

**TRANSCRIPTIONAL REGULATION
OF HUMAN UDP-
GLUCURONOSYLTTRANSFERASES**

Dione Anne Gardner-Stephen

B. Biotech. (Hons)

Department of Clinical Pharmacology

Faculty of Health Sciences, School of Medicine

Flinders University

A thesis submitted in fulfilment of the requirements for the

degree of Doctor of Philosophy

2008

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SUMMARY

The UDP-glucuronosyltransferases (UGTs) are a superfamily of enzymes that glucuronidate small, lipophilic molecules, thereby altering their biological activity and excretion. In humans, important examples of UGT substrates include molecules of both endogenous and xenobiotic origin; thus, UGTs are considered essential contributors to homeostatic regulation and an important defence mechanism against chemical insult. In keeping with both roles, UGTs are most strongly expressed in the liver, a predominant organ involved in detoxification.

Rates of glucuronidation in humans are neither uniform among individuals, nor constant in an individual over time. Genetic determinants and non-endogenous signals are both known to influence the expression of UGTs, which in turn may affect the efficacy of certain pharmaceutical treatments or alter long-term risk of developing disease. Thus, this thesis focuses on the transcriptional regulation of *UGT* genes in humans, particularly on mechanisms that are likely to be relevant to their expression and variation in the liver. Two major approaches were used: firstly, extensive studies of several *UGT* promoters were performed to identify and characterise transcriptional elements that are important for UGT expression; and secondly, important hepatic transcription factors were investigated as potential regulators of *UGT* genes.

UGT1A3, *UGT1A4* and *UGT1A5* are a subset of highly related, but independently regulated, genes of the human *UGT1* subfamily. *UGT1A3* and *UGT1A4* are expressed in the liver, whereas *UGT1A5* is not. The presented analysis of the *UGT1A3*, *UGT1A4* and *UGT1A5* proximal promoters demonstrates that a hepatocyte nuclear factor (HNF)1-binding site common to all three promoters is important for

UGT1A3 and *UGT1A4* promoter activity *in vitro*, but is insufficient to drive *UGT1A5* expression. Two additional elements required for the maximal activity of the *UGT1A3* promoter were also identified that may distinguish this gene from *UGT1A4*. *UGT1A3* was investigated further, focusing on mechanisms that may contribute to interindividual variation in *UGT1A3* expression. Polymorphisms in the *UGT1A3* proximal promoter were identified and their functional consequences tested. Known variants of HNF1 α were also tested for altered activity towards the *UGT1A3* gene.

UGT1A9 is the only hepatic member of the *UGT1A7-1A10* subgroup of *UGT1* enzymes. Previous work had identified HNF1-binding sites in all four genes, and HNF4 α as an *UGT1A9*-specific regulator. The work presented herein extends these findings to show that HNF1 factors and HNF4 α synergistically regulate *UGT1A9*, and that HNF4 α is not the only transcription factor responsible for the unique presence of *UGT1A9* in the liver.

Liver-enriched transcription factors screened as potential *UGT* regulators were chosen from the HNF1, HNF4, HNF6, FoxA and C/EBP protein families. Functional interactions newly identified by this work were HNF4 α with *UGT1A1* and *UGT1A6*, HNF6 with *UGT1A4* and *UGT2B11*, FoxA1 and FoxA3 with *UGT2B11*, *UGT2B15* and *UGT2B28* and C/EBP α with *UGT2B17*. Observations were also made regarding different patterns of interaction between each *UGT* and the transcription factors tested, particularly HNF1 α .

These studies significantly advance the understanding of the transcriptional control of human *UGT* genes. In time, it is hoped that a detailed knowledge of UGTs will be useful in developing better therapeutic and prophylactic medical treatments.

DECLARATION

I certify that this thesis does not incorporate without acknowledgement any material previously submitted for a degree or diploma in any university; and that to the best of my knowledge and belief it does not contain any material previously published or written by another person except where due reference is made in the text.

Dione Gardner-Stephen

ACKNOWLEDGEMENTS

I wish to convey sincere, heartfelt gratitude to all those who have made this thesis possible. Whether specifically listed below or otherwise, your encouragement, support, feedback and sacrifices have been invaluable; I am and continue to be most grateful.

Firstly, I offer profuse thanks to my supervisor, Professor Peter Mackenzie. Thank you for not only encouraging me to take on this project, but also for following through with friendly, effective guidance and constant availability. I have long admired your ability to balance excellent science with other important commitments, especially your family.

Also to my other colleagues, both past and present, I owe a great debt of thanks for their work and friendship. In particular, I thank Dr. Rikke Lewinsky and Dr. Philip Gregory, for providing much of the groundwork on which this thesis is built. Extra thanks are also due to Phil for teaching me many of the techniques used in this project. I am also grateful to Anne Rogers and Joanna Treloar for their excellent technical assistance, to Heather Aubert and Karli Goodwin for their unsurpassed administrative support, and to the numerous other friends and colleagues in the Department of Clinical Pharmacology who have made my PhD candidature a pleasant and productive one.

To my husband, best friend and co-PhD-student, Paul, I am forever grateful. Your love, support, encouragement and (worn out) listening ear mean more to me than words could ever express. I love you dearly and I hope you find some use for all the molecular biology you have accidentally learnt in the last few years! To our unborn child, I owe the great debt of motivation: your impending arrival was a great

incentive to finish this thesis and a very welcome distraction from the more mundane aspects of “writing-up”. I also want to recognise the contributions that my immediate and extended family, my friends and my church family have all made to my well-being over the course of my PhD. Thank you to you all. Finally, I willingly acknowledge the claim that Christ has on my life and praise Him for His unfailing provision for me; past, present and future.

PUBLICATIONS ARISING DIRECTLY FROM THIS THESIS

Gardner-Stephen, D.A. and Mackenzie, P.I. (2007) Isolation of the UDP-glucuronosyltransferase 1A3 and 1A4 proximal promoters and characterization of their dependence on the transcription factor hepatocyte nuclear factor 1alpha. *Drug Metab. Dispos.* **35**: 116-120.

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AWARDS IN SUPPORT OF THIS THESIS

Australasian Society of Clinical and Experimental Pharmacologists and Toxicologists Percy Student Poster Prize: Australian Health and Medical Research Congress 2004.

Australian Society for Biochemistry and Molecular Biology Student Poster Prize: ComBio2005 Combined National Conference 2005.

Australasian Society of Clinical and Experimental Pharmacologists and Toxicologists Peter Meffin Student Poster Prize (honourable mention): National Joint Meeting of the Australasian Society of Clinical and Experimental Pharmacologists and Toxicologists and the Australasian Pharmaceutical Science Association 2005.

Outstanding Laboratory Research Presentation Oral Prize: Flinders Cancer Control Alliance Research Day 2007.

ABBREVIATIONS

ADH	alcohol dehydrogenase
AF	activation function
AhR	aryl hydrocarbon receptor
apo	apolipoprotein
ATCC	American Type Culture Collection
ATP	adenosine triphosphate
BAC	bacterial artificial chromosome
β-ME	β-mercaptoethanol
BSA	bovine serum albumin
bZIP	basic region leucine zipper
C/EBP	CCAAT/enhancer binding protein
CAR	constitutive androstane receptor
CBP	CREB-binding protein
CDCA	chenodeoxycholic acid
Cdx	caudal-related homeodomain protein
CIP	calf intestinal alkaline phosphatase
CMV	cytomegalovirus
CoA	coenzyme A
cpm	counts per minute
CREB	cAMP-response-element-binding protein
CYP	cytochrome P450
DBP	D-site binding protein
DCoH	dimerisation co-factor of HNF1
DD	dihydrodiol dehydrogenase
DMEM	Dulbecco's modified Eagle's medium
DMSO	dimethyl sulphoxide
dNTP	deoxynucleotide-triphosphate
DTT	dithiothreitol
<i>E. coli</i>	<i>Escherichia coli</i>
EDTA	ethylenediaminetetra-acetic acid
EMSA	electrophoretic mobility-shift assay
ER β	oestrogen receptor β
fabp	fatty acid-binding protein
FoxA	forkhead box A
FXR	farnesoid X receptor
glut2	glucose transporter 2
GR	glucocorticoid receptor
GRIP	glucocorticoid receptor interacting protein
HAT	histone acetyltransferase
HCV	hepatitis C virus
HDAC	histone deacetylase
HNF	hepatocyte nuclear factor
IL	interleukin
Inr	initiator
LAP	liver-enriched transcriptional activator protein
LB	Luria broth

LETF	liver-enriched transcription factor
LIP	liver-enriched transcriptional inhibitory protein
LXR	liver X receptor
MODY	mature onset diabetes of the young
MRP	multidrug resistance protein
NCoR	nuclear receptor co-repressor
NNAL	4-(methylnitrosamino)-1-(3-pyridyl)-1-butanol
NRRE	nuclear receptor response element
NSAID	non-steroidal anti-inflammatory drug
OAT	organic anion transporter
Oct	octamer transcription factor
P/CAF	p300/CBP-associated factor
PBREM	phenobarbital response enhancer module
PBS	phosphate buffered saline
pBSII	pBlueScript II
PCR	polymerase chain reaction
PGC	PPAR-gamma co-activator
PhIP	2-amino-1-methyl-6-phenylimidazo[4,5- <i>b</i>]pyridine
POU	Pit-1, Oct-1 and Oct-2, and Unc-86
PPAR	peroxisome-proliferator-activated receptor
PXR	pregnane X receptor
QPCR	quantitative real-time PCR
rRNA	ribosomal RNA
rs	reference SNP
RXR	retinoid X receptor
SDS	sodium dodecyl sulphate
SHP	small heterodimer partner
siRNA	small interfering RNA
SMP	skim milk powder
SMRT	silencing mediator of retinoid and thyroid hormone receptor
SN-38	7-ethyl-10-hydroxycamptothecine
SNAP	<i>S</i> -nitroso- <i>N</i> -acetyl penicillamine
SNP	single nucleotide polymorphism
SRC	steroid receptor co-activator
TBE	tris-borate EDTA
TBST	tris-buffered saline/tween-20
TFII	transcription factor II
Tris	tris[hydroxymethyl]aminomethane
TSA	trichostatin A
TSS	transcription start site
UDP	uridine diphosphate
UGT	UDP-glucuronosyltransferase
XRE	xenobiotic response element