

A joint population pharmacokinetic model of total and unbound temocillin serum concentrations in haemodialysis patients

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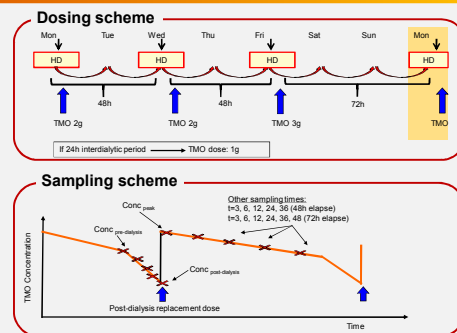


Background and Objectives

- ✓ Temocillin is a narrow-spectrum anti-Gram-negative beta-lactam marketed since the '80s witnessing renewed interest as a carbapenem-sparing drug, due to resistance to degradation by most β lactamases[1].
- ✓ Temocillin PK in hemodialysis patients has not been investigated yet.
- ✓ The purpose of this study was to develop a model describing the PK of total and unbound temocillin serum concentrations in end stage renal disease (ESRD) patients undergoing hemodialysis.
- ✓ In addition, this study aims to evaluate by simulation, the clinical performance of current dosing regimens, considering that β -lactam efficacy is best predicted by the proportion of the dosing interval during which unbound concentrations remain above the MIC (minimal inhibitory concentration) of the offending organism.

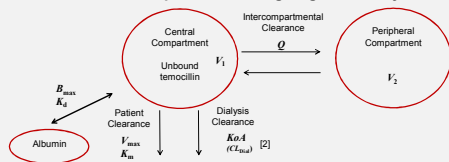
Methods

- ✓ Single-center, open-label, non-randomized study
- ✓ 16 patients were administered a dose of 1, 2, or 3g of temocillin (total of 61 doses) followed by an interdialytic period (off-dialysis) of 20, 44, or 68h, respectively, and dialysis period of 4h.
- ✓ 429 serum samples were collected to measure total and unbound concentrations.
- ✓ A population PK model was constructed and evaluated by a bootstrap analysis (internal evaluation, 1000 runs) and visual predictive check. A 1000-subject Monte Carlo simulation was conducted to determine 95% probability of target attainment (PTA95) versus MIC, based on 40% time above MIC ($fT > MIC$) for measured unbound drug.
- ✓ Data analyses were performed using NONMEM 7.3, Pirana, PsN and R.



Results

Schematic overview of the mechanism-based final PK model for temocillin in ESRD patients undergoing hemodialysis



Compartment 1
Off-dialysis

$$\frac{dA_1}{dt} = -\frac{V_{max}}{K_m + A_1} - \frac{A_1}{V_1} - Q \cdot \frac{A_1}{V_1} + \frac{A_2}{V_2}$$

On-dialysis

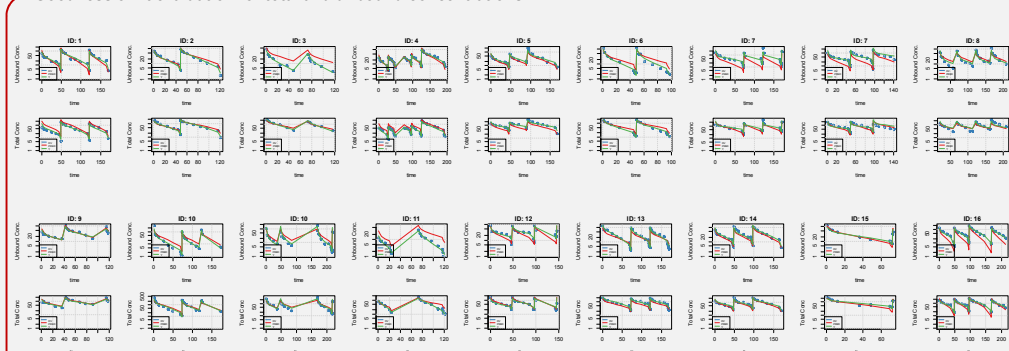
$$\frac{dA_1}{dt} = -\frac{V_{max}}{K_m + A_1} - \frac{A_1}{V_1} - Q \cdot \frac{A_1}{V_1} + \frac{A_2}{V_2} - CL_{dial} \cdot \frac{A_1}{V_1}$$

Compartment 2

$$\frac{dA_2}{dt} = Q \cdot \frac{A_1}{V_1} - \frac{A_2}{V_2}$$

$CL_{dial} = BFR \cdot (EXP(K_d \cdot BFR / (1 - BFR / DFR)) - 1) / (EXP(K_d \cdot BFR / (1 - BFR / DFR)) - BFR / DFR)$ [2]
BFR: blood flow rate (L/h); DFR: dialysis flow rate (L/h); K_d : mass transfer area coefficient (L/h)

Goodness of fit evaluation for total and unbound concentrations



DV = observed concentrations; Y = individual predicted concentrations; PRED = population-predicted concentrations

Final PK Parameter Estimates

Parameter	Estimate (RSE %)	Bootstrap median (95% CI) [†]	IIV CV% (RSE%)
Structural model			
V_1 (L) ^a	23.5 (10)	24.3 (20.9 - 28.7)	38.2 (19)
V_2 (L) ^a	24.9 (13)	25.7 (21.4 - 31.7)	37.3 (32)
Q (L/h) ^a	4.03 (12)	4.04 (2.8 - 4.5)	-
K_d (mL/min)	7.77 (16)	7.8 (5.9-9.9)	-
V_{max} (mg/h)	161 (37)	142.9 (101.1-188.1)	34.8 (25)
K_m (mg/h)	81.1 (51%)	68.5 (40.5-94.8)	52.3 (26)
K_d (mg/L)	32.8 (18)	36.3 (25.7 - 54.3)	81.9 (21)
B_{max} (mg/L)	114 (12)	121.0 (100.2 - 146.1)	42.1 (26)
Residual variability			
Proportional Error CV% unbound conc	23.9 (17)	23.7 (20.1 - 26.2)	-
Proportional Error CV% total conc	19.5 (18)	19.1 (16.3 - 21.5)	-

[†]estimated by applying the final PopPK model to 1000 re-sampled datasets

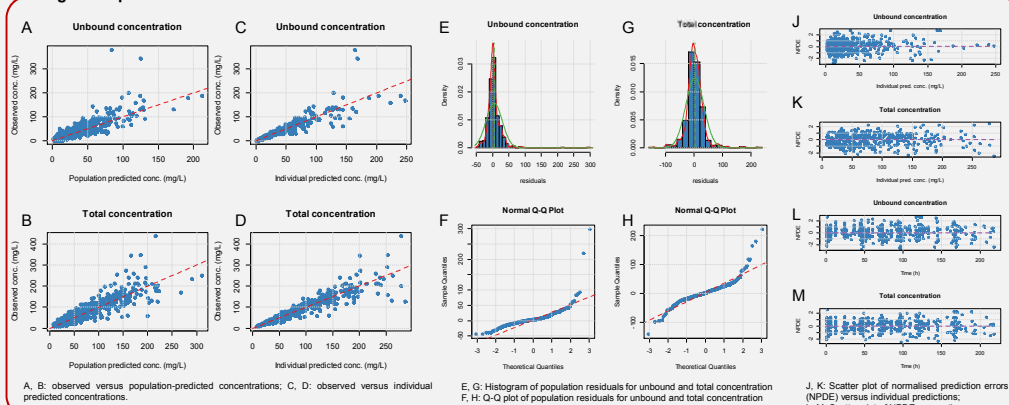
^aparameter allometric weight scaled.

^b $CL_{dial} = BFR \cdot (EXP(K_d \cdot BFR / (1 - BFR / DFR)) - 1) / (EXP(K_d \cdot BFR / (1 - BFR / DFR)) - BFR / DFR)$ [2]

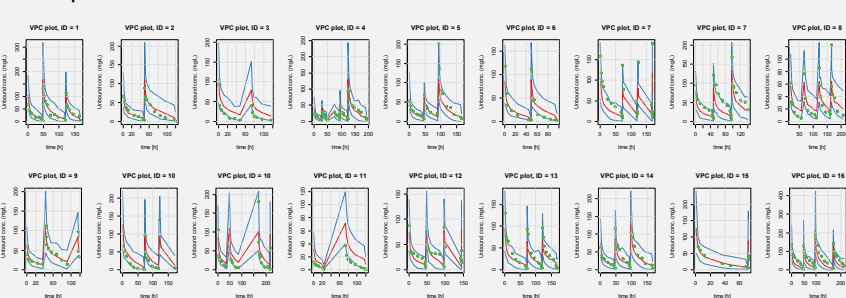
RSE, relative standard error; CV, coefficient of variation; IIV, interindividual variability; Q, intercompartmental clearance;

K_d : mass transfer area coefficient (L/h); V_{max} , maximum elimination rate of the system; K_m , drug concentration that produces 50% of the maximal elimination rate of the system; K_d , unbound drug concentration corresponding to half maximal binding; B_{max} , maximal binding capacity.

Diagnostic plots

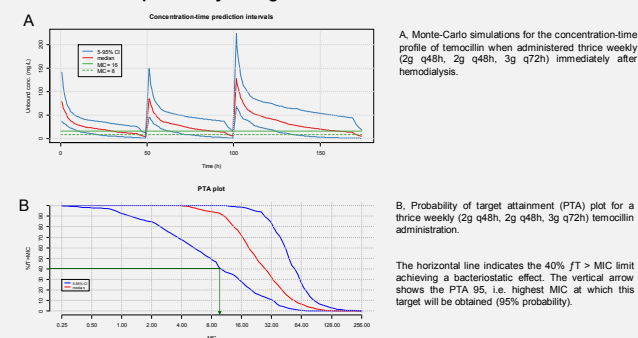


Visual predictive checks



VPCs displaying observed data (green dots) and prediction intervals for simulated data (blue: 5%-95%, red: median).

Simulations and probability of target attainment



Conclusions

- ✓ Temocillin PK off-dialysis was best described by a two-compartment model, non-linear binding to albumin (Langmuir model) and mixed order elimination. Dialysis clearance was best described by Michaelis equation. [2]
- ✓ The visual predictive checks indicated acceptable performance for simulation purposes, to support future studies.
- ✓ Simulations of a typical thrice weekly hemodialysis regimen, with temocillin administered immediately after dialysis, show that patients would be adequately treated (40% $fT > MIC$) for a MIC $\leq$ 8mg/L. However, for higher MICs like 16mg/L, patients might run the risk of sub-therapeutic drug exposure.

- ✓ Once the total temocillin serum concentrations are known, the unbound concentrations, which are pharmacologically active, can be predicted.
- ✓ This model might serve as a useful tool to provide guidance in the optimization of temocillin dosing regimens in hemodialysis patients.

[1] Livermore DM, Tulkens PM. Temocillin revived. J Antimicrob Chemother (2009); 63: 243-5.

[2] Michaels AS. Operating parameters and performance criteria for hemodialyzers and other membrane-separation devices. Trans Am Soc Artif Intern Organs (1966) 12:387-92.