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 48.3 h 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 <i>Streptococcus</i>	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

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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%CI: 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/a¹; Andrew Sullivan, n/a¹; Jahnavi Gandhi, n/a¹; Sarah Gruszka, n/a¹; Brian Turczyk, PhD¹; Dmitriy Khodakov, PhD¹; ¹TORUS

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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

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