# What is the Level of Expression of CYP2D6 in Human Liver? Influence of Different Calibration Standards on the Estimation of CYP2D6 Abundance





## INTRODUCTION

- Human hepatic CYP abundance is required for the scaling of in vitro data from recombinant human CYP systems (rhCYP) to in vivo metabolic drug clearance (Equation 1). Within this process, estimates of CYP expression are also used to determine Intersystem Extrapolation Factors (ISEFs), measures of the relative activity (per unit CYP) of the enzymes in human liver and rhCYP microsomes (Equation 2) (Proctor et al., 2004).
- CYP enzymes are present in liver as apoprotein (non-catalytic) and holoprotein (haem containing, catalytically active form). When rhCYP systems are used as standards for CYP quantification, the holo:apoprotein ratio is assumed to be similar to that in liver microsomes (HLM).

## AIMS

- To assess the variability in reported CYP2D6 abundance and determine if this is related to the use of different standards with different ratios of holo:apo CYP2D6 protein.
- Standard specific values of CYP2D6 abundance will be assigned to an uncharacterised pool of human liver microsomes (HLM) in order to investigate the effect of standard on values of ISEF.

### METHODS

- CYP2D6 abundance values were collated by searching two electronic databases ("MEDLINE" and "Web of Knowledge") and the studies were grouped according to the calibration standard used; BD baculovirus Supersomes<sup>™</sup> (BD SUP, n=2), CYP2D6 purified from human liver microsomes (HLM PUR, n=2), lymphoblastoid (LYMPH, n=2) and yeast (YEAST, n=3)). Weighted mean abundances were calculated for each group and the heterogeneity of the abundance values was assessed (Perrett *et al.*, 2007).
- ISEFs were calculated using the mean CYP2D6 abundance from each standard type and mean in vitro kinetic data for the CYP2D6 probe substrates debrisoquine, bufuralol and dextromethorphan (Simcyp internal data, unpublished), Equation 2.

### H.F.Perrett<sup>\*1</sup>, Z.E.Barter<sup>1,2</sup>, M.S.Lennard<sup>1</sup>, G.T.Tucker<sup>1,2</sup> and A.Rostami-Hodjegan<sup>1,2</sup>

### \*Correspondence: mdp05hfp@sheffield.ac.uk

<sup>1</sup>Academic Unit of Clinical Pharmacology, University of Sheffield, <sup>2</sup>Simcyp Limited, Blades Enterprise Centre, Sheffield,



Study	n	Mean CYP2D6 abundance (pmol/mg)	Standard
Nakajima <i>et al</i> ., 1999 Olesen <i>et al</i> ., 2001 Mean	6 10	6 8 73	BD SUP BD SUP
Zanger <i>et al</i> ., 2001 Coller <i>et al</i> ., 2002 <b>Mean</b>	71 50	8 8 8 8.0	HLM PUR HLM PUR
Shimada <i>et al</i> ., 1994 Venkatakrishnan <i>et al</i> ., 2000 <b>Mean</b>	30 11	9 10 <b>9.4</b>	LYMPH LYMPH
Perrett <i>et al.</i> (unpub) Imaoka <i>et al</i> ., 1996 Isobe <i>et al</i> ., 2005 <b>Mean</b>	58 16 3	10 14 18 <b>11.1</b>	YEAST YEAST YEAST
Total Weighted Mean		9.1	
$CL_{int}(L/h) = \left[\sum_{j=1}^{n} \left(\sum_{i=1}^{n} \frac{ SEF_{ji} \times Vmax(rhCYP_{j})_{i} \times CYP_{j}abundance}{K_{m}(rhCYP_{j})_{i}}\right)\right] \times MPPGL \times Liver w eigenvectors and the second secon$			
Equation 1: In vitro-in vivo extrapolation of rhCYP determined CL <sub>int</sub>			

CL<sub>intii</sub>(HLM) (ml/min/mg)

 $\mathsf{ISEF}_{\mathsf{ii}} = -$ 

CYP<sub>i</sub>abundance(HLM) (pmol CYP/mg) CL<sub>inti</sub>(rhCYP); (ml/min/pm ol CYP)

Equation 2: Calculation of ISEF using data from HLM and rhCYP **incubations.** Where the i<sup>th</sup> pathway is metabolised by the j<sup>th</sup> CYP isoform, MPPGL = Microsomal Protein per gram of Liver

Figure 1: Effect of standard and probe substrate on values of CYP2D6 ISEF

### Table 1: Literature values of CYP2D6 abundance

### RESULTS

- found between studies.
- the difference.

### DISCUSSION

- Perrett *et al.*, 2006).
- ones shown here, have yet to be determined.
- than the choice of CYP2D6 probe substrate.

### REFERENCES

Coller et al., (2002) Br J Clin Pharmacol. 54(2):157 Imaoka et al., (1996) Biochem Pharmacol. 51:1041 Isobe et al., (2005) Biological & Pharmaceutical Bulletin. 28(4):634 Nakajima et al., (1999) Drug Metab Dispos. 27(12):1381 Olesen et al., (2001) J Clin Pharmacol. 41(8):823 Shimada et al., (1994) J Pharmacol Exp Ther., 270(1):414 Perrett et al., (2006) Drug Metab Rev. 38:109 Perrett et al., (2007) Drug Metab Dispos. 35:1733 Proctor et al., (2004) Xenobiotica. 34(2):151 Venkatakrishnan et al., (2000) Drug Metab Dispos. 28(12):1493 Wilson et al., (2005) Drug Metab Rev. 37:77 Zanger et al., (2001) Pharmacogenetics. 11(7):573



The University Sheffield.

Mean values of apparent liver microsomal abundance of CYP2D6 ranged from 6 to 18 pmol/mg protein (Table 1). Values obtained using BD SUP as a standard gave similar results (7.3) pmol/mg) to HLM PUR (8 pmol/mg). Using HLM PUR as the standard gave values which appeared lower than those obtained using LYMPH (9.4 pmol/mg) and YEAST (11.1 pmol/mg) standards. However, no significant heterogeneity was

Application of different standard specific CYP2D6 abundances translated into ISEF values ranging from 0.91 (YEAST) to 1.39 (BD SUP) (Figure 1), a 1.5-fold difference. The mean ISEF for probe substrates were 0.98 (bufuralol), 1.16 (dextromethorphan) and 1.23 (debrisoquine), a 1.2-fold

A trend for rhCYP2D6 standards to produce similar or higher values of abundance compared to those estimated using standards based on purified enzyme contrasts to tour previous finding with respect to CYP3A4/5 systems (Wilson et al., 2005,

We have recently shown that CYP2D6 holoprotein is present at lower levels in preparations purified from human liver than in e.coli rhCYP systems (Perrett et al., 2007). However, holoprotein levels for other rhCYP2D6 systems, including the

• The choice of CYP2D6 standard used to quantify CYP2D6 abundance in a HLM pool has more influence on ISEF values