

Abstract

Background: Semi-synthetic tetracyclines with C-9 modifications have been reported that overcome resistance by efflux and ribosomal protection. Using a total synthesis approach, systematic modification of the tetracycline D-ring led to the discovery of **TP-434**, a novel broad-spectrum fluorocycline.

Method: Compounds were synthesized *via* a tandem Michael-Dieckmann reaction with systematic modification of the tetracycline D-ring to optimize potency and pharmacology. Protein synthesis inhibition was confirmed in a coupled transcription/translation assay and antibacterial activities were evaluated using CLSI guidelines. *In vivo* efficacy after IV dosing was determined in a mouse systemic infection model challenged with ESBL⁺ *E. coli* or in a neutropenic thigh model infected with *S. aureus* SA191 *tet*(M).

Results: Among the fluorocyclines, **TP-434** had the best overall properties. **TP-434** was an equipotent inhibitor of protein synthesis \pm ribosomal protection (TetM). Molecular modeling of **TP-434** into the 30S ribosomal crystal structure indicates key binding interactions in the A-site.

Compound	MIC (μ g/mL)										
	SA101 ATCC 29213	SA161 MRSA <i>tet</i> (M)	SA158 <i>tet</i> (K)	EF159 <i>tet</i> (M)	SP160 <i>tet</i> (M)	EC155 ESBL	EC133 ESBL	KP153 <i>tet</i> (A)	KP457 ESBL	AB250 <i>tet</i> (B)	PM112 ATCC 35659
TP-434	0.016	0.016	0.016	0.016	0.016	1	0.13	0.5	0.5	2	0.25
Tetracycline	0.5	32	>32	>32	>32	>32	0.13	>32	4	>32	32
Tigecycline	0.063	0.13	0.063	0.063	0.016	0.5	0.13	1	1	4	1
Levofloxacin	0.13	16	0.25	2	0.5	1	>32	2	64	32	0.031

SA: *S. aureus*; SP: *S. pneumoniae*; EF: *E. faecium*; EC: *E. coli*; AB: *A. baumannii*; KP: *K. pneumoniae*; PM: *P. mirabilis*; MRSA: methicillin-resistant *S. aureus*; ESBL: extended-spectrum β -lactamase producing

The mouse septicemia PD₅₀ challenged with *E. coli* was 1.2 mg/kg for **TP-434** versus 3.5 mg/kg for tigecycline. In the *S. aureus* neutropenic thigh model, **TP-434** provided a 3 log₁₀ reduction in bioburden at a dose of 3 mg/kg while tigecycline and vancomycin required 17 and 10 mg/kg, respectively.

Conclusion: The *in vitro* antibacterial activity against MDR gram-positive and gram-negative pathogens and the efficacy in established animal models of infection warrant development of **TP-434** as a single therapy treatment option.

Methods

Bacterial Strains. Strains with defined tetracycline-resistant mechanisms were obtained from M. Roberts (Univ. Washington, bicyclic enone 6¹ *via* a Michael-Dieckmann annulation according to Scheme 1. The Seattle, WA). *E. coli* EC133 was obtained from CMI (Wilsonville, OR) synthesis of other fluorocycline analogs followed similar procedures. Tigecycline was and *S. aureus* SA191 was obtained from ViviSource (Waltham, MA), prepared according to published procedures.² Other marketed antibiotics were from other strains were from the American Type Culture Collection (ATCC) Sigma-Aldrich or USP.

In vitro Susceptibility. Compounds were dissolved in water and assayed in microtiter plates according to CLSI standards.

In vitro coupled E. coli transcription/translation assay. Anti-translational activity (IC₅₀ values) was assessed in an *E. coli in vitro* coupled transcription/translation assay (TnT) with a firefly luciferase readout (Promega, Madison, WI). Purified TetM (2-3 μ M) was added to TnT reactions to evaluate ribosome protection effects *in vitro*.

Mouse Systemic Infection Studies. Mice received treatment *via* intravenous (IV) injection 1 hour post intraperitoneal (IP) infection. At termination of study, percent survival was calculated and the dose (mg/kg) affecting 50% survival, the protective dose 50% (PD₅₀), was reported along with 95% confidence intervals as calculated by Probit analysis using GraphPad Prism version 4.03 (GraphPad Software).

Mouse Thigh Infection. Mice were rendered neutropenic through two consecutive IP injections of cyclophosphamide of 150 and 100 mg/kg on days -4 and -1, respectively. Mice were infected with approximately 5 x 10⁵ CFU/mL of bacteria in a 0.1 mL volume into the right thigh. At 1.5 hours post-infection mice received treatment *via* IV injection. One group of infected mice were euthanized and thighs processed for bacterial titers to serve as T = 0 controls. Twenty-four hours post-treatment, the remaining mice were euthanized, thighs aseptically removed, weighed, homogenized, serially diluted and CFUs per gram of thigh were calculated. The amount of test article required to achieve 1, 2, and 3 log₁₀ reductions from 24 hour control thighs was determined.

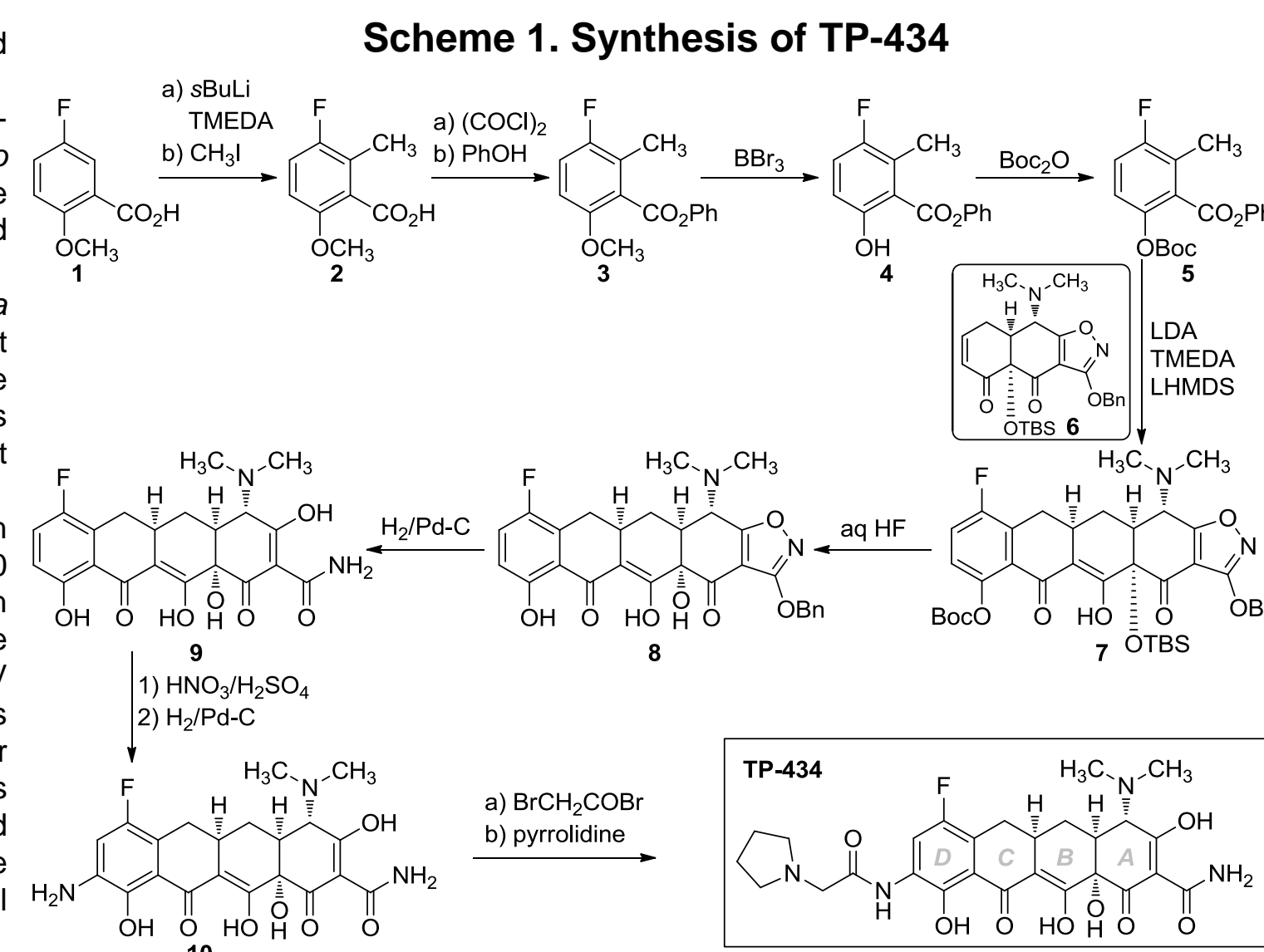
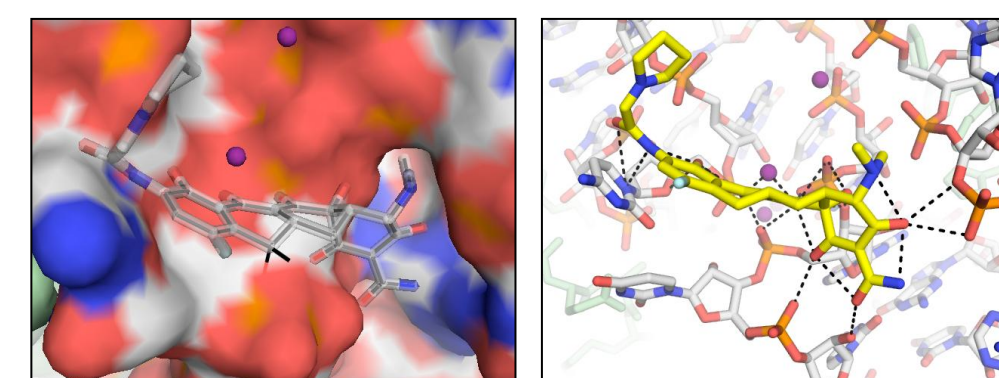


Table 1. *In vitro* Activity of TP-434 and Analogs

ID	R	MIC (μ g/mL)														
		SA101 ATCC 29213	SA100 ATCC 13709	SA161 MRSA <i>tet</i> (M)	SA158 <i>tet</i> (K)	EF103 ATCC 29212	EF159 <i>tet</i> (M)	SP106 ATCC 49619	SP160 <i>tet</i> (M)	EC107 ATCC 25922	EC155 <i>tet</i> (A)	AB110 ATCC 19606	PA111 ATCC 27853	EC108 ATCC 13047	KP109 ATCC 13883	KP153 <i>tet</i> (A)
TP-772	H ₃ C-NH ₂	0.063	0.13	0.25	1	0.063	0.13	0.016	0.016	0.25	16	2	8	0.5	1	8
TP-435	F ₂ C-NH ₂	1	1	2	4	2	4	0.5	1	16	>32	2	>32	>32	32	>32
TP-221	H ₃ C-NH ₂	0.13	0.25	0.25	0.063	0.063	0.13	0.016	0.016	0.25	2	0.5	16	1	1	2
TP-715	H ₃ C-NH ₂	4	4	>32	>32	8	>32	0.25	2	16	>32	8	>32	>32	32	>32
TP-535	H ₃ C-NH ₂	0.016	0.5	0.13	0.25	0.016	0.031	0.016	0.016	0.13	8	0.13	8	1	0.5	8
TP-434	H ₃ C-NH ₂	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	0.016	1	0.031	8	0.13	0.13	0.5
TP-921	H ₃ C-NH ₂	8	8	16	32	8	16	2	8	>32	>32	>32	>32	>32	>32	>32
TP-561	H ₃ C-NH ₂	0.5	0.5	1	0.5	0.25	0.5	0.016	0.016	1	4	0.13	32	4	2	4
TP-002	H ₃ C-NH ₂	0.063	0.063	0.5	1	0.25	0.5	0.031	0.13	1	>32	0.5	32	8	4	32
Tigecycline	H ₃ C-NH ₂	0.063	0.063	0.13	0.063	0.031	0.063	0.016	0.016	0.031	0.5	0.25	8	0.25	0.13	1

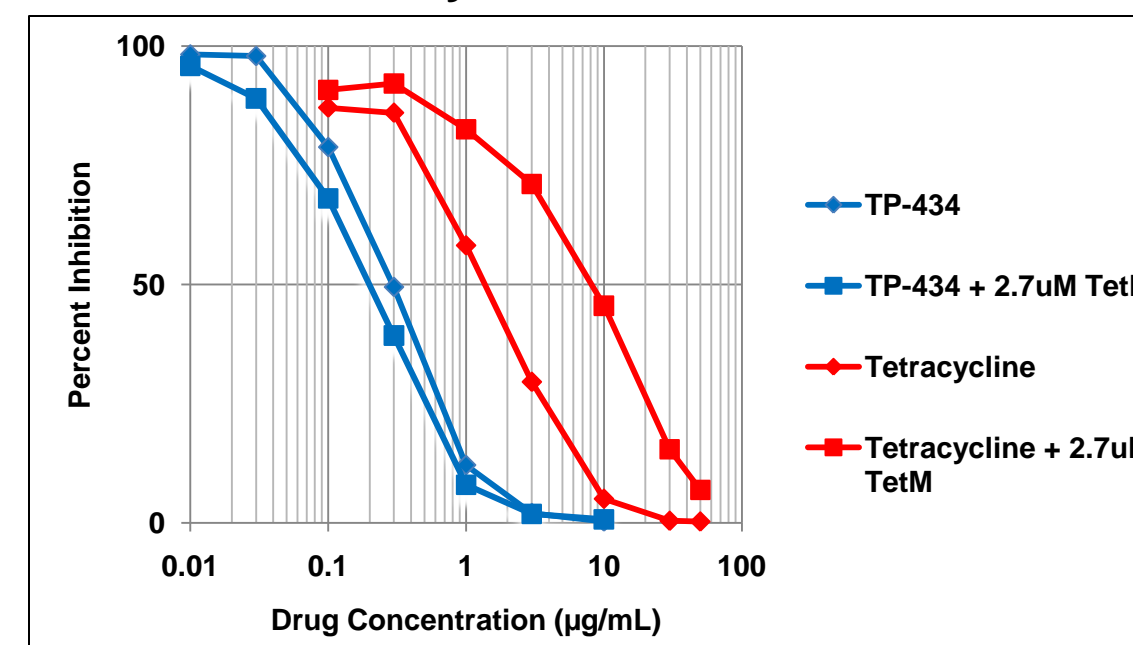
AB: *Acinetobacter baumannii*; EC: *Escherichia coli*; ECI: *Enterobacter cloacae*; EF: *Enterococcus faecalis*; KP: *Klebsiella pneumoniae*; PA: *Pseudomonas aeruginosa*; SA: *Staphylococcus aureus*; SP: *Streptococcus pneumoniae*.

Figure 1. Molecular Modeling of TP-434 in the 30S Ribosomal A-site



TP-434 is docked into the binding pocket of the 30S ribosomal A-site, assuming a similar binding mode to tetracycline. The ball-and-stick model on the right panel illustrates potential hydrogen bonds and participation of one of the Mg cations (purple spheres) in the hydrogen-bonding network.

Figure 2. TP-434 Inhibits Protein Synthesis in the Presence of Tet(M)



Results

Table 2. *In vitro* Activity of TP-434 and Comparators against *ESKAPE* Pathogens³

Organism	N	MIC range (μ g/mL)						
		TP-434	Carbapenem ^a	Fluoroquinolone ^b	3 rd Gen Cep ^c	Gentamicin	Piperacillin/Tazobactam	Tigecycline
<i>Klebsiella pneumoniae</i>	208	0.13-16 0.5/2	0.063->32 0.5/16	\leq 0.016->32 1/>32	\leq 0.016->64 32/>32	\leq 0.25->32 4/>32	1->128 8/>128	0.13-16 0.5/4
ESBL ⁺ <i>Klebsiella pneumoniae</i>	91	0.13-8 0.5/1	0.03->32 0.5/>32	0.03->32 8/>32	0.13->64 >32/>64	\leq 0.25->32 >8/>32	2->128 >64/>128	0.13-8 1/4
Carbapenem-resistant <i>K. pneumoniae</i>	19	0.13-16 0.5/1	4->32 32/>32	4->32 >32/>32	32->32 >32/>32	2->32 >32/>32	>128/>128 >128/>128	0.25-16 1/1
<i>Acinetobacter baumannii</i>	89	\leq 0.016-4 0.5/2	0.12->32 1/>32	0.02->32 8/>16	0.12->16 >16/>16	0.5->32 32/>32	1->128 >128/>128	\leq 0.016-8 1/4
<i>Pseudomonas aeruginosa</i>	88	1->64 8/16	0.12->32 1/16	0.06->2 0.25/>2	1->16 >16/>16	0.12->32 2/16	1->128 8/>128	1->16 16/>16
<i>Enterobacter cloacae</i>	134	0.03-4 0.5/2	0.06-32 0.5/4	0.008->32 0.25/>4	0.03->64 >16/>64	\leq 0.25->32 0.5/>8	0.5->128 >64/>128	0.06-8 0.5/4
<i>Enterobacter aerogenes</i>	30	0.25-2 0.25/0.25	\leq 1-2 \leq 1/1	\leq 0.25-0.5 \leq 0.25/0.25	\leq 0.5->64 \leq 0.5/16	\leq 0.25-1 \leq 0.25/0.5	\leq 0.5->64 2/16	0.25-4 0.5/0.5

Green boxes indicate that the MIC₉₀ of TP-434 < MIC₉₀ of tigecycline
^ameropenem, ertapenem, imipenem; ^blevofloxacin, ciprofloxacin; ^ccefazidime, ceftriaxone; ESBL⁺ = extended spectrum β -lactamase producing isolates

Table 3. *In vitro* Activity of TP-434 and Comparators against *ESKAPE* Pathogens³

-continued

Organism	N	MIC range (μ g/mL)					
		TP-434	Linezolid	Daptomycin	Vancomycin	Levofloxacin	Tigecycline
<i>E. faecium</i> Vancomycin-Susceptible	51	0.03-0.5 0.06/0.12	1-4 2/2	2-8 4/8	0.5-2 1/1	0.25->32 >32/>32	0.03-0.25 0.06/0.12
<i>E. faecium</i> Vancomycin-Resistant	43	0.03-0.12 0.06/0.06	2-4 4/4	2-16 8/16	>64->64 >64->64	>32->32 >32/>32	0.03-0.12 0.06/0.06
MRSA	137	\leq 0.015-0.5 0.06/0.12	1-4 2/4	0.5-1 1/1	0.5-1 1/1	0.12->32 >32/>32	0.06-0.5 0.12/0.12

Conclusions

- **TP-434** belongs to a diverse collection of novel tetracyclines generated by Tetraphase's fully synthetic platform and is the first fluorocycline selected for development as a broad spectrum antibacterial agent
- **TP-434** is an equipotent inhibitor of protein synthesis in the presence or absence of Tet(M)
- **TP-434** is broadly active against all ESKAPE pathogens (except *Pseudomonas*), including ESBL-producing and carbapenem-resistant *Enterobacteriaceae*
- **TP-434** is currently undergoing clinical trials

References

- 1) M.G. Charest, C.D. Lerner, J.D. Brubaker, D.R. Siegel, A.G. Myers, *Science*, **308**, 395 (2005).
- 2) P.-E. Sum, V.J. Lee, R.T. Testa, J.J. Hlavka, G.A. Ellestad, J.D. Bloom, Y. Gluzman, F.P. Tally, *J. Med. Chem.*, **37**, 184 (1994).
- 3) L.B. Rice, *J. Infect. Dis.*, **197**, 1079 (2008).

Figure 3. Activity of TP-434 in a Murine Septicemia Model Challenged with Extended-spectrum β -lactamase (SHV) Producing *E. coli* EC133 *tet*(B)

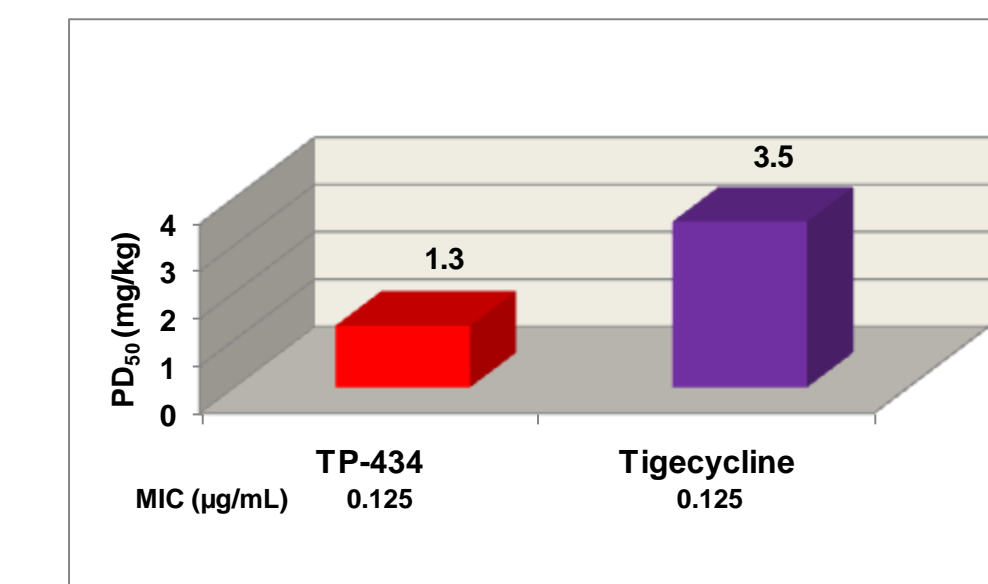


Figure 4. Activity of TP-434 in a Neutropenic Thigh Model Challenged with MRSA SA191 *tet*(M)

