is 0.27%, compared with the previously reported rate of 2.5% that included resistance to ertapenem or MER.

Conclusion. Implementing CRE PCR testing to identify CP-CRE organisms resulted in a significant reduction in utilization of anti-CRE agents for CREIs. Additionally, the testing algorithm allowed for accurate reporting of our local CRE prevalence. By avoiding CA, MV, or TG in patients without CP-CREs, this has the potential to optimize therapy while reducing collateral damage associated with broad-spectrum agents.

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2131. Multicenter Evaluation of Meropenem/Vaborbactam MIC Results for *Enterobacteriaceae* Using MicroScan Dried Gram-Negative MIC Panels

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Background. A multicenter study was performed to evaluate the accuracy of meropenem/vaborbactam on a MicroScan Dried Gram-negative MIC (MSDGN) Panel when compared with a frozen CLSI broth microdilution reference panel.

Methods. For efficacy, an evaluation was conducted at three US sites by comparing MIC values obtained using the MSDGN to MICs using a CLSI broth microdilution reference panel. A total of 560 *Enterobacteriaceae* clinical isolates were tested using the turbidity and Prompt** methods of inoculation. For challenge, 95 *Enterobacteriaceae* isolates were tested on MSDGN panels at one site. For reproducibility, a subset of 14 organisms was tested on MSDGN panels at each site. MSDGN panels were incubated at 35 ± 2°C and read on the WalkAway System, the autoSCAN-4 instrument, and read visually. Read times for the MSDGN panels were at 16–20 hours. Frozen reference panels, prepared according to CLSI/ISO methodology, were inoculated using the turbidity inoculation method. All frozen reference panels were incubated at 35 ± 2°C and read visually. Frozen reference panels were read at 16–20 hours. FDA/CLSI breakpoints (μg/ml) used for interpretation of MIC results were: *Enterobacteriaceae* ≤ 4/8 S, 8/8 I, and ≥ 16/8 R.

Results. When compared with frozen reference panel results, essential and categorical agreements for isolates tested in the Efficacy and Challenge are as follows (see table). Reproducibility among the three sites were greater than 95% for all read methods for both the turbidity and Prompt* inoculation methods.

Conclusion. This multicenter study showed that meropenem/vaborbactam MIC results for *Enterobacteriaceae* obtained with the MSDGN panel correlate well with MICs obtained using frozen reference panels using FDA/CLSI interpretive criteria. * PROMPT® is a registered trademark of 3M Company, St. Paul, MN, USA. Beckman Coulter, the stylized logo and the Beckman Coulter product and service marks mentioned herein are trademarks or registered trademarks of Beckman Coulter, Inc. in the United States and other countries. Vabomere® (Meropenem/Vaborbactam) is a registered trademark of Melinta Therapeutics, Inc.

Read Method	Essential Agreement %		Categorical Agreement %		Very Major Error (VMJ) %		Major Error (MAJ) %		Minor Error (MIN) %	
	T	P	T	P	T	P	T	P	T	P
Visually	97.9 (641/655)	96.5 (632/655)	98.5 (645/655)	99.1 (649/655)	3.2 (1/31)	0 (0/31)	0 (0/619)	0 (0/619)	1.4 (9/655)	0.9 (6/655)
WalkAway	98.2 (643/655)	98.3 (644/655)	98.5 (645/655)	99.1 (649/655)	3.2 (1/31)	0 (0/31)	0 (0/619)	0 (0/619)	1.4 (9/655)	0.9 (6/655)
autoSCAN-4	97.9 (641/655)	97.3 (637/655)	98.5 (645/655)	99.1 (649/655)	3.2 (1/31)	0 (0/31)	0 (0/619)	0 (0/619)	1.4 (9/655)	0.9 (6/655)
T = Turbidity inoculation method, P = Prompt inoculation method										

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

2132. Multicenter Evaluation of Eravacycline MIC Results for *Enterobacteriaceae* Using MicroScan Dried Gram-Negative MIC Panels

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Background. A multicenter study was performed to evaluate the accuracy of eravacycline on a MicroScan Dried Gram-negative MIC (MSDGN) Panel when compared with a frozen CLSI broth microdilution reference panel.

Methods. For efficacy, an evaluation was conducted at three sites by comparing MIC values obtained using the MSDGN to MICs using a CLSI broth microdilution reference panel. A total of 414 *Enterobacteriaceae* clinical isolates were tested using the turbidity and Prompt** methods of inoculation. For challenge, 79 *Enterobacteriaceae* isolates were tested on MSDGN panels at one site. For reproducibility, a subset of 11 organisms was tested on MSDGN panels at each site. MSDGN panels were incubated at 35 ± 2°C and read on the WalkAway System, the autoSCAN-4 instrument, and read visually. Read times for the MSDGN panels were at 16–20 hours. Frozen reference panels, prepared according to CLSI/ISO methodology, were inoculated using the turbidity inoculation method. All frozen reference panels were incubated at 35 ± 2°C and read visually. Frozen reference panels were read at 16–20 hours. FDA breakpoints (μg/mL) used for interpretation of MIC results were: *Enterobacteriaceae* ≤ 0.5 S. Potential major and very major errors were calculated using the NS result in place of resistant (R).

Results. When compared with frozen reference panel results, essential and categorical agreements for isolates tested in the Efficacy and Challenge are as follows (see table). Reproducibility among the three sites were greater than 95% for all read methods for both the turbidity and Prompt inoculation methods.

Conclusion. This multicenter study showed that eravacycline MIC results for *Enterobacteriaceae* obtained with the MSDGN panel correlate well with MICs obtained using frozen reference panels using FDA interpretive criteria. * PROMPT® is a registered trademark of 3M Company, St. Paul, MN USA. Beckman Coulter, the stylized logo and the Beckman Coulter product and service marks mentioned herein are trademarks or registered trademarks of Beckman Coulter, Inc. in the United States and other countries. Xerava™ (Eravacycline) is a registered trademark of Tetraphase Pharmaceuticals, Inc.

Read Method	Essential Agreement %		Categorical Agreement %		**Potential Very Major Error (VMJ) %		Potential Major Error (MAJ) %	
	T	P	T	P	T	P	T	P
Visually	99.0 (488/493)	97.0 (478/493)	98.8 (487/493)	98.2 (484/493)	0.0 (0/44)	0.0 (0/44)	0.4 (2/449)	1.3 (6/449)
WalkAway	98.0 (483/493)	96.8 (477/493)	98.2 (484/493)	98.4 (485/493)	0.0 (0/44)	0.0 (0/44)	1.3 (6/449)	1.6 (7/449)
autoSCAN-4	96.1 (474/493)	92.3 (455/493)	98.4 (485/493)	98.0 (483/493)	0.0 (0/44)	0.0 (0/44)	0.4 (2/449)	1.1 (5/449)
T = Turbidity inoculation method, P = Prompt inoculation method								

**Calculation of Potential VMJ excluding 1 well errors

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

2133. Clinical Impact of Implementation of Rapid Diagnostic Testing of Blood Cultures on Patient Outcomes

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Background. Rapid diagnostic testing (RDT) in microbiology labs shortens the time to identification of bacteria in blood cultures. This study evaluates the impact of implementation of Cepheid® GeneXpert® to detect methicillin-resistant *Staphylococcus aureus* and *S. aureus* in Gram-positive blood cultures.

Methods. Patients with positive blood cultures for *Staphylococcus* spp. before (November 2015–August 2016) and after (November 2017–8/2018) implementation of a new rapid diagnostic technology were evaluated. RDT results were reviewed once daily by the antimicrobial stewardship team. The primary outcome was time to appropriate antimicrobial therapy. Secondary outcomes included the duration of antimicrobial therapy from time of positive culture, duration of vancomycin therapy, and length of hospital stay (LOS).

Results. A total of 113 patients were in the pre- and 73 patients were in the post-implementation cohort. Patients treated post-RDT demonstrated significantly shorter median time to appropriate therapy (20.6 hours vs. 49.8 hours, $P = 0.03$) and numerically shorter median duration of vancomycin therapy (3.0 days vs. 1.0 days, $P = 0.32$). These numerical differences were present despite the post-RDT cohort having significantly more MSSA and MRSA infections. Differences in duration of antimicrobial therapy were not statistically significant. Patients treated pre-RDT demonstrated a shorter median LOS than those treated post-implementation (7.0 days vs. 8.5 days, $P = 0.03$).

Conclusion. The use of RDT significantly decreased time to appropriate antimicrobial therapy. Patients in the post-RDT cohort had longer LOS, which may due to a higher incidence of *S. aureus* infections, compared with coagulase-negative *Staphylococcus*, in this cohort These results are promising for future RDT interventions.

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2134. Differential Changes in Breath Volatile Metabolites to Identify Carbapenem-Resistant Enterobacteriaceae (CRE) in a Murine Pneumonia Model

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Background. CRE infections cause significant mortality, in large part because rapid identification of these infections is challenging. We tested the hypothesis that CRE and their isogenic carbapenem-susceptible counterparts have differential metabolic responses to carbapenem therapy.

Methods. We generated isogenic pairs of *E. coli*, *E. cloacae*, and *K. pneumoniae* by inserting a bla_{NDM-1}-containing plasmid into carbapenem-susceptible *E. coli*, *E. cloacae*, and *K. pneumoniae*. We confirmed phenotypic meropenem (MPM) resistance per CLSI breakpoints for Enterobacteriaceae (MIC ≥4) in the NDM-1$^+$ member and susceptibility (MIC≤1) in the NDM-1$^-$ member of each pair. We administered 2×10^8 CFU of each isolate intranasally to 23–28 g male C57BL/6J mice, infecting 6 mice with the NDM-1$^+$ member and 6 with the NDM-1$^-$ member of each species pair (12 mice per bacterial species). 24 hours after infection, we treated 3 mice in each NDM-1$^+$ and NDM-1$^-$ bacterial species cohort with MPM over 4 hours, and the other 3 mice in each cohort with saline over 4 hours as controls, confirming adequate infection (a target of 10^6 CFU/g of lung tissue) in quantitative lung homogenate cultures. We then collected breath samples from each mouse via tracheostomy using a murine ventilator, identifying all volatile metabolites in each sample using thermal desorption-gas chromatography/tandem mass spectrometry. We used Wilcoxon tests to examine differences in metabolite abundance between MPM and saline-treated control mice in the NDM-1$^+$ and NDM-1$^-$ a member of each species pair, with a two-sided *P*-value threshold of < 0.1.

Results. Several breath volatile metabolites changed differentially within each NDM-1$^+$/NDM-1$^-$ pair, outlined in Table 1 (*E. coli*), Table 2 (*E. cloacae*), and Table 3 (*K. pneumoniae*). Each listed metabolite that changed with MPM did not change with MPM in mice infected with each isogenic counterpart

Conclusion. There are differential *in vivo* metabolic responses with effective vs. ineffective treatment of mice with pneumonia caused by *E. coli, E. cloacae*, and *K. pneumoniae* pairs that are genetically identical other than bla_{NDM-1}; this differential treatment response can potentially be used to identify these infections.

Table 1. Differentially changing breath metabolites in mice infected with NDM-1$^+$ vs. NDM-1$^-$ *Escherichia coli.*

	***Escherichia coli* bla_{NDM-1}^+**	***Escherichia coli* bla_{NDM-1}^-**
Breath Volatile Metabolite	**Direction of change in abundance with MPM treatment**	**Direction of change in abundance with MPM treatment**
2-methyldodecane	Increased	ND
2,4-dimethylundecane	Increased	ND
Camphor	Increased	ND
2,6,10-trimethyldodecane	Increased	ND
Bicyclo[2.2.1]heptane-2,3-diol, 1,7,7-trimethyl-, (2-endo,3-exo)-	Increased	ND
Undecanal	Increased	ND
Octanal	ND	Increased
3-methyldodecane	ND	Increased
Acetaldehyde	ND	Decreased

***MPM**: meropenem, **ND**: no difference in abundance between MPM and saline Treatment.

Table 2. Differentially changing breath metabolites in mice infected with NDM-1$^+$ vs. NDM-1$^-$ *Enterobacter cloacae.*

	***Enterobacter cloacae* bla_{NDM-1}^+**	***Enterobacter cloacae* bla_{NDM-1}^-**
Breath Volatile Metabolite	**Direction of change in abundance with MPM treatment**	**Change in abundance with meropenem treatment**
2,3,7-trimethyldecane	Increased	ND
2,4-dimethylundecane	Increased	ND
3-methyldodecane	Increased	ND
6-ethylundecane	Increased	ND
2,6,10,14-tetramethylpentadecane	Increased	ND
2,4-Dimethoxybenzylalcohol	Increased	ND
3-methyldodecane	Increased	ND
Benzyl methacrylate	Decreased	ND
Undecanal	Decreased	ND
1-methylnonylbenzene	Increased	ND
butylcyclooctane	ND	Increased
2-ethenylbicyclo[2.1.1]hexan-2-ol	ND	Increased
Decane	ND	Increased
1,3-Octanediol	ND	Increased
Undecanal	ND	Increased
2-methylpropanalmethylhydrazone	ND	Increased
2-(R)-Octanol	ND	Increased
Sulfurous acid, cyclohexylmethyl tridecyl ester	ND	Increased
(1-methylethyl) benzene	ND	Increased
2,6,10-trimethyldodecane	ND	Increased
2-(R)-Butanol	ND	Increased
Ethanol	ND	Increased
2-methylbutane	ND	increased
2-hexyl-1-decanol	ND	Decreased
Tetradecanal	ND	Decreased

***MPM**: meropenem, **ND**: no difference in abundance between MPM and saline Treatment

Table 3. Differentially changing breath metabolites in mice infected with NDM-1$^+$ vs. NDM-1$^-$ *Klebsiella pneumoniae*.

	***Klebsiella pneumoniae* bla_{NDM-1}^+**	***Klebsiella pneumoniae* bla_{NDM-1}^-**
Breath Volatile Metabolite	**Direction of change in abundance with MPM treatment**	**Direction of change in abundance with MPM treatment**
2-methylbutane	Increased	ND
2-methyl-2-propyl-1,3-propanediol	Increased	ND
ethylcyclopentane	Decreased	ND
3-methylphenol	Decreased	Increased
Acetic acid, hydrazide	ND	Increased
Methyl Isobutyl Ketone	ND	Increased
N-methyleneethenamine	ND	Increased
1-methyl-3-propylbenzene	ND	Increased
2,4,6-trimethyldecane	ND	Increased
Octane	ND	Increased
α-methyl, β-ethenyl-Benzeneethanol	ND	Increased
1,3-dimethylbenzene	ND	Increased
2-hexyl-1-decanol	ND	Increased
1-ethyl-3-methylbenzene	ND	Increased
2-nitro-3-Pyridinecarbonitrile	ND	Increased
4-methyl-3-[2-pentenyl]-Tetrahydrofuran-2-one	ND	Increased
Carbonic acid butylphenylester	ND	Increased
3-hydroxybutanal	ND	Increased
Mesitylene	ND	Increased
Methylstyrene	ND	Increased
3-methyl-5-propylnonane	ND	Increased
1,3-bis(1,1-dimethylethyl)benzene	ND	Increased
Acetic Acid	ND	Decreased

***MPM**: meropenem, **ND**: no difference in abundance between MPM and saline treatment

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2135. *Streptococcus pneumoniae* DNA (*lytA*) Detection in Clinical Samples Sent for a Respiratory Viral Polymerase Chain Reaction: Is There Bacterial-Viral Association?

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Background. Streptococcus pneumoniae (SPNEU) is a major cause of community-acquired pneumonia and frequently complicates respiratory viral infections. Clinical differentiation of viral and bacterial respiratory tract infection can be difficult, as can predicting which patients with respiratory viral infection will develop bacterial infection. A SPNEU polymerase chain reaction (PCR) to specific DNA region lytA may be able to determine which patients with viral infections may develop bacterial infection.

Methods. Stored nucleic acid extracts from clinical samples collected and tested for respiratory viral PCR (RVP) in 2015 and 2016 were tested for SPNEU lytA DNA using standard laboratory procedure. Analyses of demographic data, RVP and SPNEU PCR result were performed to determine relevant associations.

Results. 1581 stored clinical RVP samples were tested for SPNEU DNA with PCR to lytA, 1550 of these had complete RVP panel results available for analysis. RVP samples from patients 0–5 years old were more likely to have a viral or bacterial pathogen detected than > 5 years old (78% vs. 45%, $P < 0.001$). Of 1,550 samples analyzed with SPNEU PCR, 19% were positive for SPNEU, this was more likely in those 0–5 years old than > 5 years old (50% vs. 10%, $P < 0.0001$). In 0–5 years old, SPNEU was more frequently detected when multiple pathogens were detected on RVP vs. those with no pathogen (63% vs. 43%, $P = 0.031$). In > 5 years old, compared with no pathogen samples, the presence of multiple pathogens, any single pathogen, influenza, rhinovirus and Bordetella pertussis were significantly associated with higher SPNEU positivity rates. Median SPNEU PCR DNA load was higher in multiple pathogen and single pathogen samples than in no pathogen RVP samples.

Conclusion. We have demonstrated an association between common respiratory pathogens and detection of SPNEU DNA via PCR. This association is strongest in samples with multiple RVP pathogens, suggesting additional nasopharyngeal inflammation may contribute to SPNEU presence in the nasopharynx. Previous data have focused on those 0–5 years old, we have demonstrated an SPNEU-viral association in those > 5 years old. This tool may be clinically useful to determine which individuals with viral respiratory tract infection will progress to bacterial pneumonia and warrants further investigation.

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2136. Rapid Antimicrobial Susceptibility Testing using ATP Luminescence and Machine Learning Methods

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