

In vitro global surveillance of eravacycline and comparators against Enterobacteriaceae, *Acinetobacter baumannii*, *Stenotrophomonas maltophilia*, including multidrug-resistant (MDR) isolates, over a three-year period (2013-15)

Matteo Bassetti, MD, PhD¹, Ralph Corey, MD², Yohei Doi, MD, PhD³, Ian Morrissey, PhD⁴, Trudy Grossman, PhD⁵, Melanie Olesky, PhD⁶, and Joyce Sutcliffe, PhD⁵

¹Santa Maria Misericordia Hospital, Udine, Italy, ²Duke University Medical Center, Durham, NC, ³Division of Infectious Diseases, University of Pittsburgh School of Medicine, Pittsburgh, PA, ⁴IHMA Europe Sàrl, Epalinges, Switzerland, ⁵Consultant to Tetrphase Pharmaceuticals, Watertown, MA, ⁶Tetrphase Pharmaceuticals, Inc., Watertown, MA



Contact:
Tetrphase Pharmaceuticals Medical Information (TPMI)
medinfo@tphphase.com
617-715-3600

Introduction

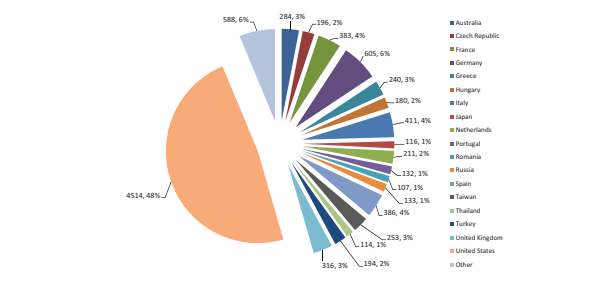
Gram-negative bacteria are common causes of intra-abdominal infections and urinary tract infections, and resistance amongst these pathogens is increasing.¹ Eravacycline (ERV) is a novel, fully-synthetic fluorocycline antibiotic of the tetracycline class in development for the treatment of serious infections, including those caused by multidrug-resistant (MDR) pathogens. ERV is in phase 3 clinical development for the treatment of complicated intra-abdominal infections (cIAI) and complicated urinary tract infections (cUTI), including pyelonephritis.

The purpose of this study was to evaluate activity of ERV and comparators against global isolates of Enterobacteriaceae (ENT), *A. baumannii* (AB), and *S. maltophilia* (SM), including those resistant to carbapenems (CR) or 3rd/4th generation cephalosporins (ESC-R), over a three-year surveillance period.

Methods

- A total of 9363 clinical isolates, collected from 2013-2015 from 205 hospitals, were tested.
- Clinical isolates were from global locations, with 48% from countries within North America (specifically, the United States), 41% from within Europe, 7% from within Asia, and 4% from within the South Pacific (Fig. 1).
- Most isolates were collected from respiratory, GI, GU, and bodily fluid sources followed by skin/wound infections (Fig. 2).
- Minimal inhibitory concentration (MIC) endpoints were determined by broth microdilution according to CLSI guidelines.²
- Quality control testing was performed each day of testing as specified by the CLSI using *Escherichia coli* ATCC 25922, *E. coli* ATCC 35218 and *P. aeruginosa* ATCC 27853.
- Antibiotic susceptibility was determined using CLSI 2015 breakpoints³, with the exception of tigecycline (TGC), where FDA breakpoints were used.⁴
- MDR was defined as resistant to at least 1 agent in 3 or more antibiotic categories.
- ESC-R was defined as resistant to ceftioxone, ceftaxime, ceftazidime, or cefepime.
- CR was defined as resistant to imipenem (2013-2014 isolates) or meropenem (2015 isolates).

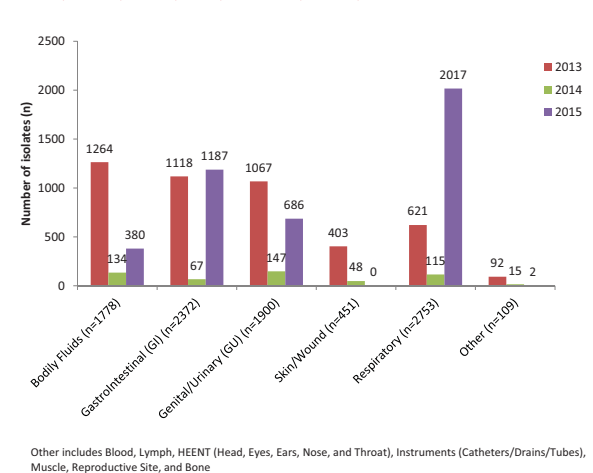
Figure 1. Isolate counts (n, %) by country of origin for the 9,363 isolates collected from 2013-2015



Countries included as "Other" (Austria, Croatia, Denmark, Hong Kong, Ireland, Latvia, Lithuania, New Zealand, Serbia, Singapore, Sweden, and Switzerland) had less than 56 isolates each.

Methods (cont'd)

Figure 2. Isolate counts by source of infection and year for the 9,363 isolates collected in 2013 (n=4,565), 2014 (n=526) and 2015 (n=4,272)



Other includes Blood, Lymph, HEENT (Head, Eyes, Ears, Nose, and Throat), Instruments (Catheters/Drains/Tubes), Muscle, Reproductive Site, and Bone

Results

- ERV MIC_{50/90} values for combined ENT were 0.5/2 mg/L (Table 1). The MIC₉₀ values against MDR (Table 2) and ESC-R (Table 3) were identical to the combined population.
 - Amongst most ENT pathogens, ERV MIC₉₀ values increased by 1 doubling-dilution for resistant phenotypes (Tables 1-4).
 - MIC₉₀ values were no higher than 2 mg/L for ENT isolates with the following exceptions: MDR and ESC-R *S. marcescens*, MDR and ESC-R *Proteus mirabilis*, MDR Indole-positive *Proteaceae*, and CR *Enterobacter* spp. had ERV MIC₉₀ values of 4 mg/L.
- ERV MIC_{50/90} values for combined AB were 0.5/2 mg/L (Table 1), and 1/2 mg/L for MDR, ESC-R, and CR AB (Tables 2-4).
- ERV MIC_{50/90} values for combined SM were 1/2 mg/L (Table 1) and 2/8 mg/L for MDR SM (Table 2).
- Based on MIC₉₀ values, the potency of ERV was up to 4-fold greater than that of TGC against these Gram-negative organisms.
- Cumulative MIC distribution patterns for ENT organisms were relatively consistent over the three-year period (Fig. 3). A one doubling-dilution shift was seen for SM and AB in the 0.12 – 1 mg/L ranges from 2013 to 2015. For both organisms, the number of 2014 isolates was low compared with 2015.

Results (cont'd)

Table 1. Summary antimicrobial activity of eravacycline and comparator agents against Enterobacteriaceae (n=7576), *S. maltophilia* (n=690), and *A. baumannii* (n=1097) isolates collected from 2013-2015

Organism (n)/Antimicrobial Agent	MIC (mg/L)				
	MIC ₅₀	MIC ₉₀	Range	Max	%
Enterobacteriaceae (7576)					
Aeromonas	<0.5	>16	<0.03	>16	84.9%
Coligepha	<0.5	>16	<0.03	>16	95.8%
Ceftazidime	<0.5	>16	<0.03	>16	85.4%
Ceftioxone	<0.5	>16	<0.03	>16	80.6%
Colistin	0.5	>16	<0.12	>4	—
Enterobacter spp. (1097)					
Aeromonas	<0.5	>16	<0.03	>16	84.7%
Coligepha	<0.5	>16	<0.008	>16	88.3%
Ceftazidime	<0.5	>16	<0.03	>16	88.4%
Ceftioxone	<0.5	>16	<0.03	>16	84.6%
Colistin	0.5	>16	<0.12	>4	—
S. maltophilia (690)					
Aeromonas	<0.5	>16	<0.03	>16	84.7%
Coligepha	<0.5	>16	<0.008	>16	89.3%
Ceftazidime	<0.5	>16	<0.03	>16	87.3%
Ceftioxone	<0.5	>16	<0.03	>16	82.3%
Colistin	0.5	>16	<0.12	>4	—
A. baumannii (1097)					
Aeromonas	<0.5	>16	<0.03	>16	72.3%
Coligepha	<0.5	>16	<0.008	>16	82.3%
Ceftazidime	<0.5	>16	<0.03	>16	72.3%
Ceftioxone	<0.5	>16	<0.03	>16	66.9%
Colistin	0.5	>16	<0.12	>4	—

Table 2. Summary antimicrobial activity of eravacycline and comparator agents against MDR Enterobacteriaceae (n=1235), *S. maltophilia* (n=36), and *A. baumannii* (n=801) isolates collected from 2013-2015

Organism (n)/Antimicrobial Agent	MIC (mg/L)				
	MIC ₅₀	MIC ₉₀	Range	Max	%
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	20.3%
Coligepha	>16	>16	<0.03	>16	57.3%
Ceftazidime	>16	>16	<0.03	>16	22.8%
Ceftioxone	>16	>16	<0.03	>16	3.9%
Colistin	0.5	>16	<0.12	>4	—
Enterobacter spp. (287)					
Aeromonas	>16	>16	<0.03	>16	4.9%
Coligepha	>16	>16	<0.03	>16	27.2%
Ceftazidime	>16	>16	<0.03	>16	21.1%
Ceftioxone	>16	>16	<0.03	>16	2.1%
Colistin	0.5	>16	<0.12	>4	—
S. maltophilia (36)					
Aeromonas	>16	>16	<0.03	>16	63%
Coligepha	>16	>16	<0.03	>16	42.2%
Piperacillin/azobactam	64	>128	1	>128	32.8%
Tetracycline	8	>16	0.5	>16	89.6%
Tigecycline	1	>16	0.12	>16	92.3%
Enterobacter spp. (536)					
Aeromonas	>16	>16	<0.03	>16	13.3%
Coligepha	>16	>16	<0.03	>16	75%
Ceftazidime	>16	>16	<0.03	>16	10.3%
Ceftioxone	>16	>16	<0.03	>16	10.3%
Colistin	0.5	>16	<0.12	>4	—
A. baumannii (801)					
Aeromonas	>16	>16	<0.03	>16	85.8%
Coligepha	>16	>16	<0.03	>16	87.1%
Piperacillin/azobactam	>16	>16	<0.03	>16	26.8%
Tetracycline	>16	>16	<0.03	>16	75.6%
Tigecycline	>16	>16	<0.03	>16	93.3%
Enterobacter spp. (1097)					
Aeromonas	>16	>16	<0.03	>16	12.2%
Coligepha	>16	>16	<0.03	>16	23.2%
Ceftazidime	>16	>16	<0.03	>16	23.3%
Ceftioxone	>16	>16	<0.03	>16	17.3%
Colistin	0.5	>16	<0.12	>4	—
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	12.2%
Coligepha	>16	>16	<0.03	>16	23.2%
Ceftazidime	>16	>16	<0.03	>16	23.3%
Ceftioxone	>16	>16	<0.03	>16	17.3%
Colistin	0.5	>16	<0.12	>4	—
Enterobacter spp. (287)					
Aeromonas	>16	>16	<0.03	>16	6.4%
Coligepha	>16	>16	<0.03	>16	7.9%
Ceftazidime	>16	>16	<0.03	>16	10.3%
Ceftioxone	>16	>16	<0.03	>16	10.3%
Colistin	0.5	>16	<0.12	>4	—
S. maltophilia (36)					
Aeromonas	>16	>16	<0.03	>16	51.4%
Coligepha	>16	>16	<0.03	>16	20.6%
Piperacillin/azobactam	64	>128	1	>128	81.8%
Tetracycline	8	>16	0.5	>16	77.8%
Tigecycline	0.25	>16	0.12	>16	99.5%
Enterobacter spp. (536)					
Aeromonas	>16	>16	<0.03	>16	6.4%
Coligepha	>16	>16	<0.03	>16	7.9%
Ceftazidime	>16	>16	<0.03	>16	10.3%
Ceftioxone	>16	>16	<0.03	>16	10.3%
Colistin	0.5	>16	<0.12	>4	—
A. baumannii (801)					
Aeromonas	>16	>16	<0.03	>16	90.5%
Coligepha	>16	>16	<0.03	>16	80%
Piperacillin/azobactam	64	>128	1	>128	23.8%
Tetracycline	2	>16	0.12	>16	74.5%
Tigecycline	0.5	>16	0.25	>16	94.3%
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	36%
Coligepha	>16	>16	<0.03	>16	50%
Ceftazidime	>16	>16	<0.03	>16	62.7%
Ceftioxone	>16	>16	<0.03	>16	4%
Colistin	>16	>16	<0.12	>4	—
Enterobacter spp. (287)					
Aeromonas	>16	>16	<0.03	>16	94.7%
Coligepha	>16	>16	<0.03	>16	81.9%
Ceftazidime	>16	>16	<0.03	>16	83%
Ceftioxone	>16	>16	<0.03	>16	67.8%
Colistin	>16	>16	<0.12	>4	—
S. maltophilia (36)					
Aeromonas	>16	>16	<0.03	>16	55%
Coligepha	>16	>16	<0.03	>16	40.4%
Piperacillin/azobactam	1	>16	<0.03	>16	93.6%
Tetracycline	8	>16	0.5	>16	78.6%
Tigecycline	1	>16	0.12	>16	92.3%
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	77.7%
Coligepha	>16	>16	<0.03	>16	77.7%
Ceftazidime	>16	>16	<0.03	>16	39.7%
Ceftioxone	>16	>16	<0.03	>16	27.8%
Colistin	>16	>16	<0.12	>4	—
Enterobacter spp. (536)					
Aeromonas	>16	>16	<0.03	>16	39.7%
Coligepha	>16	>16	<0.03	>16	27.8%
Piperacillin/azobactam	1	>16	<0.03	>16	94.8%
Tetracycline	8	>16	0.5	>16	64%
Tigecycline	4	>16	0.12	>16	24.1%
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	80.4%
Coligepha	>16	>16	<0.03	>16	76.8%
Ceftazidime	>16	>16	<0.03	>16	58.9%
Ceftioxone	>16	>16	<0.03	>16	2.7%
Colistin	>16	>16	<0.12	>4	—
Enterobacter spp. (287)					
Aeromonas	>16	>16	<0.03	>16	11%
Coligepha	>16	>16	<0.03	>16	71.4%
Ceftazidime	>16	>16	<0.03	>16	72.8%
Ceftioxone	>16	>16	<0.03	>16	89.3%
Tetracycline	8	>16	0.5	>16	80.4%
Tigecycline	4	>16	0.12	>16	62.9%
A. baumannii (801)					
Aeromonas	64	>128	1	>128	4.7%
Coligepha	64	>128	1	>128	2.6%
Ceftazidime	1	>16	<0.03	>16	0.3%
Ceftioxone	1	>16	<0.03	>16	93.9%
Colistin	>16	>16	<0.12	>4	—
Enterobacteriaceae (1406)					
Aeromonas	>16	>16	<0.03	>16	19.3%
Coligepha	>16	>16	<0.03	>16	3.3%
Ceftazidime	>128	>128	>128	>128	2.1%
Ceftioxone	>128	>128	>128	>128	1.8%
Tigecycline	2	>16	0.25	>16</	