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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.

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

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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.

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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)

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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.

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

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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%.

No cross reactivity was observed with any of the malarial species tested. *Babesia* MO1, *Babesia duncani* and all bacterial isolates tested were negative by the BMPCR. Intra-run, inter-run and day to day reproducibility of the assay was 100%.

Conclusion. The *B. microti* real time PCR assay developed by Northwell Health Laboratories is rapid, sensitive, specific and reproducible. With the sample to result turnaround time of 2.5 hours and hands on time of only 5 minutes per sample, BMPCR can be used as screening assay for *B. microti* in clinical laboratories.

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

2088. A Novel Diagnostic Method for Malaria Using Loop Mediated Isothermal Amplification (LAMP) and MinION Nanopore Sequencer

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Background. Simply and accurately diagnostic tool for Malaria is required for clinical diagnosis and epidemiological survey. We have developed a novel diagnostic tool for Malaria using loop mediated isothermal amplification (LAMP) with MinION nanopore sequencer.

Methods. In this study, we have designed human *Plasmodium* parasites-specific LAMP primers targeting for the lesion of 18S rDNA gene, which were locating on the conserved sequences across all five *Plasmodium* species; *Plasmodium falciparum, P. vivax, P. ovale* (*P.o. wallikeri and P.o crutisi*), *P. knowlesi and P. malariae*, containing each species-specific sequence within F1-B1 primer pairs. The sensitivities were evaluated using 10-fold serially diluted plasmids harboring the sequences of 18S rDNA. We also applied our protocol to human blood samples collected and stored with FTA elute cards derived from 30 Malaria patients, who are clinically diagnosed as Malaria in Indonesia. Its analytical sensitivities and specificities were also evaluated while comparing the results of previously described nested PCR methods. Finally, we performed amplicon sequencing of our LAMP methods using MinION nanopore sequencer to identify each *Plasmodium* species.

Results. Our LAMP method could amplify all targeting 18S rDNA gene on constructed plasmids and its detection limits were 10 - 100 copies/reaction respectively. In clinical samples, obtained LAMP results were completely consistent with the results of nested PCR. Additionally, identifications of *Plasmodium* species based on the sequence analysis with MinION were also consistent with the sequence of each constructed plasmid and could consistently confirmed its *Plasmodium* species with the highest homology of reference *Plasmodium*parasite sequence.

Conclusion. Our innovative diagnostic technology with LAMP and MinION could become a powerful tool for identification of *Plasmodium* parasites even in resource-limited situation.

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2089. Accelerating Time to Pathogen-adapted Antibiotic Treatment through Culture-independent Antimicrobial Susceptibility Testing in Patients Suffering from Sepsis

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Background. Accurate and fast pathogen identification and consecutive antimicrobial susceptibility testing (AST) is of vital importance for patient outcome in patients suffering from sepsis.

Methods. The Accelerate Pheno™ system is a new, fully automated, culture-independent diagnostic method for both pathogen identification (ID) and antimicrobial susceptibility testing (AST). We analyzed positive blood cultures from critically ill patients with new onset of sepsis according to the new sepsis guidelines, using both conventional standard methods (VITEK, MALDI-TOF) and Accelerate Pheno™ system. ID/AST results of the Accelerate Pheno™ system were not reported to treating physicians as part of our internal evaluation process.

Results. Accelerate Pheno™ system correctly detected 74 pathogens [Gram-negative (GN) (n = 27), Gram-positive (GP) (n = 47)] straight out of 84 positive blood culture bottles. Gram-negative (GN) pathogens were identified as *E. coli* (n = 15; concordance rate 100%), *K. pneumonia* (n = 7; 71,4 %), *S. marcescens* (n = 3; 100%), *E. cloacae* (n = 2; 50%), *P. mirabilis* (n = 1; 100%) and *P. aeruginosa* (n = 1; 33%). Gram-positive pathogens were identified as CNS (n = 24; 82,6%), *S. aureus* (n = 15; 88,2%), *E. faecium* (n = 6; 100%) and *E. faecalis* (n = 2; 100%). The Accelerate Pheno™ system generated a GN-AST result in 70,4 % (19 of 27 samples) and a GP-AST result in 61,7 % (29 of 47 samples) when compared with routine AST. Growth control, analysis and mechanical failure led to reduced results in comparison to conventional ID/AST. Accelerate Pheno™ delivered correct MIC-results for most of the panel antibiotics [e.g., meropenem: 83,3%, gentamicin: 88,9%, ertapenem: 100%].

Conclusion. The use of the Accelerate Pheno™ system significantly improved time-to-ID/AST and would have led to a reduced time-to-treatment in patients suffering from sepsis if results would have been reported. The system currently has some weakness in the detection of polymicrobial and streptococcal infections but due to the short hands-on-time, culture-independence and fast generation of results, it represents a promising new diagnostic method for the consecutive antibiotic treatment of septic patients.

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2090. T-Cell Immunity Panel Measures CMV-Specific CD4 and CD8 T-Cell Responses

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Background. Infection and disease from human cytomegalovirus (CMV) is a major complicating factor for both solid organ and hematopoietic stem cell transplant recipients. Antiviral therapy is often used to control CMV infections, but presents problems of toxicity, antiviral resistance and excessive costs. Currently, treating physicians are limited in the information and data available to assess a patient's ability to control a potential CMV infection post-transplant. Recent studies have shown that measuring a patient's CMV specific T cell mediated immunity may provide valuable information to physicians for monitoring CMV infection/disease in transplant patients and may aid in determining which patients need antiviral therapy.

Methods. For this purpose, a flow cytometry assay was developed to determine the percentages of CD4+ and CD8+ T cells that respond to stimulation with CMV antigen. Assessment of CMV specific response is based upon the cellular activation surface marker CD69 in conjunction with IFNg, TNFα, and IL-2 cytokine production. Three CMV antigens were used to assess patient immunity; a whole viral lysate, a peptide pool of pp65, and a peptide pool of IE-1.

Results. Our data indicate that CD8 T cells respond primarily to the pp65 and/or IE-1 peptide pools while the CD4 T cells respond primarily to the viral lysate. Detection of both CD4 and CD8 responding populations at levels above background, ≥ 0.2% of the parent population, indicates that a patient's immune system has previously been exposed to CMV. Validation of 23 CMV seropositive samples demonstrated immune responses for all 23 samples above 0.2% for at least one of the three intra-cellular cytokines and at least one of the three CMV antigens. Validation of five CMV seronegative samples demonstrated immune responses below 0.2% (when excluding underlying, unrelated immune responses). Included for each sample is a positive (Staphylococcal Enterotoxin type B) control to assess patient's overall ability to mount an immune response and negative (media) control to capture the presence of an underlying immune response.

Conclusion. This assay evaluates a patient's pre-existing CMV specific T cell immunity and their global T cell function.

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2091. Application of Laser Light Scattering Technology in Rapid Diagnosis of Urinary Tract Infections and Antimicrobial Susceptibility Testing in a Tertiary Children's Hospital

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Background. Timely and accurate microbiology testing is crucial in the diagnosis and management of urinary tract infections (UTIs). The ability to rapidly screen for potential UTIs can lead to early rule out and judicious use of antimicrobial therapy. This study examines the application of laser scattering for bacterial detection and antimicrobial susceptibility testing (AST) directly from urine.

Methods. Residual urine samples collected for routine culture were tested using the BacterioScan™ 216Dx™ UTI System and 216R AST System. Continuous collection of light refraction patterns generated growth curve that was used to determine whether the sample was likely positive or negative for bacteria. Further curve analysis ruled out mixed flora at lower concentrations, and "qualified" samples were identified directly on MALDI-TOF MS. AST for ampicillin, cefazolin, ceftriaxone and ciprofloxacin was performed concurrently on the instrument. Samples were incubated for up to 16 hours with results available as early as 2 hours.