of 33 isolates were tested phenotypically. We found 3 isolates with truncations in both genes. These isolates had metronidazole MICs >256. The presence of one or both intact genes did not always result in low MICs, indicating that there may be significant point mutations that contribute to resistance. Rifampin was not tested phenotypically, but no mutations in *rpoB* were found. In summary, the correlation of WGS and phenotypic testing was 100% for amoxicillin and clarithromycin, 97% for levofloxacin, 91% for tetracycline ($n = 33$), and 67% for metronidazole ($n = 24$).

Conclusion. WGS provides a detailed analysis of *H. pylori* resistance and a broader analysis of antimicrobials that may be of clinical value. Additional studies are needed for genotypic prediction of metronidazole resistance.

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2166. Performance Study on the New ETEST® Piperacillin/Tazobactam (P/T) MIC Strip

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Background. Piperacillin/Tazobactam combination is a first-line antibiotic and carbapenem sparing option for severe infections due to Enterobacteriaceae, *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. ETEST® strips allow to determine antimicrobial Minimum Inhibitory Concentration (MIC). ETEST® Piperacillin/Tazobactam (Ptc) was developped in 1995 against agar dilution reference method. Since then, resistance to Piperacillin/Tazobactam has been increasing and broth microdilution (BMD) substituted for agar dilution as the reference method. The new ETEST® P/T strip for determining MIC of Enterobacteriaceae, *P. aeruginosa* and *A. baumannii* was developed against BMD using a panel of recent strains well genotypically characterized. The aim of this study was to compare the performance of both strips on a panel of challenging strains harboring different-resistant mechanisms.

Methods. A total of 64 strains were tested using ETEST® P/T, ETEST® PTc and BMD: 48 Enterobacteriaceae including 25 resistant strains and 16 *P. aeruginosa* including 11 resistant strains. The results were analyzed for essential (EA) and category (CA) agreements, minor (mE), major (ME) and very major (VME) error rates using FDA/CLSI 2019 breakpoints (Enterobacteriaceae, *P. aeruginosa*: ≤ 16/4(S); ≥ 128/4(R) µg/mL).

Results. Although the panel of strains was challenging including different resistant mechanisms (acquired penicillinase, high-level cephalosporinase, acquired cephalosporinase, ESBL, carbapenemase), the new ETEST® P/T performance was significantly improved for Enterobacteriaceae with an EA at 92,2% without ME or VME. This improvement was also linked to the easiest reading (significant decrease of micrcolonies in the ellipse zone). For P. aeruginosa, the performance was similar between the two strips but the new ETEST® P/T was better correlated with the BMD and showed an EA of 100%. The results are summarized in the table.

Conclusion. The new ETEST® P/T improved the MIC determination and resistance detection, as well as the reading of MIC end points for the routine use. This study emphasizes the need to check the performance of the antimicrobial susceptibility testing products by testing strains reflecting the current epidemiology.

		% EA	% CA	% mE	% ME	% VME
Enterobacteriaceae	New ETEST® P/T	92.2	82.8	17.2	0	0
	ETEST® PTc	70.3	70.3	20.3	0	23.1
Pseudomonas aeruginosa	New ETEST® P/T	100	87.5	12.5	0	0
	ETEST® PTc	93.8	75	25	0	0

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2167. Evaluation of Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy for Rapid and Reagent-Free Identification of *Burkholderia* spp.

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Background. *Burkholderia cepacia* complex including *B. gladioli* are opportunistic pathogenic bacteria affecting the immunocompromised population. For prognosis and appropriate treatment, rapid and accurate species identification is particularly important for those diagnosed with cystic fibrosis (CF). Conventional biochemical identification techniques are insensitive and problematic for identifying *Burkholderia* spp., leading to common misidentification or inconclusive results. Recent studies have successfully employed attenuated total reflectance-Fourier transform infrared (ATR-FTIR) spectroscopy for rapid, reagent-free and cost-effective microbial identification. In the present study, identification of *Burkholderia* spp. by this technique is investigated.

Methods. A total of 59 isolates belonging to 7 species of *Burkholderia* were included in this study; all these isolates had been well-characterized by VITEK 2, 16S rRNA sequencing, random amplification of polymorphic DNA (*recA* typing) and/or matrix-assisted laser desorption/ionization time of flight mass spectrometry. ATR-FTIR spectra were acquired directly from colonies on 5% blood agar plates.

Results. A spectral database containing ATR-FTIR spectra of over 4300 bacterial isolates, encompassing over 70 genera and 190 species, was updated to include spectra of 39 isolates collected in this study and employed in the identification of the other isolates ($n = 20$). All isolates were correctly identified as *Burkholderia* by a multitier search approach. For *Burkholderia* species identification, spectra belonging to 39 isolates representative of all 7 species were used to construct a spectral database employed to identify the other 20 isolates [*B. anthina* ($n = 2$), *B. gladioli* ($n = 8$), *B. multivorans* ($n = 7$), and *B. vietnamiensis* ($n = 3$)]. Compared with VITEK 2 (30% correct species identification), ATR-FTIR spectroscopy correctly identified all but one isolate, resulting in overall correct species identification of 95%. Prospectively (10 months), 5 of 1100 isolates collected were identified as *Burkholderia* spp. by ATR-FTIR spectroscopy in concordance with VITEK 2.

Conclusion. ATR-FTIR spectroscopy can provide the means of rapid *Burkholderia* spp. identification for appropriate treatment of those diagnosed with CF.

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2168. Comparison of Rapid Diagnostic Tests for Bloodstream Infections Using Desirability of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT)

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Background. Rapid diagnostic tests (RDTs) for bloodstream infection (BSIs) are increasingly common. Decisions regarding which RDT to implement remains a clinical challenge given the diversity of organisms and resistance mechanisms detected by different platforms. The desirability of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT) has been proposed as a framework to compare RDT platforms but reports of clinical application are lacking. This study compared potential antibiotic decisions based on results of two different RDTs for BSI using DOOR-MAT.

Methods. Retrospective study at University of Maryland Medical Center from August 2018 to April 2019 comparing Verigene® BC (VBC) to GenMark Dx ePlex® BCID for clinical blood cultures. VBC was part of standard of care, ePlex was run on discarded fresh or frozen blood samples. In this theoretical analysis, RDT result and local susceptibility data were applied by two Infectious Diseases pharmacists to make decisions regarding antibiotic selection in a blinded manner. Cohen's Kappa statistic summarized overall agreement. DOOR-MAT, a partial credit scoring system, was applied to decisions based on final organism/susceptibility results (Figure 1). Scores were averaged between reviewers and mean scores compared between RDT systems using the *t*-test. Additionally, a sensitivity analysis with varied point assignment among Gram-negatives (AmpC-producers) was conducted.

Results. 110 clinical isolates were included; 41 Gram-negative, 69 Gram-positive organisms. Overall agreement was 82% for VBC and 83% for ePlex. The average score for VBC was 86.1 (SD 31.3) compared with ePlex 92.9 (SD 22.9), $P = 0.004$. Among Gram-negatives, the average score for VBC was 79.9 (SD 32.1) compared with ePlex 88.1 (SD 28.8), $P = 0.032$. Among GPs the average score for VBC was 89.9 (SD 30.4) compared with ePlex 95.8 (SD 18.3), $P = 0.048$. Sensitivity analysis demonstrated an average score for of 89.9 (SD 30.4) for VBC compared with 95.8 (SD 18.3) for ePlex, $P = 0.27$.

Conclusion. The use of a partial credit scoring system such as the DOOR-MAT allows for comparisons between RDT systems beyond sensitivity and specificity allowing for enhanced clinical interpretation. In this theoretical comparison, the Genmark ePlex BCID scored higher among both GP and GN organisms.

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