Prediction of Diclofenac Pharmacokinetics using Early Drug Discovery In Vitro Data in a Mechanistic Dog Physiologically-Based Pharmacokinetic Model - 'Simcyp Dog'.

SIMPLE From Virtual populations

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Introduction

Beagle dogs are used as a surrogate for human testing in toxicity of drugs and chemicals and specifically as a model for assessing oral drug absorption. *Simcyp Dog V3.0* is an *in silico* physiologically based absorption, distribution, metabolism and excretion Simulator. The model provides a platform and database for mechanistic modelling and simulation of the processes of oral absorption, tissue distribution, metabolism and excretion of drugs in a *10kg 'virtual' beagle dog*. It combines experimental data generated routinely during preclinical drug discovery and development from *in vitro* enzyme and cellular systems, and relevant physicochemical attributes of compound and dosage form to predict the fate of the drug *in vivo* in beagle dogs used routinely as a pre-clinical model in drug discovery.

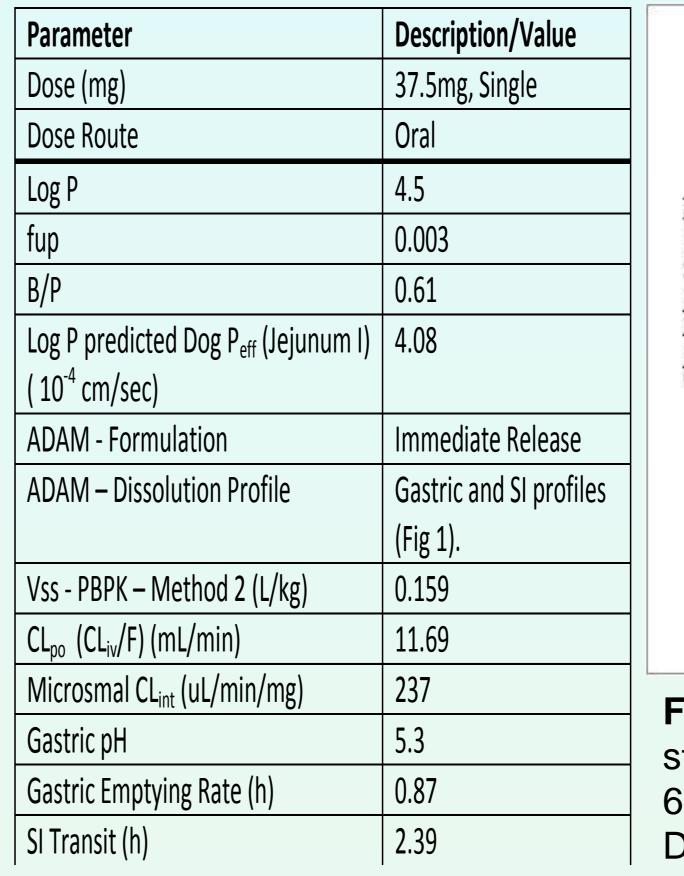
Purpose

To evaluate the performance of Simcyp Dog V3.0 to predict the Plasma Concentration-Time Profile of Diclofenac using Physico-Chemical and In Vitro Dog Liver Microsomal Metabolism Data.

Methods

Simcyp Dog V3.0 was used to predict the Plasma Concentration-Time profiles for an Orally administered Immediate Release formulation of Diclofenac in a 10kg 'virtual' beagle dog. The simulated trial was based on an *in vivo* trial¹ comprising *n*=6 beagle dogs orally administered a conventional diclofenac tablet. Simcyp Dog V3.0 utilised *In Vitro* Dissolution data (Figure 1) at pH 4 and pH 6.8 provided within the *in vivo* study with the Advanced Dissolution Absorption and Metabolism model (ADAM), the Physico-Chemical data for diclofenac such as LogP used to predict drug absorption and tissue distribution (Rodgers & Rowland Method), and kinetic metabolic data 'intrinsic clearances (CL_{int}) generated in Dog Liver Microsomes. This data is routinely generated in an Early Drug Discovery setting and the principle of *In Vitro In Vivo* Extrapolation (IVIVE)² was applied. A gastric pH of 5.3 used within the dog model was the value measured within the *in vivo* trial. The other key simulation parameters are provided in Table 1.

Table 1. Key Simulation Parameters



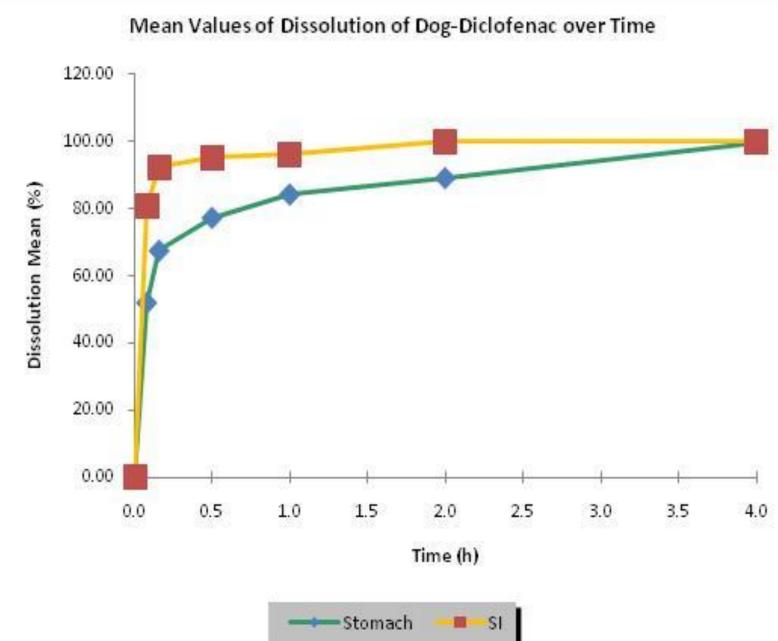


Figure 1. *In vitro* dissolution profiles for both stomach (pH 4) and small intestine (SI) (pH 6.8) used within the ADAM model in Simcyp Dog simulations.

Results

Figure 2 shows that simulations utilising an *in vivo* CL_{po} (CL_{iv}/F) and microsomal CL_{int} (IVIVE), successfully capture the *in vivo* profiles and that these profiles fall within the variability (deviation bars) of the *in vivo* study. The majority of the *in vivo* time points fall within the 5th and 95th centiles simulated by Simcyp dog.

The predicted PK parameters fall between a range of 0.83 and 1.33 fold different to those values calculated *in vivo* (table 2) for both *in vivo* CL_{po} and microsomal CL_{int} simulations, with the Mic CL_{int} simulation providing an AUC 0.96 fold that of the *in vivo* trial. Using only *in vitro* data routinely generated in an early drug discovery setting, the Mic CL_{int} simulation shows that it is possible to predict an *in vivo* diclofenac concentration time profile in a 'virtual' beagle dog successfully.

Table 2. Summary of pharmacokinetics parameters for the *in vivo* study and Simcyp Dog simulations using oral clearance (CI_{po}) and intrinsic clearance (CL_{int}) from dog liver microsomes (and CV% (within parentheses).

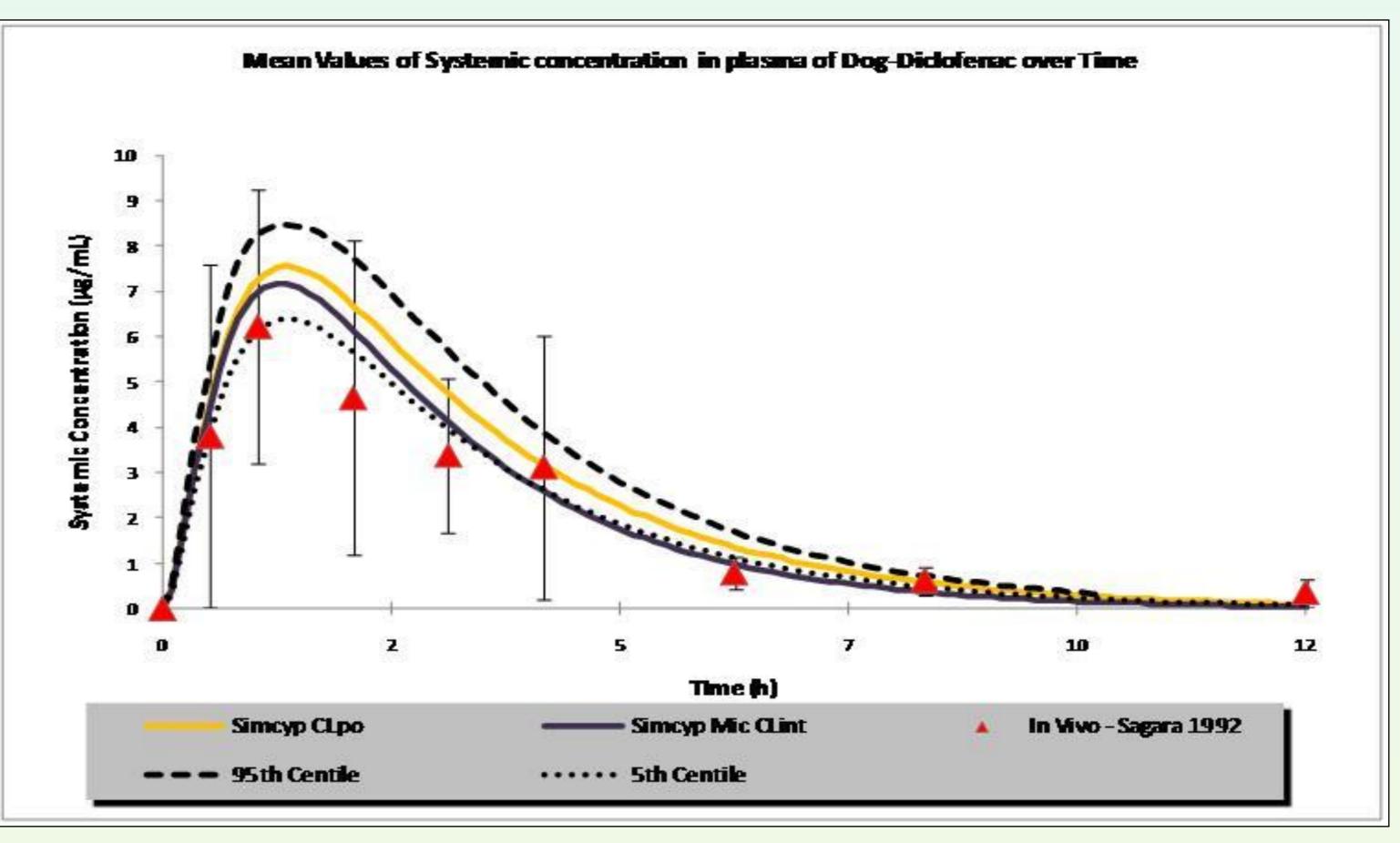


Figure 2. Diclofenac plasma concentration time profiles for the *in vivo* study (triangles) and Simcyp Dog simulations using oral clearance (Simcyp CL_{po} , yellow line) and intrinsic clearance (CL_{int}) from dog liver microsomes (Simcyp Mic CL_{int} , purple line), the - - - dashed line, reflects the 95th centile profile for Simcyp dog simulations (*n*=6) and the ----- dotted line, reflects the 5th centile profile for Simcyp dog simulations (*n*=6). Each *in vivo* point reflects the mean \pm standard deviation.

	T _{max} (h) (CV%)	Fold (<i>In</i> <i>Vivo</i> /Simcyp)	C _{max} (µg/mL) (CV%)	Fold (<i>In</i> <i>Vivo</i> /Simcyp)	AUC (µg/mL/h)	Fold (<i>In</i> <i>Vivo</i> /Simcyp)
In Vivo	1.6 ± 1.3 (81%)	_	8.1 ± 3.4 (42%)	_	23.6 ± 7.7 (33%)	_
Simcyp - CL _{po}	1.3 ± 0.09 (7%)	1.23	7.56 ± 0.94 (12%)	1.07	28.6 ± 3.81 (13%)	0.83
Simcyp - Microsomal CL _{int}	1.2 ± 0.13 (11%)	1.33	7.17 ± 0.89 (12%)	1.13	24.6 ± 3.28 (13%)	0.96
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- References
- 1. Sagara et al 1992, Chem Pharm Bull, 40(12), 3303-3306
- 2. Gibson G. G. & Rostami-Hodjegan 2007, Xenobiotica, Oct-Nov; 37 (10-11): 1013-1014.