Genetic Independence of Fat Depots in Cattle

Andrew R. Egarr

B.Biotech (Hons)

October, 2011

This thesis is presented for the degree of

Doctor of Philosophy

School of Animal and Veterinary Sciences

The University of Adelaide

Table of Contents

Index of Figures

Index of Tables

Abbreviations

BTA	cattle chromosome
dATP	2’ deoxyadenosine 5’-triphosphate
dCTP	2’ deoxycytosine 5’-triphosphate
dGTP	2’ deoxyguanosine 5’-triphosphate
DNA	deoxyribonucleic acid
dNTP	deoxyribonucleotide-triphosphate
dTTP	2’ deoxythymidine 5’-triphosphate
EBV	Estimated breeding value
EMA	Eye muscle area (*Longissimus dorsi*)
emaam	Eye muscle area (*Longissimus dorsi*)
hscw	hot standard carcass weight
HRM	High Resolution Melt
IMF	Intramuscular fat
marbam	AUS-MEAT marble score
mbms / msamb	Meat Standards Australia marble score
mbusms	USDA marble score
RFI	Residual Feed Intake
TAE	tris acetate ethylenediaminetetra-acetic acid
w/v	weight per volume

Abstract

The amount and distribution of adipose tissue is important to cattle production. Fat influences the animal's reproductive efficiency and determines its carcass value. As a cow's reproductive efficiency is associated with a level of overall fatness, not just a particular fat depot, being able to re-partition fat to a more valuable depot while reducing fat in less valuable depots would be advantageous. Most previous research involving fat deposition in cattle focussed on subcutaneous and intramuscular fat, and usually evaluated these in relation to total fat or carcass weight rather than the relationship between individual fat depots. The hypothesis that there is a genetic basis for variation in fat distribution in cattle and a weak relationship between fat depots independent of anatomical site was tested. The principal aim of this research was to gain a better understanding of the mechanisms controlling fat deposition in cattle, including any relationship between fat depots.

Marbling features (e.g. shape and orientation) and seam (intermuscular) fat area were quantified using image analysis. The seam fat area and other carcass fat measurements were used to examine the relationship between fat depots. Candidate genes for fat deposition traits were identified and sequenced in Jersey – Limousin mapping sires to find single nucleotide polymorphisms (SNPs). In all, 33 SNPs from 11 candidate genes for fat deposition were selected for association studies in the sire progeny.

There was large variation in all of the measures but the variation was largely independent of other marbling factors. The seam fat area data were used to identify a quantitative trait locus on chromosome 19, and subsequently identify candidate genes for seam fat area. In general, there were low correlations between fat traits suggesting the relationship between the depots was not strong. The fixed effects of cohort, breed

and *myostatin* variant affected general fat deposition. However, sire affected fat distribution, as no sire had progeny consistently higher or lower for all fat traits. These results suggest there is only a weak genetic link between the fat depots.

The size of effect was small for most of the SNPs associated with fat deposition, although there were some candidate genes with sizeable effects, for example, *tyrosine kinase, endothelial (TEK1)* (channel fat, 28%) and *ß, ß-carotene 15, 15'-monooxygenase (BCMO1)* (subcutaneous fat, 20%). Moreover, the combined effect of all SNPs affecting a single trait explained 38% (channel fat), 26% (seam fat and subcutaneous fat) and 23% (omental fat) of the phenotypic variation. Interestingly, although some genes were associated with variation in more than one fat trait, no one gene was associated with all fat traits or overall fatness.

The major conclusion from the research described herein is that there is genetic influence on fat deposition in addition to the effects of age, breed and management, the deposition of fat into the various adipose sites is controlled in an independent manner genetically and there appears to be no one gene that affects deposition in all sites. There were four principal results that support this conclusion; 1) there were low correlations between fat traits, 2) there were no sires with progeny consistently high or low for all fat traits, 3) the QTL for the various fat depots did not overlap with each other, and 4) no SNP was associated with all fat traits. These results indicate that there is large scope for selecting for and against individual fat traits without altering other fat depots.

Declaration

I, Andrew Egarr certify 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.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library catalogue and also through web search engines, unless permission has been granted by the University to restrict access for a period of time.

Andrew R. Egarr
October 2011

Dedication

I dedicate this work to my wife Bronwyn, the love of my life.

Acknowledgements

The time spent on this project has been interesting, enlightening and fulfilling, if at times frustrating. However, this would not have been possible on my own, and I am indebted to many people who have been part of the process.

First and foremost are my supervisors. As my principal supervisor, Dr. Cynthia Bottema has always been available for advice and direction, while also allowing me to follow my own path. Her encouragement, feedback, patience, support and concern for her students' welfare have been very much appreciated. I have also enjoyed great support and encouragement from Associate Professor Wayne Pitchford. His practical approach, advice, guidance and patience with my attempts to learn statistical methods have been invaluable. Your individual talents have complemented each other, and made this time memorable.

This project utilised data from three cattle herds. I am grateful to the J.S. Davies Bequest that provided the funds necessary to establish the Davies Gene Mapping herd, and to those who have gone before me, who measured, sampled and analysed this valuable resource. These people have paved the way for the mining of much information in cattle genetics by many students. I also thank Dr Neil Cullen, Dr Chris Morris and others at AgResearch (NZ) who supplied data from the AgResearch Gene Mapping herd; to Dr Robert Herd, Dr John Thompson and the NSW Department of Industry and Investment for making samples available from steers of the Trangie Residual Feed Intake herd, Jason Siddell who organised the collection of the Trangie samples and the commercial feedlot for their cooperation.

I am also grateful to both the University of Adelaide and the CRC for Beef Genetic Technologies for financial support during my project and the opportunities to attend conferences and improve my education throughout this time. I also acknowledge the

Walter and Dorothy Duncan Trust for financial support to assist my travelling to Amsterdam for the International Society for Animal Genetics (ISAG) conference, and the ISAG committee for awarding me an Early Career Scientist Bursary for the same conference.

I am thankful to those who have assisted me with aspects of my project; Dr Zibby Kruk, who completed the bulk of photographing the steaks from the Trangie experiment, and instructed me in extracting fat from muscle samples. Also, Associate Professor Murk Bottema who developed the software to quantify the marbling characteristics, seam fat and muscle areas of the steak images.

I thank all of the students who have been part of the research group throughout my time here. Madan Naik who helped me settle in, gave direction when needed and became a good friend, Rugang Tian, Lei-Yao Chang, Irida Novianti, Nadiatur Zulkifli and Alireza Abdolmohammadi who provided conversation, humour and valued friendship. Dr. Brian Siebert has been a great source of information regarding fatty acids in general and intramuscular fat specifically, and Dr. Graham Webb has been very helpful with general advice around the laboratory. Their experience must never be under-valued.

A special mention must go to David Lines and Stephen Lee. We may be from different generations but we have shared the highs and lows of our projects and life in general. Your friendship has been priceless and will not be forgotten.

My family have provided great support throughout this time. Erin, Sean and Sara have made many adjustments and accepted an often preoccupied and sometimes absent father. Thank you for your support and for being a constant reminder of what really is important in life. Holding all of this together has been my wife Bronwyn. I have been truly blessed with a patient, supportive, tolerant and loving wife. Thank you for giving

me the space to indulge my dreams and always believing in my ability. Your encouragement and support have never wavered; you are the one constant in an otherwise unpredictable life. Thank you for being my refuge, support and for at least trying to look interested when I talked about my work.

It may surprise those around me, but underlying all of this has been my faith. I have often questioned my situation but as I look back it all becomes clear, and I am sure that with the passage of time it will all make perfect sense.

Andrew Egarr

October 2011

What appears as a thoroughly systematic piece of scientific work is actually the final product: a cleanly washed offspring that tells us very little about the chaotic mess that fermented in the mental womb of its creator.

Auner Treinin.