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Introduction

Cyclosporine can take on a hydrophilic and hydrophobic conformation

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- Simulations only account for the hydrophilic conformation, but in vivo, cyclosporine is dynamic
- The goal of the study is to use GastroPlus™ to simulate the IV and oral pharmacokinetics of cyclosporine and understand the conformational changes in vivo
- Beyond cyclosporine, another goal is to develop a reliable systematic approach that can be applied to any other drug

Methods

- Literature data for cyclosporine were collected for physiochemical parameters, metabolizing enzymes, and transporters that affect cyclosporine pharmacokinetics
- Experimental parameters were introduced into GastroPlus[™] based on decision tree approach to determine appropriate changes
- The model was built in four main steps:
- Fit the distribution for the IV administration 1) while including non-mechanistic clearance
- 2) Fit mechanistic clearance (enzyme kinetics) for IV administration
- Fit absorption in oral administration 3)
- Evaluate gut and liver metabolism 4)

Model Development

- The IV model was fitted by adjusting the Fup and RBP from 22.3% and 0.73 (predicted) to 5% and 0.17 (experimental)
- CYP3A4 Vmax in the liver was adjusted from 9.16×10⁻⁵ mg/s/mg-enzyme (experimental) to 1.374×10⁻² mg/s/mg-enzyme (fitted) (units shown as in GastroPlus[™])
- Peff was adjusted to 12.049×10⁻⁴ cm/s (experimental); this large increase from 0.8×10^{-4} cm/s (default) is justified since GastroPlus™ treats cyclosporine as more hydrophilic
- Fup should be the same in the IV and oral model; however, since cyclosporine is dynamic, the change from 5% (IV) to 0.5% (oral) may reflect different conformations of cyclosporine

A Physiologically-Based Pharmacokinetic (PBPK) Model of Cyclosporine: Method Standardization and Improved Understanding of Conformational Effects

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Results						
IV		Oral				
		Figure	Tmax (hr)	Cmax (ng/ml)	AUC (ng*hr/ml)	
Cmax (ng/ml)	AUC (ng*hr/ml)	4	6.16	651.6	8394.4	
700		5	0.4	760.27	1275	
703	5393	6	2	369.2	1256.6	
1322	6535	7	2	3451.2	11000	
1399	6442	8	2	2727.9	10900	
1000		9	2	2035.2	7082.1	
1404	6573	Exp	1.79	1986.7	8101.1	
Total metabolism 300 250 Liver metabolism 200 150 Gut metabolism 100 50						
			Fig 10: Metabolism of cyclosporine by			

0 2 4 6 8 10 12 14 16 18 20 22 24 CYP3A4 Simulation Time (h)

Discussion

The developed cyclosporine model is largely based on experimental data

- A systematic approach was used for
- development of the model
- A key difference between the IV and oral
- models was the much lower **Fup** in the oral model
- A lower Fup indicates that a more hydrophobic conformer is present
- In oral delivery, the cyclosporine has to be in the hydrophobic form to be absorbed
- In IV delivery, we anticipate that most will still be in the hydrophobic form, but there will be some of the hydrophilic form will be present Therefore, the requirement of a change in Fup from IV to oral model may be a consequence of the different conformations of cyclosporine that are present in vivo

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Acknowledgment

We thank Simulations Plus for providing a license for GastroPlus™ through the University+ program.