

# Can Clinical Dosing Regimens Provide “Anti-mutant” Fluoroquinolone Concentrations? Predictions Using *In Vitro* Dynamic Models

EV0055

ALEXANDER FIRSOV\*<sup>1</sup>, ELENA STRUKOVA<sup>1</sup>, YURY PORTNOY<sup>1</sup>, DARYA SHLYKOVA<sup>1</sup>, STEPHEN ZINNER<sup>2</sup>,  
Department of Pharmacokinetics & Pharmacodynamics, Gause Institute of New Antibiotics, Moscow, Russia<sup>1</sup>;  
Mount Auburn Hospital, Harvard Medical School, Cambridge, MA, USA<sup>2</sup>

## Introduction

● *In vitro* studies performed mostly with fluoroquinolone-exposed *Staphylococcus aureus* allowed delineation of bell-shaped relationships between the enrichment of resistant mutants and the ratio of the 24-hour area under the curve ( $AUC_{24}$ ) to the MIC [1-4].

● To explore if similar relationships apply to Gram-negative bacteria, the pharmacodynamics of ciprofloxacin were studied against *Escherichia coli*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* over a wide range of antibiotic exposures.

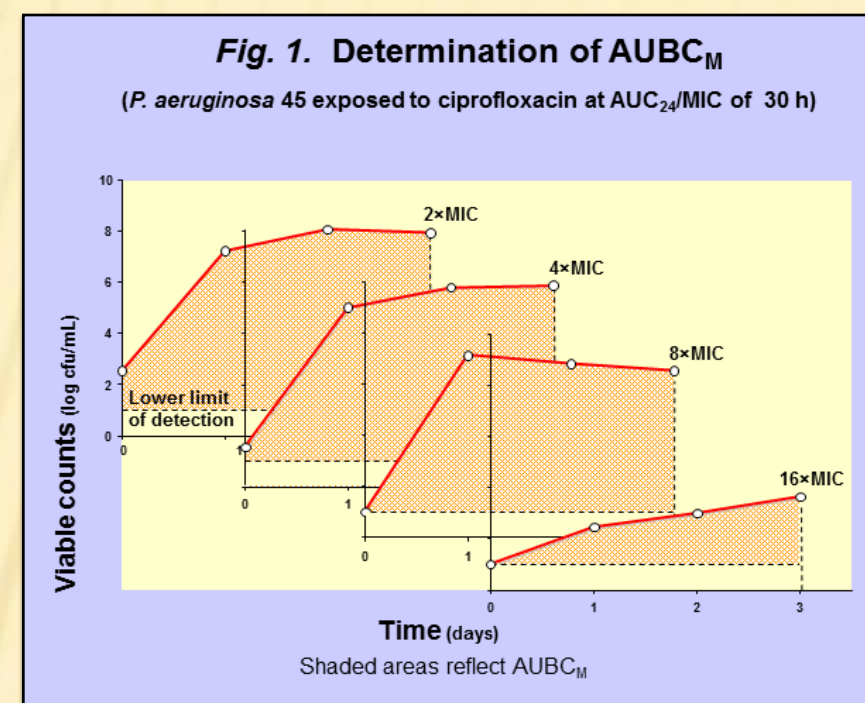
## Methods

● Four strains of *E. coli*, ATCC 25922, 4300, 4454 (MICs 0.008 mg/L) and GM 2995 (MIC 0.016 mg/L), three strains of *K. pneumoniae*, 185 (MIC 0.125 mg/L), 1145 (MIC 0.5 mg/L) and 1885 (MIC 2 mg/L) and four strains of *P. aeruginosa*, 45 (MIC 0.125 mg/L), 279, 395 and 817 (MICs 0.5 mg/L) were selected for the study.

● A series of mono-exponential profiles that mimic twice-daily administration of ciprofloxacin (half-life 4 h) was simulated for 3 consecutive days in an *in vitro* dynamic model [5] over a >100-fold range of the  $AUC_{24}/MIC$  ratio.

● The enrichment of resistant mutants was monitored by plating on media with 2×, 4×, 8× and 16× MIC of ciprofloxacin. Time courses of resistant mutants were characterized by the area under the bacterial mutant concentration – time curve ( $AUC_{24,M}$ ) [5] corrected for the area under the lower limit of detection (Fig. 1).

● To relate  $AUC_{24,M}$  to the simulated  $AUC_{24}/MIC$ s, a modified Gaussian type function was used. Using a descending portion of the  $AUC_{24,M}$ – $AUC_{24}/MIC$  curve for each bacterial species strain, the “anti-mutant”  $AUC_{24}/MIC$  ratio was taken as the point where the Gaussian curve reaches the level of  $AUC_{24,M} = 30 \log(\text{cfu/mL}) \times \text{h}$ .

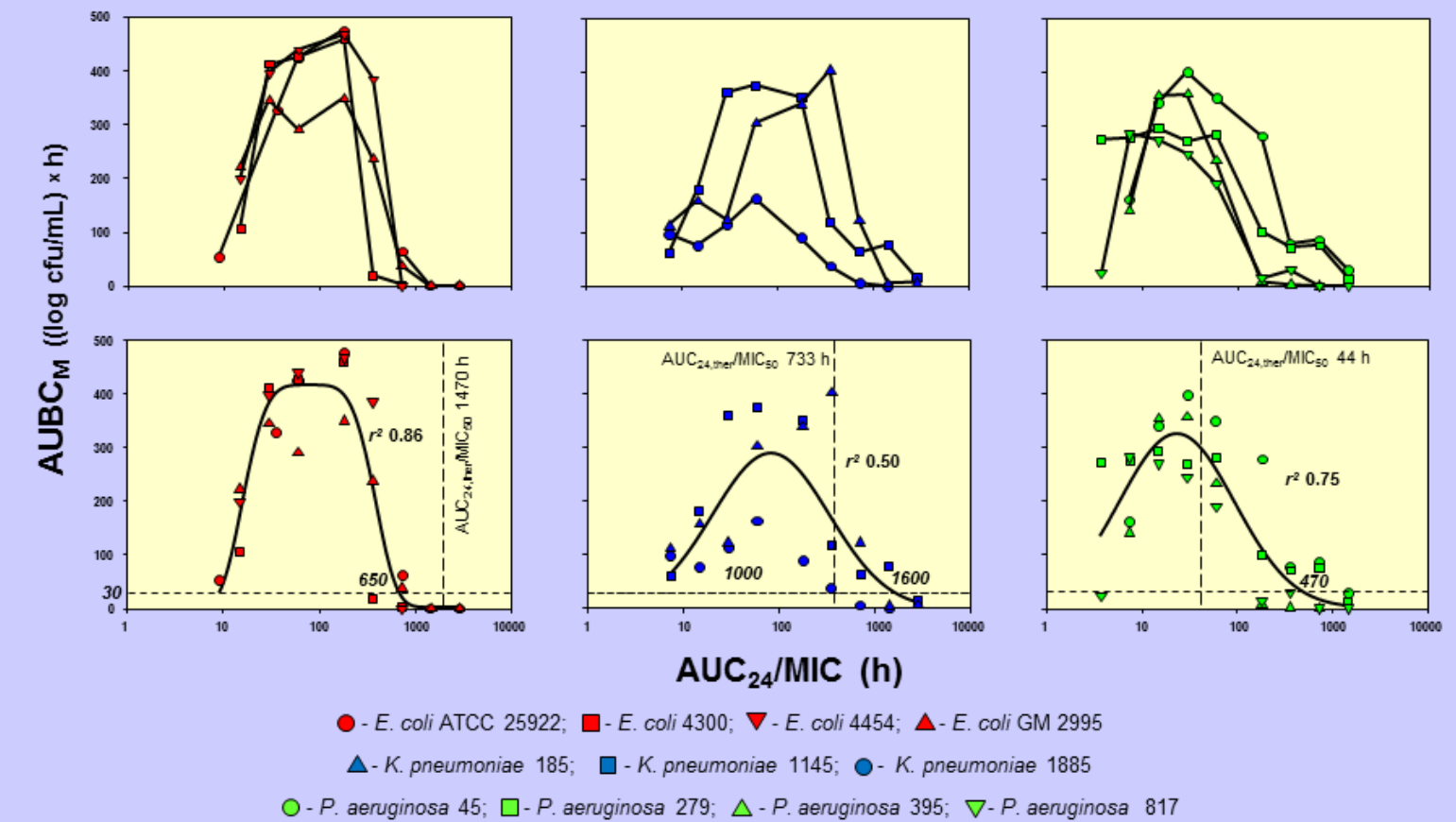


## Results

●  $AUC_{24}/MIC$  relationships with  $AUC_{24,M}$  were bell-shaped with each organism (upper portion of Fig. 2.). Gaussian functions fit combined data on all strains of *E. coli*, *K. pneumoniae* or *P. aeruginosa* ( $r^2$  0.86, 0.50 and 0.75, respectively) – see bottom portion of Fig. 2. The respective “anti-mutant”  $AUC_{24}/MIC$ s were 650, 1600 and 470 h.

● The “anti-mutant”  $AUC_{24}/MIC$  was less than clinically achievable  $AUC_{24,ther}/MIC_{50}$  ratio only for *E. coli* {1470 h (22 mg×h/L [6]/0.016 mg/L [7])} but not *K. pneumoniae* {730 h (22/0.03 [7])} and *P. aeruginosa* {44 h (22/0.5 [8-10])}.

**Fig. 2.  $AUC_{24}/MIC$ -dependent effects of ciprofloxacin on *E. coli*, *K. pneumoniae* and *P. aeruginosa* resistant to 4×MIC**



## Conclusions

● Like *S. aureus*,  $AUC_{24}/MIC$ -resistance relationships with *E. coli*, *K. pneumoniae* and *P. aeruginosa* are bell-shaped.

● Based on these relationships, “anti-mutant”  $AUC_{24}/MIC$  ratios can be achieved at clinically attainable  $AUC_{24,ther}/MIC_{50}$ s for *E. coli*, but not *K. pneumoniae* and *P. aeruginosa*.

## References:

- [1] Firsov AA, Vostrov SN, Lubenko IY et al. 2003. Antimicrob. Agents Chemother. 47:1604-13.
- [2] Firsov AA, Vostrov SN, Lubenko IY et al. 2004. J. Antimicrob. Chemother, 54:178-86.
- [3] Oonishi Y, Mitsuyama O, Yamaguchi K. 2007. J. Antimicrob. Chemother. 60:1030-7.

- [4] Tam VH, Louie A, Deziel MR et al. 2007. Antimicrob. Agents Chemother. 51:744-7.
- [5] Firsov AA, Smirnova MV, Strukova EN et al. 2008. Int. J. Antimicrob. Agents. 32:488-93.
- [6] Firsov AA, Lubenko IY, Vostrov SN et al. 2005. Antimicrob. Agents Chemother. 49: 2642-7.
- [7] Gales AC, Jones RN, Gordon KA et al. 2000. J. Antimicrob. Chemother. 45:295-303.
- [8] Zelenitsky SA, Rubinstein E, Ariano RE et al. 2013. J. Antimicrob. Chemother. 68 (Suppl. 1):i67–i72.
- [9] Howard W, Biedenbach DJ, Jones RN. 2002. Clin. Microbiol. Infect. 8:340-4.
- [10] Mikamo H, Tanaka K, Watanabe K et al. 2006. J. Antibiot. 59:355-63.