was performed to evaluate the expected impact of the BCID-GP panel on the time to organism identification, AST results, and optimization of antimicrobial therapy.

Results. A total of 80 patients were included in the final analysis (Table 1). *S. epidermidis* was the most common bacteria identified, followed by *S. aureus*, and other coagulase-negative staphylococci. Thirty-nine patients with staphylococci (48.8%) had the *mecA* gene detected and 2 patients with *E. faecium* had the *vanA* gene detected. The BCID-GP panel saved a mean of 24.4 hours (h) to identification and 48.3h to susceptibility testing compared to standard methods across all patients. In 38 patients (47.5%), the BCID-GP panel result could have enabled an earlier change in antibiotic therapy. Table 2 highlights opportunities to optimize antimicrobial therapy 53.4h earlier for 16 (20%) patients with organisms expressing AMR genes, 29.2h earlier for 8 (10%) patients infected with organisms, such as streptococci, with very low resistance rates, and to stop antimicrobial therapy 42.9h earlier for 14 (17.5%) patients with contaminated blood cultures.

Table 1. Patient demographics and co-morbidities.

Variable	Total (N=80)
Age (Mean)	54.1
Male – No. (%)	43 (53.8)
Race/Ethnicity – No. (%)	
• White	43 (53.8)
• Black	35 (43.8)
• Hispanic/Latino	2 (2.5)
Immunosuppression – No. (%)	
• Solid malignancy	6 (7.5)
• Hematologic malignancy	4 (5)
• SOT	7 (8.9)
• HSCT	3 (3.8)
• Other	4 (5)
Diabetes – No. (%)	32 (40)
Cardiovascular disease – No. (%)	26 (32.5)
Chronic lung disease – No. (%)	11 (13.8)
CKD – No. (%)	12 (15)
ESRD – No. (%)	7 (8.8)
Cirrhosis – No. (%)	3 (3.8)
IVDU – No. (%)	1 (1.3)
Mechanical ventilation – No. (%)	15 (18.8)
ECMO – No. (%)	1 (1.3)
Trauma at time of admission – No. (%)	8 (10)
Burn at time of admission – No. (%)	1 (1.3)
Pitt Bacteremia Score (Mean)	2.46

Table 2. Time of antibiotic change and time saved.

Potential change to antibiotics	No. of patients	Mean time saved (hours)
Stop for earlier ID of contaminant species	14	42.9
Change GP antibiotic based on presence or absence of resistance gene	16	53.4
Change GP antibiotic based on earlier ID of *Streptococcus*	8	29.2

Conclusion. The BCID-GP panel could have enabled earlier optimization or stopping of antibiotics in many patients with significant time savings compared to standard laboratory methods.

Disclosures. **Todd P. McCarty, MD**, **Cidara** (Grant/Research Support)**GenMark** (Grant/Research Support, Other Financial or Material Support, Honoraria for Research Presentation)**T2 Biosystems** (Consultant) **Sixto M. Leal, Jr., MD, PhD**, **Abnova** (Grant/Research Support)**AltImmune** (Grant/Research Support)**Amplyx Pharmaceuticals** (Grant/Research Support)**Astellas Pharmaceuticals** (Grant/Research Support)**CNINE Dx** (Grant/Research Support)**GenMark Diagnostics** (Grant/Research Support, Other Financial or Material Support, Honoraria-Research Presentation)**IHMA** (Grant/Research Support)**IMMY Dx** (Grant/Research Support)**JMI/Sentry** (Grant/Research Support)**mFluiDx Dx** (Grant/Research Support)**SpeeDx Dx** (Grant/Research Support)**Tetraphase Pharmaceuticals** (Grant/Research Support)

1028. Performance and Patient Acceptability Evaluation of the Chembio DPP® HIV-Syphilis Assay in an Emergency Department

Kendall N. Maliszewski[1]; Yu-Hsiang Hsieh, PhD[1]; Deanna Myer, BS[1]; Danielle A. Perez, MS[1]; Charlotte A. Gaydos, MS, MPH, DrPH[1]; Yukari C. Manabe, MD[2]; Erin Ricketts, MSPH[1]; Richard E. Rothman, PhD, MD[3]; [1]Johns Hopkins University, Baltimore, Maryland; [2]Johns Hopkins, Baltimore, MD; [3]Johns Hopkins University School of Medicine, Baltimore, MD

Session: P-58. New Approaches to Diagnostics

Background. Emergency departments (EDs) serve as sentinel settings for diagnosing sexually transmitted infections (STIs), including HIV and syphilis. We aimed to assess performance and patient acceptability of a point-of-care (POC) test, the Chembio Dual Path Platform (DPP®) HIV-Syphilis Assay, in an urban ED in Baltimore.

Methods. 170 patients were enrolled via convenience sampling from Oct 2019 – March 2020 and Jan 2021 – June 2021. Patients eligible were < 70 yrs, men who have sex with men, pregnant without care, had STI concerns, or history of drug use. Subjects received standard of care (SOC) HIV and syphilis testing under institutional laboratory algorithms. Subjects were then tested with the finger-stick POC test and completed a survey, both before and after the POC test to assess subjects' attitudes about the POC test.

Results. Comparing the SOC and POC results, 165/170 (97.1%) were test concordant. 3 syphilis POC results were false negative, but reported successful treatment over 10 years prior to enrollment (treponemal antibody remains after treatment). 1 HIV result was false negative and 1 was false positive. Overall the sensitivity and specificity of the HIV POC test were 96.8% (95%CI: 83.3%, 99.9%) and 99.3% (95% CI: 96.1%, 100%), and for syphilis were 85.7% (95%Cl: 63.7%, 97.0%) or 100% (95%CI: 81.5%, 100%), if excluding 3 persons having been successfully treated, and 100% (95% CI: 97.6%, 100%) respectively.

The pre-test survey found 67% and 77% of participants were comfortable with a finger-stick test and agreed the POC test result would be as good as the SOC test result, which increased to 96% and 86% in the post-test, respectively, ($p < 0.05$). At post-test, 86% reported they would feel confident to perform this test at home and 81% would use it at least once per year if it were available. 97% reported they were more likely to seek treatment if receiving a positive result during their ED visit and 91% reported it would reduce their stress/anxiety if receiving a negative test result in the ED.

Conclusion. Our findings demonstrated satisfactory performance and high patient acceptability of the Chembio DPP® HIV-Syphilis Assay. Given the test is FDA approved, implementation studies are needed to determine whether adoption of this POC test will benefit patients and be consistent with ED workflows.

Disclosures. **Richard E. Rothman, PhD, MD**, **Chem bio** (Grant/Research Support)

1029. Torus Synestia Nucleic Acid Analysis Platform for Fast, High Multiplex Analysis of Nucleic Acids With Single-Nucleotide Discrimination Level

Tyler Rockwood, n/a[1]; Andrew Sullivan, n/a[1]; Jahnavi Gandhi, n/a[1]; Sarah Gruszka, n/a[1]; Brian Turczyk, PhD[1]; Dmitriy Khodakov, PhD[1]; [1]TORUS BIOSYSTEMS, INC., Cambridge, Massachusetts

Session: P-58. New Approaches to Diagnostics

Background. Nucleic acid amplification testing (NAAT) is an essential tool both for biomedical research and for clinical molecular diagnostics. Currently, there are multiple NAAT platforms available, each offering certain performance and utility advantages and disadvantages as compared to each other. Next generation NAAT platforms aim to deliver increased target detection sensitivity and specificity, low limits of target detection, quantitative high multiplex target capacity, rapid time to results, and simple sample-to-answer workflow.

Methods. Here we describe the Torus Synestia System, a NAAT platform capable of rapid, highly multiplexed amplification and detection of both DNA and RNA targets. The platform comprises a small, portable (~ 2kg) amplification and detection device and a disposable single-use cartridge housing a PCR amplification chamber with an integrated label-free microarray for real-time data acquisition and interpretation. The platform offers a 30-min turnaround time with a detection limit of 10 DNA/RNA molecules per assay and single nucleotide discrimination.

Results. We demonstrate the Synestia System performance and utility with three distinct molecular applications: 1) detection of 20 genetic loci and 30 single nucleotide polymorphisms in human genomic DNA; 2) detection and genotyping of 43 unique bacterial species associated with human urinary tract infections; and 3) detection and profiling human respiratory viral pathogens including SARS-CoV-1/2, seasonal coronaviruses, Influenza A/B, and human respiratory syncytial viruses. In addition, the single-nucleotide specificity of our label-free microarray probes allowed for robust identification and discrimination of newly emerging SARS-CoV-2 lineages, such as B.1.1.7 (a.k.a. UK), B.1.351 (a.k.a. South African), P.1 (a.k.a. Brazilian), and B.1.617 (a.k.a. Indian).

Conclusion. The Torus Synestia System has broad applicability in both clinical and research environments. We are confident that the Torus Synestia System will revolutionize syndromic diagnostics at the point of care (PoC) and lead to improved response times during future epidemic and pandemic pathogen outbreaks.

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

1030. Chasing the Long Tail of Infectious Diseases: Detecting *Capnocytophaga canimorsus* and *Pasteurella multocida* Infections with A Plasma-based Microbial Cell-Free DNA Next Generation Sequencing Test

Nicholas R. Degner, MD, MPH, MS[1]; Ricardo Galvan-Castillo, MD[1]; Jose Alexander, MD, D(ABMM), FCCM, CIC, SM, MB(ASCP), BCMAS[2]; Aparna Arun, MD[2]; Christiaan R. de Vries, MD, PhD[3]; Ann Macintyre, DO[3]; Bradley Perkins, MD[2]; Asim A. Ahmed, MD[4]; Matthew Smollin, PharmD[2]; [1]Karius Inc., San Francisco, California; [2]Karius, Inc., Orlando, Florida; [3]Karius, Redwood City, California; [4]Karius, Inc, Redwood City, CA

Session: P-58. New Approaches to Diagnostics

Background. *Capnocytophaga canimorsus* (*Cc*) and *Pasteurella multocida* (*Pm*) are gram negative bacterial commensal pathogens typically from dogs or cats that can cause severe infection in humans when spread through licks, scratches or bites. The diagnosis of these infections can be limited by: (1) their fastidious nature and difficulty to culture; (2) the nonspecific manifestations of the infections; and (3) the unreliability of dog or cat exposure history. Open-ended microbial cell free DNA (mcfDNA) next-generation sequencing (NGS) offers a potential solution to overcome these limitations.

Methods. The Karius Test™ (KT) developed and validated in Karius's CLIA certified/CAP accredited lab in Redwood City, CA detects mcfDNA in plasma. After mcfDNA is extracted and NGS performed, human reads are removed, and remaining sequences are aligned to a curated database of > 1500 organisms. McfDNA from organisms present above a statistical threshold are reported and quantified in molecules/µL (MPM). KT detections of *Cc* and *Pm* were reviewed from August 2017 - present; clinical information was obtained with test requisition or consultation upon result reporting.

Results. KT detected 5 cases of *Cc* (25,039 MPM +/- 41,062) and 8 cases of *Pm* (33,264 MPM +/- 69,301) (Table 1). All detections of *Cc* were in adults (60% male) and included 2 cases of culture-negative endocarditis (one with known liver disease) and one case of sepsis with diffuse rash. *Pm* detections occurred in 6 adults and 2 children (75% male) and included 2 cases of culture-negative endocarditis, and single cases each of endovascular graft infection, pneumonia, fever of unknown origin, and a cranial dog bite complicated by an abscess. Two patients had immunocompromising conditions including neuroblastoma and aplastic anemia.

Table 1. *Capnocytophaga canimorsus* and *Pasteurella multocida* detections by the Karius Test™

Case	Age	Sex	IC	Liver disease	Exposure	Clinical Context	Karius Test Result	MPM (RI<10)
1	Adult	M	No	Yes	Dog	Culture-negative native valve endocarditis	*Capnocytophaga canimorsus*	86,130
2	Adult	M	No	No	No	Culture-negative prosthetic valve endocarditis	*Capnocytophaga canimorsus*	12,055
3	Adult	F	No	No	Dog	Sepsis with diffuse rash	*Capnocytophaga canimorsus*	Not available*
4	Adult	F	Unknown	Unknown	Unknown	Not obtained	*Capnocytophaga canimorsus*	531
5	Adult	M	Unknown	Unknown	Unknown	Not obtained	*Capnocytophaga canimorsus*	1,438
6	Adult	M	No	No	No	Endovascular graft infection	*Pasteurella multocida*	195,385
7	Adult	M	Yes	No	Farm	Fever of Unknown Origin	*Pasteurella multocida*	99
8	Pediatric	M	Yes	No	No	Pneumonia	*Pasteurella multocida*	26
9	Adult	F	No	Yes	Cat	Culture-negative prosthetic valve endocarditis	*Pasteurella multocida*	4,140
10	Adult	M	No	No	No	Culture-negative native valve endocarditis	*Pasteurella multocida*	774
11	Pediatric	M	No	No	Dog	Dog bite to head complicated by abscess	*Pasteurella multocida*	27
12	Adult	M	Unknown	Unknown	Unknown	Not obtained	*Pasteurella multocida*	65,401
13	Adult	F	Unknown	Unknown	Unknown	Not obtained	*Pasteurella multocida*	261

MPM: Molecules per microliter; RI: Reference interval which denotes the 97.5th %tile of the MPM for each microbe in a cohort of 684 healthy subjects; IC: Immunocompromised
*Sample did not meet minimum sequencing depth requirements for quantification

Conclusion. Unbiased, plasma-based mcfDNA NGS provides a rapid, non-invasive test to diagnose diverse clinical infections by *Cc* and *Pm*. These cases highlight the potential of the KT to diagnose infections caused by fastidious/unculturable pathogens with non-specific clinical manifestations and broad differential diagnoses.

Disclosures. **Nicholas R. Degner, MD, MPH, MS**, **Karius Inc.** (Employee, Shareholder) **Ricardo Galvan-Castillo, MD**, **Karius Inc.** (Employee, Shareholder) **Jose Alexander, MD, D(ABMM), FCCM, CIC, SM, MB(ASCP), BCMAS**, **Karius** (Employee) **Aparna Arun, MD**, **Karius** (Employee) **Ann Macintyre, DO**, **Karius, Inc.** (Employee) **Bradley Perkins, MD**, **Karius, Inc.** (Employee) **Asim A. Ahmed, MD**, **Karius, Inc.** (Employee) **Matthew Smollin, PharmD**, **Karius, Inc.** (Employee)

1031. Utility of Broad-Range Polymerase Chain Reaction Sequencing for Infectious Diseases Clinical Decision Making: A Pediatric Center Experience

Caitlin Naureckas Li, MD[1]; Mari M. Nakamura, MD, MPH[2]; [1]Boston Children's Hospital, Harvard Medical School, Boston, Massachusetts; [2]Boston Children's Hospital, Harvard medical school, Jamaica Plain, MA

Session: P-58. New Approaches to Diagnostics

Background. Broad-range polymerase chain reaction (PCR) sequencing is a promising tool for diagnosis of infectious conditions when traditional microbiologic strategies fail to identify a pathogen. Data on the optimal clinical scenarios in which to use this tool are limited.

Methods. We assessed the rate of organism identification from broad-range PCR testing sent from our quaternary care children's hospital between March 2017 and June 2020. We completed a retrospective chart review to evaluate patients' baseline demographic and clinical features as well as clinical significance of results (defined as influencing antimicrobial management) by specimen type.

Results. Among 184 total samples, 111 (60%) were obtained from immunocompromised patients. The median age of patients at the time of sample collection was 11.4 years (IQR 6.5-16.0). 128/181 (71%) samples were from patients known to be on ≥ 1 antimicrobial, including prophylaxis, in the 24 hours prior to sample collection. 52/184 (28%) patients ultimately had an infectious disease diagnosed by another testing modality. The most common PCR sample types were bronchoalveolar lavage (BAL) fluid (35), lung tissue (20), and bone (14). An organism was identified from 41 (22%) samples, but positive results for only 8 samples (4%) led to a change in antimicrobial management: addition of agents in 4 cases, cessation of agents in 2, and transition from one agent to another in 2. Negative results for 3 (2%) samples led to discontinuation of antimicrobials. Organisms were identified from 11 (31%) BAL samples, of which only 2 (6%) were judged to be clinically significant. No results from lung tissue, CSF (11), skin biopsies (6), or joint fluid (4) affected antimicrobial management.

	Organism identified, impact on antimicrobial management	Organism identified, no impact on antimicrobial management	No organism identified
Receipt of antimicrobials during 24 hours prior to sample collection, n (%)[a]	6 (4.7%)	24 (18.8%)	98 (76.6%)
Infectious disease diagnosed by other modality, n (%)	2 (3.8%)	12 (23.1%)	38 (73.1%)
Sample Type, n (%)[b]			
Pleural fluid	1 (14.3%)	3 (42.9%)	3 (42.9%)
Cardiac Hardware/ Cardiac Tissue	1 (9.1%)	1 (9.1%)	9 (81.8%)
Abscess	1 (8.3%)	4 (33.3%)	7 (58.3%)
Lymph Node	1 (7.7%)	1 (7.7%)	11 (84.6%)
BAL	2 (5.7%)	14 (40.0%)	19 (54.3%)
Lung	0 (0%)	1 (5.0%)	19 (95.0%)
Bone	0 (0%)	1 (7.1%)	13 (92.9%)
CSF	0 (0%)	1 (9.1%)	10 (90.9%)
Liver Tissue	0 (0%)	1 (11.1%)	8 (88.9%)
Other	1(1.9%)	7 (13.5%)	44 (84.6%)

a. Three samples were obtained outside of our institution, so data are unavailable on whether the patient was on antimicrobials at the time testing was sent
b. For one sample sent from explanted cardiac hardware, one from bone, and one from liver tissue, antibiotics were stopped after BRPCR did not identify an organism

Conclusion. We found that only 6% of broad-range PCR results influenced antimicrobial management in a diverse pediatric cohort. Our findings suggest that many positive results, especially in BAL fluid, do not lead to changes in antimicrobial management. Additional work is necessary to characterize the ideal clinical scenarios in which broad-range PCR should be used as over a quarter of patients had a causative infectious disease identified by another modality.

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

1032. Evaluation of a Multiplex Rapid Diagnostic Panel in Respiratory Specimens from Critically Ill Patients with Hospital-Acquired Pneumonia

Bradley J. Erich, PharmD[1]; Abdullah Kilic, MD[2]; Elizabeth Palavecino, MD[3]; John Williamson, PharmD[3]; James Johnson, PharmD[3]; Chris Ohl, MD[4]; Vera Luther, MD[4]; Vera Luther, MD[4]; James Beardsley, PharmD[3]; [1]The University of Kansas Health System, Kansas City, Kansas; [2]Wake Forest Baptist Health, Winston-Salem, North Carolina; [3]Wake Forest Baptist Health System, Winston Salem, North Carolina; [4]Wake Forest School of Medicine, Winston Salem, NC

Session: P-58. New Approaches to Diagnostics

Background. Rapid diagnostic tests can be a valuable aide in clinical decision-making but often cost more than traditional cultures. Prior to its implementation at our institution, we sought to evaluate the potential clinical and financial impact of using the FilmArray® Pneumonia Panel® (FP panel) in patients with hospital-acquired pneumonia (HAP).

Methods. This was a retrospective, observational, comparative study conducted at an 885-bed academic medical center. Respiratory samples obtained by bronchoalveolar lavage or tracheal aspiration from adult intensive care unit (ICU) patients with a diagnosis of HAP from Nov 2019 – Feb 2020 were tested by the FP panel in addition to routine cultures. Medical records were reviewed to determine potential changes in antimicrobial therapy if FP panel results were known by the treatment team in real time. A cost analysis was also performed incorporating the cost of the FP panel and the savings associated with the potential avoidance of antibiotics and other rapid diagnostic tests normalized per patient.

Results. 56 patients met study criteria. FP panel results could have prompted a change in therapy in 36 (64.3%) patients, with a mean reduction in time to optimized therapy of approximately 51 hours. The panel identified 3 cases where the causative pathogen was not treated by empiric therapy and 34 opportunities for antibiotic de-escalation, the most common being the discontinuation of empiric vancomycin. 36 patients had been tested with a Respiratory Virus Panel, which could have been avoided if the FP panel was used. The potential therapy impact based on specific ICU and respiratory culture results is summarized in Table 1. The cost analysis calculated an additional cost of $10 per patient associated with using the FP panel.

Table 1. Potential Changes in Therapy Based on Patient Location and Culture Result

Location	Potential Therapy Change, n (%)
Medical ICU	**13/24 (54.2)**
Positive culture	11/20 (55)
Negative culture	2/4 (50)
Surgical ICU	**12/20 (60)**
Positive culture	9/15 (60)
Negative culture	3/5 (60)
Trauma ICU	**11/12 (91.7)**
Positive culture	6/7 (85.7)
Negative culture	5/5 (100)

Conclusion. The FP panel could have prompted a change in therapy in about two-thirds of patients studied. Its potential benefits include quicker time to optimized therapy, reduced exposure to and cost of broad-spectrum antimicrobials, and reduced cost of other rapid diagnostic tests.

Disclosures. **James Johnson, PharmD**, **FLGT** (Shareholder) **Vera Luther, MD**, Nothing to disclose