

**Molecular Characterisation of Primary Wool Follicle
Initiation in Merino Sheep**

Hayley Ann McGrice BBiotech (HONS)

June, 2009

This thesis is submitted in partial fulfilment of the award of PhD in the
Discipline of Agricultural and Animal Science, School of Agriculture, Food and
Wine,
University of Adelaide, South Australia

Table of Contents

Abstract	ii
Declaration	iv
Acknowledgements	v
Abbreviations	vii
Chapter 1 Introduction and Literature Review	2
1.1 Introduction	2
1.2 Structure and Development of the Wool Follicle	4
1.2.1 Structure and Function of Mammalian Skin	4
1.2.2 Wool Follicle Types	5
1.2.2.1 Primary Follicles	6
1.2.2.2 Secondary and Secondary-Derived Follicles	6
1.2.2.3 Secondary to Primary Ratio (S/P ratio)	8
1.2.3 Molecular Basis of Primary Follicle Neogenesis	8
1.2.3.1 First Dermal Signal: Formation of the Epidermal Placode	9
1.2.3.2 First Epidermal Signal: Formation of the Dermal Condensate	13
1.2.3.3 Down growth of the epidermal placode	13
1.2.3.4 Formation of the dermal papilla	14
1.2.3.5 Formation of the Follicle Bulb	14
1.2.3.6 Inner Root Sheath (IRS)	15
1.2.3.7 Outer Root Sheath (ORS)	16
1.2.3.8 Follicle Accessory Structures	16
1.2.3.8.1 Sebaceous Gland	16

3.2	Specific Methods.....	34
3.2.1	Matings.....	34
3.2.2	Generation of Foetal Skin Series	34
3.2.3	Crown Rump Length Measurements	35
3.2.4	Processing, Embedding and Sectioning.....	36
3.2.5	Haematoxylin and Eosin Staining.....	37
3.2.6	SacPic Staining	38
3.2.7	Histology Images	39
3.2.8	Statistical Analysis	39
3.3	Results	40
3.3.1	Foetal Measurements	40
3.3.1.1	Foetal Data Comparison with a Previous Study	43
3.3.2	Histological Characterisation.....	45
3.4	Discussion.....	48
3.4.1	Foetal Sample Series	48
3.4.2	Histological Characterisation.....	51
3.5	Conclusion.....	52
Chapter 4	: Quantitative PCR Analysis of Whole Skin.....	54
4.1	Introduction	54
4.1.1	Normalisation of qRT-PCR data: geNorm.....	55
4.1.2	Candidate Genes for qPCR Analysis of Wool Follicle Initiation.....	56
4.1.2.1	Actin-based Fibroblast Migration	56
4.1.2.2	Skin Stem Cell Markers	56
4.1.2.3	Cell Proliferation	58
4.1.2.4	Tumor Necrosis Factor Signalling in Hair Follicle Development.....	59
4.1.2.5	Sonic Hedgehog Signalling in Hair Follicle Development.....	60

4.2	Aim.....	62
4.3	Specific Methods.....	62
4.3.1	qRT-PCR	62
4.3.2	geNorm Analysis and Normalisation of qPCR data	63
4.3.3	Statistical Analysis of Relative Expression Patterns.....	64
4.4	Results	64
4.4.1	RNA extractions	64
4.4.2	geNorm Analysis.....	66
4.4.3	Gene Expression Analysis.....	70
4.4.3.1	Migration Markers.....	70
4.4.3.2	Stem Cell Markers	72
4.4.3.3	Proliferation Markers	74
4.4.3.4	Tumor Necrosis Factor Signalling Pathway Members.....	76
4.4.3.5	Sonic Hedgehog Signalling Pathway	82
4.4.3.6	Gene Expression Correlations	84
4.5	Discussion	85
4.5.1	Gene Expression Analysis of Candidate Migration Markers	87
4.5.2	Gene Expression Analysis of Candidate Stem Cell Markers	88
4.5.3	Gene Expression Analysis of Candidate Cell Proliferation Markers.....	89
4.5.4	Ectodysplasin Signaling During Primary Wool Follicle Initiation	90
4.5.5	Gene expression analysis of Sonic Hedgehog and Patched-1 during primary follicle development	94
4.5.6	Differences in Gene Expression between the Midside and Rump	95
4.6	Conclusion.....	97
Chapter 5	: Laser Capture Microdissection of Foetal Sheep Skin	99
5.1	Introduction	99

5.2	Aim.....	100
5.3	Specific Methods.....	100
5.3.1	Frozen tissue sectioning and fixation.....	100
5.3.2	Haematoxylin and Eosin staining of frozen sections for laser capture microdissection	100
5.3.3	Laser Capture Microdissection Protocol	101
5.3.4	RNA extraction from laser captured tissue	102
5.3.4.1	TRIZOL and RNAqueous Micro Extraction Protocols	102
5.3.4.2	Qiagen RNeasy Micro Extraction Kit	103
5.3.5	Estimation of RNA quality and quantity	103
5.3.6	Reverse Transcription of RNA	104
5.3.7	Cells Direct One-Step Kit	104
5.4	Results	104
5.4.1	Optimisation of Sectioning and Staining for Laser Capture Microdissection.....	104
5.4.2	Optimisation of RNA extraction and RT-PCR of Laser Capture Microdissected Material	107
5.4.3	Optimisation of Slide Type for Laser Pressure Catapulting.....	112
5.4.4	Laser capture microdissection and qRT-PCR analysis of follicle regions vs. non-follicle regions of foetal sheep skin.	116
5.5	Discussion	121
5.6	Conclusion.....	129
Chapter 6	General Discussion	131
6.1	Introduction	131
6.2	Future Work	145
6.3	Conclusion.....	147

Appendix I: General Solutions, Buffers and Stains.....	149
Appendix II: Primers.....	153
References.....	155

Abstract

Primary wool follicles are initiated in the skin of sheep foetuses at approximately day 50 of gestation as the result of complex reciprocal molecular interactions between the mesenchyme and overlying epithelium. The lifetime wool production potential and fibre diameter of the Merino sheep is dependent on the total number of follicles initiated *in utero*. Understanding the molecular events that surround primary wool follicle initiation may provide approaches to enhance or manipulate this process in order to maximise the profitability of wool production enterprises.

In order to study the morphological and molecular changes occurring during early wool follicle development, a foetal skin series spanning primary follicle initiation was generated. Foetal skin was sampled from the shoulder, midside and rump of four foetuses at 8 time points between day 43 and day 68 of gestation. Histological characterisation of the shoulder skin samples revealed that primary epidermal placodes emerged at around day 53, dermal condensates were visible from day 57 and downgrowth of the follicle began at day 68. An equation relating age of the foetus (day of gestation post AI) and crown-rump length, specific to Merino foetuses, was developed for use in future studies of this nature.

Molecular markers of fibroblast migration, epidermal and dermal stem cells and cell proliferation were selected to test the hypothesis that dermal condensates are initiated at discrete sites beneath the epidermis as a result of a combination of migration and arrangement of multipotent pre-papilla cells. Quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis of *RAC1* and *RHOa* (migration markers), *β 1-integrin* and *alkaline phosphatase* (stem cell markers), *proliferative nuclear cell antigen* and *cyclinB1* (proliferation markers), *patched-1*, selected tumor necrosis factor (TNF) signalling molecules and eleven reference genes was conducted using midside and rump skin samples from each of four foetuses from the 8 time points. geNorm analysis of the reference and target genes revealed that the migration markers *RAC1* and *RHOa* along with *GAPDH* were the most stably

expressed genes in this sample series. Significant changes in mRNA expression were detected for *β1-integrin*, *alkaline phosphatase*, *patched-1* and the TNF members *EDA*, *EDAR*, *TROY* and *TRAF6*. Many of these significant differences in expression coincided with key morphological events. Significant differences in expression were also detected between the midside and rump samples for numerous transcripts.

Laser capture microdissection (LCM) was implemented for analysis of the target transcripts within particular structures of foetal sheep skin. Frozen tissue sectioning, staining, LCM, RNA extraction and cDNA synthesis were optimised for qRT-PCR analysis of endogenous controls and selected TNF transcripts. Several RNA extraction methods and reverse transcription approaches were trialled to ensure optimum extraction and reverse transcription efficiency for this tissue type. Exogenous mRNA transcripts were also incorporated prior to RNA extraction and reverse transcription to track reaction efficiency between samples. A comparison of different slide types revealed that laser pressure catapulting from membrane slides was an absolute requirement for foetal skin tissue studies. Follicle regions (including the epidermal placode and dermal condensate) and the adjacent non-follicle regions were laser captured from foetal skin, and the mRNA expression levels of *patched-1* and selected TNF members was compared. Preliminary qRT-PCR analysis using this technique revealed that *EDAR*, *TROY* and *PTCHI* mRNA levels were higher in the follicle regions than the non-follicle regions.

The TNF signalling pathway appears to play an important role in primary wool follicle initiation and patterning at different sites on the body. Spatial differences in expression of some of these regulators may be involved in initiating different types of follicles. The molecular events surrounding primary wool follicle initiation also show a high degree of conservation between sheep, humans, and mice. Considering the high degree of DNA sequence conservation as well as the histological, signalling and cycling similarities between sheep and humans, sheep may represent a better model for the study of human hair follicle initiation and disease than the currently used mice and rat models.

Declaration

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

I give consent to this copy of my thesis, when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

Date

Hayley Ann McGrice

Acknowledgements

First and foremost I would like to thank Australian Wool Innovation for their scholarship and research funding. Without your financial support this thesis would not have been possible.

A loud and resounding thank you must go to my supervisors Dr Cynthia Bottema, Dr Greg Natrass and Prof Philip Hynd. Cindy you were always there for me and I can't thank you enough for everything you have done for me over the last four years. The speed at which you read and returned my chapters to me was absolutely amazing and the lengths that you went to in order to support me during my PhD candidature were above and beyond the call of duty, so thank you, from the bottom of my heart. To my technical supervisor Greg, thank you for listening to and answering my silly questions over and over again and for all your advice and assistance in the lab, especially in the large scale qRT-PCR experiment design and undertaking. The chats we had over a quite beer on a Friday afternoon were probably the most valuable in terms of understanding and interpreting the "disco" science. Phil, thank you for nurturing my love of writing on the whiteboard, you have a unique gift for helping people to build and get excited about crazy hypotheses. Your wordsmith skills were also greatly appreciated when writing the conference abstracts and of course, this thesis. The three of you were an excellent supervision team and I greatly appreciate all your support.

Special thanks to Dr Simon Bawden for initially creating the project, awakening my interest in wool research and for your continued guidance and advice during an extremely challenging PhD candidature. Thank you also to Dr Stephanie Dunn and Clive McLaughlin from the SARDI molecular team for your technical advice, assistance and friendship, I think we had about as much fun as anyone could have in a molecular lab!

To Dr Michelle Hebart and A.Prof Wayne Pitchford, thank you a thousand times over for your assistance with the statistical analysis and interpretation, stats are not my strong point and I definitely could not have done this without you.

A special mention must also go to Natasha Edwards, Dr Melanie McDowall, and the Roseworthy wool group. Thank you for all your friendship, laboratory assistance and constructive feedback when preparing conference presentations as well as helping me to build explanations for the results along the way.

To all the farm staff at Turretfield Research Centre, thank you for your expertise and assistance with the animal sampling and for your friendship.

To my best friend and office buddy Dr Rebecca Forder, we laughed and we cried together as we rode the PhD rollercoaster. Thank you for being an excellent shoulder to cry on, an open sympathetic ear, someone to laugh with and an excellent role model when it came to finishing this thesis. Thanks also for assisting me with the tissue collection and for your help with the thesis formatting, not to mention the baby sitting that helped get me over the line. On that note, thank you also to Nana Sue and Uncle Gary John for your assistance with Colby care; babies and thesis writing do not mix! I could not have done this without the Forder's.

Thank you also to Tone for being there for me during the emotionally challenging animal sampling and for putting up with the stress fuelled outbursts at various times along the way. Twas a long PhD road for us both!

Last but by no means least, special thanks goes to my Mum and Kylie, you guys were there for me when everything went wrong, you both helped me get back on my feet, and for that I will forever be in your debt. I nearly gave it all up and it was your support and strength that got me through the roughest patch of my life. Thank you for all the babysitting too mum, you're a class 1A mum and Nana.

Thank you all from the bottom of my heart!

Abbreviations

°C	degrees Celsius
μl	microlitres
μm	micrometres
ACTB	β-Actin
ALP	Alkaline phosphatase
BCC	basal cell carcinoma
BMP	bone morphogenic proteins
bp	base pairs
CAT	chloramphenicol transferase
CD34	CD34 antigen
Cdc42	Cell Division Cycle related family member 42
cDNA	complementary DNA
CDK-1	cyclin dependent kinase 1
CIDR	controlled internal releasing device
cm	centimetres
COLL3AIII	collagen type 3AIII
CoV	coefficient of variation
CRL	crown rump length
C _t	cycle threshold
CYC B1	cyclin B1
d	day
EDA	ectodysplasin A1
EDAR	ectodysplasin A1 receptor
EDARADD	ectodysplasin A1 receptor death domain
EDTA	ethylenediaminetetraacetic acid

EM	epithelial:mesenchymal
FD	fibre diameter
FGF	Fibroblast growth factor
FGFR	FGF receptor
GAPDH	glyceraldehyde 3-phosphate dehydrogenase
GLI1	GLI family zinc finger 1
GSP	gene specific primers
GTP	guanosine-5'-triphosphate
hrs	hours
IKK	I κ B kinase complex
IRS	inner root sheath
KRT5	keratin-5
LCM	laser capture microdissection
LEF/TCF	lymphoid enhancer-binding factor/T cell factor
LPC	laser pressure catapulted
LUC	luciferase
mA	milliamps
MIB-1	mind bomb-1
mins	minutes
mM	millimolar
mm	millimetres
NF- κ β	nuclear factor-kappa-beta
ng	nanograms
nm	nanometres
nmol	nanomoles
OCT	optimal cutting temperature
oligo dTVN	oligonucleotide dTNV combination

PALM	photo-activated localisation microscopy
PCNA	proliferative cell nuclear antigen
PBS	phosphate buffered saline
PCR	polymerase chain reaction
PTCH1	patched-1
qRT-PCR	quantitative reverse transcriptase PCR
RAC1	ras-related C3 botulinum toxin substrate 1
RHOa	Ras homolog gene family, member A
RLT buffer	RNeasy lysis buffer
RO	reverse osmosis
RPL19	Ribosomal protein large 19
RT	remnant tissue
SAS	statistical analysis software
sec	seconds
SEM	standard error of the mean
SHH	sonic hedgehog
S:P ratio	secondary to primary ratio
TE buffer	Tris-EDTA buffer
TGF- β 2	Transforming growth factor –beta 2
TNF	Tumor necrosis factor
TRAF	Tumor necrosis factor associated factors
TROY	tumor necrosis factor receptor superfamily, member 19
V	volts
WNT	wingless-type
XEDAR	X-linked ectodysplasin receptor
YWHAZ	tyrosine 3-monooxygenase /tryptophan 5-monooxygenase activation protein, zeta polypeptide

This thesis is dedicated to my mum Jan and my daughter Colby

Thank you for teaching me the value of education mum,

may I instil the same important values in Colby.