

# Genetic Independence of Fat Depots in Cattle

Andrew R. Egarr

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# Table of Contents

Table of Contents.....	ii
Index of Figures .....	viii
Index of Tables.....	xi
Abbreviations .....	xiv
Abstract.....	xv
Declaration.....	xvii
Dedication .....	xviii
Acknowledgements.....	xix
Chapter 1 Introduction and literature review .....	1
1.1 Background .....	2
1.2 White adipose tissue versus brown adipose tissue.....	4
1.3 White fat depots .....	4
1.4 Cattle breed differences in fat distribution .....	7
1.5 Adipogenesis.....	9
1.6 Transdifferentiation.....	11
1.7 Hyperplasia versus hypertrophy.....	12
1.8 Manipulation of fat distribution by diet.....	13
1.9 Genes/proteins involved in adipogenesis.....	15
1.9.1 Transcription factors.....	15
1.9.1.1 CCAAT/enhancer binding proteins (C/EBP).....	15
1.9.1.2 Peroxisome proliferator-activated receptor gamma (PPARG).....	17
1.9.1.3 Adipocyte determination and differentiation factor-1 (ADD1) .....	19
1.9.1.4 Fos, jun and c-myc .....	19
1.9.2 Extracellular agents.....	20
1.9.2.1 Glucocorticoids .....	20
1.9.2.2 Thyroid hormones.....	20
1.9.2.3 Fatty Acids.....	20
1.9.2.4 Insulin .....	21
1.9.2.5 Growth hormone.....	21
1.9.2.6 Other growth factors .....	21
1.9.2.7 Retinoids.....	22
1.9.3 Adipokines.....	22
1.9.3.1 Prostaglandins.....	23

1.9.3.2	Leptin .....	23
1.9.3.3	Adiponectin .....	24
1.10	Quantitative Trait Loci .....	24
1.10.1	Molecular markers .....	25
1.10.2	Comparative genomics .....	26
1.10.3	Candidate genes .....	27
1.11	Marker Assisted Selection .....	28
1.11.1	Whole genome selection .....	29
1.12	Hypothesis .....	30
Chapter 2	General methods .....	32
2.1	Cattle .....	33
2.1.1	Davies Gene Mapping Herd .....	33
2.1.2	AgResearch Gene Mapping Project .....	34
2.1.3	Trangie Residual Feed Intake (RFI) trial herd .....	35
2.1.4	Data .....	36
2.1.4.1	Carcass measurements .....	36
2.1.4.2	Traits .....	36
2.1.4.3	Intramuscular fat extraction .....	37
2.1.4.4	Melting point of intramuscular fat .....	38
2.2	Polymerase chain reaction .....	39
2.2.1	Primer design .....	39
2.2.2	Polymerase Chain Reaction .....	39
2.2.2.1	Reaction mix .....	39
2.2.2.2	Thermal cycling .....	40
2.2.2.3	Reaction optimisation .....	40
2.2.2.4	Agarose gel electrophoresis .....	41
2.3	Contributions to this project .....	41
Chapter 3	Image analysis .....	43
3.1	Introduction .....	44
3.2	Methods .....	46
3.2.1	Cattle .....	46
3.2.2	Image analysis – Davies Gene Mapping Herd .....	46
3.2.2.1	Image capture .....	46
3.2.2.2	Image processing .....	46
3.2.3	Image analysis – Trangie Residual Feed Intake Herd .....	47

3.2.3.1	Image capture.....	47
3.2.3.2	Image processing .....	48
3.2.3.3	Image analysis.....	48
3.2.4	Quantitative Trait Loci analysis.....	49
3.3	Results .....	50
3.3.1	Intermuscular (seam) fat.....	50
3.3.1.1	Davies Gene Mapping Herd .....	50
3.3.1.2	Trangie Residual Feed Intake Selection Line .....	52
3.3.1.3	Intermuscular fat area variation .....	53
3.3.1.4	Quantitative Trait Loci.....	55
3.3.2	Intramuscular fat.....	57
3.3.2.1	Davies Gene mapping Herd .....	57
3.3.2.2	Trangie Residual Feed Intake (RFI) Selection Line.....	60
3.3.2.3	Fleck characteristics .....	62
3.4	Discussion .....	70
Chapter 4	Fat distribution traits .....	72
4.1	Introduction.....	73
4.2	Methods.....	75
4.2.1	Cattle .....	75
4.2.2	Data analysis.....	75
4.3	Results .....	77
4.3.1	Summary statistics .....	77
4.3.2	Significance effects.....	78
4.3.3	Trait variation.....	82
4.3.4	Effect of carcass weight.....	86
4.3.5	Cohort effects .....	87
4.3.6	Breed effects .....	92
4.3.7	Sire effects.....	94
4.3.8	Myostatin genotype effects.....	99
4.3.9	Trait Phenotypic Correlations .....	101
4.3.10	Trait clusters .....	105
4.4	Discussion .....	111
4.4.1	Carcass weight and fat deposition.....	112
4.4.2	Cohort, slaughter group and pen effects .....	112
4.4.3	Breed effect .....	115

4.4.4	Sire effect .....	116
4.4.5	Myostatin genotype effect.....	118
4.4.6	Phenotypic correlations .....	119
4.4.7	Cluster analysis .....	124
4.4.8	Principal Component Analysis.....	124
4.5	Conclusion.....	128
Chapter 5	Candidate genes .....	130
5.1	Introduction.....	131
5.2	Methods.....	133
5.2.1	Cattle .....	133
5.2.2	Sequencing.....	133
5.2.2.1	Polymerase chain reaction .....	133
5.2.2.2	Preparation of DNA product for sequencing .....	133
5.2.3	Sequencing reaction.....	134
5.3	Results and Discussion .....	136
5.3.1	Candidate genes .....	136
5.3.1.1	Adipogenesis and lipogenesis .....	136
5.3.1.2	Angiogenesis and vascularisation .....	141
5.3.1.3	Muscle development and structure.....	142
5.3.2	Other candidate genes .....	144
5.3.2.1	Vitamin A pathway .....	144
5.3.2.2	Lipid metabolism.....	145
5.3.2.3	Unknown function .....	146
5.3.3	Sequencing.....	146
5.3.4	Candidate gene variants.....	147
5.3.5	Inferred genotypes.....	151
5.3.6	Mononucleotide DNA regions.....	152
5.3.7	Density of Single Nucleotide Polymorphisms .....	156
5.3.8	Single Nucleotide Polymorphisms .....	158
Chapter 6	Genotyping and association analysis .....	161
6.1	Introduction.....	162
6.2	Methods.....	164
6.2.1	Genotyping .....	164
6.2.1.1	Genotyping reaction mix .....	164
6.2.1.2	High Resolution Melt.....	164

6.2.1.3	Allele Specific Polymerase Chain Reaction.....	165
6.2.2	Data analysis.....	165
6.3	Results.....	167
6.3.1	High Resolution Melt Analysis.....	167
6.3.2	Allele Specific Polymerase Chain Reaction.....	171
6.3.3	HRM genotyping of two SNPs within one PCR fragment.....	172
6.3.4	Genotype frequencies.....	176
6.3.5	Association studies.....	177
6.3.6	Single nucleotide polymorphism effects.....	181
6.3.7	Correlations.....	184
6.3.8	Cluster analysis.....	186
6.3.9	Within gene SNP interactions.....	187
6.3.10	Between gene SNP interactions.....	189
6.4	Discussion.....	193
6.4.1	Single nucleotide polymorphisms for association studies.....	193
6.4.2	High resolution melt analysis (HRM).....	194
6.4.3	Association studies.....	197
6.4.3.1	Individual SNPs.....	197
6.4.3.2	Interactions between SNPs.....	204
6.4.3.3	Correlations.....	205
6.4.3.4	Cluster analysis.....	210
6.4.3.5	Single nucleotide polymorphism effects.....	211
6.5	Conclusion.....	213
Chapter 7	General discussion.....	215
7.1	Background.....	216
7.2	Fat deposition QTL.....	218
7.3	Image analysis.....	219
7.4	Fat distribution.....	221
7.5	Genetic associated lipodystrophies in humans.....	224
7.6	Independence of fat depots.....	226
7.7	Genes affecting fat distribution in cattle.....	231
7.7.1	Gene associations.....	234
7.8	Project limitations.....	237
7.9	Future directions.....	241
7.9.1	Validate SNPs.....	241

7.9.2	Gene expression .....	242
7.9.3	Epigenetics .....	242
7.9.4	Vascularisation .....	243
7.10	Conclusions .....	244
Appendices .....		246
Appendix A	Polymerase Chain Reaction methods.....	246
Appendix A.1	Polymerase Chain Reaction mixes.....	246
Appendix A.2	Polymerase Chain Reaction programs .....	247
Appendix B	Correlation within cohorts of various image analysis results from Davies Gene Mapping Herd.....	249
Appendix C	Comparison of correlations between marble score and image analysis with differing thresholds and parameters in separate marble score ranges. ....	250
Appendix D	Correlations between image analysis fleck characteristics.....	251
Appendix E	Comparison of fat depots and ema with and without carcass weight as covariate .....	252
Appendix F	SNP effects: cohort + breed + sire + SNP .....	253
Appendix G	SNP effects: cohort + breed + sire + hscw + SNP .....	255
Appendix H	SNP effect: cohort + BOD + sire + BOD.mstn + SNP + SNP.mstn – SNP effect .....	256
Appendix I	SNP effect: cohort + BOD + sire + BOD.mstn + SNP + SNP.mstn – SNP:mstn interaction .....	258
Appendix J	SNP interactions within gene.....	260
Appendix K	Interactions between genes associated with variation in fat depots, P-values .....	261
Appendix L	<i>Myostatin</i> F94L variant genotype effect on muscle and fat traits (F probabilities) Davies Gene Mapping herd.....	278
Appendix M	Primers for sequencing and genotyping .....	279
References.....		284

## Index of Figures

Figure 1.1: Percentage of fat in each depot of mature Friesian cattle.	5
Figure 3.1: Method used for processing images, Davies Gene Mapping herd.	47
Figure 3.2: Method used for processing images, Trangie RFI selection line.	49
Figure 3.3: Images of steaks illustrating the difficulty in delineating intermuscular fat in the Davies Gene Mapping herd.	51
Figure 3.4: Image of steak indicating the muscles at the 10th/11th rib site, Davies Gene Mapping herd.	51
Figure 3.5: images of steak indicating the areas used to calculate intermuscular fat area.	52
Figure 3.6: Alternative delineation of the intermuscular and subcutaneous fat border, Trangie RFI Selection line.	53
Figure 3.7: Intermuscular fat Quantitative Trait Locus on BTA 2.	57
Figure 3.8: Intermuscular fat Quantitative Trait Locus on BTA 19.	57
Figure 3.9: Images of steaks showing no glare (A) and glare (B).	59
Figure 3.10: Diagrammatic representation of average eccentricity of marbling flecks, Trangie Residual Feed Intake line.	63
Figure 3.12: Number of fat flecks in each range of eccentricity, ratios from 1 – 15.	64
Figure 3.13: Number of flecks in each normalised ellipticity range.	65
Figure 3.14: Schematic of quarters used to assess marble fleck placement.	68
Figure 3.15: Average number of fat flecks in each quarter of the <i>M. longissimus dorsi</i> .	69
Figure 4.1: Davies gene mapping herd cohort effects.	89
Figure 4.2: AgResearch gene mapping herd slaughter group effects.	90
Figure 4.3: Pen effects on muscle and fat deposition traits in the Trangie RFI steers.	92
Figure 4.4: Breed of dam effects in the Davies gene mapping herd.	93
Figure 4.5: Breed of dam effects in the AgResearch gene mapping herd.	93
Figure 4.6: Sire effects in the Davies gene mapping herd.	94
Figure 4.7: Sire effects in the AgResearch gene mapping herd.	95
Figure 4.8: Best linear unbiased prediction of Trangie sire effects on intermuscular fat (seam fat) and intramuscular fat %.	98
Figure 4.9: Best linear unbiased prediction of Trangie sire effects on rib fat and intramuscular fat %.	98
Figure 4.10: Best linear unbiased prediction of Trangie sire effects on rib fat and intermuscular fat (seam fat).	98



Figure 4.11: Myostatin genotype effects in the Davies gene mapping herd.	99
Figure 4.12: Myostatin genotype effects in the AgResearch gene mapping herd.	100
Figure 4.13: Cluster analysis diagram for the Davies gene mapping herd.	106
Figure 4.14: Cluster analysis diagram for the AgResearch gene mapping herd.	107
Figure 4.15: Davies gene mapping herd principal component 1 v principal component 2 (eigenvector x proportion x 100).	109
Figure 4.16: Davies gene mapping herd, principal component 2 v principal component 3 (eigenvector x proportion x 100).	109
Figure 4.17: AgResearch gene mapping herd, principal component 1 v principal component 2 (eigenvector x proportion x 100).	110
Figure 4.18: AgResearch gene mapping herd, principal component 2 v principal component 3 (eigenvector x proportion x 100).	110
Figure 5.1: Schematic of adipogenesis	137
Figure 5.2: Chromatograms showing TEK1 polymorphism 34 in mapping sires.	152
Figure 5.3: Chromatograms showing effects of mononucleotide repeats.	153
Figure 6.1: Nearest-neighbour symmetry at a G/C SNP.	163
Figure 6.2: Melt curve of SNP PPARG-2.	167
Figure 6.3: Melt curve analysis of SNP PPARG-2.	167
Figure 6.4: Melt curve of SNP TEK1-4	168
Figure 6.5: Melt curve analysis of SNP TEK1-4	168
Figure 6.6: ENO3-11 quantitation curve for PCR amplification prior to HRM.	169
Figure 6.7: ENO3-11 HRM melt curve.	169
Figure 6.8: ENO3-11 HRM difference graph.	170
Figure 6.9: ENO3-11 HRM melt curve analysis.	170
Figure 6.10: DNA sequence chromatogram showing CC and CG genotypes	170
Figure 6.11: ESR1-2 allele specific PCR quantitation curve.	171
Figure 6.12: Image of agarose gel showing result of multiplexed allele specific PCR trial of known genotypes.	172
Figure 6.13: NCOA7 SNP 1 and 2 HRM melt curve.	172
Figure 6.14: NCOA7 SNP 1 and 2 HRM melt curve without homozygous controls.	173
Figure 6.15: NCOA7 SNP 1 and 2 HRM melt curve analysis.	173
Figure 6.16: NCOA7 SNP 1 and 2 HRM melt curve analysis without homozygous controls.	174
Figure 6.17: NCOA7 SNP1 and 2 HRM difference graph. Sample compared to AA genotype.	174

Figure 6.18: NCOA7 SNP1 and 2 HRM difference graph. Sample compared to GA genotype.	175
Figure 6.19: NCOA7 SNP1 and 2 HRM difference graph. Samples compared to GG genotype.	175
Figure 6.20: Sequence chromatograms of five genotypes at NCOA7 -1 and 2 SNPs.	176
Figure 6.21: Least squares means of BCMO1-4 SNP effect on subcutaneous (P8) fat.	183
Figure 6.22: Least squares means of BCMO1-4 SNP effect on omental fat.	183
Figure 6.23: Least squares means of BCMO1-4 SNP effect on channel fat.	183
Figure 6.24: Cluster analysis of genetic correlations, Davies Gene Mapping herd.	186

## Index of Tables

Table 1.1: Breed comparisons of carcass composition measurements.	8
Table 2.1: Cohort details, Davies Gene mapping herd.	34
Table 2.2: Slaughter date, sex and number in each slaughter group, AgResearch Gene Mapping herd.	35
Table 3.1: Intermuscular (seam) fat area (mm <sup>2</sup> ) results, Davies Gene Mapping herd and Trangie RFI Selection line.	54
Table 3.2: Raw correlations between intermuscular (seam) fat area and other measured traits.	55
Table 3.3: Intermuscular (seam) fat quantitative trait loci from the across sire family linkage analyses, without (A) and with (B) myostatin F94L genotype as a fixed effect.	56
Table 3.4: Correlations between image analysis and marble score or intramuscular fat %, Davies Gene mapping herd.	59
Table 3.5: Comparison of QTL detected using different quality images with the established marbling and intramuscular fat % Quantitative Trait Loci.	60
Table 3.6: Number and percentage of marble flecks in each fleck area (10mm <sup>2</sup> ) range	61
Table 3.7: Correlations of marble fleck area and number with marble score and intramuscular fat %.	61
Table 3.8: Correlations using 5 – 100mm thresholds with selected marble score ranges, Trangie RFI Selection Line.	62
Table 3.9: Fleck characteristics, Trangie RFI Selection Line.	63
Table 3.10: Number of fat flecks in each range of eccentricity, ratios from 1 – 15.	64
Table 3.11: Number of flecks in each normalised ellipticity range.	65
Table 3.12: Eccentricity and ellipticity correlations with marble score and intramuscular fat %	66
Table 3.13: Heritabilities of fleck characteristics, Trangie RFI herd.	67
Table 3.14: Genetic correlations of fleck characteristics, Trangie RFI herd.	67
Table 3.15: Fleck position correlations with marble score and intramuscular fat %	68
Table 3.16: Average number of flecks in each quarter of <i>M. longissimus dorsi</i> , Trangie RFI Selection Line.	69
Table 4.1: Summary of trait data from the Davies gene mapping herd.	77
Table 4.2: Summary of trait data from the AgResearch gene mapping herd.	78
Table 4.3: Summary of trait data from the Trangie RFI steers.	78
Table 4.4: Tests of significance (F-probabilities) for the Davies gene mapping herd.	79

Table 4.5: Tests of significance (F-probabilities) for the Davies gene mapping herd with carcass weight as a covariate.	79
Table 4.6: Tests of significance (F-probabilities) for the AgResearch gene mapping herd.	81
Table 4.7: Tests of significance (F-probabilities) for the AgResearch gene mapping herd with carcass weight as a covariate.	81
Table 4.8: Tests of significance (F-probabilities) for the Trangie RFI steers.	82
Table 4.9: Tests of significance (F-probabilities) for the Trangie RFI steers with carcass weight as a covariate.	82
Table 4.10: Least squares means of muscle and fat traits in the Davies gene mapping herd.	83
Table 4.11: Least squares means of muscle and fat traits in the AgResearch gene mapping herd.	84
Table 4.12: Least squares means of muscle and fat traits in the Trangie RFI steers.	86
Table 4.13: Regression coefficients of hot standard carcass weight with standard errors and percent changes of traits for the Davies gene mapping herd.	86
Table 4.14: Regression coefficients of hot standard carcass weight with standard errors and percent changes of traits for the AgResearch gene mapping herd.	87
Table 4.15: Regression coefficients of hot standard carcass weight with standard errors and percent changes of traits for the Trangie RFI steers.	87
Table 4.16: Trangie RFI herd sire effects	96
Table 4.17: Heritabilities of fat traits and eye muscle area, Trangie RFI herd	97
Table 4.18: Genetic correlations of fat traits and eye muscle area, Trangie RFI herd	97
Table 4.19: Residual correlations between traits in the Davies gene mapping herd.	103
Table 4.20: Residual correlations between traits in the AgResearch gene mapping herd.	104
Table 4.21: Residual correlations between traits and estimated breeding values (EBV) in the steers from the Trangie RFI herd.	105
Table 4.22: Clusters formed for fat traits in Davies and AgResearch gene mapping herds.	105
Table 4.23: Eigenvalues and proportions of fat principal components in the Davies gene mapping herd.	107
Table 4.24: Eigenvalues and proportions of fat principal components in the AgResearch gene mapping herd.	108
Table 5.1: Fat deposition candidate genes sequenced for polymorphisms.	136

Table 5.2: Candidate genes and regions sequenced.	148
Table 5.3: Variants identified in the candidate genes.	149
Table 5.4: Mapping sire genotypes	154
Table 6.1: Genotyped single nucleotide polymorphisms and allele frequencies.	177
Table 6.2: Traits affected by SNPs (F probability)	179
Table 6.3: Single nucleotide polymorphism effects, including additive and dominance.	182
Table 6.4: Genetic correlations calculated from SNPs for fat and muscle traits.	185
Table 6.5: Within gene SNP interactions (significance).	188
Table 6.6: Interactions between genes. All SNPs within each gene are included.	190
Table 6.7: Comparison of genetic correlations between carcass traits from the Davies Gene Mapping herd with previously published genetic correlations.	207
Table 6.8: Comparison of fatty acid composition genetic correlations with previously published genetic correlations.	209
Table 7.1: Fat deposition quantitative trait loci from the National Animal Genome Research Program database, accessed 2011.	219
Table 7.2: Fat deposition quantitative trait loci from the Davies Gene Mapping herd.	219

## 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 ( <i>Longissimus dorsi</i> )
emaam	Eye muscle area ( <i>Longissimus dorsi</i> )
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  $\beta$ ,  *$\beta$ -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.

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Andrew R. Egarr  
October 2011

## **Dedication**

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

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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.