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35<sup>th</sup> ESCMID – Vienna, Austria, 11-15 April 2025

## BACKGROUND

Cefepime is a fourth-generation cephalosporin antibiotic approved for clinical use since 1994. Taniborbactam is a new boronate-based  $\beta$ -lactamase inhibitor to be combined with cefepime. Cefepime-taniborbactam (FTB) is active against most isolates of serine- and metallo- $\beta$ -lactamase producing *Enterobacterales* and *Pseudomonas aeruginosa* and is in development for the treatment of complicated urinary tract infections/acute pyelonephritis and hospital-acquired/ventilator-associated bacterial pneumonia.

## OBJECTIVE

The aim of this study was to perform a comparative evaluation of ETEST<sup>®</sup> cefepime-taniborbactam (ETEST FTB) with the Clinical and Laboratory Standards Institute (CLSI) broth microdilution (BMD) reference method using a large panel of clinical strains.

## METHODS

- A panel of 99 *Enterobacterales* and 27 *P. aeruginosa* with different resistance mechanisms (including ESBL, high level cephalosporinase, carbapenemase production and porin alteration/impermeability) and 4 ATCC quality control strains were tested. The details of species and QC strains are presented in tables 1 and 2.
- The strains were provided by bioMérieux's internal collection, supplemented by strains supplied by Venatorx pharmaceuticals.

Species	Number of strains
<i>Enterobacter cloacae</i> complex	12
<i>Escherichia coli</i>	16
<i>Klebsiella pneumoniae</i>	12
<i>Proteus mirabilis</i>	10
<i>Pseudomonas aeruginosa</i>	27
<i>Serratia marcescens</i>	10
<i>Citrobacter freundii</i> complex	5
<i>Citrobacter koseri</i>	5
<i>Klebsiella aerogenes</i>	5
<i>Klebsiella oxytoca</i>	5
<i>Morganella morganii</i>	5
<i>Proteus vulgaris</i>	5
<i>Providencia rettgeri</i>	5
<i>Providencia stuartii</i>	4

Table 1 – Detail of species

QC Strains	Collection number	QC Range CLSI M100 – Ed34 ( $\mu$ g/mL)
<i>Escherichia coli</i>	ATCC <sup>®</sup> 25922 <sup>TM</sup>	0.032/4 – 0.125/4
<i>Escherichia coli</i>	NCTC <sup>®</sup> 13353 <sup>TM</sup>	0.125/4 – 1/4
<i>Klebsiella pneumoniae</i>	ATCC <sup>®</sup> 700603 <sup>TM</sup>	0.125/4 – 0.5/4
<i>Pseudomonas aeruginosa</i>	ATCC <sup>®</sup> 27853 <sup>TM</sup>	0.5/4 – 4/4

Table 2 – CLSI QC strains for cefepime-taniborbactam

- BMD was performed using the CLSI standards M100 – 34th Edition – 2024 and M07 – 12th Edition – 2024. ETEST<sup>®</sup> FTB was evaluated using the standard ETEST<sup>®</sup> MIC procedure for aerobic strains (inoculum 0.5 McFarland from 18/24h cultures on Columbia agar + 5% sheep blood, testing on Mueller Hinton agar medium, incubation at 35°C during 16-20h in ambient air).
- For BMD, the MIC endpoint corresponded to the lowest concentration of cefepime-taniborbactam that showed complete inhibition of growth. For ETEST<sup>®</sup> FTB, the MIC endpoint corresponded to the value where the respective inhibition ellipses intersected the strip or where haze, macrocolonies or microcolonies within 3mm of the strip disappeared (bactericidal reading).
- Results were analysed using ISO standard 20776-2 (2021) for essential agreement (EA) and bias, and FDA AST Guidance (2009) for essential agreement (EA), category agreement (CA), major error rate (ME) and very major error rate (VME) using cefepime-taniborbactam provisional breakpoints ( $S \leq 16/4$  and  $R \geq 32/4$   $\mu$ g/mL).

## RESULTS

- The MICs for QC strains were within the CLSI ranges (EUCAST ranges not yet published) with reproducible results.



Figure 1  
*E. coli* ATCC 25922  
MIC = 0.047  $\mu$ g/mL  
Read at complete inhibition of haze



Figure 2  
*E. coli* NCTC 13353  
MIC = 0.38  $\mu$ g/mL



Figure 3  
*K. pneumoniae* ATCC 700603  
MIC = 0.19  $\mu$ g/mL



Figure 4  
*P. aeruginosa* ATCC 27853  
MIC = 1  $\mu$ g/mL

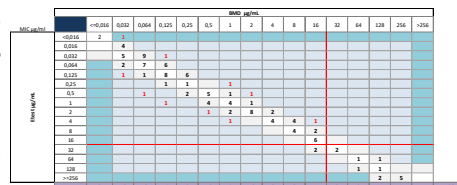


Table 3 – Distribution diagram between ETEST<sup>®</sup> FTB and BMD – All strains

- The essential agreement [ $\pm 1$  dilution] for all strains between ETEST<sup>®</sup> FTB and BMD MICs was **92.1%**, with no significant bias (-19.2% for *Enterobacterales* and -4.9% for *Pseudomonas aeruginosa*).
- Cefepime-taniborbactam exhibits activity against most carbapenem-resistant strains of *Enterobacterales* and *P. aeruginosa*. Among the 126 strains tested, 57 were Intermediate or Resistant to meropenem (i.e., meropenem CLSI breakpoints: MIC  $\geq 2$   $\mu$ g/mL for *Enterobacterales* and MIC  $\geq 4$   $\mu$ g/mL for *P. aeruginosa*). ETEST<sup>®</sup> FTB performance was therefore also assessed against these strains of interest (strains with elevated carbapenem MICs).

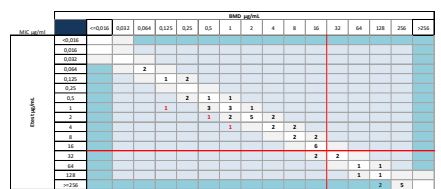


Table 4 – Distribution diagram between ETEST<sup>®</sup> FTB and BMD – Strains of interest (i.e., meropenem MIC  $\geq 2$   $\mu$ g/mL for *Enterobacterales* and MIC  $\geq 4$   $\mu$ g/mL for *P. aeruginosa*)

- For these strains of interest, the essential agreement [ $\pm 1$  dilution] between ETEST<sup>®</sup> FTB and BMD MICs was **94.7%**, with no significant bias (+7.9% for *Enterobacterales* and +10.9% for *Pseudomonas aeruginosa*).

The list of strains not within essential agreement is presented in Table 5 (all strains).

Species	Resistance profile	ETEST <sup>®</sup> FTB MIC ( $\mu$ g/mL)	BMD FTB MIC ( $\mu$ g/mL)	Doubling dilution difference
<i>Enterobacter cloacae</i> complex	Carbapenemase (VIM)	2	0.5	+2
<i>Escherichia coli</i>	Acquired cephalosporinase	0.032	0.125	-2
<i>Klebsiella pneumoniae</i>	Carbapenemase (KPC)	0.25	1	-2
<i>Serratia marcescens</i>	Undetermined	4	16	-2
<i>Pseudomonas aeruginosa</i>	Wild type	0.5	2	-2
<i>Citrobacter freundii</i> complex	ESBL	< 0.016	0.032	-2
<i>Citrobacter freundii</i> complex	Carbapenemase (KPC)	4	1	+2
<i>Morganella morganii</i>	Carbapenemase (NDM)	1	0.125	+3
<i>Proteus vulgaris</i>	Undetermined	0.5	0.064	+3
<i>Proteus vulgaris</i>	Undetermined	0.125	0.032	+2

Table 5 : Detail of discrepant strains in terms of essential agreement

- The categorical agreement was **98.4%** with 124/126 concordant strains between both methods (see tables 6a and 6b). The major error rate was 1.8%. Only 2 strains showed category discrepant results although they are concordant in essential agreement (see detail in table 7). There were no very major errors observed.

ETEST <sup>®</sup> FTB / BMD	ETEST			%	Number of strains	Total
	S	R	Total			
BMD	S	R	Total			
	111	2	113			
	0	13	13			
	Total	111	15	126		

Tables 6a and 6b : Category agreement between ETEST<sup>®</sup> FTB and BMD

Species	Resistance profile	ETEST <sup>®</sup> FTB MIC ( $\mu$ g/mL)	BMD FTB MIC ( $\mu$ g/mL)	ETEST <sup>®</sup> category	BMD category
<i>Escherichia coli</i>	Carbapenemase (IMP)	32	16	R	S
<i>Escherichia coli</i>	Carbapenemase (NDM)	32	16	R	S

Table 7 : Detail of discrepant strains in terms of category agreement

## CONCLUSION

ETEST<sup>®</sup> FTB performed similarly to the CLSI reference BMD method and MIC endpoints for both methods were generally easy to read. With a 15 doubling dilution range and simplicity of use, ETEST<sup>®</sup> FTB may become a valuable tool for MIC testing to inform clinical drug use for *Enterobacterales* and *P. aeruginosa* once cefepime-taniborbactam is approved for clinical use. These results still need to be validated by clinical trials before review and clearance by regulatory authorities for *in vitro* diagnostic use.

This project has been funded in whole or in part with federal funds from the Department of Health and Human Services; Administration for Strategic Preparedness and Response, Biomedical Advanced Research and Development Authority, under contract numbers HHSO100201900007C and 75A50122C00080.