

Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

Regulation of protein synthesis in the mammary gland

A thesis presented in partial fulfilment of the requirements for the degree of

Doctor of Philosophy

in
Animal Science

at Massey University
Palmerston North
New Zealand

**Amanda Aparecida Hayashi
2007**

This thesis is dedicated to my parents
Mandi Hayashi and Ivaci Hayashi

For your unconditional love

"It is the simple things in life that are the most extraordinary, only wise men are able to understand them."

Paulo Coelho

ABSTRACT

This thesis examines the signaling pathways involved in the regulation of milk protein synthesis in the lactating mammary gland and their control. The protein synthetic machinery can be regulated during the transcription, translation and degradation stages of mRNA processing. Translation control in eukaryotes involves changes in the activity or other functional properties of the translation factors. These include proteins involved in initiation, peptide-chain elongation and termination of mRNA processing. Changes in the nutritional, physiological and hormonal status of the body are sensed by receptors that signal to a central protein, known as mammalian target of rapamycin (mTOR). The mTOR signaling pathway then activates or inhibits the activity of translation factors and kinases involved in the initiation and elongation stage of translation.

A major objective of this thesis was to elucidate which genes and pathways are involved in the regulation of milk protein synthesis in the mammary gland and the mechanism(s) that regulate their action. The results presented here show that changes in milk protein production occurring during lactation in response to external stimuli are potentially regulated at the level of translation or subsequent processing rather than by transcriptional regulation (mRNA abundance).

The results also show that in response to growth hormone (GH) treatment, which increased the yield of milk protein, the phosphorylation status of the ribosomal protein S6 (S6) is increased as well as the protein abundance of eukaryotic elongation factor 2 (eEF2) and eukaryotic initiation factor 4E (eIF4E). These results suggest an important

relationship between milk protein yield and changes in the initiation and elongation stages of translation.

Another major finding was the elucidation that mTOR is involved in the signaling pathways activated by GH and that this effect involves signaling through the PI-3 kinase pathway. In these experiments, increased protein synthesis was potentially achieved with the use of GH. Thus, this study suggests the mTOR signaling pathway is a key mediator of the GH effects in protein synthesis stimulation.

Finally, the requirement for a functional mTOR signaling (TOS) motif in the eukaryotic initiation factor 4E binding protein (4E-BP1) was identified. This finding could help the identification of other proteins that may be controlled by mTOR and consequently are regulators of mRNA translation.

In summary, this thesis unveils key signaling pathways involved in the regulation of milk protein synthesis and provides further insight into the control of the mTOR signaling pathway. These findings open new frontiers for the manipulation of milk composition.

ACKNOWLEDGEMENTS

I would like to thank my supervisors from AgResearch, Dr. Sue McCoard, Dr. Nicole Roy, Dr. Warren McNabb and Dr. David Pacheco for all their intellectual support and supervision over these past years. I would like to record my gratitude to Dr Sue McCoard for her guidance and insights from the very early stage of this research as well as crucial contribution during the writing process. I thank her for encouragement during the final phases of my work and her fruitful feedback for my thesis. Dr. Nicole Roy was the first friendly face to greet me when I arrived in New Zealand and has always been a tremendous help no matter the task or circumstance. I am grateful for their time and effort listening to and supervising me.

I am indebted to my Massey University supervisor; Professor Duncan Mackenzie, for generously and constantly providing me with his invaluable guidance, advice and remarkable experience. I would also like to express my sincere gratitude to Professor Chris Proud for the treasured training I received at his lab and for furnishing me with his knowledge that nourished my education and research. Thank you all for helping me during these years of PhD study.

I am also very thankful to the AgResearch technical team; Kate Broadley, Peter Schreurs, Jason Peters, Bruce Sinclair, Bryan Treloar and Matt Deighton for their expert assistance. Thanks to the AgResearch post-docs and students; Katia Nones, Silas Vilas-Boas, Bianca Knoch, Ben Vladimir and Leoni, for their friendship and help. Thanks to the bioinformatics team and statistics group. Special thanks to the best secretaries in the world; Catherine Cameron and Denise Martin for being so competent and helpful.

Thanks to all members of Professor Proud's laboratory. Thanks to my dear friend and mentor Bruno Fonseca for the fruitful discussions and teaching. Thanks to Dr. Ewan Smith for your kindness; Danielle Krebs for your friendship and all other members from the lab; Min, Yanni, Maria, Josep, Brandon, Craig, Kailun, Suzan, Yun Young and Constance for making the lab a friendly and enjoyable working place.

I am sincerely thankful to CAPES, Brazilian PhD scholarship, which funded my four years of PhD studies. I acknowledge AgResearch Investment for financially supporting this work.

To my friends, whom have provided me with moral support.

I would like to thank my 'big family'; mum dad and sisters, for their love, dedication and emotional support throughout my life. Your love and dedication were my strength during these PhD years. Finally, thanks to my 'small family', Amer, for your love, dedication and patience necessary during this time without which I could not finish this thesis.

TABLE OF CONTENTS

ABSTRACT	I
ACKNOWLEDGEMENTS	III
TABLE OF CONTENTS.....	V
LIST OF TABLES	IX
LIST OF FIGURES.....	X
ABBREVIATIONS.....	XII
GENERAL INTRODUCTION.....	XV
CHAPTER 1: LITERATURE REVIEW.....	1
1.1. INTRODUCTION.....	2
1.2. MAMMARY GLAND	2
1.3. HOMEORHESIS	3
<i>1.3.1. Hormonal control of lactation</i>	4
<i>1.3.1.1. Growth hormone and homeorhesis</i>	7
1.4. MILK COMPOSITION.....	8
<i>1.4.1. Milk protein composition</i>	9
<i>1.4.1.1. Caseins.....</i>	9
<i>1.4.1.1.1. α_{S1}-casein.....</i>	10
<i>1.4.1.1.2. α_{S2}-casein.....</i>	10
<i>1.4.1.1.3. β-casein.....</i>	10
<i>1.4.1.1.4. κ-casein</i>	11
<i>1.4.1.2. Whey proteins</i>	11
<i>1.4.1.2.1. β-lactoglobulin.....</i>	11
<i>1.4.1.2.2. α-lactalbumin.....</i>	12
1.5. TREATMENTS TO AFFECT MILK PROTEIN SYNTHESIS.....	12
<i>1.5.1. Growth hormone.....</i>	13
<i>1.5.2. Atropine</i>	14
1.6. REGULATION OF THE MILK PROTEIN GENES	16
<i>1.6.1. Transcription</i>	17
<i>1.6.1.1. Transcriptional control of milk protein synthesis.....</i>	19
<i>1.6.1.1.1. Regulatory elements</i>	20
<i>1.6.1.1.2. Hormonal control.....</i>	21
<i>1.6.2. Translation.....</i>	22
<i>1.6.2.1. General overview of eukaryotic translation</i>	23
<i>1.6.2.1.1. Eukaryotic ribosome.....</i>	26
<i>1.6.2.1.2. Initiation.....</i>	27
<i>1.6.2.1.3. Elongation.....</i>	29
<i>1.6.2.1.4. Termination.....</i>	30
<i>1.6.2.2. Regulation of Eukaryotic mRNA Translation</i>	31
<i>1.6.2.2.1. Regulation of Translation Initiation</i>	32
<i>1.6.2.2.2 Regulation of eIF2 and Met tRNA_i recruitment to the ribosome</i>	32
<i>1.6.2.3. Regulation of eIF4E</i>	33
<i>1.6.2.4. eIF4E binding proteins (4E-BPs)</i>	34
<i>1.6.2.5. Regulation of translation elongation</i>	36
<i>1.6.2.6. Regulation of the S6 kinases</i>	38
<i>1.6.2.7. Signaling cascades involved in the regulation of translation – PI 3-Kinase signaling</i>	39
<i>1.6.2.8. Signaling cascades involved in the regulation of translation - MAP kinase signaling</i>	39
<i>1.6.2.9. Signaling cascades involved in the regulation of translation - mTOR signaling</i>	40
<i>1.6.2.10. The role of the translational regulatory factors in the regulation of lactation and milk protein synthesis</i>	42
1.7. RATIONALE FOR THE STUDY.....	43

CHAPTER 2: ELUCIDATION OF PATHWAYS INVOLVED IN THE REGULATION OF MILK PROTEIN SYNTHESIS	45
2.1. ABSTRACT	46
2.2. INTRODUCTION	47
2.3. MATERIAL AND METHODS	50
2.3.1. RNA extraction and purification	50
2.3.2. Microarray experiment	51
2.3.2.1. cDNA and fluorescent labelling	51
2.3.2.2. Array Preparation	53
2.3.2.3. Slide Hybridization and Scanning	54
2.3.2.4. Microarray Design, Normalization and Analysis	55
2.3.3. Quantitative real-time polymerase chain reaction	59
2.3.3.1. cDNA synthesis	59
2.3.3.2. Primers	60
2.3.3.3. PCR assay conditions	62
2.3.4. Agarose Gel	63
2.4. RESULTS	65
2.4.1. Gene expression profiles of mammary gland tissue	65
2.4.2. Regulation of milk protein genes	67
2.4.3. Functional grouping	67
2.4.3.1. Ingenuity pathway analyses	69
2.4.3.2. FUNC analyses software	69
2.4.4. Differentially expressed genes involved in the regulation of protein synthesis	70
2.4.5. Potential pathways involved in the regulation of milk protein synthesis	77
2.5. DISCUSSION	79
CHAPTER 3: RIBOSOMAL PROTEIN S6 IS INVOLVED IN CHANGES IN MILK PROTEIN YIELD CAUSED BY GROWTH HORMONE	85
3.1. ABSTRACT	86
3.2. INTRODUCTION	87
3.3. MATERIALS AND METHODS	90
3.3.1. Animals and experimental design	90
3.3.2. Total RNA extraction	90
3.3.3. qRT-PCR	90
3.3.4. Primers	90
3.3.5. Protein extraction from tissues	92
3.3.6. Determination of protein concentration	92
3.3.7. SDS-PAGE	93
3.3.8. Staining, fixing and drying polyacrylamide gels	93
3.3.9. Electrotransfer	94
3.3.10. Western blot analysis	94
3.3.11. Primary antisera	95
3.4. RESULTS	97
3.4.1. Gene expression of mTOR signaling	97
3.4.2. Effect of GH treatment on phospho-S6 and total S6	98
3.4.3. Effect of GH treatment on phospho-4E-BP1, total 4E-BP1 and total eIF4E	98
3.4.4. Effect of GH on the phospho- and total eEF2 and eEF2K	99
3.5. DISCUSSION	105
CHAPTER 4: STUDY OF THE MOLECULAR MECHANISM INVOLVED IN THE ATROPINE EFFECTS ON MILK PROTEIN SYNTHESIS IN LACTATING DAIRY COWS	111
4.1. ABSTRACT	112
4.2. INTRODUCTION	113
4.3. MATERIALS AND METHODS	116
4.3.1. Animals and experimental design	116
4.3.2. Total RNA extraction	116
4.3.3. Quantitative real-time polymerase chain reaction	116
4.3.4. Primers	116
4.3.5. Protein extraction from tissues	116
4.3.6. Determination of protein concentration	117

4.3.7. SDS-PAGE.....	117
4.3.8. Staining, fixing and drying polyacrylamide gels.....	117
4.3.9. Electrotransfer.....	117
4.3.10. Western blot analysis	117
4.3.11. Primary Antisera.....	117
4.4. RESULTS	118
4.4.1. Gene expression.....	118
4.4.2. Effect of atropine on translation initiation	119
4.4.3. Effect of atropine on translation elongation.....	120
4.5. DISCUSSION	125
CHAPTER 5 :THE RAPID ACTIVATION OF PROTEIN SYNTHESIS BY GH REQUIRES SIGNALING THROUGH THE MTOR.....	129
5.1. ABSTRACT	130
5.2. INTRODUCTION	132
5.3. MATERIALS AND METHODS	136
5.3.1. Cell culture (<i>H4IIE</i>)	136
5.3.2. Cell culture and treatment	136
5.3.3. Protein extraction from <i>H4IIE</i> hepatoma cells	137
5.3.4. Determination of protein concentration	138
5.3.5. <i>m⁷GTP-Sepharose Chromatography</i>	138
5.3.6. SDS-PAGE.....	138
5.3.7 Staining, fixing and drying polyacrylamide gels	139
5.3.8 Electrotransfer.....	139
5.3.9. Western blot analysis.....	139
5.3.10. Primary Antisera.....	139
5.3.11. Production and Purification of Polyclonal antibodies.....	139
5.3.12. Protein synthesis measurement.....	140
5.4. RESULTS	141
5.4.1. GH regulates multiple effectors of mTOR signaling	141
5.4.2. GH activates two pathways that can function upstream of mTOR	148
5.4.3. GH activates mTOR via PI 3-kinase	150
5.4.4. mTOR controls early and late stages of GH-induced eEF2 dephosphorylation	155
5.4.5. Rapamycin inhibits the activation of protein synthesis by GH	157
5.5. DISCUSSION	159
CHAPTER 6: THE ROLE OF EEF2 IN THE ACTIVATION OF PROTEIN SYNTHESIS BY GH.....	163
6.1. ABSTRACT	164
6.2. INTRODUCTION.....	165
6.3. MATERIAL AND METHODS	167
6.3.1. Tissue culture cell lines (<i>H4IIE</i>)	167
6.3.2. SiRNA molecules	167
6.3.3. Transient transfection of <i>H4IIE</i> cells.....	167
6.3.4. Cell treatment and preparation of cell lysates	168
6.3.5. Determination of protein concentration	168
6.3.6. SDS-PAGE.....	168
6.3.7 Staining, fixing and drying polyacrylamide gels	168
6.3.8 Electrotransfer.....	169
6.3.9. Western blot analysis.....	169
6.3.10. Primary Antisera.....	169
6.3.11. Production and Purification of Polyclonal antibodies.....	169
6.3.12. Protein synthesis measurement.....	169
6.4. RESULTS	170
6.4.1. eEF2K knock down in <i>H4IIE</i> cells.....	170
6.4.2. Transfection and starvation	172
6.4.3. Protein synthesis.....	175
6.5. DISCUSSION	105
CHAPTER 7: ANALYSIS OF THE INTERACTION AND REGULATORY MOTIFS IN 4E-BP1.....	181
7.1. ABSTRACT	182

7.2. INTRODUCTION	183
7.3. MATERIAL AND METHODS	187
7.3.1. Vectors	187
7.3.2. Induction and expression of fusion proteins in <i>E. coli</i>	187
7.3.4. Preparation of soluble and insoluble proteins from <i>E. coli</i>	188
7.3.5. Purification of soluble GST-fusion protein produced in <i>E. coli</i>	188
7.3.6. Polymerase chain reaction (PCR)	189
7.3.7. Determination of nucleic acid concentrations	189
7.3.8. Automated DNA sequence analysis	190
7.3.9. Agarose gel electrophoresis	190
7.3.10. Purification of DNA from agarose gels	190
7.3.11. Site direct mutagenesis	191
7.3.12. Bacterial strains	191
7.3.13. Preparation of competent cells	191
7.3.14. Transformation and selection of competent cells	192
7.3.15. Plasmid DNA preparation	193
7.3.16. Human Embryonic Kidney (HEK) 293 Cell Culture	193
7.3.17. Transient transfection of HEK 293 cells	194
7.3.18. Cell treatment and preparation of cell lysates	194
7.3.19. Determination of protein concentration	195
7.3.20. SDS-PAGE	195
7.3.21. Staining, fixing and drying polyacrylamide gels	195
7.3.22. Electrotransfer	196
7.3.23. Western blot analysis	196
7.3.24. Primary Antisera	196
7.3.25. Far Western Blotting using Raptor lysate	196
7.4. RESULTS	198
7.4.1 Regions of 4E-BP1 involved in binding to raptor	198
7.4.2. Defining what constitutes a functional TOS motif	200
7.5. DISCUSSION	208
CHAPTER 8: GENERAL DISCUSSION	211
8.1. METHODOLOGICAL CONSIDERATIONS	212
8.2. GENERAL DISCUSSION	219
8.3. FUTURE DIRECTIONS	223
APPENDIX A: ANIMAL MODELS TO STUDY THE MOLECULAR MECHANISMS INVOLVED IN THE REGULATION OF MAMMARY PROTEIN SYNTHESIS	225
A.1. ABSTRACT	226
A.2. INTRODUCTION	227
A.3. MATERIAL AND METHODS	229
A.3.1. Animals, diets and treatment	229
A.3.2. Milking and milk samples	232
A.3.3. HPLC method	232
A.3.4. Blood sampling	233
A.3.5. Collection of tissue samples	233
A.3.6. Statistical analysis	234
A.4. RESULTS	236
A.4.1. GH experiment - Milk yield and composition	236
A.4.2. GH experiment - Hormone concentration	236
A.4.3. Atropine experiment - Milk yield and composition	240
A.4.4. Atropine experiment - Hormone concentration	240
A.5. DISCUSSION	243
APPENDIX B.....	245
REFERENCES	270

LIST OF TABLES

Chapter 1:

Table 1.1:	<i>Eukaryotic translation factors involved in the initiation, elongation and termination.</i> 24
-------------------	--

Chapter 2:

Table 2.1:	<i>Primers used in quantitative real-time RT-PCR assays</i> 61
Table 2.2:	<i>qRT-PCR fold change for the reference genes</i> 64
Table 2.3:	<i>Summary of total gene expression changes in response to GH and atropine treatment (vs. control)</i> 66
Table 2.4:	<i>Microarray and qRT-PCR gene expression of milk protein genes from GH vs control or atropine vs. control cows</i> 68
Table 2.5:	<i>Differentially expressed genes involved in the protein synthesis in response to GH treatment vs. control. Genes are ordered in relation to fold difference in expression</i> 74
Table 2.6:	<i>Differentially expressed genes involved in the protein synthesis in response to atropine treatment vs. control. Genes are ordered in relation to fold difference in expression</i> 75

Chapter 3:

Table 3.1:	<i>Sequence of primer sets used for qRT-PCR</i> 91
Table 3.2:	<i>List of polyclonal antibodies used</i> 96

Chapter 7:

Table 7. 1:	<i>Known or potential TOS motifs in selected proteins of <i>H. sapiens</i>. Italics indicate putative TOS motifs: others have been shown to function in their respective proteins</i> 203
--------------------	---

Appendix A:

Table A.1:	<i>Diet ingredient and composition</i> 231
Table A.2:	<i>Milk yield and composition in control and GH-treated cows after 6 days of treatment</i> 237
Table A.3:	<i>Milk protein concentration and yield in control and GH-treated cows after 6 days of treatment</i> 238
Table A.4:	<i>Milk composition in control and atropine treated cows 8 hours after intravenous infusion of atropine sulphate</i> 241
Table A.5:	<i>Milk protein concentration in control- and atropine-treated cows 8 hours after intravenous infusion of atropine sulphate</i> 242

Appendix B:

Table B.1:	<i>Complete list of differentially expressed genes in response to GH treatment vs. control. Genes are ordered in relation to fold difference in expression</i> 246
Table B.2:	<i>Complete list of differentially expressed genes in response to atropine treatment vs. control. Genes are ordered in relation to fold difference in expression</i> 255
Table B.3:	<i>Significant associations between gene sets and ontological annotations. Category of genes up-regulated in response to GH treatment</i> 265
Table B.4:	<i>Significant associations between gene sets and ontological annotations. Category of genes down-regulated in response to GH treatment</i> 266
Table B.5:	<i>Significant associations between gene sets and ontological annotations. Category of genes up-regulated in response to Atropine treatment</i> 267
Table B.6:	<i>Significant associations between gene sets and ontological annotations. Category of genes down-regulated in response to Atropine treatment</i> 268

LIST OF FIGURES

Chapter 1:

<i>Fig. 1.1:</i> Transcriptional control.....	18
<i>Fig. 1.2:</i> Schematic diagram of the three phases of eukaryotic mRNA translation	26
<i>Fig. 1.3:</i> Simplified model for translation initiation complex.....	27
<i>Fig. 1.4:</i> Formation active eIF4F complex.....	29
<i>Fig. 1.5:</i> Simplified model for translation elongation.....	30
<i>Fig. 1.6:</i> Simplified model for translation termination.....	31
<i>Fig. 1.7:</i> Hierarchical phosphorylation of 4E-BP1.....	36

Chapter 2:

<i>Fig. 2.1:</i> RNA quality after Trizol extraction	52
<i>Fig. 2.2:</i> Schematic representation of the steps performed in a microarray experiment.....	56
<i>Fig. 2.3:</i> Representation of loop design used in microarray studies.....	57
<i>Fig. 2.4:</i> The figure represents the most significant categories of genes differentially expressed in response to GH treatment.....	71
<i>Fig. 2.5:</i> The figure represents the most significant categories of genes differentially expressed in response to atropine treatment.....	72
<i>Fig. 2.6:</i> The figure shows categories up- and down-regulated in response to the treatments and the percentage of genes differentially expressed that fall inside the categories listed.....	73
<i>Fig. 2.7:</i> Illustration of the microarray results for members of the mTOR signaling pathway	78
<i>Fig. 2.8:</i> Illustration of the different points of control of milk protein synthesis regulation.	84

Chapter 3:

<i>Fig. 3.1:</i> qRT-PCR results comparing GH-treated and control animals.	100
<i>Fig. 3.2:</i> qRT-PCR results comparing GH-treated and control animals.	101
<i>Fig. 3.3:</i> GH treatment stimulated phosphorylation of S6 in the mammary gland	102
<i>Fig. 3.4:</i> GH treatment increased the abundance of eIF4E in the mammary gland but did not affect the phosphorylation of 4E-BP1.....	103
<i>Fig. 3.5:</i> GH treatment did not change phosphorylation status of eEF2 and eEF2K but increased total eEF2	104

Chapter 4:

<i>Fig. 4.1:</i> Total mammary gland RNA from atropine-treated and control animals was subjected to qRT-PCR analysis.	121
<i>Fig. 4.2:</i> Total mammary gland RNA from atropine-treated and control animals was subjected to qRT-PCR analysis.	122
<i>Fig. 4.3:</i> Atropine treatment effect on the total eIF4E and phosphorylation of 4E-BP1	123
<i>Fig. 4.4:</i> Atropine treatment effect on the phosphorylation status of eEF2 and eEF2K.....	124

Chapter 5:

<i>Fig. 5.1:</i> Effects of serum starvation of H4IIE cells on targets of the mTOR pathway.....	142
<i>Fig. 5.2:</i> GH stimulates S6, eEF2 and 4E-BP1.....	145
<i>Fig. 5.3:</i> Analyses of eIF4E, 4E-BP1 and eIF4G using affinity chromatography on m^7GTP -Sepharose..	146
<i>Fig. 5.4:</i> GH stimulates S6, 4E-BP1, ERK and Akt. Rapamycin effects on downstream targets of mTOR.....	147
<i>Fig. 5.5:</i> GH stimulates ERK and Akt pathways.....	149
<i>Fig. 5.6:</i> Blocking PI 3-kinase, but not ERK signaling, inhibits the activation of mTORC1 signaling by GH.....	152
<i>Fig. 5.7:</i> GH regulates the mTOR through activation of the PI 3-kinase signaling pathway.....	153
<i>Fig. 5.8:</i> GH activates TSC2 phosphorylation.....	154
<i>Fig. 5.9:</i> Both phases of the GH effect on eEF2 phosphorylation are blocked by rapamycin.....	156

Fig. 5.10: mTOR is required for the activation of protein synthesis by GH in H4IIE cells 158
Chapter 6:

- Fig. 6.1:** H4IIE cells transfected with different concentrations of eEF2K siRNA molecule 171
Fig. 6.2: H4IIE cells transfected with two different concentrations of eEF2K siRNA molecule for 40 hours and starved for 16 hours 173
Fig. 6.3: H4IIE cells transfected with two different concentrations of eEF2K siRNA molecule for 70 hours and starved for 30 hours 174
Fig. 6.4: siRNA mediated knockdown of eEF2K in H4IIE cells inhibits the stimulation of protein synthesis in response to GH treatment 177

Chapter 7:

- Fig. 7.1:** Schematic diagram of 4E-BP1 showing the RAIP and TOS motifs, the region that binds eIF4E and the four phosphorylation sites 186
Fig. 7.2: Analysis of binding of raptor to variants based on 4E-BP1 199
Fig. 7.3: Overlay assay used to assess the binding of raptor to GST or GST to which a four alanine spacer and the TOS motif (FEMDI) was attached 201
Fig. 7.4: Ability of TOS motifs variants to support the binding of 4E-BP1 to raptor 206
Fig. 7.5: Phosphorylation of 4E-BP1 variants expressed in HEK293 cells 207

Appendix A:

- Fig. A.1:** Schematic representation of the tissue and milk sampling timing from GH-, atropine- and control-treated cows 235
Fig. A.2: Daily milk yield (A) and protein yield (B) in control and GH-treated cows over 6 days following the injection of a slow release formulation of GH on day 0 239

ABBREVIATIONS

4E-BP1	Eukaryotic initiation factor 4E-binding protein 1
ATP	Adenosine triphosphate
BES	N, N-bis [2-Hydroxyethyl]-2 aminoethanesulfonic acid
BSA	Bovine serum albumin
cDNA	Complementary DNA
Ct	Cycles to threshold
DMEM	Dulbecco's modified Eagle's medium
DMSO	Dimethyl sulphoxide
DNA	Deoxyribonucleic acid
dNTP	Deoxyribonucleotide triphosphate
DTT	Dithiothreitol
ECL	Enhanced chemiluminescence
EDTA	Ethylenediamine tetraacetic acid
eEF2	Eukaryotic elongation factor 2
eEF2K	Eukaryotic elongation factor 2 kinase
eIF	Eukaryotic initiation factor
eIF4E	Eukaryotic initiation factor 4E
eRF	Eukaryotic release factor
ERK	Extracellular signal-regulated protein kinase
EST	Expressed sequence tag
FCS	Foetal calf serum
FDR	False discovery rate
GDP	Guanosine diphosphate
GH	Growth hormone
GHR	GH receptor
GO	Gene ontology
GTP	Guanosine triphosphate
IGF	Insulin-like growth factor
IGFBP	Insulin-like growth factor binding protein
IPA	Ingenuity pathway analysis
IPTG	Isopropyl-β-thiogalactopyranoside

IRES	Internal ribosomal entry segments
JAK	Janus kinase
JNK	c-Jun N-terminal kinase
m⁷GTP	7-methyl-GTP
MAPK	MAP kinase
mRNA	Messenger RNA
mTOR	Mammalian target of rapamycin
NADPH	Nicotamide adonine dinucleotide phosphate
NCBI	National Center for Biotechnology Information
PBS	Phosphate-buffered saline
PCR	Polymerase chain reaction
PI 3-kinase	Phosphatidylinositol 3-kinase
PIP₂	Phosphatidynositol 4,5-biphosphate
PKB	Protein kinase B
PTEN	Phosphatase and tensin homologue deleted on chromosome 10
PVDF	Polyvinylidene difluoride
qRT-PCR	Quantitative real time PCR
REST	Relative expression software tool
RNA	Ribonucleic acid
S6	Ribosomal protein S6
SDS-PAGE	Sodium dodecyl sulphate polyacrylamide gel electrophoresis
STAT	Signal transduction and transcriptional activation
Rheb	Ras homolog enriched in brain
dsRNA	Double-stranded RNA
RNAi	RNA interference
P90^{RSK}	P90 ribosomal S6 kinase
RNAi	RNA interference
siRNA	Small interfering RNAs
EGF	Epidermal growth factor
CoREs	Composite response elements
C/EBP	CAAT\enhancer binding protein
NF-1	Nuclear factor 1
YY-1	Yin Yang-1

GSK3	Glycogen synthase kinase 3
S6K	Ribosomal S6 kinase
S6	Ribosomal protein S6
P70S6K	P70S6 kinase
TCA	Trichloroacetic acid
GPAM	Mitochondrial glycerol-3-phosphate acyltransferase
MGEA5	Meningioma-expressed antigen 5
KRT15	K15 intermediate filament type I keratin
PKC	Protein kinase C
Raptor	Regulatory associated protein of mTOR
TOS	TOR signaling motif
HPLC	High pressure liquid chromatography
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
Mac-T	Mammary alveolar cells with large-T antigen
H4IIE	Rat hepatoma cell line
HEK293	Human embryonic kidney cell line
TPA	Phorbol-12-myristate-13-acetate
t-RNA	Transfer RNA
t-RNA_i	Initiator tRNA
TSC	Tuberous sclerosis complex
UTR	Untranslated region

GENERAL INTRODUCTION

Background

The New Zealand dairy industry is the country's biggest agricultural industry, accounting for 23% of New Zealand's total export earnings (www.investnewzealand.govt.nz/common/files/Dairy_Feb06.pdf). The application of new biotechnologies in the dairy industry is essential for sustaining the competitiveness and profitability of New Zealand in the global market. A number of studies have successfully demonstrated the physiological changes that occur in response to treatments that perturb the milk synthetic machinery. However, the elucidation of the molecular mechanisms, specifically those of the signaling pathways and genes, involved in the regulation of protein synthesis in the mammary gland are still being explored.

Protein synthesis is mainly regulated through the phosphorylation or binding ability of the initiation and elongation components of the mRNA translational machinery. Although there is ample evidence that certain exogenous stimuli change milk protein synthesis in lactating cows and it is clear that mRNA translation is important for the regulation of protein synthesis, there are no studies demonstrating that these stimuli affect the translation initiation and elongation factors and hence protein synthesis in the mammary gland.

During protein synthesis a tightly regulated step occurs during the initiation and elongation of the mRNA translation which involves the mammalian target of rapamycin (mTOR) signaling pathway. The start of initiation is controlled by the formation of the eukaryotic initiation factor (eIF) 4F complex, which requires the eIF4E protein. The

biological activation of the eIF4E protein is regulated by a family of translation repressor proteins, the eIF4E binding proteins (4E-BPs) proteins. mTOR regulates the phosphorylation of 4E-BP1, which occurs in multiple sites. However, the residues involved in the interaction between mTOR and 4E-BP1 and the nature of the interaction are still unclear.

Objectives

The main objectives of this thesis were to identify the pathways and genes involved in the regulation of milk protein synthesis and to understand their roles in the mammary gland during lactation in response to exogenous stimuli like growth hormone and atropine. A second objective was to study the regulation and interaction of 4E-BP1 and mTOR, the main identified regulators of protein synthesis in other tissues. A better understanding of the 4E-BP1-mTOR interaction will help to identify new downstream targets for the mTOR signaling cascade and consequently new proteins involved in the protein synthesis machinery.

It is anticipated that the knowledge gained from this research will open up possibilities to develop new technologies to manipulate milk composition and yield with potential economic benefits to the dairy industry.