



<http://researchspace.auckland.ac.nz>

ResearchSpace@Auckland

Copyright Statement

The digital copy of this thesis is protected by the Copyright Act 1994 (New Zealand).

This thesis may be consulted by you, provided you comply with the provisions of the Act and the following conditions of use:

- Any use you make of these documents or images must be for research or private study purposes only, and you may not make them available to any other person.
- Authors control the copyright of their thesis. You will recognise the author's right to be identified as the author of this thesis, and due acknowledgement will be made to the author where appropriate.
- You will obtain the author's permission before publishing any material from their thesis.

To request permissions please use the Feedback form on our webpage.

<http://researchspace.auckland.ac.nz/feedback>

General copyright and disclaimer

In addition to the above conditions, authors give their consent for the digital copy of their work to be used subject to the conditions specified on the Library Thesis Consent Form.

**ENZYME ACTIVITIES ASSOCIATED WITH
GONADOTROPIC HORMONES**

Mirella Maria Daja

A thesis submitted in fulfilment
of the requirements for the degree of
Doctor of Philosophy in Biochemistry,
University of Auckland,
September 1993.

*"Science is always wrong.
It never solves a problem without creating ten more".*

George Bernard Shaw

ABSTRACT

A structural relationship between gonadotropic hormones and certain types of enzymes has been suggested in previous studies and an investigation into the possibility of enzymatic activity associated with the gonadotropic hormones has been the primary focus of the research presented in this thesis.

Partial sequence homology between human chorionic gonadotropin (hCG) and α -chymotrypsin prompted the recent proposal of a tertiary structure of hCG using α -chymotrypsin as a folding template, which suggested the possibility of intrinsic peptidase activity associated with hCG. Highly purified hCG (CR127) was assayed for enzymatic activity against a range of synthetic peptide substrates and was found to exhibit Arg-specific peptidase activity. This activity was almost completely inhibited by diisopropylfluorophosphate (DFP), soybean trypsin inhibitor (STI), N-tosyl-L-phenylalanine chloromethyl ketone (TPCK) and to a lesser extent by N- α -p-tosyl-L-lysine chloromethyl ketone (TLCK), which indicated that the observed protease activity was serine protease-like. To establish whether this activity was intrinsic to the hormone or due to contaminants, extensive purification procedures were carried out. Hydrophobic interaction chromatography (HIC) and soybean trypsin inhibitor-affinity chromatography were found to effectively separate the protease activity from the hormone, indicating the presence of exogenous protease contaminants in the highly purified preparation of hCG. Further analysis by [³H]-DFP labelling of hCG and SDS-PAGE of the isolated contaminants revealed the presence of possible serine proteases with apparent molecular masses of 60 and 20 kD.

Because serine proteases are known to stimulate cAMP production in the same target cells, it was necessary to determine the effects of the contaminating proteases on the receptor binding of hCG and cAMP production. The presence of these contaminants was found to have no apparent effect on the receptor binding capability of hCG, however the *in vitro* biological activity of hCG as determined by maximal cAMP production was decreased after HIC-HPLC purification of the hormone. These observations suggested that the serine protease-like contaminants contributed to the total cAMP production, thereby introducing significant error in biological assays that use hCG (CR127).

The possible intrinsic enzymatic activity of hCG against its receptor as a natural substrate was further investigated. A membrane-bound receptor preparation was isolated from porcine ovaries and a receptor binding assay successfully established. The effects of hCG

binding upon the membrane-bound receptor were studied and receptor proteolysis was observed. However, this proteolysis could not be definitively attributed to the actions of hCG. A purified receptor was subsequently prepared by hCG-affinity chromatography and analysed by SDS-PAGE with detection by autoradiography and silver staining. The purified receptor was found to have undergone proteolysis during the purification procedure, presumably following incubation with the hCG affinity matrix.

Recent reports of the presence of homologous amino acid sequences in the active site of thioredoxin and the β -subunit of the gonadotropic hormones luteinizing hormone (LH) and follicle stimulating hormone (FSH), and subsequent demonstration of thioredoxin-like activity associated with these hormones, prompted an investigation into the possibility of thioredoxin-like activity associated with hCG. LH, FSH and hCG were all assayed for their ability to promote reactivation of reduced and denatured RNase. Although LH was shown to be capable of reactivating reduced RNase, the level of activity detected was significantly lower than that previously reported, whereas FSH and hCG were not found to be capable of this thioredoxin-like activity. These results suggested that the previously reported thioredoxin-like activity may be due to contamination of the hormone preparation, by the ubiquitous enzyme thioredoxin.

The possibility of LH possessing intrinsic dithiol-disulphide interchange activity was investigated further using [^3H]-iodoacetic acid. RNase/LH were incubated in an attempt to quench a dithiol intermediate. Preliminary results suggested that the presence of LH in this reaction increased the amount of protein radiolabelled, however, the isolation of a radiolabelled dithiol intermediate which could be conclusively identified as LH was not forthcoming.

Furthermore the lack of RNase reactivation activity in hCG, suggests that the putative thioredoxin-like activity of LH, if intrinsic, may not be involved in receptor activation and/or signal transduction, as hCG and LH share the same receptor and should therefore have a similar mechanism of activation.

ACKNOWLEDGEMENTS

This thesis is not only the conclusion of three years work, but also a reflection of the great help and support shown to me over the years by a great many people.

I would firstly like to thank my supervisor Professor A.G.C. Renwick and my co-supervisors Dr Ken Scott and Dr Jun Hiyama for all their guidance and support throughout the years. A special thanks to Dr Jun Hiyama, who was not only my co-supervisor but a valued colleague and supportive influence throughout my studies; for all the knowledge and experience I have acquired through your constant guidance, I am grateful.

I must thank the University Grants Committee for my post graduate scholarship which enabled me to undertake and complete my PhD and I acknowledge the Medical Research Council of New Zealand and the University of Auckland Graduate Research Fund for their assistance. I would especially like to thank the Department of Biochemistry for providing the extra support which was always needed and always welcome.

Various aspects of this work could not have been carried out without the valued help of many people. I am grateful to Dr. David Harding for providing synthetic peptide substrates, Dr. David Christie and Ms Catriona Knight for carrying out amino acid sequence analysis and Dr. T. H. Ji of the Department of Molecular Biology at the University of Wyoming for kindly performing receptor binding and cAMP assays. To Mr John Reyland and staff of the Auckland Municipal Abattoir I am deeply indebted for all their help and for not making me go out on the line and get the 'little fellas'.

To the various staff and students both past and present of the Department of Biochemistry (especially Ms Sue Buglass, Dr. Gerhard Weisshaar, John Soo Ping Chow, Oliver Hofmann, Penny Sowerby, Sushila Manilal, Hugh Senior and Tim Ng), I am grateful for your friendship and support which have made my many years as a member of this department enjoyable (most of the time anyway!). My thanks also to David Hieber for reading this thesis so many, many times and for providing much appreciated advice and comments. I would also like to thank Dr. Nigel Birch and Dr. David Christie who were always willing to help whenever I was in need.

I am grateful to Star for allowing me to vent my frustrations in clay and for being not only a great teacher but also a great friend. To Lucille for friendships newly found, Ruth for being my cosmic twin and to my dearest friends Kiri and Annemarie, I am truly indebted for all of your support and encouragement, least of all for putting up with me and all my stressful moments throughout the years. To Diana, I am eternally grateful for all the 'spiritual guidance' but especially for being my closest friend, and to Mark who had something to do with starting this all so many years ago -you have a lot to answer for!! To my dear friend David for giving so generously of your time and friendship, I am eternally grateful. All I can say is that we're *still* talking to each other but more importantly- Thank You. To Paul, for teaching me that one plus one equal one, and for your support a planet away- TDS.

I would like to thank all of my family but my special thanks go to my mother, without whose constant support, encouragement and faith in me, this day would not have come. For every step you suffered with me and for every success we celebrated, I am and always will be eternally grateful. *Ti ringrazio con tutto il cuore.*

TABLE OF CONTENTS

Abstract	ii
Acknowledgements	iv
Table of contents	vi
List of tables	x
List of figures	xi
Abbreviations	xiii

Chapter One: Introduction

1.1	Glycoprotein hormone function	1
1.2	Glycoprotein hormone structure	3
1.2.1	α -subunit structure	3
1.2.2	β -subunit structure	3
1.2.3	Putative α - and β -subunit interaction sites	5
1.3	Heterogeneity of glycoprotein hormones	5
1.4	Biosynthesis of glycoprotein hormones	7
1.4.1	α -subunit gene	7
1.4.2	β -subunit gene	8
1.5	Carbohydrate structures of glycoprotein hormones	8
1.5.1	Carbohydrate structures of hCG	11
1.5.2	Carbohydrate structures of LH	13
1.5.3	Carbohydrate structures of FSH	13
1.5.4	Carbohydrate structures of TSH	14
1.6	Functions of N-linked oligosaccharides of glycoprotein hormones	14
1.7	Putative enzymatic activity associated with the glycoprotein hormones	16
1.7.1	Serine protease activity	16
1.7.2	Dithiol-disulphide interchange	17

1.7.3	Dithiol-disulphide interchange associated with gonadotropic hormones	20
1.8	G proteins	21
1.9	Glycoprotein hormone receptors	22
1.9.1	Receptor binding regions in LH/hCG	26
1.10	Aims	29
Chapter Two:	Detection of protease activity associated with human chorionic gonadotropin	
2.1	Introduction	30
2.2	Materials and Methods	32
2.2.1	Materials	32
2.2.2	Esterase activity	33
2.2.3	Dissociation of hCG into α - and β -subunits	33
2.2.4	Reassociation of hCG α - and β -subunits	33
2.2.5	Peptidase activity	34
2.2.6	Inhibition studies	34
2.2.7	Further purification of hCG by HPLC	35
2.2.8	Effect of protease contaminants on hCG incubation	36
2.2.9	Analysis of peptidase contaminants by RP-HPLC	36
2.2.10	Receptor binding and cAMP stimulation assays	36
2.2.11	Gel electrophoresis	37
2.2.12	Amino acid sequence analysis	37
2.3	Results and Discussion	38
2.3.1	Peptidase activity	38
2.3.2	Effect of hormone and substrate concentrations on peptidase activity	42
2.3.3	Inhibition	42
2.3.4	Purification of hCG	47
2.3.5	Characterization of contaminants	47
2.3.6	Effects of protease contaminants on hCG incubation	51
2.3.7	Receptor binding and cAMP stimulation assays	51

Chapter Three: The proteolytic effect of human chorionic gonadotropin upon its receptor

3.1	Introduction	55
3.2	Materials and Methods	57
3.2.1	Materials	57
3.2.2	Iodination of hCG*	57
3.2.3	Isolation of membrane-bound hCG/LH receptor	58
3.2.4	Isolation of soluble hCG/LH receptor	58
3.2.5	Isolation of purified hCG/LH receptor	58
3.2.6	Receptor binding assay: temperature assessment	59
3.2.7	Receptor binding assay: receptor and [¹²⁵ I]-hCG* concentration dependence	59
3.2.8	Proteolytic cleavage of the receptor/[¹²⁵ I]-hCG* complex	60
3.2.9	Ligand blotting	60
3.3	Results and Discussion	61
3.3.1	Isolation of a membrane-bound hCG/LH receptor	61
3.3.2	Establishment of a receptor binding assay	62
3.3.3	Proteolytic action of hCG* against its receptor	66
3.3.4	Solubilization and purification of the hCG/LH receptor	70

Chapter Four: Characterization of thioredoxin-like activity associated with gonadotropic hormones

4.1	Introduction	75
4.2	Materials and Methods	77
4.2.1	Materials	77
4.2.2	HPLC purification of RNase	77
4.2.3	Reduction and denaturation of RNase	77
4.2.4	Reactivation of reduced and denatured RNase	78
4.2.5	Determination of RNase activity	78
4.2.6	S-[³ H]-carboxymethylation of RNase	78
4.2.7	S-[³ H]-carboxymethylation of RNase/LH	79

4.3	Results and Discussion	81
4.3.1	Reactivation of reduced and denatured RNase and determination of RNase activity	81
4.3.2	S-[³ H]-carboxymethylation of RNase	85
4.3.3	S-[³ H]-carboxymethylation of RNase/LH	86
4.3.4	Analysis of S-[³ H]-carboxymethylation of RNase/LH by SDS-PAGE	89
4.3.5	S-[³ H]-carboxymethylation of RNase/LH by RP-HPLC	92
4.3.6	Future directions	98
Chapter Five:	Conclusion	100
References:		106
Appendix:	Publication	127

LIST OF TABLES

Table 2.1	Peptidase activity of various glycoprotein hormones assayed with the substrate Bz-Phe-Val-Arg-pNA	40
Table 3.1	Purification of porcine hCG/LH receptor	71
Table 4.1	N-terminal sequence analysis of the radiolabelled fraction isolated by RP-HPLC	97

LIST OF FIGURES

Figure 1.1	Amino acid sequence of the human α -subunit	4
Figure 1.2	Amino acid sequence of the human β -subunit	6
Figure 1.3	General structures of N-linked sugar chains	9
Figure 1.4	Proposed structures of the asparagine-linked oligosaccharides of hCG	12
Figure 1.5	The primary structure of protein disulphide isomerase (PDI)	19
Figure 1.6	Diagram representative of the hCG/LH receptor	25
Figure 2.1	Peptidase activity of hCG (CR127) with synthetic peptide substrates	39
Figure 2.2	Peptidase activity of reassociated hCG (CR127) and its subunits	41
Figure 2.3	Inhibition of peptidase activity associated with hCG (CR127)	44
Figure 2.4	Autoradiography of [³ H]-DFP labelled hCG (CR127)	45
Figure 2.5	Soybean trypsin inhibitor-agarose purification of hCG (CR127)	46
Figure 2.6	Gel-filtration and anion-exchange chromatographic analysis of hCG and the associated peptidase activity	48
Figure 2.7	Purification of hCG (CR127)	49
Figure 2.8	HIC-HPLC purification of the contaminating proteases	50
Figure 2.9	Receptor binding and cAMP assay of hCG (CR127) and hCG*	52
Figure 3.1	Temperature dependence of receptor binding assay	63
Figure 3.2	Receptor concentration dependence of receptor binding assay	64
Figure 3.3	[¹²⁵ I]-hCG* concentration dependence of receptor binding assay	65
Figure 3.4	Receptor binding assay for membrane-bound receptor	67
Figure 3.5	Autoradiography of hCG/LH receptor proteolysis	68
Figure 3.6	Receptor binding assay for soluble receptor	72

Figure 3.7	Autoradiography and SDS-PAGE silver stain of the purified hCG/LH receptor preparation	73
Figure 4.1	Reactivation of reduced and denatured RNase	82
Figure 4.2	The reactivation of reduced and denatured RNase as a function of the concentrations of LH and hCG	84
Figure 4.3	Incorporation of [³ H]-IAA into RNase	87
Figure 4.4	Incorporation of [³ H]-IAA into RNase, LH and RNase/LH	88
Figure 4.5	Autoradiography of [³ H]-IAA labelled RNase/LH	90
Figure 4.6	SDS-PAGE analysis of RNase and LH	91
Figure 4.7	RP-HPLC analysis of RNase/LH	93
Figure 4.8	Analysis of [³ H]-IAA incorporation into RNase and LH by RP-HPLC	94
Figure 4.9	Isolation of [³ H]-labelled protein by RP-HPLC	96

ABBREVIATIONS

¹ H-NMR	proton nuclear magnetic resonance
BSA	bovine serum albumin
cAMP	adenosine 3', 5'-cyclic monophosphate
cCMP	cytidine 2':3'-cyclic monophosphate
cpm	counts per minute
DFP	diisopropylfluorophosphate
EDTA	ethylenediaminetetraacetic acid
h	hours
HIC	hydrophobic interaction chromatography
HPLC	high performance liquid chromatography
IAA	iodoacetic acid
kD	kilodaltons
MOPS	3-(N-Morpholino)propanesulfonic acid
PDI	protein disulphide isomerase
PEG	polyethylene glycol
PMSF	phenylmethylsulphonyl fluoride
RNase	ribonuclease A
RP	reverse phase
SDS-PAGE	sodium dodecyl sulphate polyacrylamide gel electrophoresis
STI	soybean trypsin inhibitor
TEA	triethylamine
TFA	trifluoroacetic acid
TLCK	N- α -p-tosyl-L-lysine chloromethyl ketone
TPCK	N-tosyl-L-phenylalanine chloromethyl ketone
Tris	tris (hydroxymethyl) aminomethane
w/v	weight per volume