

Using quantitative systems pharmacology to evaluate the drug efficacy of COX-2 and 5-LOX inhibitors in therapeutic situations

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SUPPLEMENTARY INFORMATION

PBPK model development

Properties of diclofenac, celecoxib, zileuton, licofelone, rifampicin and their metabolites are identified in literature and are used to establish the human PBPK models (Supplementary Table S2). In some cases, logP and Fu values as well as initial intestinal permeabilities provided by the modeling software¹ are slightly adjusted to best describe the clinical PK data. To represent the ADME behavior several active transport processes, metabolizing reactions, and clearance processes are considered in the respective model structure (Fig. 2, Supplementary Table S3). Relative abundances of relevant transporters and enzymes are estimated by using tissue-specific gene expression data.² Since diclofenac and its metabolites are highly bound to plasma proteins, an endothelial barrier between the plasma and the interstitial space is assumed for all organs (brain: 8.53E-05 cm/s (diclofenac), 8.24E-05 cm/s (3'-hydroxy-diclofenac), 8.79E-05 cm/s (4'-hydroxy-diclofenac), 1.44E-05 cm/s (5-hydroxy-diclofenac), 2.4E-7 cm/s (diclofenac-acyl-glucuronide), other organs/tissues: 0.05 cm/s) except the liver. The best-performing distribution models provided in the modeling software are used to determine intracellular-to-plasma partition coefficients (celecoxib: Rodgers and Rowland^{3,4}; diclofenac: PK-Sim Standard; licofelone: PK-Sim Standard; rifampicin: Schmitt⁵; zileuton: PK-Sim Standard) as well as permeabilities between the interstitial and the cellular space (celecoxib: PK-Sim Standard¹; diclofenac: PK-Sim Standard; licofelone: PK-Sim Standard; rifampicin: charge dependent Schmitt⁵; zileuton: PK-Sim Standard).

Developed PBPK models are validated by comparing simulated drug concentrations with clinical PK data from literature⁶⁻²¹. Thereby, PBPK model parameters are kept unchanged, besides parameters specifying the clinical study design (e.g. the dose level). Since CYP2C9 genetic polymorphisms have an influence on the pharmacokinetics of celecoxib, different kinetic parameters are used to take into account the differences in drug plasma concentrations for the CYP2C9 genotypes (Supplementary Table S3).

Model quality is assessed by visually inspecting simulated and experimental drug concentrations. In addition, normalized root-mean-square deviation (RMSD)²² as well as coefficient of determination (R^2) are calculated, and percentage deviations between simulated and experimental Cmax and AUC(0→∞) are evaluated (Supplementary Fig. S1).

SUPPLEMENTARY FIGURE LEGENDS

Supplementary Fig. S1 PBPK model assessment.

Observed vs. predicted plots, normalized RMSD value, coefficient of determination (R^2), deviations of C_{max} and $AUC(0-\infty)$ values determined by comparing experimental PK data with simulated drug concentration-time profiles. References and dose levels of the experimental data are shown above each plot. Root-mean-square deviation, RMSD; area under the curve, AUC; maximal concentration, C_{max} ; Diclofenac, DFN; hydroxy, OH; acyl glucuronide, AGLU; celecoxib, CEL; carboxy, COOH; glucuronide, GLU; zileuton, ZLT; sulfoxide, SO; licofelone, LCF; rifampicin, RIF; desacetyl, DA.

Supplementary Fig. S2 Rifampicin-induced activation dynamics of CYP3A4.

a Intracellular concentrations of unbound rifampicin are simulated in the liver following oral administration of 600 mg q.d. over one week. b Rifampicin-induced induction of CYP3A4 mRNA expression levels and CYP3A4 enzyme activity. Once daily, "q.d".;

Supplementary Fig. S3 Conceptual overview of the QSP PBPK/PD approach.

PBPK models in-house developed by use of PK-Sim are coupled with existing SBML models from literature by using the MoBi toolbox for MATLAB and the IQM toolbox to perform PBPK/PD simulations.

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