-tissue infections can manifest in a variety of ways, ranging from a self-resolving abscess to a rapidly spreading necrotizing soft-tissue infection (NSTI). Based on culture data, the microbiology of both infections are similar, both involving Gram-positive cocci such as *Staphylococcus* species. This begs the question – why would different patients start with seemingly similar infections and end with drastically different clinical courses? One factor is the patient's immune response, but it does not fully account for many NSTIs that occur in otherwise healthy individuals. We hypothesize that anaerobes, which are difficult to detect via culture and thus are under-detected, worsen the infection, favoring the NSTI pathology. Our objective in this study was to better understand the impact of anaerobes in NSTIs.

Methods. We enrolled adult patients that had been diagnosed either with NSTIs or abscesses. We collected samples of their infections via routine skin debridements or incision and drains, respectively. We then extracted DNA from each sample and sequenced the variable regions 1–2 of the 16S rRNA. The sequences were compared against an in house database and for species identification.

Results. From December 2011 to the present, we have collected 26 NSTI samples and 19 abscess samples. We found that a higher proportion of obligate anaerobes in the wound is correlated with increased BMI and mortality in NSTIs. The wound microbiomes of patients who died from their infections also seem to cluster together. Moreover, our preliminary data suggest that NSTIs may also have a higher proportion of obligate anaerobes and higher microbial diversity compared with abscess infections. Lastly, we noted significant disconcordance between data obtained by our institution clinical microbiology laboratory and our 16S data.

Conclusion. The presence of obligate anaerobes, traditionally difficult to detect via culture, plays a significant role in the development and worsened clinical outcome of NSTIs. Their presence may be one of the determining factors that favor the NSTI pathology over the easily-treated abscess. If true, this should lead to more aggressive and comprehensive anaerobe coverage in NSTIs, especially in culture-negative infections.

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

2086. Evaluation of a Multiplex PCR Assay with Molecular Beacon Probes to Rapidly Detect Bacterial Pathogens Directly in Bronchial Alveolar Lavage (BAL) Samples from Patients with Hospital-Acquired Pneumonia (HAP)

Kalyan D. Chavda, PhD[1]; Michael Satlin, MD, MS[2]; Liang Chen, PhD[1]; Bhakti Chavda, MS[1]; Claudia Manca, PhD[1]; Lars Westblade, PhD[3]; Stephen G Jenkins, PhD[4]; Thomas J. Walsh, MD[5] and Barry N. Kreiswirth, PhD[1]; [1]Public Health Research Institute, Rutgers New Jersey Medical School, Newark, New Jersey, [2]NewYork-Presbyterian Hospital/Weill Cornell Medical Center, New York, New York, [3]Weill Cornell Medicine, New York, New York, [4]Pathology and Laboratory Medicine, Weill Cornell Medicine, New York, New York, [5]Internal Medicine/Infectious Diseases, Weill Cornell Medicine, New York, New York

Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Bacterial pneumonia is a common complication in hospitalized patients and it is associated with high morbidity and mortality. Standard culture-based methods may take 2–3 days to identify the etiologies of HAP, leading to delays in appropriate therapy. A rapid molecular assay that could diagnose the etiology of bacterial pneumonia directly from BAL samples within a few hours could facilitate faster and more directed administration of antimicrobial therapy.

Methods. BAL samples were collected from hospitalized patients with suspected pneumonia, including ventilated patients, from December 2016 through April 2017. Genomic DNA was isolated from BAL samples using NucliSENS® easyMAG®. A panel of target-specific molecular beacon probes in a real time PCR assay (MB-PCR) was used to identify the following pathogens: universal bacterial Identification (16S rRNA), *E. coli* (*uidA*), *K. pneumoniae* (*gapA*), *S. aureus* (*spa*), *P. aeruginosa* (*rpsL*), *A. baumannii* (Ab-ITS) and the following resistance determinants: ESBLs (CTX-M, TEM and SHV), carbapenemases (NDM, VIM, IMP, OXA-48 and KPC) and *mec*A. The results of MB-PCR were then compared with quantitative culture results performed by the clinical microbiological lab.

Results. We evaluated 53 BAL samples to identify the bacterial pathogen and key resistance determinants. Thirty-one samples yielded growth of $\geq 1 \times 10^4$ CFU/mL of bacteria by quantitative culture. The bacterial identification using MB-PCR for 16S rRNA correctly identified the presence of bacteria in all 31 samples (100% sensitivity). The MB-PCR identified *P. aeruginosa* ($n = 5$), *S. aureus* ($n = 5$), *E. coli* ($n = 1$), *A. baumannii* ($n = 1$), and *K. pneumoniae* ($n = 1$) in BAL samples that yielded $\geq 1 \times 10^4$ CFU/mL of the same pathogen by culture (100% sensitivity). The MB-PCR also identified bla_{TEM}-harboring *E. coli* that grew ampicillin-resistant *E. coli* by culture. The specificity of the16S rRNA probe was 70%, as 7/53 BAL were false positive, whereas the specificity for the MB-PCR was 100% for *P. aeruginosa*, *S. aureus*, *E. coli*, and *A. baumannii*, and 98% for *K. pneumoniae*.

Conclusion. Multiplex MB-PCR assay is a rapid, sensitive and specific tool for detection of common bacterial causes of nosocomial pneumonia and important resistance determinants directly from BAL samples.

Disclosures. **M. Satlin**, Hardy Diagnostics: Investigator, Research support; **S. G. Jenkins**, Cormedix: Consultant, Consulting fee; Bayer: Consultant, Consulting feeMerck: Grant Investigator and Scientific Advisor, Research grant; **T. J. Walsh**, The Medicines Company: Consultant and Investigator, Consulting fee and Research grant Astellas: Consultant and Investigator, Consulting fee and Research grant Allergan: Consultant and Investigator, Consulting fee and Research grant Merck: Consultant and Investigator, Consulting fee and Research grant

2087. A Novel Real Time PCR Assay for the Detection of *Babesia microti* in a Highly Endemic Area Using Luminex Aries System

Alamelu Chandrasekaran, PhD[1]; Fan Zhang, MD[1]; Ansamma Joseph, PhD[1]; Maureen Bythrow, BS[1]; Reeti Khare, PhD, D(ABMM)[1,2] and Stefan Juretschko, PhD, D(ABMM)[1,2]; [1]Pathology and Laboratory Medicine, Northwell Health Laboratories, Lake Success, New York, [2]Hofstra Northwell School of Medicine, Hempstead, New York

Session: 237. Diagnostics - Novel Diagnostics
Saturday, October 7, 2017: 12:30 PM

Background. Babesiosis is a tick-borne infection of erythrocytes caused by parasites of the genus *Babesia*. In United States most of the reported cases occur in the Northeast and upper Midwestern states, New York being an endemic area. Majority of the cases in the United States is due to infection with *Babesia microti.* Most patients with babesiosis are asymptomatic or have a mild illness, but some may develop fatal illness. Current laboratory diagnosis of Babesiosis including parasitemia is by microscopic demonstration of intraerythrocytic *Babesia* parasites in blood films which requires specially trained personnel. We have developed a simple and rapid PCR assay for the detection of *B. microti* 18S rRNA gene (BMPCR) which can be used as an alternative screening assay.

Methods. BMPCR assay was developed based on Luminex Multicode technology using Luminex Aries instrument and in-house developed primers. *Babesia* positive clinical samples confirmed by NY State Department of Health and clinical samples negative for *Babesia* were used to determine accuracy. Specificity was evaluated using malaria positive samples, several bacterial isolates, selected *B. microti* strains and other *Babesia* species. Limit of Detection was determined using known copies of *B. microti* DNA. Reproducibility of the assay was assessed by testing samples on different days and runs by different analysts.

Results. Accuracy of the BMPCR assay was 100% for the 30 *Babesia* positive and 30 negative samples. All *B. microti* ATCC strains were positive by BMPCR. 95% LOD of the assay as determined by probit analysis was 1177 copies/50µl of blood. Sensitivity of the assay was higher than that of microscopic detection and specificity was 100%.