



## Translation of Pre-Clinical Pharmacokinetic Parameters in the Determination of Dosing in First Time in Human Studies

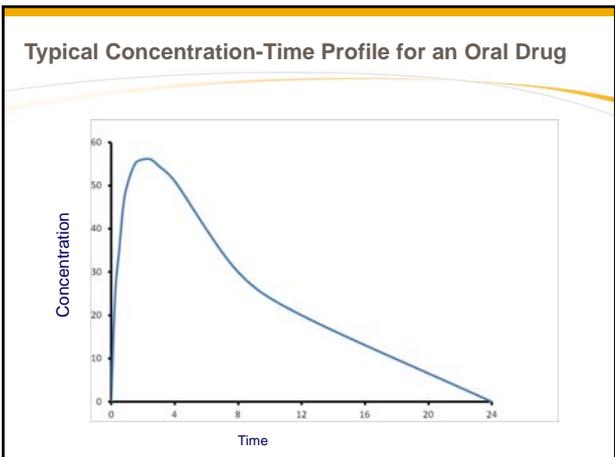
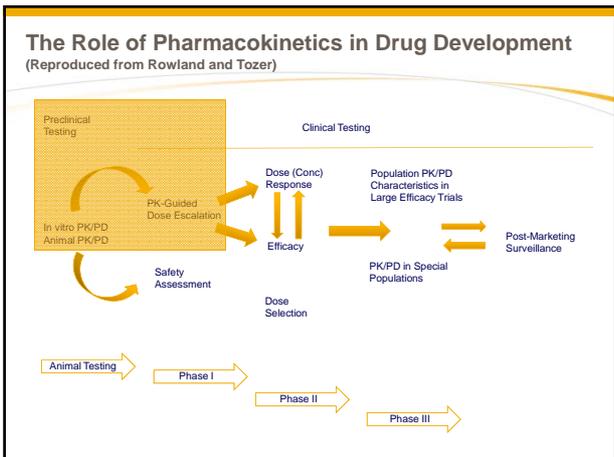
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 Biannual non-clinical statistics conference  
 September 2012, Potsdam

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### What am I going to talk about

- The role of pharmacokinetics in drug development
  - From pre-clinical through the clinical development spectrum
  - A typical PK profile for an orally administered drug
- How PK is used to choose dose
  - FDA Guidance on Minimum Recommended Starting Dose
  - Use of PK data and simple allometric scaling
- Methods for prediction of FTIH dose from pre-clinical PK
  - PhRMA Clinical and Preclinical Development Committee (CPCDC)
- On-going GSK work
  - Methods of prediction, data set collection, statistical comparisons

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## How is PK Used to Select a Starting Dose

### Guidance for Industry Estimating the Maximum Safe Starting Dose in Initial Clinical Trials for Therapeutics in Adult Healthy Volunteers

U.S. Department of Health and Human Services  
Food and Drug Administration  
Center for Drug Evaluation and Research (CDER)  
July 2006  
Pharmacokinetics and Toxicology



## Method by Reigner and Blesch (2002)

- Instead of using dose Reigner and Blesch use systemic exposure – e.g. AUC
- The desired systemic exposure = that which corresponds to the NOAEL
- If available from more than one species – the species with the lowest AUC is used
- Uses clearance of the drug in humans predicted by allometric scaling

$$SD = AUC_p \times CL_h$$

- Where
  - SD = Starting Dose
  - AUC<sub>p</sub> = Pre-clinical AUC
  - CL<sub>h</sub> = Human clearance estimated using allometric scaling

## Allometric Scaling

- The theory of allometric scaling assumes you treat a species as a large animal
- $Y = aTBW^b$  or  $\ln(a) + b \cdot \ln(TBW)$
- One common slope and one common intercept
- Slope is dictated by biological processes thus has an exponent with median a value of 0.75 or 0.67
- Intercept is a function of drug properties, thus can approximate to clearance
- If true can scale from one species



$$CL_{Human} = CL_{Animal} \times \left[ \frac{Weight_{Human}}{Weight_{Animal}} \right]^{0.75}$$



## PhRMA Clinical and Preclinical Development Committee

### PhRMA CPE/CDC Initiative on Predictive Models of Human Pharmacokinetics, Part 1: Goals, Properties of the PhRMA Dataset, and Comparison with Literature Datasets

PhRMA's mission is to provide quality products, services to patients and healthcare providers. The PhRMA Clinical and Preclinical Development Committee (CPE/CDC) is a key component of PhRMA's commitment to the industry and to the public. The CPE/CDC is a multi-stakeholder organization that brings together industry, academia, and regulatory agencies to address key issues in the development of predictive models of human pharmacokinetics. The CPE/CDC is currently focused on the development of a predictive model of human pharmacokinetics based on preclinical data. The CPE/CDC is currently focused on the development of a predictive model of human pharmacokinetics based on preclinical data. The CPE/CDC is currently focused on the development of a predictive model of human pharmacokinetics based on preclinical data.

- Limited Duration Key Issues Team - Predictive Models of Human PK
  - Assess prediction methods
  - Verify impact of protein binding
  - Compare monkey with Rat and Dog
  - Predict PK properties and full plasma profiles
  - Evaluate the prediction methods based on the degree of accuracy
  - Provide a mechanistic understanding of why one method provides better predictions than another

## Methods to Compare Plasma Clearance

- Allometry
- Simple and multiexponential allometry
- $F_u$  corrected intercept
- Rule of exponent
- Normalized allometry
- Single species scaling
- Two-species scaling
- Animal-human proportionality
- Calculation methods
- QSAR equation based on molecular descriptors and preclinical CL *in vivo* data
- Microsomes and hepatocytes

## Eight Statistical Parameters

- Number of predictions/drugs
- % less than two-fold error of deviation
- % less than three-fold error of deviation
- % more than ten-fold error of deviation
- Absolute fold errors
- Root mean square error
- Concordance correlation coefficient

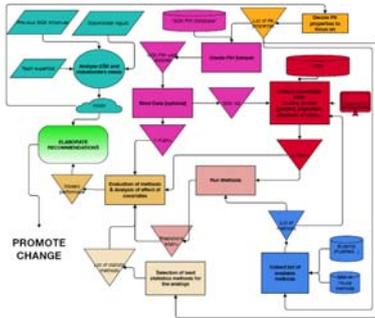
## Conclusions from looking at Clearance

- Prediction of human CL based on nonclinical CL data (allometry) was slightly more accurate than predictions based on *in vitro* data
- The  $f_u$  Intercept Correction Method (FCIM) and two-species-based allometry (rat-dog) were the best performing allometric methods.
- The best IVIVE methods for predicting human CL were the microsomal method corrected for both binding in plasma and incubation medium and hepatocyte method not corrected for any binding.
- Work is expanded to look at volume of distribution

## GSK Human Pharmacokinetics (PK) and Dose Predictions Initiative

- Overall Goal
  - Evaluate the applicability of the recommendations of the PhRMA CPCDC Predictive Models of Human PK working group within the GSK drug domain.
- Comparing those methods found to be the best performing in the prediction of FTIH PK data with GSK current methods
- Stage I – GSK dataset collection
  - Collection of in-house human PK data from FIH and clinical trials studies (reference data)
  - Collection of associated discovery and pre-clinical data
  - Calculation of human PK according to the several predictive models used by PhRMA and/or internally in GSK
- Stage II – Analysis of dataset and production of recommendations
  - Selection of statistical analysis methods for the comparison of several predictions with the reference data
  - Performance of statistical analysis and ranking of predictive methods, based not only on comparison of means but also on comparison of variability
  - Produce recommendations and publish in a peer reviewed journal
- To be completed by end 2012, further work to be carried into 2013

## Flowchart of the GSK Human Pharmacokinetics (PK) and Dose Predictions Initiative



## Statistical Methods to Be Used for Comparisons

- PhRMA ones
  - Number of predictions/drugs, % less than two-fold error of deviation, % less than three-fold error of deviation, % more than ten-fold error of deviation, Absolute fold errors, Root mean square error, Concordance correlation coefficient
- Bayesian methods –
  - we are not just interested in point estimates, the distributions for the parameters is of more interest. Look at the posterior distribution from a Bayesian analysis of the data predicted using each of the methods. How does this compare to the distribution of the FIH data.
  - Posterior predictive distribution from the Bayesian analysis of the pre-clinical – how does it compare to the FIH data.
- ??????

## Conclusions

- PK data is used to predict FIH doses but the process uses different methods each of which have plusses and minuses.
- Much work done in this area resulting in the PhRMA report
- How much has been adopted in companies and what are the relative implications?