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Activity of tebipenem against Enterobacterales, including molecularly characterized isolates causing urinary tract and bloodstream infections in the United States and United Kingdom in 2023-2024

Tebipenem demonstrated potent *in vitro* activity against the numerous subsets of molecularly characterized isolates, including those with ESBL phenotypes.

Digital poster

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Introduction

- Tebipenem (TBP) pivoxil is in clinical development as an oral carbapenem for the treatment of complicated urinary tract infections (cUTI), including acute pyelonephritis (AP)[1,2].
- Positive results from the recently completed phase 3 PIVOT-PO trial demonstrated non-inferiority of oral tebipenem compared to intravenous imipenem[3].
- This study describes the *in vitro* activity of TBP and comparator agents against molecularly characterized Enterobacterales isolates recovered from UTIs and bloodstream infections (BSIs) in the United States and United Kingdom, including ESBL and carbapenemase producing isolates.

Methods

Bacterial isolates

- A total of 4,171 Enterobacterales isolates were included in this study. Isolates were collected from 62 US sites in 2024 (3,914 isolates; 93.8%) and 3 different UK sites in 2023 (257 isolates; 6.2%). This included 3,436 isolates of *Escherichia coli, Klebsiella pneumoniae*, and *Proteus mirabilis*. The remaining 735 isolates were comprised of 14 different genera, including *Citrobacter*, *Enterobacter*, *Serratia* and other *Klebsiella* spp.
- Isolates recovered were from UTIs (3,040; 72.9%) and BSIs (1,131; 27.1%).
- Bacterial identification was confirmed by standard algorithms supported by matrix-assisted laser desorption ionization-time of flight mass spectrometry (Bruker Daltonics, Bremen, Germany).

Antimicrobial susceptibility testing

- Isolates were tested for susceptibility by broth microdilution following Clinical and Laboratory Standards Institute (CLSI) guidelines[4] and results were interpreted following European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines[5].
- All *E. coli* and *K. pneumoniae* isolates displaying MIC results ≥2 mg/L for aztreonam or ceftazidime or ceftriaxone were defined as presumptive ESBL producers (ESBL+). *P. mirabilis* isolates displaying MIC results ≥2 mg/L for cefpodoxime or ceftazidime were defined as ESBL+.
- Any isolate displaying MIC values of ≥2 mg/L for imipenem and/or meropenem or ≥1 mg/L for ertapenem, were categorized as carbapenem-nonsusceptible Enterobacterales (CNSE). Only meropenem was used for the categorization of *Morganellaceae* due to their intrinsic decreased susceptibility to imipenem.
- ESBL+ and CNSE isolates were subjected to genome sequencing and screened for plasmid-mediated AmpC (pAmpC), extended spectrum b-lactamase, and carbapenemase-producing genes.

Whole genome sequencing and screening of β-lactamase genes

- Selected isolates had total genomic DNA extracted by the fully automated *Thermo Scientific* KingFisher Flex Magnetic Particle Processor (Thermo Scientific), which was used to generate input material for library construction.
- DNA libraries were prepared using the *Illumina* DNA library construction protocol (Illumina) following the manufacturer's instructions and were sequenced on a NextSeq Sequencer (Illumina).
- FASTQ format sequencing files for each sample set were trimmed, error-corrected and assembled using *de novo* assembler SPAdes 3.15.3. An in-house software was applied to align the assembled sequences against a comprehensive in-house database containing known β-lactamase genes.

Results

- Tebipenem MIC_{50} and MIC_{90} values against the 4,171 Enterobacterales isolates from the UK and US were 0.015 mg/L and 0.06 mg/L, respectively (Table 1 and Table 2). Identical $MIC_{50/90}$ values were obtained for the 3,436 *E. coli, K. pneumoniae*, and *P. mirabilis* isolates (0.015 mg/L and 0.06 mg/L, respectively).
- Among the *E. coli*, *K. pneumoniae*, and *P. mirabilis* isolates, 577 (16.8%) met the screening criteria for ESBL phenotype (ESBL+) (Table 1 and Table 2).
- Tebipenem displayed $MIC_{50/90}$ values of 0.015/0.06 mg/L against ESBL+ isolates.
  - The $MIC_{50/90}$ values of intravenous (IV) carbapenem agents were ≤0.12/0.5 mg/L for imipenem (96.4% susceptible), 0.03/0.06 mg/L for meropenem (97.6% susceptible), and 0.03/0.25 mg/L for ertapenem (93.2% susceptible).
  - Susceptibility to non-carbapenem comparator agents ranged from 6.4% - 72.4%.
- Of the ESBL+ isolates, 538 (93.2%) were carbapenem-susceptible (ESBL+, CSE).
- ESBL+, CSE were predominantly associated with $bla_{CTX\text{-}M}$ (83.5%; 449/538). Plasmid-mediated AmpC genes without a $bla_{CTX\text{-}M}$ were detected in 8.2% (44/538) of isolates, other ESBL genes were identified in 2.0% (11/538) of isolates, and no acquired ESBL genes were found in 6.3% (34/538) of isolates.
- The CNSE phenotype represented 2.4% (101/4,171) of all isolates tested.
- Against CNSE isolates, tebipenem had $MIC_{50/90}$ values of 0.5/>8 mg/L.
  - Comparator IV carbapenem agents showed $MIC_{50/90}$ values of 1/>8 mg/L for imipenem (79.2% susceptible), 0.25/32 mg/L for meropenem (82.2% susceptible), and 2/>2 mg/L for ertapenem (19.8% susceptible).
  - Susceptibility to non-carbapenem comparator agents ranged from 13.9% - 58.4%.
- Carbapenemase genes were identified in 25/101 CNSE isolates, including bla_{KPC} (n=13), bla_{NDM} (n=8), bla_{IMI} (n=1), $bla_{OXA\text{-}48\text{-}like}$ (n=2), and bla_{NDM} + $bla_{OXA\text{-}48\text{-}like}$ (n=1).

Table 1: Activity of tebipenem and comparator agents against molecularly characterized Enterobacterales isolates collected from the United States in 2024 and the United Kingdom during 2023

Phenotype/genotype (No. of isolates)	MIC_{50}/MIC_{90} in mg/L (% susceptible by EUCAST)								
	TEB	IMI	MER	ERT	LEV	CRO	FEP	SXT[l]	TZP
All Enterobacterales[a] (4,171)	0.015/0.06 (-)	0.25/1 (97.0)	0.03/0.06 (99.6)	≤0.008/0.06 (98.1)	0.06/8 (80.7)	≤0.06/>8 (82.9)	0.06/8 (86.6)	≤0.12/>4 (74.8)	2/8 (90.9)
US Enterobacterales (3,914)	0.015/0.06 (-)	0.25/1 (96.9)	0.03/0.06 (99.5)	≤0.008/0.06 (98.0)	0.06/8 (80.4)	≤0.06/>8 (82.5)	0.06/8 (86.3)	≤0.12/>4 (74.8)	2/8 (90.9)
UK Enterobacterales (257)	0.015/0.12 (-)	≤0.12/1 (97.7)	≤0.015/0.06 (100)	0.008/0.03 (98.4)	0.03/2 (85.2)	≤0.06/>8 (87.9)	0.06/2 (89.5)	≤0.12/>4 (73.5)	2/8 (91.1)
UTI Enterobacterales (3,040)	0.015/0.06 (-)	≤0.12/1 (96.8)	0.03/0.06 (99.5)	≤0.008/0.06 (98.0)	0.06/8 (80.9)	≤0.06/>8 (83.6)	0.06/8 (86.9)	≤0.12/>4 (74.3)	2/8 (91.3)
BSI Enterobacterales (1,131)	0.015/0.12 (-)	0.25/1 (97.4)	0.03/0.06 (99.8)	0.015/0.06 (98.1)	0.06/8 (80.2)	≤0.06/>8 (81.1)	0.06/16 (85.3)	≤0.12/>4 (75.9)	2/16 (89.8)
CSE[b] (4,070)	0.015/0.06 (-)	0.25/1 (97.4)	0.03/0.06 (100)	≤0.008/0.06 (100)	0.06/8 (81.3)	≤0.06/>8 (84.6)	0.06/4 (87.9)	≤0.12/>4 (75.2)	2/8 (92.8)
CNSE[c] (101)	0.5/>8 (-)	1/>8 (79.2)	0.25/32 (82.2)	2/>2 (19.8)	0.25/>32 (58.4)	>8/>8 (13.9)	8/>32 (30.7)	0.5/>4 (58.4)	128/>128 (16.8)
non-ESBL[d] (3,594)	0.015/0.06 (-)	0.25/1 (97.1)	0.03/0.06 (99.9)	≤0.008/0.03 (98.8)	0.06/2 (87.8)	≤0.06/0.25 (95.2)	0.06/0.12 (98.0)	≤0.12/>4 (80.8)	2/8 (93.9)
EC/KP/PM isolates (3,436)	0.015/0.06 (-)	≤0.12/0.5 (96.9)	≤0.015/0.06 (99.6)	≤0.008/0.03 (98.9)	0.06/8 (78.5)	≤0.06/>8 (84.3)	0.06/16 (85.6)	≤0.12/>4 (72.0)	2/8 (93.2)
non-ESBL[e] (2,859)	0.015/0.03 (-)	≤0.12/0.5 (97.0)	≤0.015/0.03 (100)	≤0.008/0.015 (100)	0.03/4 (86.9)	≤0.06/0.12 (100)	0.06/0.12 (99.9)	≤0.12/>4 (79.1)	2/4 (97.3)
ESBL+[f] (577)	0.015/0.06 (-)	≤0.12/0.5 (96.4)	0.03/0.06 (97.6)	0.03/0.25 (93.2)	4/16 (36.7)	>8/>8 (6.4)	32/>32 (14.7)	>4/>4 (37.1)	4/64 (72.4)
ESBL+, CSE[g] (538)	0.015/0.06 (-)	≤0.12/0.5 (98.9)	0.03/0.06 (100)	0.03/0.12 (100)	4/16 (37.9)	>8/>8 (6.9)	32/>32 (15.8)	>4/>4 (37.9)	4/32 (77.7)
CTX-M[h] (449)	0.015/0.03 (-)	≤0.12/0.25 (98.9)	0.03/0.06 (100)	0.03/0.12 (100)	8/16 (32.3)	>8/>8 (0.0)	>32/>32 (2.4)	>4/>4 (31.2)	4/16 (79.3)
pAmpC[i] (44)	0.03/0.06 (-)	0.5/1 (97.7)	0.03/0.06 (100)	0.12/0.5 (100)	0.25/16 (61.4)	>8/>8 (20.5)	0.25/1 (93.2)	0.25/>4 (63.6)	8/64 (72.7)
Other[j] (11)	0.03/0.12 (-)	0.25/1 (100)	0.03/0.06 (100)	0.03/0.25 (100)	1/16 (36.4)	8/>8 (9.1)	4/>32 (36.4)	0.25/>4 (72.7)	8/>128 (63.6)
None[k] (34)	0.015/0.03 (-)	0.12/0.5 (100)	0.03/0.03 (100)	0.015/0.12 (100)	0.03/4 (82.4)	0.5/>8 (79.4)	0.12/2 (85.3)	≤0.12/>4 (82.4)	8/>128 (67.6)

- EC, *E. coli*; KP, *K. pneumoniae*; PM, *P. mirabilis*; CSE, carbapenem-susceptible; ESBL, extended-spectrum β-lactamase; CNSE, carbapenem-non-susceptible Enterobacterales; TEB, tebipenem; IMI, imipenem; MER, meropenem; ERT, ertapenem; LEV, levofloxacin; CRO, ceftriaxone; FEP, cefepime; SXT, trimethoprim-sulfamethoxazole; TZP, piperacillin-tazobactam; EUCAST (V16.0) breakpoints applied for comparator agents; "-" breakpoints not available
- [a] Includes species of *Citrobacter, Cronobacter, Enterobacter, Escherichia, Hafnia, Klebsiella, Lelliottia, Morganella, Pantoea, Pluralibacter, Proteus, Providencia, Raoultella,* and *Serratia*
- [b] Includes CSE isolates with MIC ≤1 mg/L for imipenem (not considered for Morganellaceae) and/or meropenem, or ≤0.5 mg/L for ertapenem
- [c] Includes isolates with MIC ≥2 mg/L for imipenem and/or meropenem, or ≥1 mg/L for ertapenem; 25 isolates that carried carbapenemase genes (1 $bla_{IMI\text{-}5}$, 1 $bla_{KPC\text{-}18}$, 4 $bla_{KPC\text{-}2}$, 8 $bla_{KPC\text{-}3}$, 7 $bla_{NDM\text{-}5}$, 1 $bla_{NDM\text{-}7}$, 1 $bla_{OXA\text{-}181}$, 1 $bla_{OXA\text{-}48}$, and 1 $bla_{OXA\text{-}181}$ and $bla_{NDM\text{-}4}$) and 76 isolates where no carbapenemase genes were detected
- [d] Includes all Enterobacterales that did not meet the definition of ESBL phenotype
- [e] Includes *E. coli, K. pneumoniae,* and *P. mirabilis* isolates that did not meet the definition of ESBL phenotype
- [f] Includes *E. coli* and *K. pneumoniae* isolates (with aztreonam, ceftazidime, or ceftriaxone MICs of ≥2 mg/L), and *P. mirabilis* isolates (with cefpodoxime or ceftazidime MICs of ≥2 mg/L) that meet the definition of ESBL phenotype
- [g] Includes carbapenem-susceptible *E. coli, K. pneumoniae,* and *P. mirabilis* isolates that meet the definition of ESBL phenotype
- [h] The following $bla_{CTX\text{-}M}$ alleles were detected: 2 $bla_{CTX\text{-}M\text{-}1}$, 20 $bla_{CTX\text{-}M\text{-}14}$, 313 $bla_{CTX\text{-}M\text{-}15}$, 1 $bla_{CTX\text{-}M\text{-}24}$, 82 $bla_{CTX\text{-}M\text{-}27}$, 2 $bla_{CTX\text{-}M\text{-}3}$, 3 $bla_{CTX\text{-}M\text{-}32}$, 20 $bla_{CTX\text{-}M\text{-}55}$, 3 $bla_{CTX\text{-}M\text{-}65}$, 1 $bla_{CTX\text{-}M\text{-}91}$, 1 $bla_{CTX\text{-}M\text{-}15}$ and $bla_{CTX\text{-}M\text{-}3}$, and 1 $bla_{CTX\text{-}M\text{-}15}$ and $bla_{CTX\text{-}M\text{-}55}$. Isolates may include additional ESBL alleles
- [i] The following alleles were detected: 1 $bla_{CMY\text{-}145}$, 25 $bla_{CMY\text{-}2}$, 1 $bla_{CMY\text{-}4}$, 1 $bla_{CMY\text{-}42}$, 1 $bla_{CMY\text{-}2}$ and $bla_{CMY\text{-}43}$, and 15 $bla_{DHA\text{-}1}$. Excludes isolates with CTX-M alleles.
- [j] The following alleles were detected: 1 $bla_{OXA\text{-}1/30}$, 1 $bla_{SHV\text{-}105}$, 2 $bla_{SHV\text{-}12}$, 3 $bla_{SHV\text{-}2A}$, 1 $bla_{SHV\text{-}5}$, 1 $bla_{SHV\text{-}5}$ and $bla_{SHV\text{-}7}$, 1 $bla_{TEM\text{-}10}$, 1 $bla_{TEM\text{-}19}$. Excludes isolates with CTX-M or pAmpC alleles
- [k] No ESBL alleles were detected in these isolates
- [l] Enterobacterales breakpoint of ≤2 mg/L used for *Serratia* spp.

Table 2: Frequency distribution of tebipenem MIC values against molecularly characterized Enterobacterales isolates collected from the United States in 2024 and the United Kingdom during 2023

Phenotype/genotype (No. of isolates)	No. and cumulative % of isolates inhibited at MIC (µg/mL) of:													MIC_{50}	MIC_{90}
	0.004	0.008	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	>8		
All Enterobacterales[a] (4,171)	16	753	2156	564	288	265	73	19	14	3	4	2	14	0.02	0.06
	0.4%	*18.4%*	*70.1%*	*83.6%*	*90.6%*	*96.9%*	*98.7%*	*99.1%*	*99.4%*	*99.5%*	*99.6%*	*99.7%*	*100.0%*		
US Enterobacterales (3,914)	15	684	2034	544	269	248	64	19	14	3	4	2	14	0.02	0.06
	0.4%	*17.9%*	*69.8%*	*83.7%*	*90.6%*	*96.9%*	*98.6%*	*99.1%*	*99.4%*	*99.5%*	*99.6%*	*99.6%*	*100.0%*		
UK Enterobacterales (257)	1	69	122	20	19	17	9							0.02	0.12
	0.4%	*27.2%*	*74.7%*	*82.5%*	*89.9%*	*96.5%*	*100.0%*								
UTI Enterobacterales (3,040)	11	593	1578	390	197	171	54	14	11	3	4	1	13	0.02	0.06
	0.4%	*19.9%*	*71.8%*	*84.6%*	*91.1%*	*96.7%*	*98.5%*	*98.9%*	*99.3%*	*99.4%*	*99.5%*	*99.6%*	*100.0%*		
BSI Enterobacterales (1,131)	5	160	578	174	91	94	19	5	3	0	0	1	1	0.02	0.12
	0.4%	*14.6%*	*65.7%*	*81.1%*	*89.1%*	*97.4%*	*99.1%*	*99.6%*	*99.8%*	*99.8%*	*99.8%*	*99.9%*	*100.0%*		
CSE[b] (4,070)	16	753	2153	561	271	248	63	5						0.02	0.06
	0.4%	*18.9%*	*71.8%*	*85.6%*	*92.2%*	*98.3%*	*99.9%*	*100.0%*							
CNSE[c] (101)		0	3	3	17	17	10	14	14	3	4	2	14	0.5	>8
		0.0%	*3.0%*	*5.9%*	*22.8%*	*39.6%*	*49.5%*	*63.4%*	*77.2%*	*80.2%*	*84.2%*	*86.1%*	*100.0%*		
non-ESBL[d] (3,594)	14	722	1833	439	248	245	66	13	9	0	1	2	2	0.02	0.06
	0.4%	*20.5%*	*71.5%*	*83.7%*	*90.6%*	*97.4%*	*99.2%*	*99.6%*	*99.9%*	*99.9%*	*99.9%*	*99.9%*	*100.0%*		
EC/KP/PM isolates (3,436)	16	731	1925	389	153	151	42	6	5	3	3	0	12	0.02	0.06
	0.5%	*21.7%*	*77.8%*	*89.1%*	*93.5%*	*97.9%*	*99.2%*	*99.3%*	*99.5%*	*99.6%*	*99.7%*	*99.7%*	*100.0%*		
non-ESBL[e] (2,859)	14	700	1602	264	113	131	35							0.02	0.03
	0.5%	*25.0%*	*81.0%*	*90.2%*	*94.2%*	*98.8%*	*100.0%*								
ESBL+[f] (577)	2	31	323	125	40	20	7	6	5	3	3	0	12	0.02	0.06
	0.3%	*5.7%*	*61.7%*	*83.4%*	*90.3%*	*93.8%*	*95.0%*	*96.0%*	*96.9%*	*97.4%*	*97.9%*	*97.9%*	*100.0%*		
ESBL+, CSE[g] (538)	2	31	323	124	37	15	5	1						0.02	0.06
	0.4%	*6.1%*	*66.2%*	*89.2%*	*96.1%*	*98.9%*	*99.8%*	*100.0%*							
CTX-M[h] (449)	2	27	284	97	26	9	3	1						0.02	0.03
	0.4%	*6.5%*	*69.7%*	*91.3%*	*97.1%*	*99.1%*	*99.8%*	*100.0%*							
pAmpC[i] (44)		0	14	18	8	3	1							0.03	0.06
		0.0%	*31.8%*	*72.7%*	*90.9%*	*97.7%*	*100.0%*								
Other[j] (11)		0	3	3	3	2								0.03	0.12
		0.0%	*27.3%*	*54.5%*	*81.8%*	*100.0%*									
None[k] (34)	0	4	22	6	0	1	1							0.02	0.03
	0.0%	*11.8%*	*76.5%*	*94.1%*	*94.1%*	*97.1%*	*100.0%*								

- EC, *E. coli*; KP, *K. pneumoniae*; PM, *P. mirabilis*; CSE, carbapenem susceptible; ESBL, extended spectrum-b-lactamase; CNSE, carbapenem non-susceptible Enterobacterales
- [a] Includes species of *Citrobacter, Cronobacter, Enterobacter, Escherichia, Hafnia, Klebsiella, Lelliottia, Morganella, Pantoea, Pluralibacter, Proteus, Providencia, Raoultella,* and *Serratia*
- [b] Includes CSE isolates with MIC ≤1 mg/L for imipenem (not considered for Morganellaceae) and/or meropenem, or ≤0.5 mg/L for ertapenem.
- [c] Includes isolates with MIC ≥2 mg/L for imipenem and/or meropenem, or ≥1 mg/L for ertapenem; 25 isolates that carried carbapenemase genes (1 $bla_{IMI\text{-}5}$, 1 $bla_{KPC\text{-}18}$, 4 $bla_{KPC\text{-}2}$, 8 $bla_{KPC\text{-}3}$, 7 $bla_{NDM\text{-}5}$, 1 $bla_{NDM\text{-}7}$, 1 $bla_{OXA\text{-}181}$, 1 $bla_{OXA\text{-}48}$, and 1 $bla_{OXA\text{-}181}$ and $bla_{NDM\text{-}4}$) and 76 isolates where no carbapenemase genes were detected.
- [d] Includes all Enterobacterales species that did not meet the definition of ESBL phenotype.
- [e] Includes *E. coli, K. pneumoniae,* and *P. mirabilis* isolates that did not meet the definition of ESBL phenotype.
- [f] Includes *E. coli* and *K. pneumoniae* isolates (with aztreonam, ceftazidime, or ceftriaxone MICs of ≤2 mg/L), and *P. mirabilis* isolates (with cefpodoxime or ceftazidime MICs of ≤2 mg/L) that meet the definition of ESBL phenotype
- [g] Includes carbapenem-susceptible *E. coli, K. pneumoniae,* and *P. mirabilis* isolates that meet the definition of ESBL phenotype
- [h] The following $bla_{CTX\text{-}M}$ alleles were detected: 2 $bla_{CTX\text{-}M\text{-}1}$, 20 $bla_{CTX\text{-}M\text{-}14}$, 313 $bla_{CTX\text{-}M\text{-}15}$, 1 $bla_{CTX\text{-}M\text{-}24}$, 82 $bla_{CTX\text{-}M\text{-}27}$, 2 $bla_{CTX\text{-}M\text{-}3}$, 3 $bla_{CTX\text{-}M\text{-}32}$, 20 $bla_{CTX\text{-}M\text{-}55}$, 3 $bla_{CTX\text{-}M\text{-}65}$, 1 $bla_{CTX\text{-}M\text{-}91}$, 1 $bla_{CTX\text{-}M\text{-}15}$ and $bla_{CTX\text{-}M\text{-}3}$, and 1 $bla_{CTX\text{-}M\text{-}15}$ and $bla_{CTX\text{-}M\text{-}55}$. Isolates may include additional ESBL alleles.
- [i] The following alleles were detected: 1 $bla_{CMY\text{-}145}$, 25 $bla_{CMY\text{-}2}$, 1 $bla_{CMY\text{-}4}$, 1 $bla_{CMY\text{-}42}$, 1 $bla_{CMY\text{-}2}$ and $bla_{CMY\text{-}43}$, and 15 $bla_{DHA\text{-}1}$. Excludes isolates with CTX-M alleles.
- [j] The following alleles were detected: 1 $bla_{OXA\text{-}1/30}$, 1 $bla_{SHV\text{-}105}$, 2 $bla_{SHV\text{-}12}$, 3 $bla_{SHV\text{-}2A}$, 1 $bla_{SHV\text{-}5}$, 1 $bla_{SHV\text{-}5}$ and $bla_{SHV\text{-}7}$, 1 $bla_{TEM\text{-}10}$, 1 $bla_{TEM\text{-}19}$. Excludes isolates with CTX-M or pAmpC alleles.
- [k] No ESBL alleles were detected in these isolates.

Abbreviations

AP, acute pyelonephritis
BSI, bloodstream infection
CNSE, carbapenem not susceptible Enterobacterales
CSE, carbapenem susceptible Enterobacterales
CLSI, Clinical and Laboratory Standards Institute
cUTI, complicated urinary tract infection
ESBL, extended-spectrum β-lactamase
EUCAST, European Committee on Antimicrobial Susceptibility Testing
I, Susceptible, increased exposure
MDR, multidrug resistance
MIC, Minimal inhibitory concentration
TBP, tebipenem

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Conclusions

- Tebipenem demonstrated potent *in vitro* activity against carbapenem-susceptible Enterobacterales causing UTI and BSI in the US and UK, including ESBL+ isolates.
- These data indicate that tebipenem has activity comparable to intravenous carbapenems and support the development of tebipenem as an oral treatment option for cUTI.
- Only 2.4% of isolates included in this study met criteria for CNSE, indicating a low prevalence of this resistance phenotype in this UTI/BSI sample set.

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Disclosures

R Kapoor and D Torumkuney are employees of the GSK group of companies , I Critchley is an employee of Spero Therapeutics, and TB Doyle, RE Mendes, and M Castanheira are employees of Element Materials Technology (JMI Laboratories).

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