final report

Developing CTscan parameters for objective carcase measurement program and calibrating VIAscan systems

Executive summary

This report details a jointly funded project (MLA/WAMMCO/Cedar Creek) that aimed to:

1. Collect carcase yield information from boning a sufficient number and range of lamb carcases representing a range of leading industry sires.

2. Compare these with CTscan measurements from the same animals.

3. Develop yield prediction equations from measurements made by the VIAscan Sheep Carcase System.

4. Develop a cheaper alternative to the current VIAscan calibration system.

To achieve these aims lambs from the Sheep CRCs Information Nucleus Flock were slaughtered at the Katanning (2007 drop) site and various carcase measures taken. These included VIAscan, CT scan, and a complete carcase bone-out procedure. The analysis of this data is presented within this report in two parts; in Part 1 objectives 1, 2, and 4 are reported on, and in Part 2 objective 3 is reported on.

This study has confirmed the robustness of the VIAscan prediction across a wide range of carcase weights and fatnesses. This has been demonstrated in comparison to both CTscan estimates of %Lean, and also against lean meat yield % derived from a team of trained boners. This study has also demonstrated the potential for VIAscan to predict robustly within the progeny of current industry leading sires. A method for using CTscans to provide on-going calibration of the VIAscan system has also been proposed, relying on the direct regression between VIAscan LMY% and %CT lean.

Contents

1 Part 1 - Murdoch University Report

1.1 Introduction

1.1.1 Economics of lean meat yield for the lamb industry

Australia and New Zealand are the world's leading exporters of sheep meat products (Ward 1995). Over several decades in both domestic and international markets, there has been a progressive shift in consumer preference for larger, leaner cuts of lamb with minimal fat (Ward 1995; Banks, 2002). In addition, the phenotypic characteristics of muscularity and its presentation (cut style) also influence consumer choice (Laville et al, 2004). Consequently, meat yield has become a key criteria for optimal carcase quality and in an economic context, central to profitability.

An increase in saleable meat yield requires an increase in the amount of muscle mass relative to trimable fat and bone (Jones et al, 2002). Indeed, removing excess fat trim from a carcase represents a significant cost to the sheep meat industry sector concomitant with a reduction in saleable 'best-quality' meat. Clearly, the Australian sheep meat industry sector must continue to develop and utilize industry best-practice techniques that are responsive to consumer preferences, moreover in an increasingly competitive and complex market.

Animal maturity at time of slaughter will significantly influence carcase composition. As a proportion of total body composition, bone and skeletal muscle development precedes fat deposition, hence in the final phases of growth as an animal approaches growth maturity they become proportionately fatter (Cake et al 2006; Butterfield, 1988). Thus feeding lambs for longer periods to achieve a greater carcase weight, which are required to meet primal size specifications in overseas markets, may also result in animals which present with increased fat deposition and thus have a reduced yield of saleable meat (Nsoso et al, 2000). For this reason breeding programs have targeted fast growing, muscular and lean lambs.

Carcase traits have been found to be moderate to highly heritable in sheep (Lewis et al, 2000; Simm, 2000). Hegarty et al (2005) demonstrated several traits which significantly contribute to saleable meat yield in sheep, including growth (high post-weaning weight), leanness (C-site fat depth) and muscularity (high eye muscle depth), all of which can be selected for using breeding indices. Thus selecting for specific muscling traits associated with high carcase yield provides the potential to optimize lean meat yield returns. However, accurate yield measurement is essential to assess whether these genetic parameters are impacting on carcase yield (Safari, 2005).

1.1.2 Australian Sheep Industry Co-operative Research Centre: Information Nucleus Flock

A key focus for the Australian Sheep Industry Co-operative Research Centre (Sheep CRC) is to enhance carcase saleable meat yield. In addressing this, the Sheep CRC is currently hosting a large-scale prospective phenotypic study which aims to generate Australian Sheep Breeding Values (ASBV's) for traits of economic importance. The project involves the generation of an *'Information Nucleus Resource Flock'* (INF) consisting of five thousand ewes located at eight research sites Australia wide. The INF is being used to generate progeny from leading industry sires of diverse genetic backgrounds. Various traits of economic importance, including lean meat yield, will then be measured. This will allow quantification of phenotypic variation for given traits and estimation of how much of this phenotypic variation is genetically dependent. Understanding heritability in the context of genetic and environmental interactions and identifying associations with phenotype will clearly be pivotal for developing ASBV's that can be utilized in breeding selection indexes. Central to this outcome is accurate measures of muscle yield for slaughtered

INF progeny. Furthermore, for successful adoption within industry of these high yielding genotypes, an accurate yield measurement must be available within industry.

1.1.3 Measurement systems for Yield

There are a number of 'yield determination systems' utilized in Australia. Currently price grids based around Hot Standard Carcase Weight (HSCW) and GR tissue depth (total tissue depth measured at the GR site; 110mm from the spine over the 12th rib) are offered by the bulk of Australian processors (Banks et al, 2003). Most commonly used methods rely upon a single point measurement of the carcase (GR tissue depth) as a surrogate marker of whole body fatness, and by difference muscle yield. Single site measurement of fat relies on the concept of linearity between the single measure and whole body distribution, an assumption which may be erroneous. Trezona-Murray (2008) demonstrated that in pigs point selection for leanness at a single site on the back resulted in a redistribution of fat away from this site over a number of generations, with little change in whole body fatness. Furthermore, Hegarty *et al.* (2006) reported significant divergence in fatness between fast and slow-growth lambs, with the HSCW and GR tissue depth method unable to predict lean meat yield on carcases with this level of divergence. If clusters of sheep have a skewed distribution of fat away from the single site of fat measurement through genetic selection, the predictive power of this approach would be compromised.

In Europe, the carcase classification system for lamb carcases is based on a visual fat cover and conformation score known as the 'EUROP grid' system, (Kyame & Vangen, 2007; Navajas, 2008). Carcase grading in this manner has raised concern that desirable carcase conformation tends to be confounded with fatness. In terms of payment to the producer, the premiums for 'good conformation' animals outweigh the penalties of increased fat levels when the carcase is re-assessed after slaughter. The EUROP grid system encourages production of carcases with similar weight but without consideration of muscle yield.

A direct measure of lean meat yield can be obtained by a full bone-out of the carcase. However, given that the average time for a full-body bone out is approximately forty minutes per carcase, this would be a costly and time-consuming option for collecting yield data. From an experimental view-point there would also be concern regarding accuracy between boners and between animal processing plants (Biagini, Lazzorini, 2005).

Various studies have shown X-ray computer tomography scanning (CT) as an accurate method for predicting fat, protein and ash content of both the live animal and carcases (Jones et al 2002, Jopson et al 1995, Lambe et al 2003, Lambe et al 2008). It was found that CT was also a good predictor of lean meat yield (Smith, 2007). Presently, CT technologies are costly and not easily implemented in an industry setting because of occupational health issues. However, as a research tool CT allows accurate assessment of carcase composition, irrespective of phenotypic diversity. The CT methodology is a useful benchmark when considering alternate yield prediction systems for the INF, and also as a means of calibrating other yield prediction technologies such as VIAscan.

Video Image Analysis (VIAscan) is an objective grading tool that utilises digital images to quickly and accurately assess lamb and beef carcase characteristics. The VIAscan has a good yield predictive accuracy (96% accuracy with 4% error tolerance) (Davidson, Pethick 2005). However, there may be limitations in predicting Lean Meat Yield, particularly of carcases at the extremes of weight or fatness. A further limitation within the Australian industry is that VIAscan is only available in two sheep processing plants Australia wide, making it unsuitable for the national INF yield measurement. However, at present it is the only yield prediction system that goes beyond relying on HSCW and GR tissue depth. For there to be further adoption of VIAscan within

industry, it is essential that there is on-going demonstration of its predictive power – particularly within the modern genotypes being promoted within the Sheep CRC.

1.1.4 Project Objectives

The objective of this project was to:
1. Collect carcase yield information from boning a sufficient number and range of lamb carcases and compare these with predictions from the same animals CAT-scanned.

2. Enable development of yield prediction equations from measurements made by the VIAscan Sheep Carcase System and develop a cheaper alternative to the current VIAscan calibration system.

The primary intention was to use utilise lambs from the Sheep CRCs Information Nucleus Flock (INF) to capture progeny with divergent sire genotypes, and extremes of weight and fatness.

1.1.5 Hypotheses

1. VIAscan prediction of LMY% will have more precision than GR tissue depth and HSCW.
2. The VIAscan prediction of LMY% will maintain accuracy and precision at extremes of weight and fatness, and across a diverse range of sires.
3. The VIAscan prediction of LMY% will correlate strongly with %CT lean, and show no skewing at the extremes of %CT lean measurement.

1.2 Methodology-Section

1.2.1 Data Set

The data set used for this study (termed the Katanning 2007 data set within other reports) consisted of animals taken from the 2007 drop Information Nucleus Flock (INF) lambs at Katanning (n=202), which were slaughtered within two killgroups in 2008. Progeny were selected across a liveweight strata, after ensuring that progeny from all sires within each killgroup were represented. This data set consisted entirely of cross-bred lambs that were the progeny of 35 different sires representing Terminal sire types (Poll Dorset, Suffolk, Texel, White Dorper, and White Suffolk) and Maternal sire types (Border Leicester, East Friesian). Carcases were scanned whole (Katanning 2007), and subjected to a detailed whole carcase bone-out protocol.

1.2.2 Experimental Protocol

Of the original 202 lambs available within the Katanning 2007 data set, only 168 records were used due to either poor boning recoveries or the lack of availability of VIAscan readings. These progeny were chosen to represent the complete range of sires available at the Katanning site, so that the information collected could be used in further genetic analyses. These lambs were slaughtered in two groups balanced for sire over two separate kill days. Kill days were separated by 2 months to allow the later kill group to reach heavier slaughter weights (they were also supplemented with grain during finishing), thus expanding the data range to improve robustness of the prediction model. Each slaughter was carried out under commercial conditions with hot standard carcase weight (HSCW) and GR tissue depth (measured 110mm from the midline to the lateral surface of the 12th rib) recorded. Following slaughter (day 1) the carcases were

transported to Murdoch University, weighed and CT scanned on days 2 & 3, and then trucked to the commercial boning and boned out on days 4 & 5. All carcases were kept continuously chilled until bone-out.

1.2.3 CT scanning

All carcases were weighed before being scanned. This provided an accurate weight measurement for the CT scan data to be correlated with, in addition to providing an estimation of carcase dehydration which occurred between slaughter and CT scan. This was found to not differ to the subsequent cold carcase weight measured at bone-out.

A Picker PQ 5000 spiral CT scanner, located in the Murdoch University Veterinary School barn was used to scan the carcases at the Katanning site. At scanning the carcases were bent over the mid section, with the fold in the lumbar region of the spine, with the forelimbs flexed and extended caudally, and the hindquarters flexed and level with the body to ensure that the entire carcase fitted in the scanning field. Spiral abdomen protocol was selected to include the entire body from the thoracic inlet down to the hocks in the scan. The settings for each scan are outlined as follows: pilot scan length of 512mm, the field of view set at 480, Index 20, mA 150, revs 40, pitch 1.5 and algorithm standard. The carcase was scanned in 10mm slice widths, with each slice taken 10mm apart.

1.2.4 Editing and analysis of CT images

The images produced from the CT scanner required editing prior to analysis to remove non-carcase sections and artifacts from the image, particularly the CT table where the subject reclines. Image J version 1.37v (National Institute of Health, USA) was used in conjunction with Microsoft excel to carry out this task and then partition each image into bone, muscle and fat components. The discrimination point to identify the hounsfield barriers for associating pixels with bone, muscle, or fat were -235 to 2.3 for fat, 2.4 to 164.3 for lean and >164.3 for bone. An estimate of volume using Cavalieri's method was calculated as follows;

$$\text{Volume}_{\text{Cav}} = d \times \sum_{g=1}^{m} \text{area}_g - t \times \text{area}_{max}$$

where m is the number of CT scans taken, d is the distance the CT scans are apart, in this case 1cm. The value of t is the thickness of each slice (g), in this example 1cm, and area$_{max}$ is the maximum area of any of the m scans.

The average of the hounsfield units of the pixels of each component was then determined and converted into density (kg/L) using a linear transformation (Mull 1984). This was then used along with the volume of each component to determine the weight of fat, lean and muscle which was then expressed as a percentage of total carcase weight at the time of scanning.

Given the density of the marrow tissue, it is classified as either fat or lean using the boundary discrimination method described above. Additional editing within Image J enabled the isolation of the marrow component of bone within all images. Thus the above procedures could be repeated on the "marrow only" images. This enabled back correction for these pixels, reallocating them as bone and removing their associated volumes from the lean and fat components of the first iteration of image analysis.

1.2.5 Bone-out procedure

The bone-out procedure for the Katanning 2007 data was carried out at a commercial boning room in accordance with the Authority for Uniform Specification of Meat and Livestock (AUS-MEAT) 1998. The same boners were used throughout the entire collection period, with each boner being assigned to each of the three primals for cut preparation to optimize the consistency of the trimming.

A bandsaw was used to break each carcase down into three primal components, the hind quarter, saddle and forequarter. The hind quarter was separated from the saddle by a cut through the mid-length of the 6th lumbar vertebrae. A cut between the fourth and fifth ribs separated the forequarter from the saddle. A cut between the third and fourth cervical vertebrae separated the neck from the forequarter, with the forequarters being split down the midline. The left side forequarter was divided into the breast, foreshank and the square cut shoulder. The dorsal fat crest was removed from the neck to give a 'trimmed neck', which was further separated into lean meat, bone and fat components. The foreshank and breast were further separated into their lean meat, fat and bone components. The square cut shoulder was trimmed to leave only 6mm of subcutaneous fat; this cut was then divided into an eye of shoulder and a boneless shoulder component, which is associated with lean trim.

The saddle was split and the flaps were removed through a cut made parallel to the spine. The saddle was then cut between the 12th and 13th ribs to give a short loin and rack component. The width and depth cross-sectional measurement of the *M. longissimus thoracis et lumborum (LL)* was taken and used to calculate the cross-sectional area (EMA). A single cut 25mm from the lateral edge of the (LL) was made to remove the tail of the short loin. The subcutaneous fat was trimmed and the 13th rib was also removed. From this, an 'eye of short loin' was prepared and the 'tenderloin, butt off' was removed. From the left side of the LL a bone-in trimmed rack was prepared. The bone was removed from the flaps and the lean percentage of the flaps was subsequently determined. The flank meat was removed from the hind legs and the subcutaneous fat trimmed to 6mm. The legs were then split down the midline to give a 'leg, chump on'. The left leg was broken down into butt tenderloin, round, silverside, topside, rump and shank. All cuts used were boneless and trimmed to 6mm of subcutaneous fat.

1.2.6 Statistical Analysis

Precision of the VIAscan estimate
As a means of demonstrating predictive precision, the VIAscan predicted LMY% was regressed against the actual boner derived LMY%, and the root mean square error (RMSE), and R2 values reported. For comparison the precision of a yield prediction derived from a general linear model consisting of HSCW and GR tissue depth was also reported. The VIAscan predicted LMY% was also regressed against %CT Lean, with this measure considered a highly accurate determination of whole body lean. Lastly, %CT Lean was regressed against boner derived LMY%, providing an algorithm for converting %CT Lean values into the equivalent boner LMY% values. In all cases a truncated data set (n=121) has been used, consisting of only those carcases where CT measurements have been captured. This enables direct comparison of RMSE and R2 values for the different regression equations. However, to assess the precision of the VIAscan prediction across the entire Katanning 2007 data set (n=168), refer to Figure 6, page 11 within the Cedar Creek section of this report.

Phenotypic model
The lambs used within this study were a subset of the Sheep CRC Information Nucleus Flock. Within this Sheep CRC experiment the data is being analysed using phenotypic models. This

same modelling approach was applied to the VIAscan data (n=168) and %CT Lean data (n=121) collected from the Katanning 2007 drop lambs. VIAscan® lean meat yield and %CT Lean were analysed using a linear mixed effect model (SAS Version 9.1, SAS Institute, Cary, NC, USA). Fixed effects, and their first order interactions, included sex (male, female), birth type (1, 2, 3), rear type (1, 2, 3), sire type (Merino, Maternal, Terminal), and kill group (the first killgroup (174K07) was slaughtered at 174 days of age, and the second (244K07) at 244 days of age). Sire identification, and dam identification were included as random terms. First order interactions between fixed effects were tested and removed if non-significant (P>0.05). Age of lamb and HSCW and their first order interactions with fixed effects were included as covariates. Covariates and their interactions were only retained in the model if significant (P<0.05).

The aim of this phenotypic modeling was to demonstrate similarity in the outcome of yield analysis within a population where yield was measured using a highly accurate measure (CT scan), compared to a predictive measure (VIAscan).

1.3 Results

1.3.1 Raw data ranges

As an indication of the data range present within the Katanning 2007 data set, this information is summarised within table 4.1, with their mean, standard deviation, and range presented. This table includes information for HSCW, GR tissue depth, EMA, and C-site fat depth as well as a range of other muscle, bone and fat depot weights. Also presented are the range in %CT Fat, Lean, and Bone for these carcases. Figure 4.1 clearly demonstrates the diverse range in fatness and carcase weights, up to HSCW values of 36kg, and GR tissue depths of 29mm.

Table 4.1. Summary of raw carcase data within the Katanning 2007 data set, including the tissue weights of specific cuts to provide indicative tissue weight ranges. Values are Mean ± Standard Deviation (Minimum, Maximum).

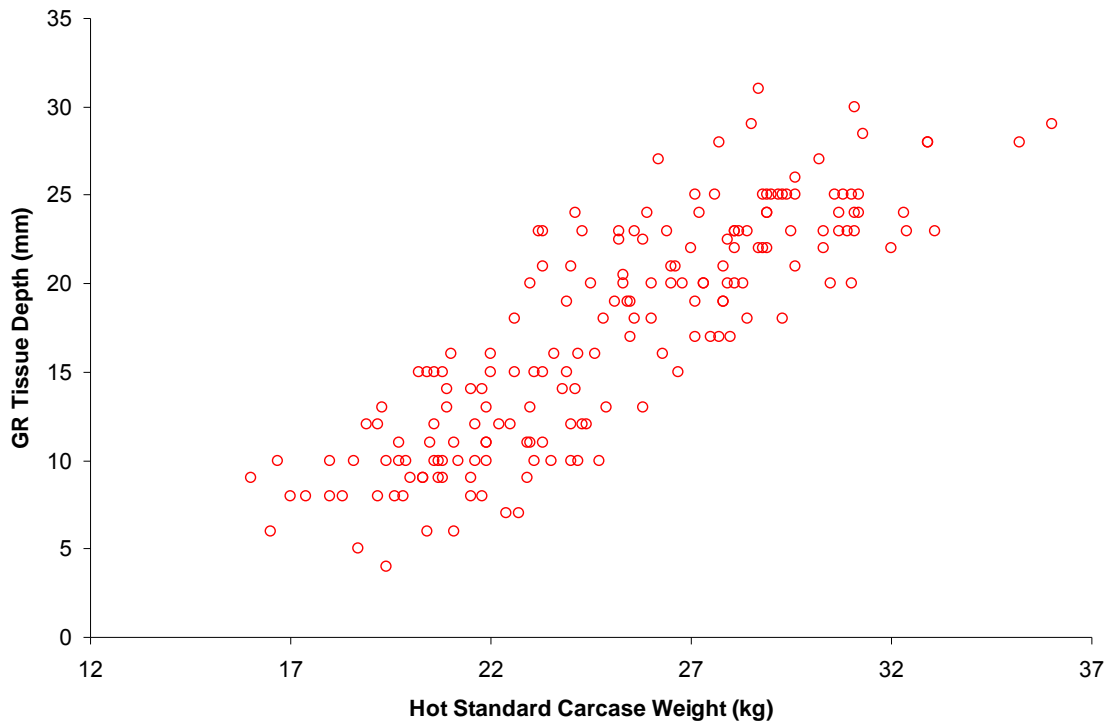|	Katanning 2007
Hot Standard Carcase Weight (kg)	24.7±4.35 (16, 36)
GR Tissue Depth (mm)	16.3±6.52 (4, 29)
Eye Muscle Area (mm^2)	14.9±2.66 (10.3, 23.5)
5th Rib Fat Depth (mm)	8.92±2.97 (2, 16)
C Site Fat Depth (mm)	5.78±2.68 (1, 14)
Topside Weight (kg)	0.65±0.10 (0.45, 0.90)
Eye of Shortloin Weight (kg)	0.38±0.07 (0.20, 0.56)
Round Weight (kg)	0.47±0.07 (0.32, 0.65)
Leg Bone Weight (kg)	0.89±0.10 (0.67, 1.14)
Shortloin Fat Weight (kg)	0.25±0.06 (0.10, 0.42)
% CT Fat	25.1±3.59 (16.6, 37.5)
% CT Lean	58.6±3.19 (50.0, 65.9)
% CT Bone	16.2±1.64 (11.5, 20.8)

Figure 4.1 HSCW versus GR tissue depth ranges for cross-bred lambs in Data Set C (n=183).

1.3.2 VIAscan performance

The carcases from the Katanning 2007 data set (n=168) were utilised to expand the prediction data set for the VIAscan® lean meat yield prediction system. In this section we demonstrate the performance of the VIAscan prediction, but only within those carcases that were CT scanned. As such the predictive precision of this system can be shown, but only in the context of its performance within its native (or training) data set (for demonstration of its transportability refer to Table 3, Page 8 of the Cedar Creek section of this report). The precision of the VIAscan system was relatively high (Figure 4.2; RMSE=1.74 and R^2 = 0.43). It also demonstrated no apparent skewing or heteroskedasticity at extremes of either weight or fatness, as demonstrated by plots of the residuals (residual = actual boners lean meat yield % - VIAscan predicted lean meat yield %) versus HSCW (Figure 4.3) and GR tissue depth (Figure 4.4). These predictions also maintained a linear relationship with %CT lean (Figure 4.5) across the entire range of lean values, again with no apparent skewing or heteroskedasticity at extremes of either weight or fatness (data not shown).

For comparison, when a combination of HSCW and GR tissue depth (current industry standard for yield prediction) are used to predict Lean Meat Yield % within this data set there is considerably less precision, with an RMSE=2.19 and R^2 =0.19.

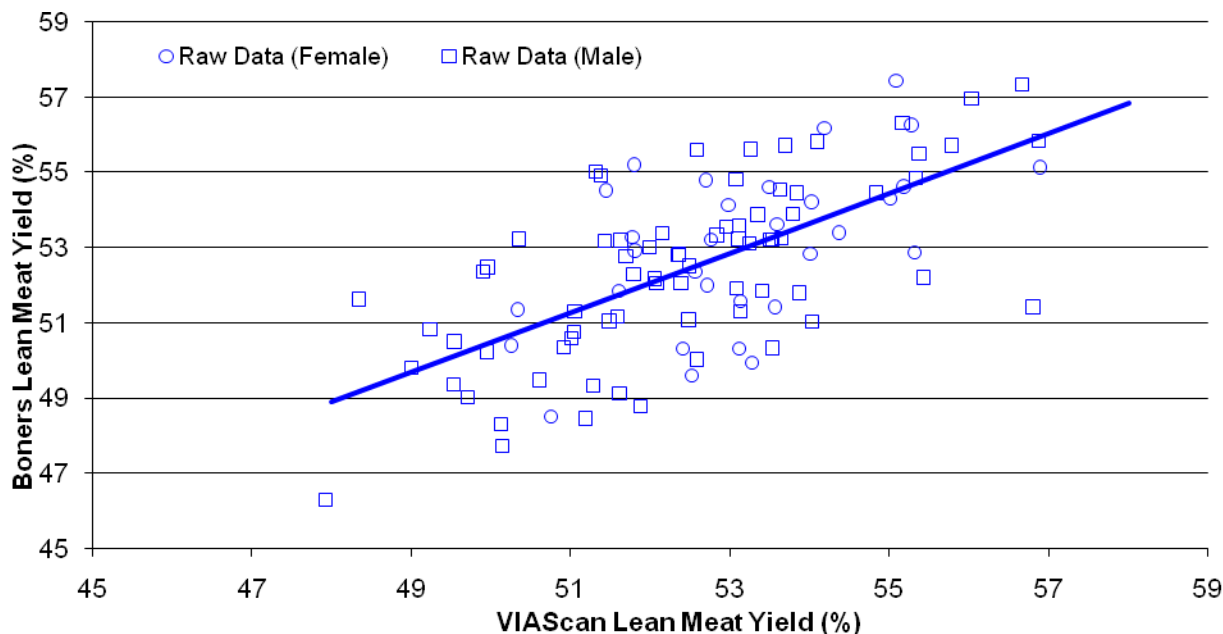Figure 4.2. The relationship between actual lean meat yield (%) determined by commercial boners and VIAscan® predicted lean meat yield % for the Katanning 2007 data set (RMSE = 1.74, and R^2 = 0.43).

Figure 4.3. Residuals for VIAscan® predicted lean meat yield % within its native data set (Katanning 2007) versus hot standard carcase weight (kg). Residual = actual boners LMY –VIAscan® predicted lean meat yield %.
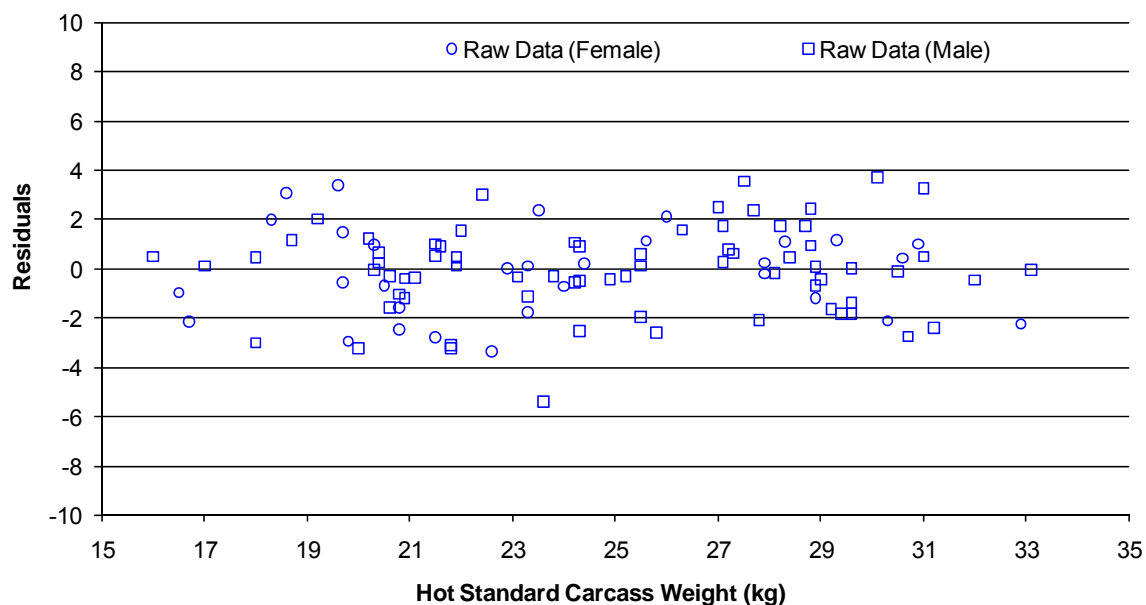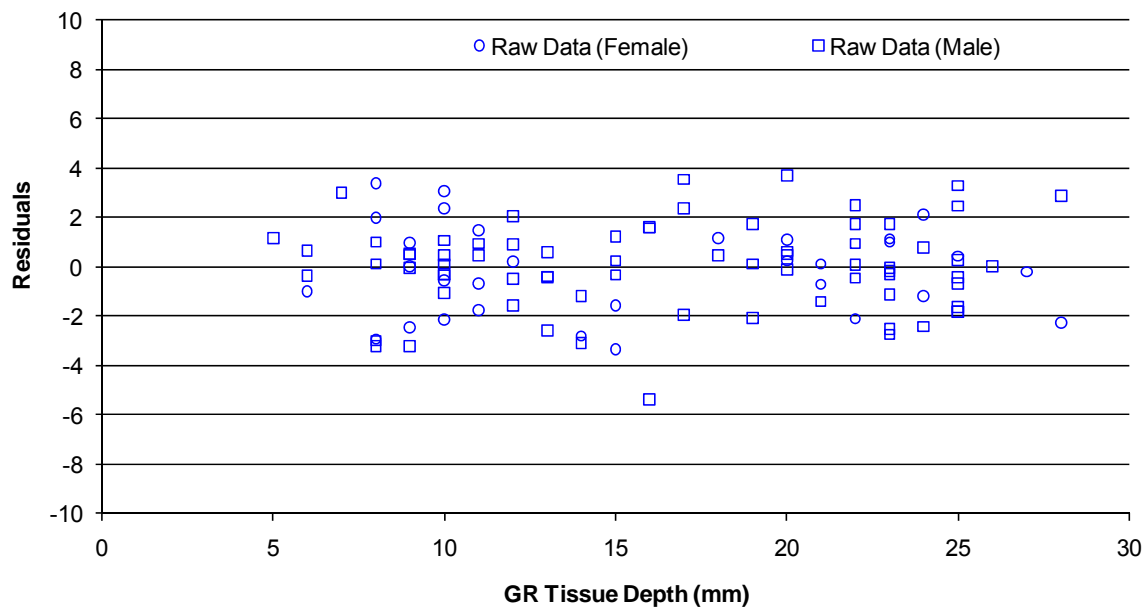
Figure 4.4. Residuals for VIAscan® predicted lean meat yield % within its native data set (Katanning 2007) versus GR tissue depth (mm). Residual = actual boners LMY –VIAscan® predicted lean meat yield %.
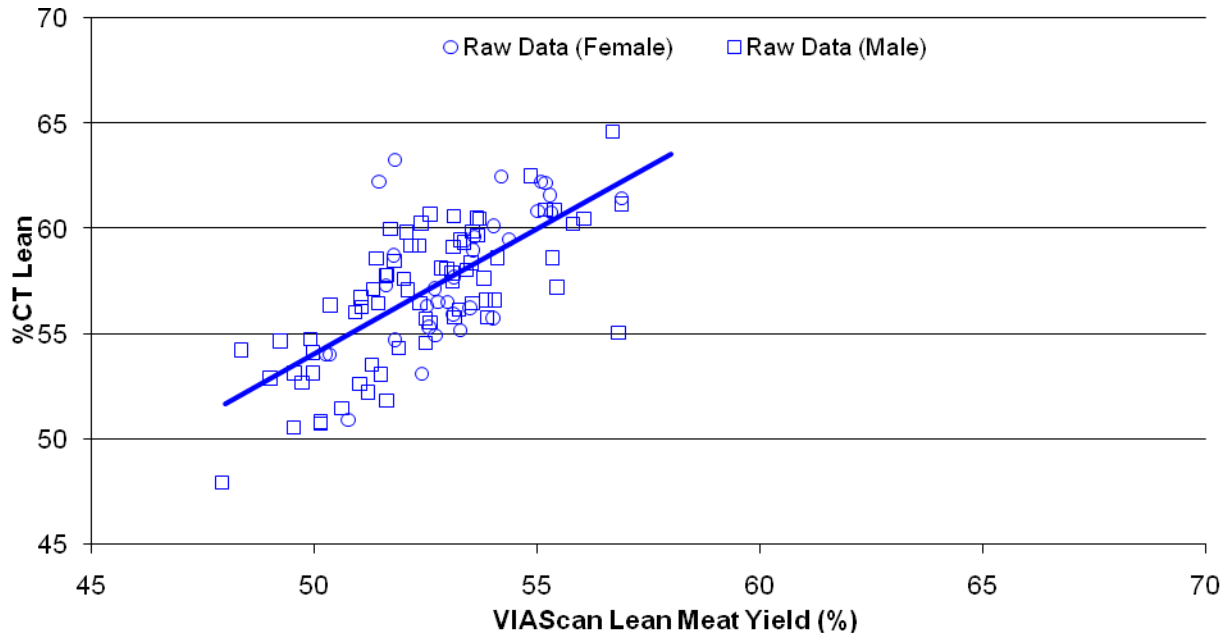

Figure 4.5. The relationship between %CT lean and lean meat yield (%) predicted by VIAscan® for the Katanning 2007 data set (RMSE = 2.34, and R^2 = 0.49).

1.3.3 Comparison of output from a phenotypic analysis of VIAscan predicted Lean Meat Yield %, versus %CT Lean.

Phenotypic models were derived for both the VIAscan LMY% data. Of the fixed effects tested, only sire type (ie Maternal or Terminal) and killgroup (ie killgroup 1 or 2) were significant ($P<0.01$; Table 4.3). Terminal sired lambs had VIAscan LMY% that were about 1.3 units higher than Maternal sired lambs, and the lambs in the younger killgroup (174K07) had VIAscan LMY% that were about 1.6 units higher than the older killgroup (244K07). No other fixed effects tested were significant within this relatively small sample size. HSCW as a covariate was only significant if killgroup was dropped from the model, and in this case each kilogram increase in HSCW resulted in a 0.21±0.028 unit fall in VIAscan LMY%.

For comparison, the same phenotypic analysis was carried out on the %CT Lean data collected from the same animals. In all cases the same fixed effects were found to impact within the model (Table 4.3), their magnitudes were similar, and the covariate for HSCW was again only significant when killgroup was excluded from the model.

Table 4.2 *Covariance parameter estimates for the linear mixed effects models for VIAscan Lean Meat Yield % and %CT Lean shown in* Table

Covariance Parameter	VIAscan LMY%		%CT Lean	
	Variance Component Estimate ±SE	Z Value	Variance Component Estimate ±SE	Z Value
Sire Identification	0.13±0.198	0.65	0.18±0.487	0.36
Dam Identification	1.27±0.524	2.42*	0	.
Residual	1.26±0.439	2.88	5.57±0.846	6.58

*$P<0.01$

Table 4.3. *F-values, and least square means or coefficients (±SE) for the effects of sire type, and kill group on VIAscan Lean Meat Yield % and %CT Lean.*

Effect	VIAscan LMY%		%CT Lean	
	F-value	LS means ±SE	F-value	LS means ±SE
Killgroup	41.9**		96.6**	
174K07 [ψ]		53.3±0.21		58.8±0.33
244K07		51.7±0.20		54.5±0.33
Sire type	15.0**		16.1**	
Maternal		51.8±0.28		55.7±0.40
Terminal		53.1±0.17		57.7±0.28

*, $P<0.05$; **, $P<0.01$. [ψ], kill group annotation represents the average age of each kill group, the site code (K=Katanning), and the year of lamb birth.

As a final demonstration of the potential for VIAscan to discriminate between the progeny of different sires, the sire estimates derived from the phenotypic model for VIAscan LMY% were plotted against the sire estimates derived from the phenotypic model for %CT Lean (Figure 4.6). The discrimination between the progeny of Terminal and Maternal sires is clear, however even

within a siretype group there was still only limited re-ranking of sires as determined by the two yield measurement technologies.
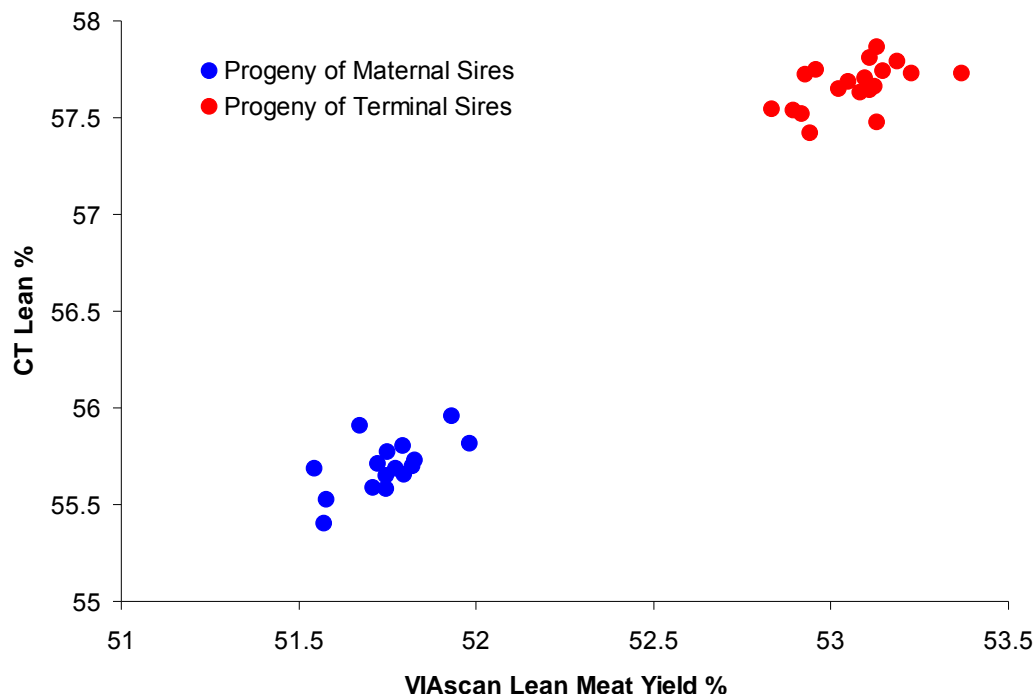

Figure 4.6. Sire estimates derived from a phenotypic model of %CT lean versus the sire estimates derived from a phenotypic model of lean meat yield (%) predicted by VIAscan®.

1.3.4 Converting %CT lean to the equivalent commercial lean meat yield.

A constraint of using %CT lean as a dependant variable is that this measurement is not directly equivalent to the lean meat yield derived from a team of commercial boners, and hence not immediately relevant to industry (as opposed to VIAscan LMY% which is). Therefore, as a point of practical reference the relationship between %CT lean and boners lean was determined (Figure 4.7). Thus to convert %CT lean into the commercial boners lean equivalent, the following equation can be used:

Commercial boners lean meat yield (%) = %CT Lean * 0.657 + 14.52.

Whilst linear, this relationship also demonstrates that a 1 unit reduction in %CT lean only corresponds to a drop of 2/3 this amount in boners lean. Thus it seems apparent that the commercial cuts from fatter animals are containing "proportionately" more fat, even after these cuts have been trimmed to equivalent levels of lean. This is most likely a reflection of the intra- and inter-muscular fat depots which will be larger in fatter animals, and yet not accessible to commercials boners for trimming. None-the-less, the variability of boners lean within the fatter animals did not increase as shown by the residuals (actual boners LMY% - %CT Lean) plotted against GR tissue depth (Figure 4.8).

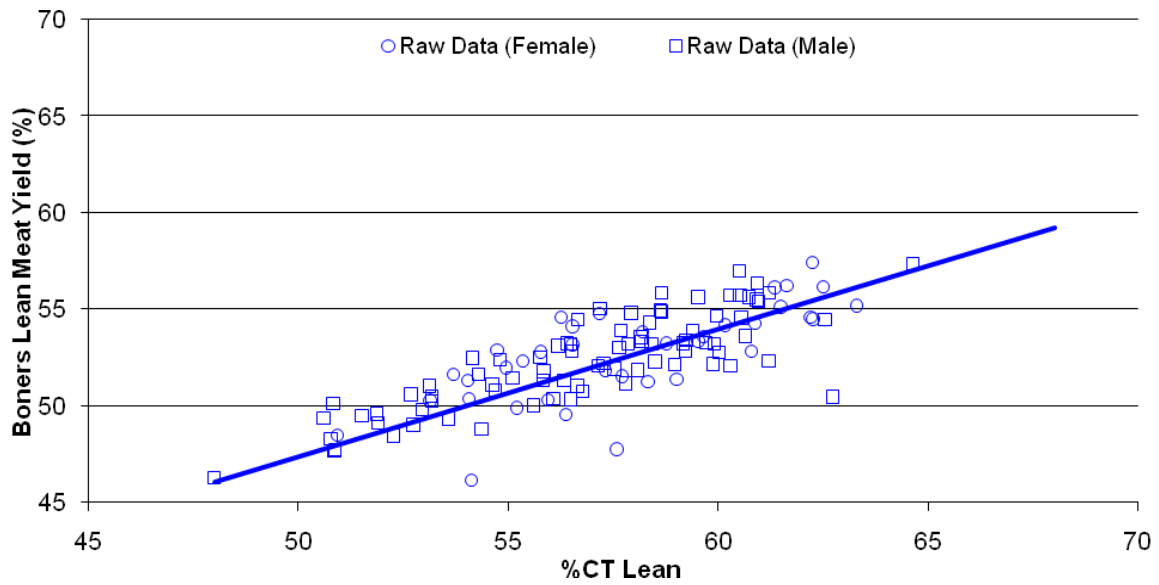Figure 4.7. The relationship between lean meat yield (%) determined by commercial boners and %CT lean for the Katanning 2007 data set (RMSE = 2.66, and R^2 = 0.41, Slope = 0.657, Intercept = 14.52).
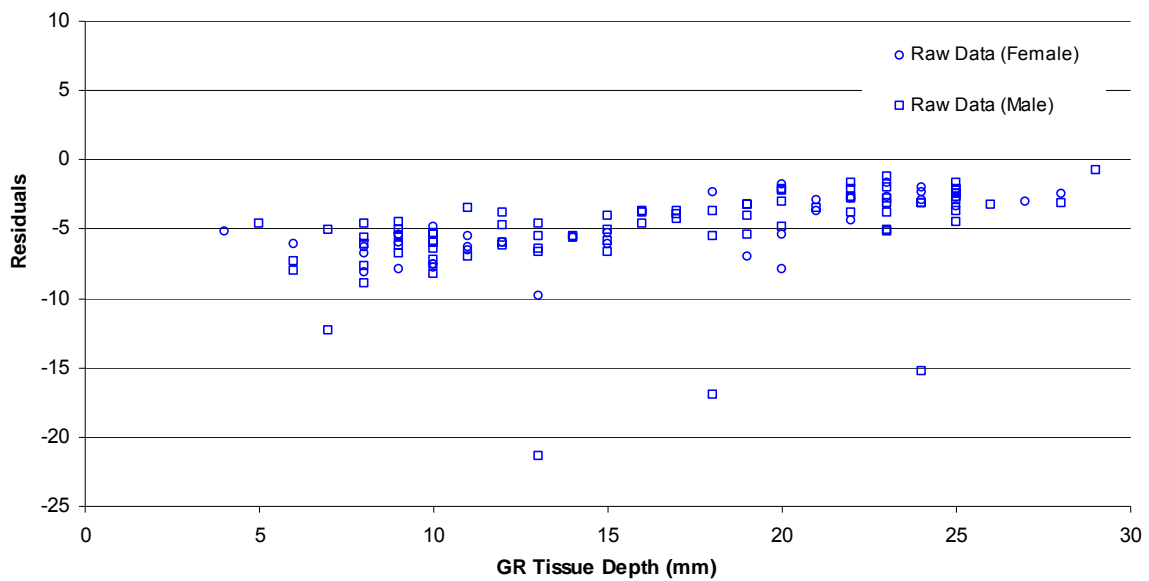

Figure 4.8. Residuals for the difference between lean meat yield (%) determined by commercial boners and %CT lean for the Katanning 2007 data set versus GR tissue depth (mm). Residual = actual boners LMY% –%CT Lean.

1.4 Discussion

1.4.1 Precision and accuracy of the VIAscan LMY% prediction algorithm

Within its native data set the VIAscan prediction of LMY% demonstrated very good precision. This precision was well in excess of that demonstrated by a model containing HSCW and GR tissue depth, which is the current industry standard for indicating carcase LMY%, thus supporting our initial hypotheses. There was also no apparent bias in the VIAscan prediction of LMY% at the extremes of either weight or fatness, thus supporting our second hypothesis. Given the large range in carcase weights and fatness, this should provide users of the VIAscan system with confidence that its predictions are robust across the commercially relevant range of carcase sizes.

1.4.2 Stability of the VIAscan LMY% prediction relative to %CT lean.

The VIAscan prediction of LMY% also compared well with %CT Lean. This relationship was linear across the entire range of %CT Lean values, demonstrating no skewing or heteroskedasticity at extremes of either LMY%, HSCW, or GR tissue depth, thus supporting our third hypothesis. Given the accuracy with which CT determines carcase lean, this result provides further confidence in the ability of VIAscan to describe lean tissue proportion within a carcase.

1.4.3 Accuracy of the VIAscan LMY% prediction algorithm across a diverse range of sires.

When the VIAscan prediction of LMY% was analysed using a phenotypic model similar to that being utilised by the analysis team within the Sheep CRC, it clearly demonstrated an ability to discriminate between the progeny of high yielding Terminal sires (ie Poll Dorset, Suffolk, Texel), and lower yielding Maternal sires (ie Border Leicester). To demonstrate confidence that these lean differences were actually present within these animals the same phenotypic analysis was applied to the corresponding %CT Lean measurements from the same carcases, and in this case a very similar result was found. Furthermore, when the sire estimates from the %CT Lean model and the VIAscan predicted LMY% model were generated, they demonstrated a very high correlation. This provides further confidence that VIAscan will predict robustly within the progeny of current industry leading sires.

1.4.4 The potential for using CT as a means of calibrating VIAscan systems.

There are two approaches that could be employed for on-going calibration of the VIAscan system utilising CT data captured on the same carcases. Firstly, the VIAscan prediction of LMY% could be regressed against the corresponding %CT Lean, similar to that shown in Figure 4.3 above. The new data should follow the same relationship, and fall within the distribution shown in this figure. Secondly, the CT data could be transformed into the corresponding boners LMY% equivalent using the formula shown in section 4.4 and derived from Figure 4.5 above. This transformed data could then be regressed against the corresponding VIAscan prediction of LMY% and should follow the same relationship as that shown in Figure 4.2 above. In principle, this transformed data could even be incorporated into the prediction database that the VIAscan algorithm is derived from. However the flaw in this second approach is associated with an issue of compounding errors. The transformation step to convert %CT Lean to the equivalent boners LMY% has error associated with it, which would then be compounded within the subsequent comparison of boners LMY% and VIAscan LMY% - also with an associated error. As such this

second approach is not recommended, and calibration should be limited to comparing %CT Lean with VIAscan prediction of LMY%.

1.4.5 Conclusion

Results of this study have confirmed the robustness of the VIAscan prediction across a wide range of carcase weights and fatnesses. This has been demonstrated in comparison to both CTscan estimates of %Lean, and also against lean meat yield % derived from a team of trained boners. This study has also demonstrated the potential for VIAscan to predict robustly within the progeny of current industry leading sires. A method for using CTscans to provide on-going calibration of the VIAscan system has also been proposed, relying on the direct regression between VIAscan LMY% and %CT lean.

1.5   References

Australian Sheep Industry Cooperative Research Centre, (2008). Information Nucleus (Pamphlet): *Cooperative Research Centre for sheep industry Innovation, 2008.*

Banks, R.G., (2002). Enhancing the value of meat from wool sheep: is there a need for specialization? *International Journal of Wool Technology*, Vol 50:584-595.

Banks, R. G., Ross, I. S., (2003). Information flow in lamb supply chains – implications for terminal sire breeding. Proceedings of the 15th conference of the Association for the Advancement of Animal Breeding and genetics, pp: 334–337.

Barnard P., (2006). Meat-prospects and markets, *Sheep CRC Conference 2006*, Eds Cronje P.B. & D.K. Maxwell, Armidale, NSW.

Biagini D., Lazzaroni C. (2005). Carcass dissection and commercial meat yield in Piemontese and Belgian Blue double-muscled young bulls, *Livestock Production Science*, Vol 98: 199-204.

Butterfield R., New Concepts of Sheep Growth. (1988). Griffin Press Ltd, Australia.

Cake M.A, Gardner G.E., M.D Boyce, (2006). Forelimb bone growth and mineral maturation as potential indices of skeletal maturity in sheep, *Australian Journal of Agricultural Research*, Vol 67: 699-706.

Davidson R., Pethick D. (2005). Benefits of VIAscan to producers and WAMMCO, *Sheep Updates,* Chief Executive Officer, Department of Agriculture, Western Australia.

De Boer H., Dumont B.L., R.W. Pomeroy & others, (1974). Manual on E.A.A.P. Reference Methods For the Assessment Of Carcass Characteristics in Cattle, *Livestock Production Science*, Vol1, pp:151-164.

Fogarty N.M., Safari E., Gilmour A.R., Ingham V.M., Atkins K.D., Mortimer S.I., Swan A.A., Brien F.D & J.C. Greef (2006). Wool and meat genetics-the joint possibilities, *Wool Meets Meat (eds. P.B. Cronjé & D. Maxwell),* Proceedings of the 2006 Australian Sheep Industry CRC Conference.

Gardner G.E., Pethick D.W., D.L. Hopkins, & others, (2006). The impact of carcase estimated breeding values on yield and quality of sheep meat, *International Journal of Sheep and Wool Science*, 54:33-39.

Garrick, D.J., (1991). Best linear unbiased prediction for across

flocks could allow even higher rates of genetic gains flock/ year breeding values. *Proceedings NZ Society. Animal Production.* 51, 411–416.

Harrington, G., Kempster, A.J., (1989). Improving Lamb carcass composition to meet modern consumer demand., In: Dyrmundsson, O.R., Thorgeirsson, S. (Eds*), Reproduction, Growth and Nutrition in Sheep.* Agricultural Research Inst., Reykjavik, Iceland, pp: 9-90.

Hegarty R.S, Warners R.D and D.W. Pethick, (2006). Genetic and nutritional regulation of lamb growth and muscle characteristics, *Australian Journal of Agricultural research*, Vol 67, pp: 721-730.

Hopkins D.L., Safari E., J.M. Thompson, (2004), Video image analysis in the Australian meat industry-precision and accuracy of predicting lean meat yield in lamb carcasses, *Meat Science*, Vol 67, pp:269-274.

 Hopkins D.L., (2008). An industry applicable model for predicting lean meat yield in lamb carcasses, *Australian Journal of Experimental Agriculture*, Vol 48, pp:1-5.

Jones H.E., Simm, G., W.S. Dingwall, (1999). Genetic relationships between visual and objective measures of carcass composition in crossbred lambs, *Animal Science,* Vol 69, pp:553-561.

Jones H.E., Simm G., R.M. Young, (2002). The use of X-ray computer tomography for measuring the muscularity of live sheep. *Animal Science*, Vol 75, pp:387-399.

Jopson N.B., Kolstad K, E Sehested & others (1995). Computed tomography as an accurate and cost effective alternative to carcase dissection. *In 'Australian Association for the Advancement of Animal Breeding and Genetics'*, pp: 635-638.

Kempster A.J., Cuthbertson A., & C Harrington, (1982). Carcase evaluation in livestock breeding, production and marketing. p:306, Granada Publishing Ltd, London.

Kennedy, B.W., Trus, D., (1993). Considerations on genetic connectedness

between management units under an animal model. *Journal of Animal Science*, Vol71:2341–2352.

Kinghorn, B.P., Shepherd, R.K., (1990). The impact of across-flock

strategies on sheep breeding structures. *In: Proceedings for the 4th World Congress on Genetics Applied to Livestock Production,* Vol. 15, pp. 7–16.

Kvame T., Vangen O., (2007). Selection for lean weight based on ultrasound and CT in a meat line of sheep, *Livestock Science*, 106,:232-242.

Lambe N.R., Young M.J. K.A McLean & others, (2003). Prediction of total body tissue weights in Scottish Blackface ewes using computed tomography scanning, *Animal Science*, Vol 76, pp:191-197.

Lambe N.R., Navajas E.A., C.P. Schofield & others, (2008). The use of various live animal measurements to predict carcass and meat quality in two divergent lamb breeds*, Sustainable Lievestock Systems Group*, Scottish Agricultural College.

Larzul, C., Lefaucheur, L., Ecolan, P., Gogue, J., Talmant, A., Sellier, P., Le Roy, P. & Monin, G. (1997). Phenotypic and genetic parameters for longissimus muscle fibre characteristics in relation to growth, carcass, and meat quality traits in Large White pigs. *Journal Animal Science,* Vol 75: 3126-3137.

Laville, E., Boiux J, T Sayd, (2004). Effects of a quantitative trait locus for muscle hypertrophy from Belgium Texel on sheep carcass conformation and muscularity, *Journal of Animal Science*, Vol 82, pp: 3128-3137.

Lewis R.M., Simm G, (2000). Selection strategies in sire referencing schemes in sheep, *LivestockProductionScience*,Vol67,pp:129-141.

Marcoux M., Pomar C., L. Faucitano, (2007). The relationship between different pork carcass lean yield definitions and the market carcass value*, Meat Science*, 75:94-102.

McFarland (2006). The development of individual management systems for prime lamb production, In 'Ovine Observer', No. 35, Department of Agriculture and Food, Narrogin.

Miles C.A., Fursey, G.A.J, A.V. Fisher, (1991). Estimation of lamb carcass composition from measurements of the speed of ultrasound in the soft tissues of live animals and carcasses, *Meat Science*, Vol 30, pp:245-256.

Mull R.T., (1984). Mass estimates by computed tomography: physical density from CT numbers, American Journal of Roentgenology, Vol 143, 99: 1101-1104.

Navajas E.A., Lambe N.R., A.V. Fisher, (2008). Muscularity and eating quality of lambs: Effects of breed, sex and selection of sires using muscularity measurements by computed tomography, *Meat Science*, Vol 79, pp:105-112.

Nsoso S.J., Young M.J., P.R. Beatson, (2000). A review of carcass conformation in sheep: assessment, genetic control and development*, Small Ruminant Research*, Vol 25, pp:89-96.

Patel, K, Amthor H, (2005). The function of Myostatin and strategies of Myostatin blockade—new hope for therapies aimed at promoting growth of skeletal muscle. *Neuromuscular Disorders*, **15**: 117-126.

Pearce KL, Ferguson M, G Gardner, (2008). Dual x-ray absorptimotery accurately predicts carcass composition from live sheep and chemical composition of live and dead sheep. *Meat Science* In press.

Plant C.L., Maden J.J.L., & P.A. Kenney, (1996). Estimating the Lean Meat Yield of Lambs, *Proceedings for Australian Society of Animal Production*, Vol 21, pp:139-142.

Pomar, C., Rivest, J., P. Jean dit Bailleul, & Marcoux M. (2001). Predicting loin-eye area from ultrasound and grading probe measurements of fat and muscle depths in pork carcasses. *Canadian Journal of Animal Science*, Vol 81, pp:429–434.

Ponnampalama E.N, Hopkins D.L., Butler K.L, F.R. Dunshea, (2007). Genotype and age effects on sheep meat production 2. Carcass Quality traits, *Australian Journal of Experimental Agriculture*, Vol 47, pp: 1147-1154.

Safari E., Fogarty N.M., A.R. Gilmour, (2005). A review of genetic parameter estimates for wool, growth, meat and reproduction traits in sheep, *Livestock Production Science*, Vol 92, pp: 271-289

Simm G., Murphy S.V, (1996). The effects of selection for lean growth in Suffolk sires on the saleable meat yield of their crossbred progeny, *Animal Science*, Vol 62, pp: 255-263.

Simm, G. (2000). Genetic improvement of cattle and sheep, Tonbridge, Farming Press.

Smith N, (2007). Use of Computer Tomography to estimate compositional changes in response to carcase estimated breeding values in Merino wethers, PhD, Murdoch University

Stanford K., Clark I. S.D.M. Jones, (1995). Use of ultrasound in prediction of carcass characteristics in lambs. *Canadian Journal Animal Science*, Vol 75, pp: 185-189

Stanford K., Jones W.D.M., M.A Price, (1998). Methods of predicting lamb carcass composition: *A review, Small Ruminant Research*, Vol 29, pp: 241-254.

Sundstrom, B. (2003). "BREEDPLAN." Agnote DAI-311 (first edition) DAI-311 (first edition).

Suster, D., Leury, B., Wark, J., Kerton, D., Ostrowska, E., & Dunshea, F. (2000). Dual Energy X-ray Absorptiometry Accurately Predicts Whole Body and Carcass Composition in Pigs. *Journal of Animal Science, 78*(Supplement 1), pg:145

Tobin, J. F., A. J. Celeste (2005). "Myostatin, a negative regulator of muscle mass: implications for muscle degenerative diseases. Current Opinion in Pharmacology 5, Vol 1: 328–332

Thompson JM, Kinghorn BP, (1992). CATMAN- A program to measure CAT-scans for prediction of body components in live animals. In ' Australian Association for the Advancement of Animal Breeding and Genetics' pp. 560-564.

Trezona, M., Mullan, B. P., D'Antuono, M., Wilson, R. H., and Williams, I. H. (2004). The causes of seasonal variation in backfat thickness of pigs in Western Australia. **Australian Journal of Agricultural Research** 55(3) 273 - 277

Trezona-Murray M., (2008). Conventional and Deep Litter Pig Production Systems: The effects on fat deposition and distribution in growing female large white X landrace pigs. PHD thesis, Murdoch University, Perth, W.A.

Walstra, P., & Merkus, G. S. M. (1996). Procedure for assessment of the lean meat percentage as a consequence of the EU reference dissection method in pig carcass classification. *Report ID-DLO 96.014, The Netherlands.*

Ward, C.E., Hildebrand T.A., (1995). Consumer perception of lamb compared with other meats. *Sheep Goat Research Journal*, Vol 11, Iss 2, pp: 64-70.

2 Part 2-Cedar Creek Report-The development of improved lean meat yield (LMY) Algorithms for VIAscan

2.1 Company Overview

Cedar Creek Company (CCC) is a specialist technology company, whose core business is the development and implementation of advanced software and hardware systems for the perishable and general food & beverage processing industries. CCC services its customer base from its head office in Brisbane, with regional offices in New Zealand and Chile, catering to a global customer base.

CCC provides the food industry with a range of software systems and associated hardware, backed by business analysis, integration, implementation and support services, to deliver real, on-going value to its clients.

CCC places strong emphasis on building ongoing business partnerships with its clients, based on a thorough understanding of their business needs and priorities that enables it to offer informed analysis and advice and to incorporate this into the design of its systems and solutions.

2.2 Project Background

This project is a component of the MLA Project: "WAM4 - Developing CAT-Scan parameters for objective carcase measurement program and calibrating VIAscan systems".

An extract from the application and contract for this over-arching project is outlined in this section to provide background to this project.

Project "WAM4 - Developing CAT-Scan parameters for objective carcase measurement program and calibrating VIAscan systems" outlines a process for laying the foundation for an unparalleled basis for the implementation of advanced Supply Chain Management in Australia's lamb industry.

The key to the potential success of this Supply Chain is the ability to accurately measure lamb carcase value (predominantly influenced by carcase yield) on-line during processing, linked to the genetic background of lambs and delivered to all members of the supply chain via the internet.

The lamb industry has been promoting efficiencies within the supply chain for some time. In the pursuit of greater efficiencies, accurate prediction of carcase composition is vital, particularly for the efficient allocation of resources during production and the optimisation of carcase recovery during processing. The prediction of carcase composition in relation to market demands is a key to underpinning the development of a value based marketing system. Establishing an environment of value based marketing is one aspect that will assist producers and processors to improve pricing efficiency and information flow within the supply chain.

Within the Australian lamb industry there has been limited investment from an industry perspective in recent years in updating the objective yield algorithms to account for changes in the genetics and the heavier carcase weight of lambs processed.

A number of detailed lamb bone-out trials have been undertaken by the Australian lamb industry to calibrate the on-line objective yield measurement technology (VIAscan®) to actual lamb yields. However, the Australian lamb industry has progressed in recent years by adopting Lambplan

principles to improve the genetic merit of existing breeds and importing some new breeds into the country. The broader range of improved genetics and management practices can now meet the increasing demands of consumers and markets as well as the pressures of production efficiencies. Current methods of on-line objective yield measurement are more than two times as accurate as the current carcase weight and fat grid system. However, in order to provide the supply chain with the most accurate and robust assessment of lamb carcase value on-line across a broad range of known contemporary genetics including extreme ASBV's, further yield calibration trials need to be undertaken on an industry basis.

VIAscan yield prediction calibrations have not been validated on evolving genetics and as such their calibration needs to be updated and validated for the initial investors to have confidence in the use of the existing VIAscan systems for carcase payment. This project will use the developing understanding of CAT-Scanning techniques to continue to evolve MLA's Objective Carcase Measurement program whilst at the same time scanning the animals that are CAT-Scanned with a VIAscan unit and hence recalibrate the existing VIAscan systems. It is anticipated that the outcomes from this project will provide owners of VIAscan systems a more cost effective way to keep their system calibrated compared with the only other method of extensive and expensive bone out trial calibrations.

The objectives of the overarching project are to:
1. collect carcase yield information from boning a sufficient number and range of lamb carcases and compare these with predictions from the same animals CAT-scanned.
2. enable development of yield prediction equations from measurements made by the VIAscan Sheep Carcase System and develop a cheaper alternative to the current VIAscan calibration system

The second of these points forms the scope and basis for this report and is described in further detail below.

The VIAscan system has operated at WAMMCO since 2005. The VIAscan regression released at the time of commissioning was based on the Castricum 2000 boning trial. This trial consisted of 7 meat breeds (1st and 2nd cross – 60% and 29% respectively) and merino lambs (10%). This dataset has provided an excellent platform to predict lean composition of Australian lambs.

For this project, Rob Davidson (WAMMCO) initiated a collaboration with Graham Gardner (Murdoch University/Sheep CRC) to utilise a subset of lambs sourced from the Sheep CRCs Information Nucleus Flock (INF). The INF uses semen from a diverse range of industry sires, most being industry leaders for a particular genetic trait. A subset of 202 XB lambs were taken from the 2007 drop at the Katanning INF site, of which 168 lambs were successfully boned (30 carcases had poor boning recoveries, 4 carcases did not have VIAscan information available). Seven sire types were represented and their contribution to the dataset is shown in

Table 1

Table 1: The proportion of sire types represented in the 2008 XB Trials (168 head).

Breed	Proportion
Border Leicester	23.1%
East Friesian	2.4%
Poll Dorset	27.2%
Suffolk	8.3%
Texel	7.1%
White Dorper	10.7%
White Suffolk	20.1%

The 2008 XB trial will supplement the Castricum dataset with additional yield data from lambs with the latest genetics currently in the lamb industry.

2.3   Objectives

The objectives of this project are to ascertain the ability of the VIAscan Sheep Carcase System to predict the yield of a broad range of Cross-Bred lambs representing the current breeds available in the Australian processing industry and implement these equations into the VIAscan System operating at WAMMCO's Katanning Plant.

2.4   Methodology, results and discussion

The 2008 XB trial was divided into two kills – Jan'08 and Mar'08. The second kill were a draft from the initial trial population that were feed on a grain based diet to achieve a greater carcase weight and fat depth.

The lambs were slaughter at Katanning, WAMMCO and were chilled over night at which time a portion were trucked directly to the boning room in Perth and the remainder were delivered to Murdoch University for CAT scanning. The carcases were boned over a 3 – 4 day period according to the boning procedure describe in the VIAscan Lamb - Lean Meat Yield Trial Manual (Cedar Creek Company Publication)

2.4.1   Carcase Composition.

This section details the relative composition of the carcases from the various bone-out trials. The reason for this investigation is to understand the potential impacts of stages of maturity of lambs and/or boning procedures on the performance of the VIAscan System to predict carcase yield.

2.4.2   Lean Meat Yield

Based on the average Lean Meat Yield (LMY), there were significant differences between trials. The LMY of Cast 2000 lambs were on average 1.3% – 2.59% greater than the other trials. The Cast 2000 lambs and Jan 08 lambs were the most alike as the difference was 1.3%. Even between the 2008 XB trials there was a difference in LMY of 1.27%.

Table 2: The averages of carcases composition, HSCW and GR for each trial. The ADJ LMY is the LMY corrected for GR.

Trials	LMY (%)	FAT (%)	BONE (%)	HSCW (kg)	GR (mm)	ADJ LMY
Cast2000	54.96	20.18	24.65	20.74	11.9	54.32
XB08_Jan	53.64	18.21	27.58	21.44	11.1	52.73
XB08_Mar	52.37	23.33	23.70	28.25	22.3	55.15

When the LMY yield was adjusted for the differences in GR between the trials, the absolute LMY yield differences were reduced, as shown in the last column in Table 2. In fact, the Mar 08 XB lambs can be seen to have higher yield than Cast 2000 at the same GR.

Relative to GR, the LMY of the Jan'08 lambs was low compared to the Cast 2000 and the Mar'08 lambs (~1.6 and ~3% respectively). Therefore at the same fat depth these lambs did not have the same muscle development, but instead had a large proportion of bone. These Jan'08 lambs were at a different stage of development compared to the Cast 2000 and the Mar '08 lambs.

The other noticeable difference between Jan'08 and Cast 2000 was that the rate of change of LMY relative to GR. The LMY decreased at a slower rate for the Jan '08 lambs. In fact, with a 13mm increase in GR the LMY dropped only ~2.7% (-0.2114% per 1mm increase in GR), whereas for the Cast 2000 trial the yield dropped ~5% (-0.3875% per 1mm increase in GR). Even though there appears to be subcutaneous fat deposited, this does not appear to be related to a decrease at the same rate as in other trials. This suggests there is less inter muscular fat in the Jan'08 lambs. Once again this may indicate these lambs were at a different point of development than the Cast 2000 and March '08 lambs.

2.4.3   VIAscan Predictions

The performance of the VIAscan System has been assessed using the Regression initially released to site in 2004 when the VIAscan was commissioned at WAMMCO, Katanning (Regr v 1).

The Regr v1 was built entirely on the 360 carcases from the Cast 2000 trial.

The performances of the VIAscan regressions are shown in
Table 3, when predicting the yield of the entire XB '08 trials. The VIAscan regression demonstrated a moderate level of transportability when predicting the LMY of the XB lambs. The R-Square (RSQ) was 25% and the Root Means Square Error (RMSE) was 2.54%. The prediction accuracy was driven by the prediction of the Shoulder and Leg yield (RSQ 33 – 35%), although the over prediction of the Leg yield (+1.02) has meant the RMSE was inflated above the standard deviation (Stdev) (Stdev 1.26 vs RMSE 1.63). Fortunately there is very little overall bias (+0.14%), as the over prediction of the leg Yield was offset by the under prediction of the Loin yield (-0.88%). However, these underlying inaccuracies have caused the LMY RMSE to be greater then the Standard deviation (2..33 vs. 2.54).and consequently only a moderate prediction performance (see Figure 1, Figure 2, Figure 3, Figure 4)

Table 3: The prediction accuracy of the VIAscan when using WAMMCO Regr v1 to predict the yield % of 2008 XB trials

	Actual Avg. (%)	Act Stdev	RMSE (%)	RSQ (%)	BIAS (%)

Leg Yield	20.82	1.26	1.63	33%	+1.02
Loin Yield	15.46	1.03	1.37	2%	-0.88
Shldr Yield	16.65	1.02	0.93	35%	0.00
Lean Meat yield (LMY)	52.92	2.33	2.54	25%	+0.14

The level of VIAscan accuracy is only moderate when cross validated on the XB '08 lambs, which supports the inclusion of additional carcases from the latest trials to assist with reducing the prediction bias and improving the overall performance.
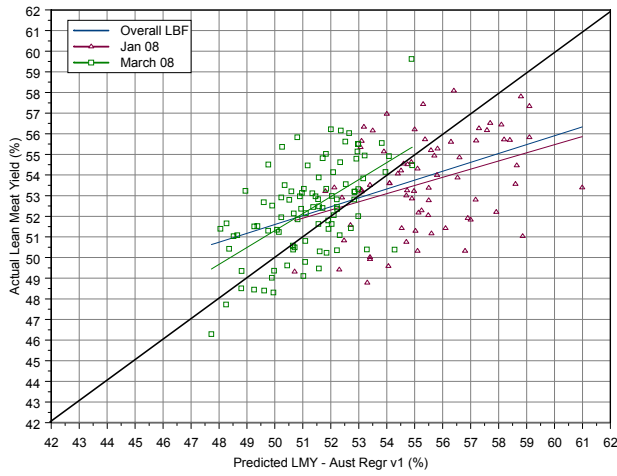
Figure 1: Actual vs Predicted LMY (Regr v1)
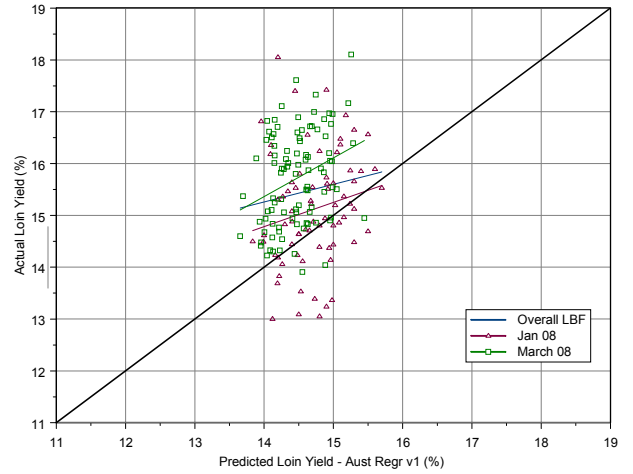
Figure 3: Actual vs Predicted Loin yield (Regr v1)
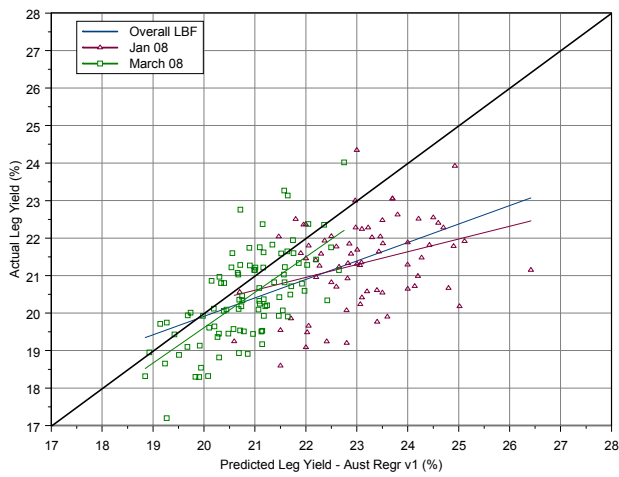
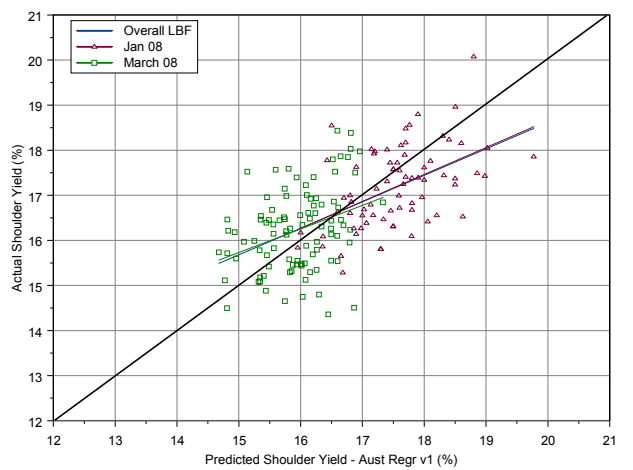**Figure 2: Actual vs Predicted Leg yield (Regr v1)**

Figure 4: Actual vs Predicted Shldr yield (Regr v1)

2.4.4 Derivation of VIAscan Regressions for WAMMCO Cross-Bred Lambs

A customised regression was developed for WAMMCO specifically for Cross-bred lambs. The Merino portion of the Cast 2000 dataset (37 head) was separated and will be combined with the 2006 Merino Dataset as part of a separate project. The entire dataset has 517 Cross-Bred carcases, and the contribution of each trial is shown in Table 4.

Table 4: The numbers of valid XB carcases from each boning trial.

Trial	No.
Cast2000	322
XB_Jan08	73
XB_Mar08	95
WAMMFeb07	27
Total	517

The VIAscan regressions predicted the percentage lean of the entire carcases and within each primal region. The Flap was excluded from the Loin which on average reduced the yield by ~4%. However the contribution of the Flap to the overall yield does vary between trials. The largest contribution was 6.5% for the March '08 trial, followed by the Jan'08 trial at 5.4%, and for the Cast 2000 and WAMMCO trials the averages were ~3.5% and ~2.5% respectively.

Table 5: The prediction accuracy of the VIAscan when predicting the percentage lean of XB carcases.

	LMY – No Flap	Leg	Loin – No Flap	Shldr
RSQ (%)	61	56	17	58
RSD (%)	2.04	1.07	0.78	0.88
Stdev	3.25	1.60	0.85	1.42
Mean	49.00	21.86	9.56	17.56
Actual Range	37.58 – 58.31	17.2 – 26.04	6.89 – 12.19	13.01 – 22.26

VIAscan predicted the LMY of the entire XB dataset with a high level of accuracy as the RSD was 2.04% and the RSQ was 61%. The RSD was well below the Stdev of the 3.25%, which indicates that the accuracy of the regression is very high. This performance surpasses that observed with New Zealand and Icelandic trials. Figure 5 shows the performance of the LMY model with respect to each trial. In Figure 6, only the WA XB lambs are displayed along with prediction accuracy. Without the Cast 2000 dataset, the remaining WA lambs had a smaller LMY distribution, which has reduced the RSQ, but the RSD is still very strong at 1.95%. The LMY of the WAMMCO '07 dataset is being over predicted, which was mainly caused by the over prediction of the shoulder yield (Figure 12). This will be discussed further later in this report.
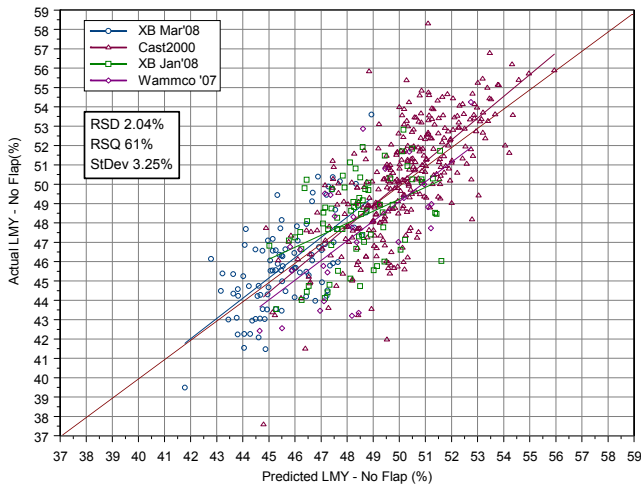
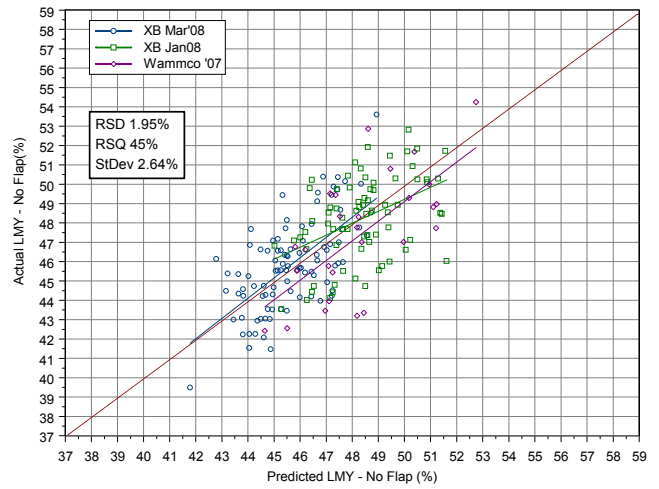**Figure 5: The Predicted vs. Actual LMY using a VIAscan equation derived on the entire XB dataset.**

Figure 6: The Predicted vs. Actual LMY of the WA lambs, using a VIAscan equation derived on the entire XB dataset

The VIAscan predicted the Leg yield with a very high accuracy, as the RSD was 1.07% and the RSQ was 56% (Figure 7,Table 5). The regression performed exceptionally well on the WA lambs, as the RSD was 0.97% and the RSQ was 48% (Figure 8).
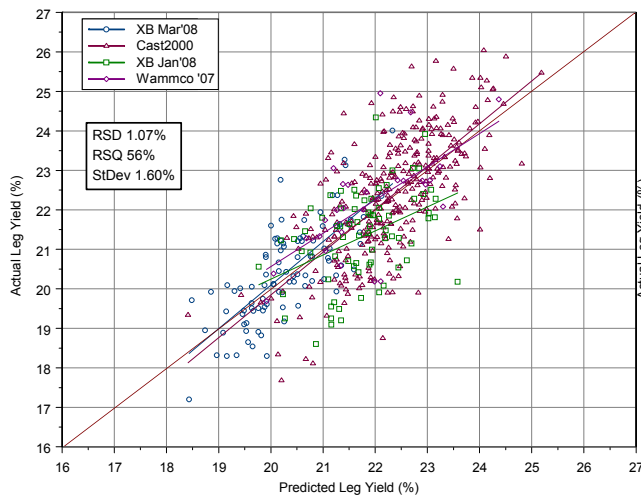

Figure 7: The Predicted vs. Actual Leg Yield using a VIAscan equation derived on the entire XB dataset.
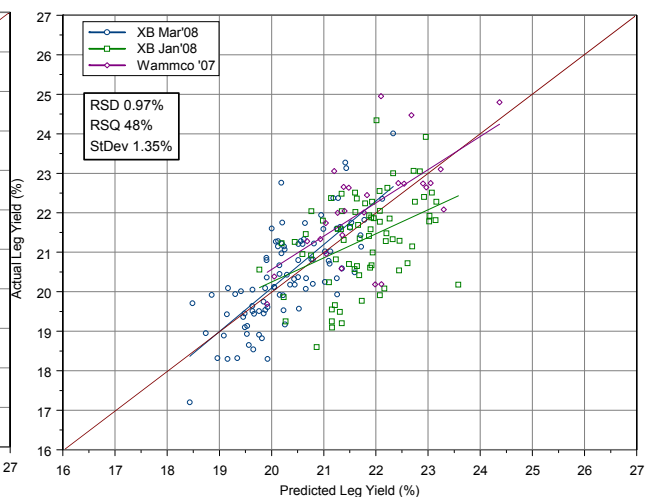

Figure 8: The Predicted vs. Actual Leg Yield of the WA lambs, using a VIAscan equation derived on the entire XB dataset

The variability in the Loin yield was very small compared to the other primals (Stdev = 0.85% cf. 1.42 – 1.6, Table 5), hence it is very difficult to predict these small levels of variation, particularly when a high yielding loin muscle does not change the shape of the carcases to the same degree as a muscular leg. The predictive ability of the Loin Yield was relatively low, as the RSD was similar to the Stdev (0.78%) and the RSQ was only 17% (Table 5).
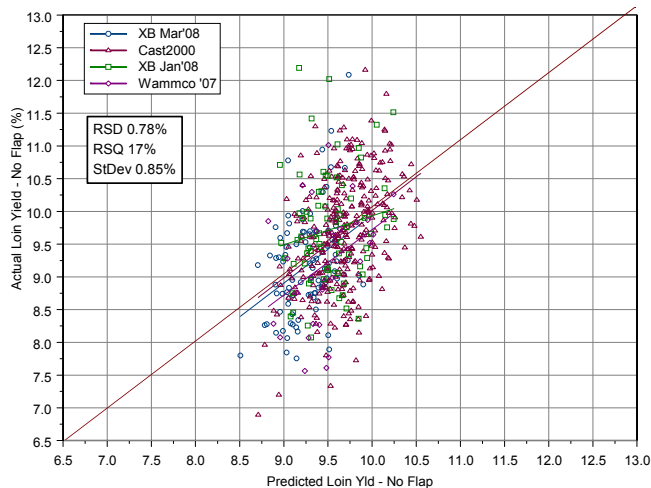

Figure 9: The Predicted vs. Actual Loin Yield (No Flap) using a VIAscan equation derived on the entire XB dataset.
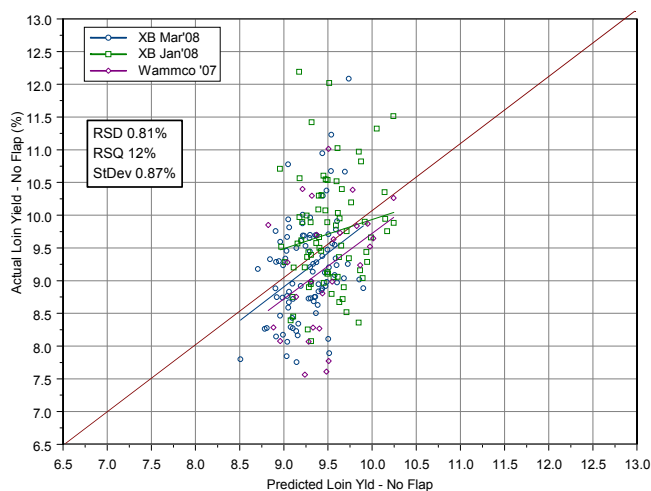

Figure 10: The Predicted vs. Actual Loin Yield (No Flap) of the WA lambs, using a VIAscan equation derived on the entire XB dataset

The VIAscan predicted the Shoulder yield with high level of accuracy as the RSD was 0.88% and the RSQ was 58% (Figure 11, Table 5). Not only does the regression exhibit a high level of accuracy, but the strength of the model further improved as the prediction range is across a large distribution of Shoulder yield. The combined XB dataset demonstrates a Shoulder yield that ranges ~ 9.2%, which provides VIAscan with an excellent prediction range.

The distribution of Shoulder yield for the WA XB lambs, was more condensed compared to the combined dataset as the stdev has decreased from 1.42 to 1.05%, However the VIAscan still provided a good prediction of the shoulder yield as the RSQ was at 37% and the RSD was 0.88% (Figure 12)
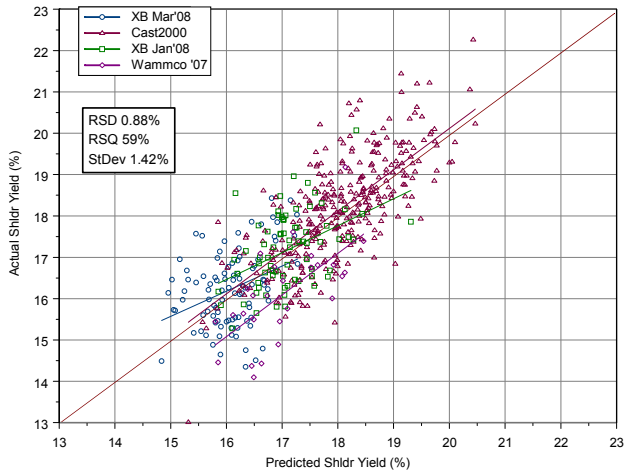
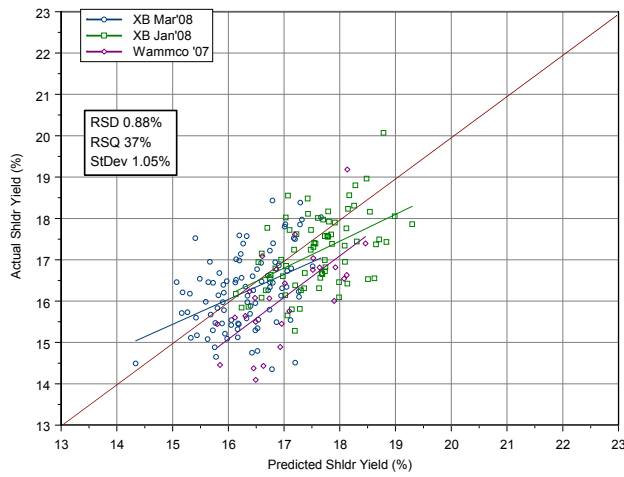**Figure 11: The Predicted vs. Actual Shldr Yield using a VIAscan equation derived on the entire XB dataset.**

Figure 12: The Predicted vs. Actual Shldr Yield of the WA lambs, using a VIAscan equation derived on the entire XB dataset

2.5 Summary

The VIAscan regressions deployed to Katanning in 2004 were based on the Castricum 2000 dataset. The regression performance had high level of prediction accuracy on the Cast 2000 data set and is comparable to models that have been derived on the latest 2008 XB.

The VIAscan regression released at commissioning was derived on Cast 2000 lambs (Regr v1). This consisted of 360 lambs majority of which were 1st and 2nd cross prime lambs.

The VIAscan (Regr v1) predicted the lean composition of the 2008 XB lambs with a moderate level of accuracy. The leg yield was slightly over predicted and the loin yield could not be described by the VIAscan due to its small degree of variation. There appeared to be significant compositional differences in the loin between trials. This was attributed to the microwave method not accounting for all the fat within the Flap, which artificial increased the loin yield as GR increased. Once the Flap was removed, the Loin yield of the 2008 XB lambs decreased as the carcases increased in fatness as expected.

The ability of the VIAscan System to predict the yield of XB lambs was greatly enhanced by combining the 2008 XB, Cast 2000 and WAMMCO '07 trials. The prediction of the LMY was excellent and surpassed the prediction accuracy observed from other trials conducted in New Zealand and Iceland. The LMY prediction accuracy was driven by the prediction of the Leg and Shoulder yield whereas the yield of the loin was still very difficult to predict. The loin yield range is only 4% compared to an 8% range in leg yields and it is likely that a large proportion of this 4% could be random due to cutting variability. Further investigation is required in developing a commercial Loin Yield regression based on rack and shortloin.

The performance of the regressions are summarised below:

Regression	RSQ	RSD
Cast 2000 LMY (2004 model) on Cast. lambs	51%	2.2%
Leg	49	1.09
Loin	21	0.99
Shldr	47	0.91
XB / Cast Regr (on combined XB data set)	46	2.23
Leg	56	1.07
Loin	24	1.02
Shldr	56	0.88

The VIAscan predicted the LMY with an RSD of ~2.2. The RSD was further improved by excluding the Flap from the yield definition.

Regression	RSQ	RSD
XB / Cast Regr (on combined XB data set) No Flap	61	2.04
Loin No Flap	17	0.78

Across all trials the VIAscan consistently predicted the Leg and shoulder yield with a high level of accuracy as the RSD ranged between 0.90 to 1.09%, and RSQ was between 47 – 58%.

The latest Cross-Bred dataset consisted of lambs from a diverse genetic base. Both trials have encapsulated genotypes with differing propensity to muscle and fatten and the cross bred lambs have been selected across 9 breeds. Thereby implementing a VIAscan regression based on these datasets, ensure they are suitable for industry application. The prediction models are capable of describing the variation in carcase composition with a high degree of accuracy.

For this reason the prediction models for Cross-bred lambs are suitable to underpin a yield based payment system across the range of lambs processed through WAMMCO. It is recommended that in line with other processing sites, that regular updates to the VIAscan predictions be conducted to maintain yield predictions relevant to the types of lambs being processed.