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Background. To prevent the spread of drug-resistant bacteria, a rapid and accurate antimicrobial susceptibility test (AST) is necessary. Recently, morphokinetic microscopy approaches have been reported as a rapid AST method. However, these still require several hours to obtain a minimum inhibitory concentration (MIC). Adenosine triphosphate (ATP) luminescence has also been reported as a rapid AST method that can detect bacterial growth more rapidly than morphokinetic approaches, since ATP in bacteria increases prior to bacterial division. In this study, we designed a new machine learning-based algorithm that predicts MIC rapidly, using a dataset that contains ATP luminescence patterns and conventional MICs determined by turbidity. Essential agreement (EA) rates between rapid and conventional MIC were then evaluated.

Methods. Sixty-three strains of *E. coli* (ATCC 25922 and clinical isolates from Toyama University Hospital) were tested. Bacterial suspensions were diluted 500-fold in Mueller–Hinton broth from 0.5 McF solutions, and the final concentration of bacteria was 3×10^5 CFU/mL. The suspensions were dispensed into a 96-well microplate, which had 12 antimicrobials in two-fold dilution series, and the microplate was incubated at 35°C. At each measurement time point, the amount of ATP in a 10 µL aliquot from each well was evaluated by our original measurement system, which can sensitively detect ATP luminescence equivalent to a single bacterium. After 22 hours, MIC was determined conventionally by measuring turbidity. A rapid MIC for each bacterium was estimated by the algorithm based on the dataset consisting of the rest of the 62 strains (leave-one-out cross validation).

Results. Table 1 shows the EA rate for the 12 antimicrobials; EA rates > 90% were achieved for 7 antimicrobials in 2 hours and for 12 antimicrobials in 3 hours. In 6 hours, an average EA rate > 97% was achieved.

Conclusion. Using the dataset, our new machine learning-based algorithm predicted MIC rapidly within 2 hours with an EA rate > 90% for 7 antimicrobials. The rapid AST detected by the ATP luminescence method will contribute toward both appropriate antimicrobial treatment and reduction in medication and admission charges. In the future, other species of bacteria will be evaluated by our ATP method.

Table 1 EA* rate (%) by ATP luminescence and machine learning

	ABPC	P / T	CAZ	CTX	CFPM	CPFX	LVFX	MINO	AMK	AZT	MEPM	IPM	Average
6 Hours	100	95.2	100	96.8	95.2	95.2	100	100	93.7	100	100	98.4	97.9
4 Hours	100	95.2	96.8	96.8	95.2	95.2	100	96.8	93.7	98.4	100	98.4	97.2
3 Hours	100	92.1	95.2	98.4	95.2	95.2	98.4	93.7	95.2	95.2	100	98.4	96.4
2 Hours	95.2	79.4	87.3	77.8	95.2	95.2	98.4	84.1	95.2	76.2	100	96.8	90.1

Abbreviations: ABPC: Ampicillin, P/T: Piperacillin/Tazobactam, CAZ: Ceftazidime, CTX: Cefotaxime, CFPM: Cefepime, CPFX: Ciprofloxacin, LVFX: Levofloxacin, MINO: Minocycline, AMK: Amikacin, AZT: Aztreonam, MEPM: Meropenem, IPM: Imipenem
***EA (Essential Agreement): Agreement within ±1 two-fold dilution of conventional MIC**

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

2137. Impact of Accelerate Pheno™ Rapid Blood Culture Detection System with Real-time Notification vs. Standard Antibiotic Stewardship on Clinical Outcomes in Bacteremic Patients

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Background. Accelerate Pheno™ blood culture detection system (AXDX) provides identification (ID) and antimicrobial susceptibility testing (AST) within 8 hours of growth in blood culture. We previously reported length of stay (LOS), time to optimal therapy (TTOT), and antibiotic days of therapy (DOT) decrease following AXDX implementation alongside an active antimicrobial stewardship program (ASP). It is unclear whether real-time notification (RTN) of results further improves these variables.

Methods. A single-center, quasi-experimental before/after study of adult bacteremic inpatients was performed after implementation of AXDX. A 2017 historical cohort was compared with two 2018 intervention cohorts. Intervention-1: AXDX performed 24/7 with results reviewed by providers or ASP as part of their normal workflow. Intervention 2: AXDX performed 24/7 with RTN to ASP 7 days per week 9a-5p and overnight results called to ASP at 9a. Interventions 1 and 2 were utilized on an alternating weekly basis during the study (February 2018–September 2018). Historical ID/AST were performed using VITEK® MS and VITEK®2. Exclusion criteria included polymicrobial or off-panel isolates, prior positive culture, and patients not admitted at the time of AST. Clinical outcomes were compared with Wilcoxon rank-sum and χ^2 analysis.

Results. 540 (83%) of 650 positive cultures performed on AXDX had on-panel organisms. 308 (57%) of these cultures and 188 (77%) of 244 reviewed historical cultures met inclusion criteria. Baseline illness severity and identified pathogens were similar between cohorts. Clinical outcomes and antimicrobial DOT are reported in Tables 1 and 2.

Conclusion. Following our implementation of AXDX, clinical outcomes including LOS, TTOT, total DOT, BGN DOT, and frequency of achieving optimal therapy were significantly improved compared with a historical cohort. Addition of RTN for AXDX results in the setting of an already active ASP did not further improve these metrics. However, compared with historical arm, AXDX with RTN did significantly impact specific subsets of antibiotic use while AXDX alone did not. This may be due to earlier vancomycin de-escalation. These results support the benefit of integration of AXDX into healthcare systems with an active ASP even without the resources to include real-time notification.

Table 1: Clinical Outcomes comparing historical, intervention-1, and intervention-2 arms

Clinical Outcomes	Historical N = 188	Intervention-1 N = 155	Intervention-2 N= 153	Historical vs Intervention-1 P value	Historical vs Intervention-2 P value	Intervention-1 vs Intervention-2 P value
LOS, days; mean (±SD)	11.89 (11.0)	9.54 (9.8)	10.08 (11.0)	**<0.01***	**<0.01***	0.68
ICU LOS, days; mean (±SD)	5.17 (6.2)	5.20 (5.9)	5.55 (8.82)	0.79	0.99	0.79
TTOT, days; mean (±SD)	2.69 (1.8)	1.58 (1.5)	1.48 (1.3)	**<0.01***	**<0.01***	0.51
Optimal Tx Achieved, n (%)	159 (84.6)	145 (93.6)	146 (95.4)	**<0.01***	**<0.01***	0.47

LOS: length of stay; ICU LOS: intensive care unit length of stay; TTOT: time to optimal therapy; Tx: treatment; Optimal Tx Achieved: directed therapy based on organism ID and AST; SD: standard deviation; *statistical significance (p value ≤0.05)

Table 2: Antimicrobial use comparing historical, intervention-1, and intervention-2 arms

Antimicrobial Use	Historical N = 188	Intervention-1 N = 155	Intervention-2 N= 153	Historical vs Intervention-1 P value	Historical vs Intervention-2 P value	Intervention-1 vs Intervention-2 P value
Total DOT, days; mean (±SD)	8.83 (6.8)	7.23 (5.6)	7.90 (6.6)	**<0.01***	**0.04***	0.47
BGP DOT, days; mean (±SD)	4.85 (5.1)	4.22 (4.6)	3.88 (4.7)	0.12	**0.02***	0.80
BGN DOT, days; mean (±SD)	6.15 (7.6)	4.54 (5.1)	4.69 (6.8)	**0.01***	**<0.01***	0.83
NBL DOT, days; mean (±SD)	2.05 (3.3)	2.23 (3.8)	2.99 (4.6)	0.57	**0.02***	0.07

DOT: days of therapy; BGP: broad gram-positive (vancomycin, daptomycin, linezolid); BGN: broad gram-negative (cefepime, piperacillin/tazobactam, levofloxacin, ciprofloxacin, meropenem, ertapenem, amikacin, tobramycin, gentamicin); NBL: narrow beta lactams (ampicillin, ampicillin/sulbactam, cefazolin, ceftriaxone); SD: standard deviation; *statistical significance (p value ≤0.05)

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

2138. Follow-up Investigation of Antibody Titers and Diagnostic Antibody Cut-Off Values in Scrub Typhus Patients in Korea

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Background. Scrub typhus is a mite-borne infectious disease caused by *Orientia tsutsugamushi*. There have been few follow-up studies assessing antibody titers using serologic tests from various commercial labs.

Methods. A prospective investigation to assess antibody titers of scrub typhus patients and seroprevalence for health checkup individuals were evaluated. The antibody titers of former patients diagnosed with scrub typhus at least 1 year and a maximum of 13 years were also investigated. The following tests were performed simultaneously: (i) immunofluorescence antibody assays (IFAs) that detect immunoglobulin(Ig) M and IgG, (ii) IFA that detects total Ig by a commercial lab, (iii) antibody tests using two commercially available kits.

Results. In prospective analyses with cutoff values set to ≥1:16 for IgM, ≥1:256 for IgG based on the KCDC's criteria, and ≥1:40 for total Ig. The antibody positive rates of 102 confirmed scrub typhus patients were 44%, 35.3%, and 57.6%, respectively, in the first week after symptom onset. Among 91 former patients recovered, the follow-up IgM, IgG, and total Ig positivity rates were 38.5% (35/91), 22% (20/91), and 76.9% (70/91), respectively. In overall cohort of 216 health checkup subjects, 4.2% (9/216) IgM and 0% (0/216) IgG seroprevalence was observed.

Conclusion. The IFA from KCDC and commercial lab, and rapid commercial kits cannot differentiate between former patients recovered from scrub typhus and current scrub typhus. In Korea and other countries where low antibody cut-off titer values have been used as criteria for diagnosing and reporting scrub typhus, upward adjustments of cut-off values may be necessary.

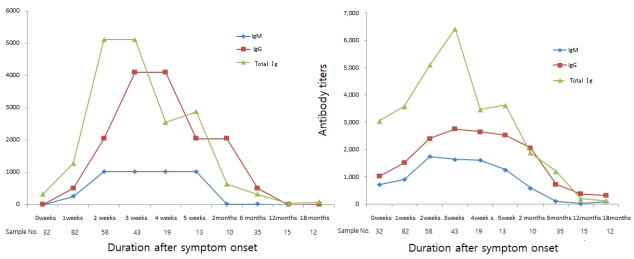

Table 1. Prospective follow-up investigation of antibody titers in patients with confirmed scrub typhus: rapid diagnostic testing by immunochromatography, as performed using commercial C company commercial kit and D company commercial kit

	6 months						12 months						18 months					
	C company kit				D company kit		C company kit				D company kit		C company kit				D company kit	
	IgM		IgG				IgM		IgG				IgM		IgG			
	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)	N	CP(%)
–	24	68.6	29	82.9	12	34.3	16	100	16	100	29	82.9	12	100	11	91.7	4	33.3
+	11	31.4	6	17.1	23	65.7	0	**0**	0	**0**	6	17.1	0	0	1	8.3	8	66.7
Total	35		35		35		16		16		35		12		12		12	

* CP=cumulative percentage

Table 2. Antibody titers in patients who had recovered from scrub typhus: follow-up investigations at several time points, as determined using the D and C company (IgG/M) kits

	1 year		2 years		3 years		4 years		5 years		6 years		7 years		8 years		9 years		10 years		11 years		12 years		13 years		Total
	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	C company IgM	D IgG	
–	16	16	2	8	7	2	18	18	10	3	3	2	7	7	3	8	8	7	5	5	5	3	3	3	6	2	3	6	6	6	6	6	3	2	2	1	3	3	2
+	0	0	14	0	1	6	0	0	8	0	0	1	0	0	4	0	0	1	0	0	0	0	0	0	0	14	3	0	0	0	0	0	3	0	0	1	0	0	1
Total	16		8		18		3		7		8		5		3		6		6		6		2		3		91

C> -: negative, +: positive, D: D company Kit

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

2139. *Rickettsia typhi* Detection in Clinical Infections by the Karius Test, a Plasma Microbial Cell-free DNA Next-Generation Sequencing Test

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Background. *Rickettsia typhi* typically causes a nonspecific syndrome characterized by fever, rash, and headache but can rarely progress to severe disease. *R. typhi* is transmitted by the rat flea and there has been an increased incidence in Houston, TX. Establishing the diagnosis can be challenging and is often made by serological studies. Prompt therapy with doxycycline is important especially in severe disease.

Methods. Karius Test results from the prior 2 years (Redwood City, CA) were reviewed for detections of *R. typhi*. The Karius Test is a CLIA-certified/CAP-accredited next-generation sequencing (NGS) plasma test that detects microbial cell free DNA (mcfDNA). After mcfDNA is extracted and NGS performed, human sequences are removed and remaining sequences are aligned to a curated pathogen database of >1,000 organisms. Organisms present above a statistical threshold are reported. Chart review was conducted on the cases of *R. typhi* identified by the Karius Test.

Results. The Karius Test detected *R. typhi* in 6 adult patients, 4 women and 2 men, from a medical center in Houston, TX. In 2 patients, *R. typhi* mcfDNA was present in the raw sequencing data but at an abundance below validated statistical thresholds. *R. typhi* mcfDNA was not found in negative controls run simultaneously with the samples. All patients presented with fever, 4 presented with headache, 3 presented with gastrointestinal symptoms, 3 developed rash, one presented with hypotension. Laboratory data were available for 5 patients. Four patients developed thrombocytopenia, 5 had anemia, 4 patients had WBC < 5, 4 had transaminase elevation and 3 developed hyponatremia. 3 out of 5 had *R. typhi* serologies sent; all 3 were positive (including two of the patients with *R. typhi* mcfDNA levels below threshold). In the two other patients the Karius test was the means of establishing the diagnosis. 3 out of 5 patients where data were available were treated with doxycyline.

Conclusion. The Karius test was able to detect *R. typhi* in a cluster of 6 patients in one medical center in Houston, TX. NGS for mcfDNA offers a rapid means of detecting *R. typhi* infection. Accurate, rapid diagnosis of *R. typhi* has important public health implications given its vector-borne mechanism of transmission.

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

2140. Utility of Respiratory Specimen Gram Stain for Predicting Final Culture Result in Patients with Clinically Diagnosed Pneumonia

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Background. Obtaining a high-quality respiratory tract specimen for Gram stain and culture in patients with suspected lower respiratory tract infections is recommended by the IDSA guidelines. However, conflicting results correlating Gram stain with final culture growth has led to questions about the utility of a respiratory specimen Gram stain. The purpose of this study was to assess the correlation of Gram stain with final culture in patients with pneumonia.

Methods. A retrospective chart review was conducted to evaluate adult inpatients with a diagnosis of pneumonia (based on the CDC surveillance definition) who had a respiratory specimen submitted for Gram stain and culture. A specimen was considered acceptable if less than ten epithelial cells were visualized under low power field. Each Gram stain was compared with the corresponding final culture. The primary outcome was to evaluate the correlation of Gram stain with final culture using positive predictive value (PPV), negative predictive value (NPV), sensitivity, and specificity. A culture was considered negative if no bacteria were isolated or if only normal flora grew. Secondary outcomes were PPV and NPV based on antibiotic exposure prior to specimen collection, semi-quantitative number of bacteria on Gram stain, and collection method. Additionally, discordance between Gram stain and final culture morphology was evaluated.

Results. A total of 269 acceptable specimens were assessed. Of the 72 specimens with a positive Gram stain, 41 yielded bacteria in final culture (PPV: 56.9%). In contrast, 154 of the 197 specimens with a negative Gram stain were associated with negative final culture (NPV: 76.7%). The NPV of Gram stain was decreased when antibiotics were given for > 24 hours pre-specimen. The PPV of Gram stain improved as an increasing amount of bacteria were reported. Less invasive collection methods had a lower PPV but a higher NPV in comparison to invasive collection methods. Finally, the discordance rate between Gram stain and final culture morphology was low.

Conclusion. This study shows inconsistent results regarding the ability of Gram stain to predict final culture. Pneumonia should continue to be managed clinically and caution taken prior to adjusting empiric antimicrobial regimens based solely on the Gram stain.

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

2141. Potential for Harm From Rapid Campylobacter Antigen Test: Quality Improvement Process Reveals 84% False-Positive STAT! Campy Stool Antigen Results

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Background. The Immunocard STAT! Campy is known to have a poor correlation with Campylobacter culture, and bloody stools are thought to be the most common cause of false-positive tests. A CDC investigation of 11 cases of Campylobacter in premature infants with non-bloody stools between March and April, 2018 at the Children's Hospital of Illinois identified a pseudo-outbreak secondary to false-positive stool antigen tests.

Methods. Beginning May 1, 2018, Immunocard STAT! Campy (Meridian BioScience) positive stools from 14-hospitals in the OSF network were sent to the OSF System lab for confirmation prior to resulting in the medical record (MR). Stool was placed into Cary Blair media and a STAT! Campy stool antigen test was repeated in the OSF System Lab. BioFire GI Panel (GIP) PCR was performed on STAT! Campy positive stools, and results reported in the MR.

Results. Between May 1, 2018 and April 30, 2019, 3,639 stools were submitted for culture. 372 tested positive by the STAT! Campy rapid antigen test and were referred for confirmation. Repeat rapid antigen tests were negative for 56% (208/372) of stools and were finalled in the MR as negative without GIP testing. GIP PCR was performed on 164 samples from 163 patients (mean age = 18). 43% (71/164) of GIP were completely negative; 16% (27/164) positive STAT! Campy antigens were confirmed by the GIP (84% were false positive). Pathogens detected by the GIP included: 30 viral infections (50% Norovirus), 27 cases of *C. difficile*, and 19 pathogenic *E. coli* (Table 1). Multiple pathogens were detected in 15% (25/163) patients (1 patient was positive for 4 pathogens). One case of Salmonella was not detected by GIP. One patient tested negative by the GIP but remained symptomatic and *C. difficile* was detected on repeat testing 10 days later.

Conclusion. *C. difficile* and Norovirus were the most common pathogens detected in stools that yielded false positive STAT! Campy results. These findings have important patient care and infection control implications. Currently neither FDA nor CDC requires Campylobacter culture (or other laboratory methods) of confirmation of positive Campylobacter stool antigen tests. Missed and incorrect diagnoses represent a significant risk of harm for patients (particularly *C. difficile* or Shiga toxin-infected patients, Table 1), and outbreaks in institutional settings.

Table 1. Shiga toxin detection: antigen vs PCR

Pathogenic *E. coli* in Stool (N=19)

	BioFire GIP		
Shiga toxin Antigen	NEG	POS	
Shiga toxin NEG	14	4	18
Shiga Toxin POS	0	1	1
	14	5	19

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