



Australian Government
Department of Agriculture



Development of selection criteria to improve carcase quality and use of haemoglobin levels in sows and piglets to improve piglet survival, performance and pork quality

Final Report
APL Project 2011/1025

June 2013

Animal Genetics and Breeding Unit (AGBU)*

Susanne Hermes
University of New England
Armidale NSW 2351

*AGBU is a joint venture between NSW Department of Primary Industries and University of New England

Disclaimer: The opinions, advice and information contained in this publication have not been provided at the request of any person but are offered by Australian Pork Limited (APL) solely for informational purposes. While APL has no reason to believe that the information contained in this publication is inaccurate, APL is unable to guarantee the accuracy of the information and, subject to any terms implied by law which cannot be excluded, accepts no responsibility for loss suffered as a result of any party's reliance on the accuracy or currency of the content of this publication. The information contained in this publication should not be relied upon for any purpose, including as a substitute for professional advice. Nothing within the publication constitutes an express or implied warranty, or representation, with respect to the accuracy or currency of the publication, any future matter or as to the value of or demand for any good.

Acknowledgements

This project is supported by funding from Australian Pork Limited and the Department of Agriculture.

This project was conducted in close collaboration with a number of Australian pig breeding companies and I gratefully acknowledge their continued and on-going support of pig genetics research in Australia.

I thank Kristy Tickle and Amy Lealiifano for their enthusiasm and dedication to collect images and primal cut weights for 2,500 pigs. Kristy Tickle was also instrumental in developing recording procedures for haemoglobin levels of pigs on farm. Thanks go to staff at Rivalea for diligent data collection and to Rob Smits, Cherie Collins and Brian Luxford for coordinating trials.

I thank Greg Davis and Brenden McClelland for implementing recording procedures of haemoglobin in sows and piglets on farm and for guiding their staff in data collection. I gratefully acknowledge the additional efforts provided by staff at Aroora and Belmont for the collection of data for this project.

I thank Joshua Dobos and Brittany McVicar for their endurance and precision in collecting over 36,000 image-analysis records. Further, the diligent data entry of on-farm records by Joshua Dobos, Brittany McVicar and Sigrid McKenzie is gratefully acknowledged.

Executive Summary

Improving selection for carcass quality

Additional return per carcass can be achieved by having more weight in the more valuable primal cuts for carcasses with the same total weight and fat depth. Australian data were required to quantify the economic benefits of higher saleable meat yield for a given carcass weight and fat depth for the Australian market and to develop selection strategies for improved carcass market value.

Primal cut weights were obtained for 2,311 carcasses which were combined with 23,210 pedigree and 16,875 performance records. A proportion of these pigs had fat and muscle depth measures available from the PorkScan™ system. It was not possible to obtain light-stripping information from the PorkScan™ system and images of the standing pig were collected instead. These images were analysed with a freely available image-analysis program (ImageJ) to obtain 14 linear or area measurements for each pig to describe conformation of live pigs three weeks prior to slaughter. In total, over 36,000 image-analysis records were obtained. Genetic analyses of data provided information about genetic and phenotypic associations between primal cut weights and other traits.

Considerable variation was observed in primal pork cuts recorded in Australian pigs. Hot carcass weight explained forty to eighty percent of the variability in individual primal cut weights. Fat depth, loin depth and weight loss explained an additional one to six percent of the variation in primal cut weights. Primal cut weights varied by four (shoulder and leg weight) and three (belly and loin weight) kilograms per carcass for carcasses with a hot carcass weight of 78.0 to 80.0 kg only. This variation in primal cut weights can be used to improve market value of pig carcasses by up to \$15 per pig beyond the current pricing system used in Australia.

A simple procedure was outlined to obtain image-analysis measures of live pigs that describe conformation of pigs using a free software package. These image-analysis measurements had predictive power for the weight of pigs or carcasses and the weight of primal cuts demonstrating the usefulness of image analysis for predicting carcass market value.

Different image-analysis measures provided complementary information for prediction of primal cut weights at a given carcass weight. The first width measurement of the middle at the tail end had a partial R-square of above 5% for all primal cut weights and cold weight. This image-analysis measure explained considerable variation for cold weight (28%), forequarter (23%), middle (23%) and belly (17%) weight. It is the most important conformation trait on the live pig to predict weight in primal cuts. Further image-analysis traits with superior predictive ability for primal cut weights were area of the leg or middle and length of the pig or shoulder.

These results should be used in any further developments of the prediction equations of the PorkScan™ light-stripping system. Further, image-analysis is used in a highly-awarded German technology (optiSCAN; hl-agrar.de) to predict weight of pigs from a hand held device. The application of this device in the Australian pig industry should be explored including evaluation of specific measures that could be used for prediction and selection of primal cut weights.

The heritability of loin depth recorded with PorkScan™ on the carcass was considerably higher than the corresponding heritability for muscle depth recorded on the live pig confirming independent results from an earlier comparison of heritability estimates between PorkScan™ and live-animal measures. Heritability estimates for fat and muscle depth on the live pig were not significant in these data. Breeders should evaluate the repeatability of these measurements on farm periodically and

genetic parameters should be re-estimated from time to time to account for the effects of selection and changes of recording procedures on estimates of genetic parameters.

Weights of primal cuts at a given carcass weight were moderately heritable. Two economic approaches were developed and compared to include primal cut weights in pig breeding objectives. It was demonstrated that more weight in the more-valuable middle contributed 9% to the breeding objective used in terminal lines. This contribution is similar to the contribution of fat depth to the breeding objective highlighting the need to include weight of primal cuts in pig breeding programs. Selection strategies for improved carcass market value that involve measurements on the live animal will be outlined to industry through the established technology-transfer pathways of AGBU to ensure that results from this project are adopted by Australian breeders.

Use of haemoglobin to improve piglet survival, performance and pork quality

Survival of piglets is an important welfare trait with significant economic importance. Higher haemoglobin levels have been shown to be phenotypically associated with improved survival. However, there is a paucity of studies investigating genetic associations between haemoglobin levels and survival of piglets and fecundity of sows.

Development of reliable procedures to record haemoglobin levels on farm was the first aim of this project. Guidelines for recording haemoglobin levels in sows, piglets and pigs were presented to industry following an initial trial comparing the ear or tail as locations to collect a droplet of blood. Subsequently two breeders were able to collect haemoglobin levels in sows and piglets along with other sow traits on farm. Average haemoglobin levels in sows varied from 107 to 114 g/L between herds. Given the variation around these means, a significant proportion of sows had a haemoglobin level below the recommended level of 100 g/L and haemoglobin levels should be increased.

Herds with higher mean haemoglobin levels in sows also had higher mean haemoglobin levels in piglets. Within herds, higher haemoglobin levels in sows were associated with higher haemoglobin levels in piglets. Further, the random effect of sow was an important effect for haemoglobin levels in piglets. These results offer opportunities to target selection and intervention strategies to maintain adequate haemoglobin levels in sows with beneficial effects on haemoglobin levels in piglets. The simple measurement procedure developed in this study should be used by breeders and producers to record and monitor haemoglobin levels in sows and piglets on farm regularly. Further, it should be evaluated whether this measure of haemoglobin could be used as a measure of acute stress because haemoglobin was slightly higher in piglets following tail docking and increase in haemoglobin due to stress has been shown previously (Dubreuil et al., 1993).

A number of weight traits of the sow and the litter as well as litter size had negative associations with haemoglobin levels indicating that higher productivity is associated with lower haemoglobin levels in piglets. Associations between number of still born piglets and haemoglobin levels were predominantly negative supporting the hypothesis that higher haemoglobin levels favour survival of piglets. A considerable number of records are required to investigate these associations reliably and data recording on farms continues to enable further investigation of the use of haemoglobin levels to improve survival of piglets and fecundity of sows.

Table of Contents

Acknowledgements	2
Executive Summary	3
Improving selection for carcase quality	3
Use of haemoglobin to improve piglet survival, performance and pork quality	4
Table of Contents.....	5
Background to Research.....	7
Improving selection for carcase quality	10
Use of haemoglobin to improve piglet survival, performance and pork quality	10
Objectives of the Research Project.....	11
Introductory Technical Information.....	12
Development of carcase selection criteria for weight of primal cuts	12
Research Methodology.....	13
Data collection.....	13
Live-animal measures from images of standing pigs.....	13
Statistical analyses	16
Discussion of Results	18
Data used for phenotypic and genetic analyses	18
Genetic parameters for primal cut weights.....	37
Options for incorporating primal cut weight traits into breeding objectives.....	47
Implications & Recommendations.....	52
Improving selection for carcase quality	52
Technical summary.....	53
Introduction.....	53
Data.....	53
Variation in primal cut weights for a fixed carcase weight	54
Prediction of primal cut weights.....	54
Prediction equations.....	54
References.....	58
Use of haemoglobin levels in sows and piglets to improve piglet survival, performance and pork quality	59
Introductory Technical Information.....	59
Research Methodology.....	61

Developing recording procedures for haemoglobin levels	61
Analyses of the first haemoglobin data	61
Analysis of haemoglobin levels and sow or piglet traits recorded by breeders	61
Discussion of Results	62
Recording haemoglobin levels in sows.....	62
Recording haemoglobin levels in piglets	63
Recording haemoglobin levels in growing pigs.....	65
A sampling comparison between the ear and the tail for testing of haemoglobin levels in piglets..	67
Within-litter variability in haemoglobin levels of piglets.....	68
Phenotypic analyses of haemoglobin levels in sows and piglets as well as traits describing sow performance and condition	69
Description of data.....	69
Associations between haemoglobin levels and sow reproductive performance	70
The effect of parity and breed on haemoglobin levels in sows.....	71
Implications & Recommendations.....	73
Technical summary	73
References.....	76
Fostering adoption of research results in the Australian pig industry	77
Publications arising	79
Industry publications and presentations	79
Book.....	79
Book chapters and Newsletter articles.....	79
Web-supported seminar.....	79
Journal paper.....	79
Refereed conference paper.....	79
Appendix I: Industry presentations in September and October 2013.....	80
Webinars on piglet survival and osteochondrosis in pigs.....	80

List of Figures

Figure A1. Main window of the program ImageJ	14
Figure A2. Windows to set the scale and measurements recorded for images	15
Figure A3. Image of pigs standing in weighing crate along with outline of various linear and area measurements that can easily be recorded with ImageJ on the digital image	16
Figure A4. Distribution of shoulder and leg weight per carcase for carcasses with a hot standard carcase weight of 78.0 to 80.0 kg	25
Figure A5. Distribution of belly weight per carcase for carcasses with a hot standard carcase weight of 78.0 to 80.0 kg	25
Figure B6. Plot of first versus second measure of haemoglobin levels recorded in sows	63
Figure B7. Plot of first versus second ear measure of haemoglobin levels recorded in piglets	65
Figure B8. Plot of first versus second tail measure of haemoglobin recorded in piglets	65
Figure B9. Plot of first versus second measure of haemoglobin levels recorded in growing pigs	66

List of Tables

Table A1. Data statistics for weight, growth and fat or muscle depth measurements recorded on the live animal and the carcase	19
Table A2. Data statistics for primal cut weights and percentages	19
Table A3. Data statistics for image analyses measures	21
Table A4. Data statistics for the angle of linear image analyses measures	21
Table A5. Data statistics for image analyses measures actually used in analyses	22
Table A6. Table A6. Data statistics for pigs slaughtered from March to May 2012	23
Table A7. Data statistics for pigs slaughtered from June to September 2012	23
Table 8. Proportion of variation (%) for primal cut weights explained by the model	24
Table A9. Pearson correlations between image-analyses measures	28
Table A10. Pearson correlations between primal cut weights or percentages and image-analyses measures	29
Table A11. Partial and model R-square for variables entered or removed to predict cold weight omitting or fitting live weight	31
Table A12. Partial and model R-square for variables entered or removed to predict leg weight omitting or fitting live weight	32
Table A13. Partial and model R-square for variables entered or removed to predict middle weight omitting or fitting live weight	33
Table A14. Partial and model R-square for variables entered or removed to predict shoulder weight omitting or fitting live weight	34
Table A15. Partial and model R-square for variables entered or removed to predict loin weight omitting or fitting live weight	35
Table A16. Partial and model R-square for variables entered or removed to predict belly weight omitting or fitting live weight	36
Table A17. Coefficients of determinations (R ²) and p-values of significant fixed effects for average daily gain (ADG), backfat (BF), muscle depth (MD), carcase fat depth (FD) and carcase loin depth (CLD)	38
Table A18. Coefficients of determinations (R ²) and p-values of significant fixed effects for primal cut weights and primal cut percentages	39
Table A19. Estimates of heritabilities (h ²) and common litter effects (c ²) estimates both with standard errors (SE) along with variance components for growth and fat or muscle depth measurements	40
Table A20. Estimates of heritabilities (h ²) and common litter effects (c ²) estimates both with standard errors (se) along with variance components for primal cut weights and percentages	41
Table A21. Estimates of genetic correlations (above diagonal) and residual and phenotypic correlations (first and second row below diagonal) between growth and fat or muscle depth measurements	42
Table A22. Estimates of genetic correlations between primal cut weights	43
Table A23. Estimates of genetic correlations between primal cut percentages – no weight adjustments	43
Table A24. Estimates of genetic correlations between primal cut percentages – weight adjustments	44
Table A25. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut weights and growth, fat or muscle measurements	45
Table A26. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut percentages (unadjusted for weight) and growth, fat or muscle measurements	45
Table A27. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut percentages (adjusted for weight) and growth, fat or muscle measurements	46
Table A28. Primal specific assumptions used in the calculations and resulting economic values derived for specific cuts	48
Table A29. Genetic regressions (bgen), economic values (EV) and the net change in carcase value for a one-kg change in each primal cut on the value of the carcase at farm gate after accounting for correlated changes in other primal cut weights (Net-change)	49
Table A30. Percent contribution of individual breeding goal traits to a terminal sire line breeding objective including weight of the middle	51

Table B31. Data statistics for sow traits	62
Table B32. Data statistics for haemoglobin levels in piglets	64
Table B33. Data statistics for haemoglobin levels in growing pigs	66
Table B34. Influence of blood sample collection location and order of sampling on Hb concentrations	67
Table B35. Variance components along with proportion of total variance due to sow	69
Table B36. Data statistics for variables recorded on sows and piglets including haemoglobin levels (Hb, g/L)	70
Table B37. Pearson correlations between haemoglobin levels and sow reproductive traits for herd B (above diagonal) and herd A (below diagonal)	71
Table B38. The effect of parity on sow traits	72

Background to Research

Improving selection for carcass quality

The payment system used in Australia uses the weight of the carcass and fat depth at the P2 site to determine the price per kg carcass weight paid to producers. This economic incentive for a specific weight range and a higher overall lean meat content in the carcass have resulted in larger and leaner cuts available to consumers across Australia in comparison to pork cuts available in the 1980s and 1990s (Müller *et al.*, 2009). The study also found only small differences in the lean meat content of pork cuts between states and areas of different socio-economic status 'due to breeding and feeding for large, lean pigs by the Australian pig industry' as the authors concluded. While the variation in the proportion of lean meat in each raw cut was modest, considerable variation was observed in the weight of cuts, fat thickness and slice thickness due to differing butchering practices. This aspect of variability has been addressed by Australian Pork Limited (APL, 2012) by providing the PorkStar training manual (Australian Pork Limited) which outlines the various retail cuts in detail.

Different prices are paid for individual pork cuts. Price differences between cuts increase as the carcass is broken down. For example, the rolling annual average wholesale price varied from \$3.24 for forequarters to \$7.59 for bellies for broken sales and from \$3.72 for boneless middles above 13 mm fat depth to \$15.49 for US ribs for carton sales (APL, Eyes and Ears, Issue #534, May 2013). At the farm gate level, carcasses may be broken down to the primal cuts and the return per carcass may be increased by optimising the weight in each primal cut.

Mérour and Hermes (2008) demonstrated variation in primal cuts for carcasses with similar weight and fatness levels. This variation in primal cuts resulted in an additional return per carcass of \$7 at the farm gate level and \$21 at the wholesale/retail level for the top 10% of pigs in comparison to the average. This evaluation was based on French data as similar data were not available in Australia at the time. The Australian pig industry lacks classification systems to measure variation in primal weights in commercial abattoirs and Australian data are required to quantify the economic benefits of higher saleable meat yield for a given carcass weight and fat depth level for the Australian market.

There have been multiple attempts by breeders to retrieve muscle depth recorded on the carcass and primal cut weights from boning rooms. Logistical constraints have resulted in only small data sets from these attempts and automated procedures are required to obtain measures of carcass quality for individual pigs. Breeders require genetic parameters for additional carcass characteristics in order to develop better selection strategies for the improvement of overall carcass quality that incorporates variation in weight of primal cuts at a fixed carcass weight.

The availability of new technologies to describe the market value of pig carcasses in abattoirs will be beneficial for providing market signals through the supply chain back to producers, who will then demand genotypes with better overall carcass quality. Currently, the full commercial value of a pig carcass is not measured objectively in the abattoir and additional carcass measures are required to better quantify carcass quality. It will be beneficial for breeding programs if information on live animals prior to selection is available.

Use of haemoglobin to improve piglet survival, performance and pork quality

Improving piglet survival remains an important goal for the Australian pig industry in order to improve welfare of pigs and farm productivity. The number of still born piglets has increased over time in Australia (Lewis and Hermes, 2013) and new tools are required to halt this unfavourable

trend. An on-farm measure of haemoglobin may be used in sows and piglets to improve survival and performance of piglets and sows. Haemoglobin levels were unexpectedly low in a recent Australian study by Payne (2009) who found that 50% of piglets not receiving creep feed were borderline anaemic. The iron levels of dams were not recorded but may have been depleted given a more recent finding by Gannon *et al.* (2011) who found a decline in haemoglobin levels in older sows. Genetic associations between haemoglobin levels in sows and piglets were not found in the literature. Further, an understanding of phenotypic relationships between haemoglobin levels and performance of sow, piglets and growing pigs can be used to improve husbandry practices in Australian pig farms.

Blood haemoglobin can be used as a selection criterion on farm to improve iron content in pork and pork quality characteristics as long as it can be measured accurately on farm (Hermesch and Jones, 2012). Repeatability and consequently heritability estimates were low for haemoglobin levels in blood and recording procedures need to be improved to increase the accuracy of the measurement technique. In addition, pig farmers require training in recording this potentially important new trait. Guidelines for procedures to record blood haemoglobin on farm will foster the adoption of this trait by industry. A better understanding of haemoglobin levels in sows and piglets will lead to a reduction of the incidence of anaemia on farm with subsequent benefits for piglet survival and sow reproductive performance.

Objectives of the Research Project

Development of carcase selection criteria for weight of primal cuts.

Use of haemoglobin levels in sows and piglets to improve piglet survival, performance and pork quality.

Fostering adoption of research results in the Australian pork industry.

Introductory Technical Information

Development of carcass selection criteria for weight of primal cuts

A number of selection criteria for better carcass quality were investigated by Isabelle Mérour during her sabbatical at AGBU using French data (Mérour *et al.*, 2009; Mérour *et al.*, 2010). The economic benefits of higher weight in more valuable primal cuts at a given carcass weight have been outlined (Hermesch and Jones, 2010). So far, adoption of new selection criteria to improve saleable meat yield has been hindered by the lack of data available in Australia.

There have been multiple attempts by breeders to retrieve muscle depth recorded on the carcass and primal cut weights from boning rooms. Logistical constraints have resulted in only small data sets from these attempts and automated procedures are required to obtain carcass data for individual pigs. The PorkScan™ system (PorkScan Pty Ltd, Canberra, ACT, Australia) provides light striping information to better describe pork carcasses (Green, 2008). Higher heritabilities were found for fat and muscle depth recorded with PorkScan™ on the carcass in comparison to corresponding measures on the live pig (Hermesch, 2011). However, light striping information has not been available for analyses.

Primal cut weights in pigs are heritable (Newcom *et al.*, 2002; van Wijk *et al.*, 2005; Gilbert *et al.*, 2007; Mérour *et al.*, 2010). However, heritability estimates were variable between studies indicating that differences in populations and cutting procedures may have affected these estimates. The weight in individual primal cuts reflects the shape of an animal as demonstrated by Fisher *et al.* (2003) who found differences in compositional characteristics during growth to commercial slaughter weight for three morphologically different pig genotypes with the same daily carcass weight gain. The authors stated that a few linear measurements do quantify major differences in proportions which were further demonstrated by Doeschl-Wilson *et al.* (2005) who quantified phenotypic relationships between body dimensions of live pigs and carcass composition. Genetic parameters for linear measurements on the live pig were not found. However, high heritability estimates have been found for carcass length (Engellandt *et al.*, 1997; Gilbert *et al.*, 2007; Mérour *et al.*, 2009) indicating that linear shape measures will respond to selection and may be used as selection criteria for primal cut weights in pigs.

Research Methodology

Data collection

Primal cut weights

The data specifically collected for this project from March to September 2012 was combined with pedigree and performance data generally available from the herd recording system at Rivalea. The final data set included primal cut weights recorded on 2,311 carcasses from castrates that belonged to four different genotypes. Pigs were born in one farm and raised in five different grow-out facilities. Lifetime growth rate, backfat depth at the P2 site and muscle depth between the third and fourth last ribs were recorded on pigs at 143.5 ± 3.84 days of age. Backfat and muscle depth were recorded using real time ultrasound. A photo of the pig standing in the weighing crate was taken four days later along with an additional weight measure for a proportion of pigs. Genetic analyses of growth, backfat and muscle depth included information from contemporaries of project animals recorded in 2012.

Pigs were slaughtered at 167.3 ± 3.65 days when fat depth was recorded at the P2 site, 65 mm from the midline of the carcass at the last thoracic rib on the carcass. Pigs were evaluated with the PorkScan™ equipment (PorkScan Pty Ltd, Canberra, ACT) from March to May 2012 which also provided a measure of loin depth at the P2 site in addition to fat depth (FD). The Hennessy Chong grading system was used from June to September 2012 to evaluate carcasses.

Primal cut weights included the three primal cuts of forequarter, middle and leg (HAM 4029, 4070 and 4011, respectively - AUS-MEAT Handbook of Australian Meat, 2005). The middle was further broken down into loin and belly primals (HAM 4101 and 4080, respectively). All primal cut weights were recorded on one side of the cold carcass about 24 hours after slaughter. The original weights were then multiplied by 2.0 to express them on a per-carcass basis. Each primal cut weight was also expressed as a percentage of cold weight as an alternative measure of primal cuts. Pigs with an age at a particular measurement point outside four standard deviations of the mean were excluded from the data as these extremes may indicate multiple data errors including pedigree errors. Any other trait measures exceeding four standard deviations from the mean were omitted from the analyses.

The pedigree included 23,219 animals over 8 generations including 869 sires and 5,342 dams. Animals with performance data originated from 327 sires and 3,694 dams. The subset of animals with primal cut weights was represented by 112 sires and 1,250 dams.

Live-animal measures from images of standing pigs

Description of procedures to record linear and area measurements on standing pigs with ImageJ.

The software package ImageJ is in the public domain and freely available from <http://rsbweb.nih.gov/ij/>. Version ImageJ 1.46r was used for the analyses of images of boars standing in a weighing crate. The main window of the program is shown below (Figure 1). The use of this program is intuitive and the following procedures were developed without needing much background information.

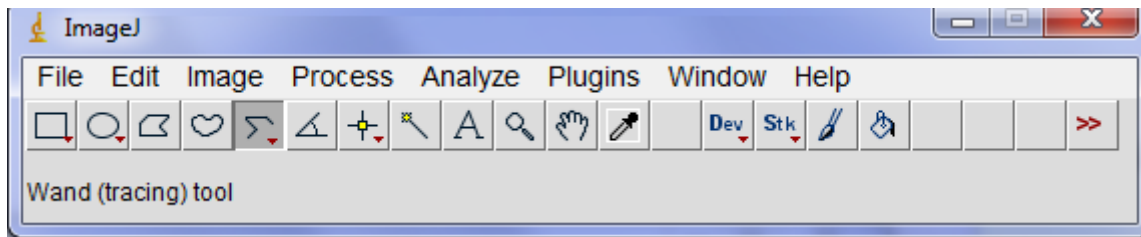


Figure A1. Main window of the program ImageJ.

Each image is opened under *File/Open*. Once the first image in a folder is opened, the next file can automatically be opened by using *File/Open next*. The properties of images can be changed and the scale of each image is defined under *Image/Scale*, which brings up the screen *Scale* as shown below in Figure 2. The X and Y scales were set to 1 using the full pixel width and height. It is important to keep this setting across all images the same to ensure that measurements are comparable across images. This setting is also important to convert measurements expressed in pixels to other units of length or area in the metric system.

Measurements are defined under *Analyze/Set Measurements*, which leads to the screen *Set Measurements* shown in Figure 2 as well. Only the area measurement was chosen as a specific measurement and the label of each image will be displayed in the result section.

Linear measurements were recorded by choosing either the *Straight line* option or the *Segmented Line* option under the line button in the *ImageJ* screen shown above. Individual options appear by using the right button of the mouse. The *Straight line* option was chosen for the first two linear measurements of the A4-sized card showing the identification of the pig and the width of the crate. Both of these two measures will be used to transfer pixel numbers to metric length units. Once the desired line has been drawn on the image, pressing *Analyze/Measure* (or Ctrl M) exports the measurement into a window listing all measurements taken on the image.

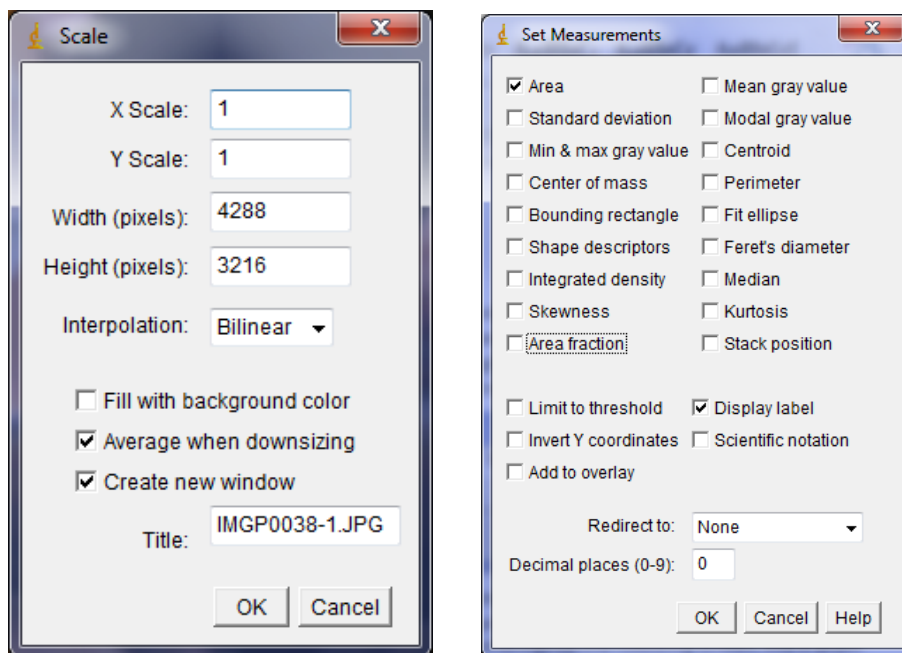


Figure A2. Windows to set the scale and measurements recorded for images

Area measurements were recorded by choosing the Polygon selection button (third button from left in *ImageJ*). This area measurement tool was preferred over the free-hand option as it allows users to follow the shape of the animal by setting focus points at desired intervals. It was found that areas could easily be traced using this tool.

List of measurements. Individual measurements are saved into a separate window that can be saved in various formats (e.g. csv file). This enables export of data into other programs. It is not possible to enter data manually in this screen. Therefore, the order of measurements was always the same for each image to ensure that all 16 measurements per animal could be exported jointly into Excel. Specific details about identification of the animal and details about each measurement were then added in Excel. Figure 3 provides a visual illustration of the various measurements.

The order of measurements were:

1. Horizontal width of A4 sheet
2. Vertical width of crate
3. Vertical width of leg – tail end
4. Vertical width of leg – middle
5. Vertical width of loin – tail end
6. Vertical width of loin – middle
7. Vertical width of loin – head end
8. Vertical width of shoulder – middle
9. Vertical width of shoulder – head end
10. Length of pig – horizontal line along the spine
11. Length of leg
12. Length of loin
13. Length of shoulder
14. Area of leg
15. Area of loin
16. Area of shoulder

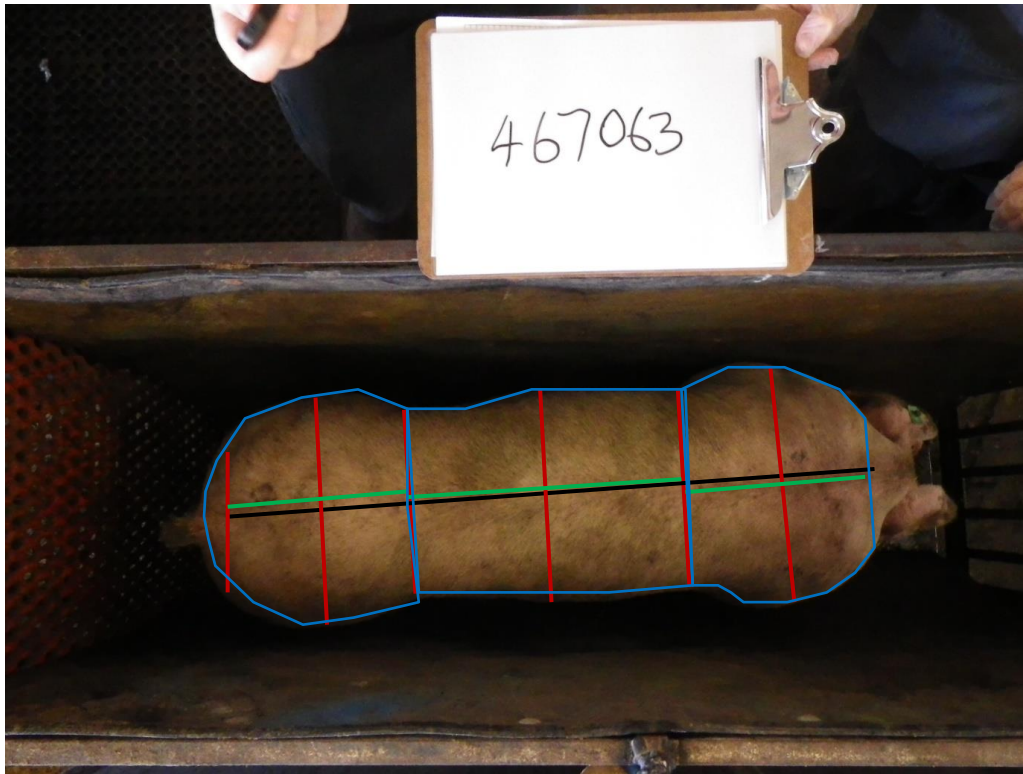


Figure A3. Image of pigs standing in weighing crate along with outline of various linear and area measurements that can easily be recorded with ImageJ on the digital image

Attempts to obtain further carcass data

The PorkScan™ system (PorkScan Pty Ltd, Canberra, ACT, Australia) provides light striping information to better describe pork carcasses (Green, 2008). However, this system was not operational at the start of the current project. A number of obstacles had been overcome prior to commencement of this project and efforts continued during this project to get the PorkScan™ light striping system operational in a commercial abattoir. Despite these considerable efforts of multiple organisations it was not possible to obtain PorkScan™ light striping information for this project.

Statistical analyses

The following mixed linear animal models were used for the analyses of traits.

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e} \quad [1]$$

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wc} + \mathbf{e} \quad [2]$$

where $\mathbf{y}$ represents the vector of observations with, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{a}$ is the vector of random additive genetic effects of animals, $\mathbf{c}$ is the vector of common litter effects and $\mathbf{e}$ is the vector of residual effects. The terms $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{W}$ are incidence matrices relating records to fixed, animal and common litter effects, respectively. The expectations of random effects were zero and the variances were assumed to be $\text{var}(\mathbf{a}) = \sigma_a^2 \mathbf{A}$, $\text{var}(\mathbf{c}) = \sigma_c^2 \mathbf{I}$, and $\text{var}(\mathbf{e}) = \sigma_e^2 \mathbf{I}$, where $\mathbf{A}$ is the

numerator relationship matrix among animals and $\mathbf{I}$ is the identity matrix. Random effects were assumed to be correlated between traits and all remaining covariances between separate random effects were assumed to be zero. Variance components were estimated with ASReml (Gilmour *et al.*, 2009) in univariate and bivariate analyses. The fixed effect model for each trait was derived using the GLM (SAS, 2011) procedure.

Discussion of Results

Data used for phenotypic and genetic analyses

Primal cut weights

Performance of the subset of project animals corresponded well with growth, fat and muscle depth measures of pigs recorded in 2012 (Table A1). Fat and muscle depth recorded on the carcass are not directly comparable to fat and muscle depth recorded on the live pig because pigs were slaughtered three weeks after measurements were taken on the live animal. The coefficients of variations (CV) were higher for fat and loin depth recorded on the carcass in comparison to the corresponding live-animal measures showing that these carcass traits were more variable relative to the mean. The later recording of carcass traits in comparison to live-animal measures may have contributed to the higher variability for fat and muscle depth. These traits are not expressed yet at an earlier growth stage.

The standard procedure to cut carcasses into the main primals in Australia led to similar weights in forequarter, leg and the middle (Table A2). Coefficients of variation were higher for loin and belly weight in comparison to the original primal weights. The weight of the carcass explained a large proportion of weight in primal cuts and expressing each primal cut weight as a percentage of the carcass weight reduced the coefficients of variation accordingly.

Table A1. Data statistics for weight, growth and fat or muscle depth measurements recorded on the live animal and the carcase (CV: coefficient of variation, %)

Variable	N	Mean	Std Dev	CV	Min.	Max.
Body weight at recording from data base, all, (kg)	16875	84.8	11.53	13.6	50	132
Body weight at recording from data base, subset, (kg)	2154	84.8	7.93	9.3	50	120
Body weight at recording from Project, subset, (kg)	1543	84.7	7.82	9.2	67	120
Body weight at taking image (kg)	1393	86.9	8.29	9.5	63	116
Average daily gain, all (g/day)	15903	572.1	70.57	12.3	304	861
Average daily gain, subset. (g/day)	2060	591.8	54.86	9.3	355	792
Backfat, all , (mm)	3610	9.7	1.22	12.7	6	15
Backfat, subset, (mm)	290	9.6	0.92	9.6	6	12.5
Muscle depth, all, (mm)	3617	38.5	3.52	9.2	25	53
Muscle depth, subset, (mm)	290	38.0	2.95	7.8	27	44
Hot carcase weight, (kg)	2311	79.0	8.28	10.5	50	107
Cold carcase weight, (kg)	2311	69.3	7.39	10.7	43	93
Carcase fat depth, (mm)	2308	10.8	2.55	23.7	4	21
Carcase loin depth, (mm)	573	50.9	6.03	11.8	28	66

Table A2. Data statistics for primal cut weights and percentages (CV: coefficient of variation, %)

Trait¹	N	Mean	Std Dev	CV	Min.	Max.
Forequarter weight, (kg)	2200	22.64	2.516	11.1	12.4	32.2
Leg weight, (kg)	2200	23.19	2.377	10.2	14.5	31.5
Middle weight, (kg)	2200	22.95	2.909	12.7	12.5	32.9
Loin weight, (kg)	2200	12.75	1.783	14.0	6.8	19.1
Belly weight, (kg)	2200	10.19	1.768	17.3	5.1	16.2
Forequarter percentage, (%)	2200	32.77	1.604	4.9	21.9	39.3
Leg percentage, (%)	2200	33.59	1.411	4.2	25.6	39.5
Middle percentage, (%)	2200	33.16	1.801	5.4	25.4	41.8
Loin percentage, (%)	2200	18.46	1.824	9.9	9.3	26.2
Belly percentage, (50	2200	14.70	1.661	11.3	8.7	22.6

¹ all traits are defined per carcase

Image-analysis measurements

Description of recorded image-analysis data

A total of 36,312 records were collected from the images of 2,283 pigs that had information about primal cut weights available. These data were collected by two operators who each analysed a proportion of weekly groups of animals. The data statistics of the original measures (in pixels) are shown in Table A3. Outliers that exceeded three standard deviations from the mean of the measurement were excluded from the analyses. The first two measures, the length of an A4 sheet and the width of the crate, were collected to calibrate each image. The dimensions of the weighing crate were 75 cm wide and 131 cm long. The low CV of 2.7 and 2.1 % indicate that the position of the camera was reasonably constant between images. Variation in this regard may have occurred from placing the camera in a slightly different position on the fixed post each week or from holding the A4 sheet at an angle.

Coefficients of variation were below 10% for most length measures (Table A3). The increased CV of the first leg-width and the last shoulder-width measures indicate measurement errors. It was often difficult to define the exact position for these measurements which contributed to measurement errors and increased variation for these measurements.

Coefficients of variation were slightly higher for horizontal length measures (Variable 10 to 13) ranging from 6.8 to 15.1%. Only the horizontal length measure of the shoulder had higher variability in comparison to other horizontal length measurements. The area of the middle was considerably larger than the area of the leg or shoulder. Variability of area measures was relatively consistent between area measurements with CV ranging from 11.8 to 13.8 %. In comparison, coefficients of variation were around 10% for weight measures in these data as shown earlier in Table A1. Overall, the variability in these traits corresponded well with variability observed for growth and weight traits.

For each length measurement, the angle of the measurement is recorded by the software package ImageJ. Exactly horizontal measures have an angle of 0 while vertical measures have an angle of -90 degrees. Length measurements recorded on the standing pig had angles close to the expectation of either 0 or -90 degrees (Table A4). However, angles were variable for all length measures between animals. Deviations from the expected angle measures indicate that pigs did not stand straight in the crate when the image was taken. This may have affected the accuracy of length measurements. Information about the angle of a length measurement may be used to define a quality control criterion for the length measures.

Table A3. Data statistics for image analyses measures (in pixels, SD: standard deviation; CV: coefficient of variation)

Variable ¹	Measure	N	Mean	SD	CV	Min	Max
1	A4 sheet	2219	1,390	36.9	2.7	1,315	1,545
2	Crate width	2237	1,873	40.1	2.1	1,758	1,993
3	Leg width 1	2247	541	104.3	19.3	301	1,854
4	Leg width 2	2260	931	56.7	6.1	760	1,224
5	Middle width 1	2254	785	54.4	6.9	618	954
6	Middle width 2	2254	864	60.4	7.0	682	1,047
7	Middle width 3	2256	835	58.3	7.0	656	1,014
8	Shoulder width 1	2257	894	61.9	6.9	711	1,080
9	Shoulder width 2	2246	527	111.4	21.1	270	878
10	Pig length	2229	2,663	181.8	6.8	2,168	3,249
11	Leg length	2231	736	65.9	9.0	544	948
12	Middle length	2254	1,293	129.2	10.0	920	1,687
13	Shoulder length	2255	685	103.6	15.1	374	1,003
14	Leg area	2245	667,341	79,051.8	11.8	452,415	1,235,812
15	Middle area	2246	1,024,662	130,798.2	12.8	695,655	1,445,472
16	Shoulder area	2261	577,735	79,465.0	13.8	346,574	992,184

¹1: Horizontal length of A4 sheet; 2: vertical width of crate; 3: vertical width of leg – tail end; 4: vertical width of leg – middle; 5: vertical width of loin – tail end; 6: vertical width of loin – middle; 7: vertical width of loin – head end; 8: vertical width of shoulder – middle; 9: vertical width of shoulder – head end; 10: length of pig – horizontal line along the spine; 11: length of leg; 12: length of loin; 13: length of shoulder; 14: area of leg; 15: area of loin; 16: area of shoulder.

Table A4. Data statistics for the angle of linear image analyses measures (SD: standard deviation)

Variable ¹	Measure	N	Mean	SD	Min	Max
1	A4 sheet	2279	-1.00	3.82	-16.1	12.7
2	Crate width	2252	-90.27	1.18	-94.0	-86.0
3	Leg width 1	2196	-89.95	5.68	-128.4	-68.0
4	Leg width 2	2257	-90.44	6.35	-114.0	-66.0
5	Middle width 1	2161	-89.84	6.81	-125.1	-64.7
6	Middle width 2	2232	-90.40	3.62	-113.0	-76.1
7	Middle width 3	2194	-91.57	7.53	-118.0	-64.9
8	Shoulder width 1	2264	-90.14	9.26	-118.9	-56.9
9	Shoulder width 2	2241	-89.24	10.06	-123.5	-45.5
10	Pig length	2241	0.17	2.36	-20.6	10.6
11	Leg length	2241	0.73	4.93	-19.0	21.0
12	Middle length	2264	0.75	2.71	-9.0	13.0
13	Shoulder length	2261	-0.15	7.32	-22.0	22.2

¹ For information on variables see Table A3.

Description of image-analysis data linked with other performance records

Fewer records were available for traits derived from image analyses because identification may have been missing for an image and data could not be linked with pedigree and other performance data. Further, some pigs did not stand straight in the crate or parts of the leg or forequarter were missing on the image and it was not possible to obtain reliable images for these pigs. The summary of data outlined in Table A5 represents records with complete information that were used in phenotypic and genetic analyses. Although the number of records was reduced for all traits, the changes in data statistics were minimal in comparison to the image-analyses traits recorded in total (Table A3).

A proportion of pigs with image-analysis traits available had been selected and therefore had no carcass data available. This reduced the number of pigs that had both live-animal measures and carcass information available.

Table A5. Data statistics for image analyses measures actually used in analyses (in pixels, SD: standard deviation; CV: coefficient of variation).

Variable ¹	Measure	N	Mean	SD	CV	Min	Max
3	Leg width 1	1865	542	102.6	18.9	301.0	812.0
4	Leg width 2	1913	931	57.4	6.2	759.5	1224.0
5	Middle width 1	1914	784	54.6	7.0	618.0	954.0
6	Middle width 2	1913	864	60.5	7.0	681.6	1047.0
7	Middle width 3	1861	834	58.4	7.0	655.8	1014.0
8	Shoulder width 1	2023	895	61.3	6.8	711.0	1080.1
9	Shoulder width 2	2012	529	112.0	21.2	270.1	878.0
10	Pig length	1891	2663	181.6	6.8	2167.6	3249.2
11	Leg length	1895	736	65.5	8.9	544.0	948.3
12	Middle length	1913	1293	130.2	10.1	920.0	1686.5
13	Shoulder length	1914	683	103.0	15.1	374.4	1002.9
14	Leg area	1904	667,806	79,283.8	11.9	452415.0	1235812.0
15	Middle area	1906	1,024,146	130,797.0	12.8	695655.0	1445472.0
16	Shoulder area	1920	576,157	78,465.1	13.6	346574.0	992184.0

¹ For information on variables see Table A3.

Variation in weight of primal cuts

Pigs were evaluated with the PorkScan™ system (PorkScan Pty Ltd, Canberra, ACT) from March to May 2012 (data set A) and with the Hennessy Chong grading system from June to September 2012 (data set B). Data statistics for the carcass traits are shown for both groups of pigs in Table A6 and Table A7. The first group of pigs were slightly heavier and had a higher mean backfat depth. Loin depth was only available for the first data set. Considerable variation was observed in all four primal cut weights. Coefficients of variations were highest for belly weight with values around 17 %.

Table A6. Table A6. Data statistics for pigs slaughtered from March to May 2012 (data set A)

Variable	N	Mean	SD	CV	Min	Max
Hot carcass weight (kg)	586	81.33	7.46	9.17	57.90	102.10
Weight loss (%)	573	12.6	1.56	12.44	6.80	17.9
Fat depth at P2 site (mm)	578	11.61	2.44	20.99	6.00	18.00
Loin depth at P2 site (mm)	589	51.03	5.75	11.26	34.00	66.00
Shoulder weight ¹ (kg)	584	11.76	1.17	9.97	8.55	15.19
Leg weight ¹ (kg)	578	11.84	1.10	9.28	8.46	14.88
Belly weight ¹ (kg)	586	5.30	0.88	16.61	3.14	7.68
Loin weight ¹ (kg)	589	6.55	0.83	12.73	3.40	9.55

¹Weight based on one side of the carcass only. N: number of pigs, SD: standard deviation, CV: Coefficient of variation, Min and Max: minimum and maximum.

Table A7. Data statistics for pigs slaughtered from June to September 2012 (data set B)

Variable	N	Mean	SD	CV	Min	Max
Hot carcass weight (kg)	1606	78.28	8.16	10.42	54.40	102.80
Weight loss (%)	1585	12.0	1.45	12.12	7.20	17.8
Fat depth at P2 site (mm)	1604	10.40	2.38	22.92	4.00	18.60
Shoulder weight ¹ (kg)	1574	11.24	1.26	11.25	7.65	15.13
Leg weight ¹ (kg)	1579	11.57	1.19	10.28	8.16	15.08
Belly weight ¹ (kg)	1542	5.03	0.87	17.40	2.54	7.70
Loin weight ¹ (kg)	1560	6.35	0.91	14.39	3.62	9.64

¹Weight based on one side of the carcass only. N: number of pigs, SD: standard deviation, CV: Coefficient of variation, Min and Max: minimum and maximum.

Factors explaining variation in primal cut weights

The proportion of variation explained by hot standard carcass weight alone was considerably higher for shoulder weight and leg weight in comparison to weight of belly and loin (Table A8). Hot standard carcass weight explained only 41 and 43% of the variation observed in weight of the loin.

Fat depth, loin depth and weight loss explained an additional three to six percent of the variation in primal cut weights observed in data set A. In comparison, the additional variation explained by these three factors varied from one to four percent in data set B. The additional variation explained by adding fat depth to the model was largest for weight of shoulder and belly, while fat depth was not significant for loin weight. Loin depth explained an additional 1.9% of the variation for loin weight and was of less importance for the other primal cut weights. Weight loss was a significant factor for all four primal cut weights. However, the proportion of additional variation explained by this factor was variable between data sets for individual primal cut weights.

Table 8. Proportion of variation (%) for primal cut weights explained by the model

Model		Shoulder	Leg	Belly	Loin
$y = \text{HSCW}$	Data A	76.5	77.3	56.9	40.9
	Data B	77.8	81.2	58.8	43.4
$y = \text{HSCW} + \text{CFD}$	Data A	77.9	77.6	58.5	40.7
	Data B	78.1	82.0	59.6	43.0
$y = \text{HSCW} + \text{CFD} + \text{WTLOSS}$	Data A	81.7	80.9	61.3	42.0
	Data B	80.5	85.3	59.7	45.2
$y = \text{HSCW} + \text{CFD} + \text{CMD}$	Data A	78.2	77.7	58.9	42.6
$Y = \text{HSCW} + \text{CFD} + \text{CMD} + \text{WTLOSS}$	Data A	82.2	81.0	62.0	43.8

Abbreviations: HSCW: host standard carcass weight; CFD: carcass fat depth; WTLOSS: weight loss; CMD: carcass loin depth.

Variation in primal cut weights at a fixed carcass weight

There was considerable variation in the four primal cut weights for a fixed carcass weight as illustrated in Figures A4 and A5. Data were limited to 201 carcasses with a hot standard carcass weight of 78.0 to 80.0 kg only. Shoulder weight and leg weight varied by about four kg per carcass ignoring the tails of each distribution. The variations in belly and loin weights were only slightly smaller with a range of three kilograms.

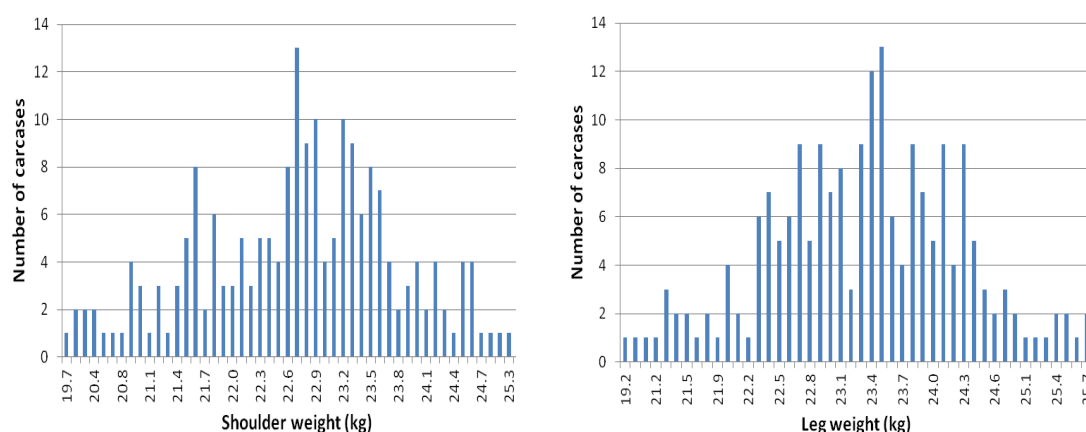


Figure A4. Distribution of shoulder and leg weight per carcass for carcasses with a hot standard carcass weight of 78.0 to 80.0 kg.

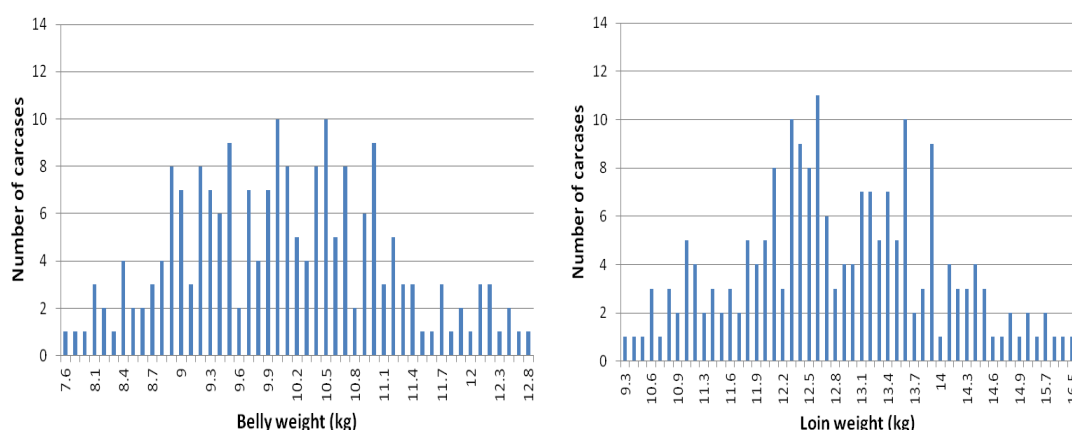


Figure A5. Distribution of belly weight per carcass for carcasses with a hot standard carcass weight of 78.0 to 80.0 kg.

Prediction of primal cut weights

Pearson correlations between image-analyses traits

Traits obtained from image analyses were grouped into trait groups describing width, length and area measurements. Pearson correlations between adjacent width measurements were highest in comparison to width measurements in general demonstrating their close associations (Table A9). In particular middle width measures were highly correlated (0.53 to 0.74). The first (WLeg1) and last (WShoulder2) width measures had higher variability and also lower correlations with other weight measures. These two most-distant measures had the strongest correlations to each other in comparison to other width measurements. This strong association may be due to the operator who had to make a subjective decision on the position for these measures. The position for these measures was less defined than positions of other width measurements. It is likely that each

operator used the same procedure for recording the first and the last width measurement which would have contributed to a stronger association between these two traits.

The length of the pig had positive correlations of 0.46 to 0.66 with other length measures of the pig due to part-whole relationships. Length of the middle was not associated with length of leg or shoulder. A longer leg was correlated with a longer shoulder (0.36).

Magnitude of Pearson correlations between area measures varied from 0.29 to 0.46. Each primal cut area had strong correlations with the length measure of that particular primal cut. Width measures of each primal cut also had high correlations with the corresponding area measurement although the magnitude of these correlations was slightly lower than the corresponding correlations between length and area measurements.

Pearson correlations between primal cut weights and image-analysis traits

Numerous image-analyses measures had high Pearson correlations ranging from 0.42 to 0.54 with cold carcass weight (Table A10). In comparison, fat and muscle depth recorded on the carcass at slaughter had correlations of 0.51 and 0.43, respectively. It should be noted though, that image analyses measures were taken three weeks prior to slaughter which is expected to have led to lower associations. Fat and muscle depth recorded at the same time on the live animal had lower correlations of 0.13 and 0.24, respectively. The image-analyses measures used in this study were very simple measures based on limited research and development. Overall, these results demonstrate that live-animal measures based on image analyses describing conformation of animals are useful predictors of the weight of pigs.

The three width measures of the middle had high associations (range: 0.42 to 0.50) with the three main primal cut weights of the leg, middle and shoulder. The first and last width measure had no predictive ability for primal cut weights with Pearson correlations ranging from -0.09 to 0.04.

In regard to length measurements, the length of the pig had highest correlations with the main primal cut weights varying from 0.42 to 0.45. The length of the leg and shoulder had higher predictive power than the length of the middle for the main primal cut weights. Length and width measurements had lower associations indicating that these measures complement each other for the predication of primal cut weights.

All three area measures also from image analyses had high Pearson correlations (range: 0.41 to 0.53) with weight of leg, middle or forequarter. Area measurements are more time consuming to record in comparison to linear measurements. Therefore, width measurements taken on the middle may be preferable to predict primal cut weights.

In summary, a number of image analyses measures had associations with primal cut weights that corresponded to the magnitude of correlations found between carcass fat or muscle depth and primal cut weights (range: 0.34 to 0.55). These correlations were higher than Pearson correlations observed between fat or muscle depth recorded on the live pig and primal cut weights, which ranged from 0.09 to 0.25.

Pearson correlations of loin or belly weight with image-analysis traits were slightly lower than associations between image-analysis measures and leg, middle or shoulder weight. However, correlations were strongest for width measures of the middle and area measurements which

correspond to Pearson correlations found between image-analyses traits and the main primal cut weights.

Pearson correlations between primal cut percentages and image-analysis traits

Primal cut percentages were derived by dividing each primal cut weight by the cold weight of the whole carcass. These traits are therefore not weight measurements per se but rather represent traits describing the relative weight of each primal cut. As a result, Pearson correlations between image-analysis traits and primal cut percentages were lower and varied from negative to positive values (Table A7). This shift in correlations was most pronounced for width measurements of the middle which had positive correlations with percentage of middle (range: 0.10 to 0.16) and negative correlations with percentage of leg (range: -0.13 to -0.12) or forequarter (range: -0.11 to -0.06). The positive association between width measures of the middle and percentage of middle weight were due to positive Pearson correlations between width of the middle and belly percentage. Width measures of the middle were not associated with loin percentage. Pigs with higher belly percentage also had higher carcass fat depth given the Pearson correlation of 0.30 between these traits.

Area of the middle had a positive correlation with percentage of middle while the other two area measurements had no significant association with the corresponding primal cut percentage trait. However, percentage of the leg had negative correlations with area of middle and forequarter. Similarly, percentage of forequarter had negative correlations with area of leg and middle. Therefore, indirect measures may be more informative than direct measures for primal cut weights at a fixed carcass weight.

A long pig has a lower leg percentage and a higher middle percentage while a short pig has a higher leg percentage and a lower middle percentage. These associations reflect the conformation of Landrace-type pigs (maternal lines) versus Pietrain-type pigs (terminal lines). Maternal lines are generally longer and have a less-pronounced leg while selection for lean meat in terminal sire lines has resulted in shorter, more muscular type of pigs. These associations are reflected in a positive Pearson correlation between carcass fat depth and middle percentage due to positive association of carcass fat depth with belly percentage and negative Pearson correlations between carcass fat depth and leg or forequarter percentage. In Australia, the middle is more valuable than the leg and the full market value of the carcass should be evaluated for different types of pigs in regard to conformation and primal cut weights.

A wider hind quarter is associated with a lower percentage of the forequarter weight and higher leg percentage. A long leg though, was associated with a low leg percentage. Further, a long shoulder was correlated with a low leg percentage and a high shoulder percentage.

Overall, the diversity of Pearson correlations between image-analyses measures and primal cut percentages demonstrates that different image measures provide complementary information for the prediction of primal cut weights at a given carcass weight.

Table A9. Pearson correlations between image-analyses measures

	Width (W)						Length (L)				Area (A)		
	Leg	Middle			Shoulder		Pig	Leg	Middle	Shoulder	Leg	Middle	Shoulder
	2	1	2	3	1	2							r
WLeg1	0.47	0.14	0.15	0.19	0.46	0.70	0.00	0.00	0.24	-0.39	0.23	0.22	-0.02
WLeg2		0.61	0.54	0.53	0.57	0.33	0.33	0.39	0.29	-0.03	0.78	0.41	0.36
WMiddle1			0.74	0.58	0.41	0.08	0.35	0.34	0.22	0.15	0.60	0.52	0.38
WMiddle2				0.66	0.47	0.05	0.24	0.27	0.15	0.09	0.51	0.49	0.40
WMiddle3					0.63	0.26	0.39	0.29	0.29	0.15	0.47	0.56	0.51
WShoulder1						0.47	0.30	0.18	0.24	-0.02	0.42	0.39	0.50
WShoulder2							0.10	-0.07	0.34	-0.30	0.09	0.35	-0.03
LPig								0.46	0.66	0.53	0.48	0.72	0.55
LLeg									0.06	0.36	0.64	0.26	0.38
LMiddle										-0.01	0.25	0.73	0.16
LShoulder											0.21	0.20	0.59
ALeg												0.41	0.46
AMiddle													0.29

Table A10. Pearson correlations between primal cut weights or percentages and image-analyses measures.

Traits ¹	Cold Wt	Leg Wt	Middle Wt	FQ Wt	Loin Wt	Belly Wt	Leg %	Middle %	FQ %	Loin %	Belly %
BF	0.13	0.09	0.09	0.12	0.05	0.10	-0.07	-0.02	0.01	-0.06	0.03
MD	0.24	0.24	0.21	0.18	0.25	0.10	0.01	0.04	<u>-0.13</u>	<u>0.12</u>	-0.08
WL _{Leg1}	-0.02	0.04	-0.05	-0.09	0.02	-0.10	<u>0.17</u>	-0.04	<u>-0.11</u>	0.07	<u>-0.12</u>
WL _{Leg2}	0.42	0.47	0.35	0.35	0.33	0.26	0.09	0.02	<u>-0.14</u>	0.02	0.00
WM _{Middle1}	0.54	0.50	0.49	0.49	0.37	0.44	<u>-0.12</u>	<u>0.10</u>	-0.06	-0.04	<u>0.15</u>
WM _{Middle2}	0.48	0.43	0.43	0.42	0.32	0.39	<u>-0.12</u>	<u>0.12</u>	-0.07	-0.03	<u>0.16</u>
WM _{Middle3}	0.49	0.46	0.48	0.44	0.39	0.41	<u>-0.13</u>	<u>0.16</u>	<u>-0.11</u>	0.04	<u>0.14</u>
W _{Shoulder1}	0.35	0.35	0.31	0.30	0.28	0.23	-0.01	0.06	-0.06	0.03	0.03
W _{Shoulder2}	-0.02	0.00	-0.03	-0.07	0.00	-0.05	0.07	-0.01	-0.08	0.03	-0.05
LPig	0.48	0.44	0.42	0.45	0.35	0.34	<u>-0.11</u>	0.08	0.00	0.01	0.07
LL _{Leg}	0.35	0.33	0.30	0.35	0.28	0.22	-0.06	0.03	0.03	0.03	0.00
LM _{Middle}	0.27	0.24	0.23	0.24	0.20	0.18	-0.05	0.04	-0.01	0.01	0.03
LS _{Shoulder}	0.34	0.28	0.30	0.37	0.22	0.29	<u>-0.16</u>	0.06	0.09	-0.05	<u>0.12</u>
AL _{Leg}	0.51	0.53	0.44	0.47	0.38	0.35	0.01	0.04	-0.06	0.00	0.05
AM _{Middle}	0.50	0.44	0.46	0.44	0.34	0.42	<u>-0.13</u>	<u>0.13</u>	-0.06	-0.03	<u>0.17</u>
A _{Shoulder}	0.48	0.45	0.41	0.48	0.33	0.35	<u>-0.10</u>	0.04	0.03	-0.03	0.08
CFD	0.51	0.40	0.55	0.41	0.40	0.51	<u>-0.30</u>	<u>0.30</u>	<u>-0.17</u>	0.02	<u>0.30</u>
CLD	0.43	0.42	0.41	0.34	0.36	0.28	-0.04	<u>0.11</u>	<u>-0.16</u>	0.05	0.05

Abbreviations of traits: BF: Backfat recorded on live pig; MD: muscle depth recorded on live pig; Wt – weight; W – Width; L – Length; A – Area; CFD: Carcase fat depth; CLD: Carcase loin depth;

Prediction of primal cut weights

The models to predict cold carcase weight and primal cut weights or percentages were developed using the regression procedure (proc reg) of the SAS system. A stepwise selection method was chosen which includes variables in the model based on their significance level at entry to the model. When another variable has been added to the model, the stepwise selection method evaluates all existing variables in the model and eliminates those that are not significant at the specified level to stay in the model. A significance level of 0.05 was chosen as a criterion for variables to enter and stay in the model.

The predictive ability of image-analysis measures is documented in Tables A11 to A16 for carcase cold weight and primal cut weights. Two scenarios were compared for each weight trait by omitting or including live weight in the prediction equation. Backfat and muscle depth were not included in the stepwise regression analyses because the number of animals with both trait groups, fat or muscle depth and image-analyses traits, were low with approximately 240 pigs.

Image-analysis measures alone accounted for 51% of the variation in cold weight and 41 to 45% of the variation in weight of the leg, middle and forequarter (Tables A11 to A16). A lower proportion of the variation was explained by image-analysis traits for weight of the loin (25%) and the belly (34%). When live weight was included in the model, the models accounted for an additional 2 to 3% of the variation in cold weight or primal cut weights.

Image-analysis measures differed in their predictive ability for individual primal cut weights. The first width measurement of the middle (WMiddle1) had a partial R-Square of above 1% for all primal cut weights and cold weight. This image-analysis measure explained considerable variation for cold weight (28%), forequarter (23%), middle (23%) and belly (17%) weight. Therefore, this is the most important conformation trait on the live pig to predict weight in primal cuts.

Area of the leg and area of the middle accounted for over 1% of the variation in five of the six cold or primal cut weights. As expected, area of the leg had the highest predictive ability for leg weight which was greater than the partial R-square of live weight (R-square of 29% versus 9%). Area of the middle also had a high R-square of 7% for leg weight.

The length of the pig had partial R-square values of over 1% for cold, forequarter, middle and loin weight varying from about 3% for loin weight to around 10% for the other three weight traits. Among the individual length measurements, only the length of the shoulder explained at least 1% of the variation in cold or primal cut weights. For length of the shoulder had the highest partial R-square value was found for belly weight (7%).

These regression analyses showed that of the 14 image-analysis traits investigated, width of the middle at the tail, area of the leg or middle and length of the pig or shoulder were the five image-analysis traits with the highest predictive ability for cold or primal cut weights.

Table A11. Partial and model R-square for variables entered or removed to predict cold weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Cold Weight	WMiddle1		0.285	0.285	<.0001	Live weighth		0.327	0.327	<.0001
	LPig		0.116	0.401	<.0001	ALeg		0.078	0.404	<.0001
	AShoulder		0.032	0.433	<.0001	LShoulder		0.058	0.462	<.0001
	ALeg		0.018	0.451	<.0001	AMiddle		0.035	0.497	<.0001
	AMiddle		0.023	0.474	<.0001	WMiddle1		0.016	0.513	<.0001
		LPig	0.000	0.474	0.4413	WShoulder2		0.009	0.522	<.0001
	WLeg1		0.023	0.497	<.0001	AShoulder		0.009	0.531	<.0001
	LShoulder		0.004	0.501	0.0016	LPig		0.004	0.534	0.0013
	WLoin3		0.004	0.504	0.0025	WLeg1		0.002	0.536	0.0159
	WShoulder2		0.003	0.507	0.0039					
	Lpig		0.002	0.509	0.0304					
	WShoulder1		0.002	0.511	0.04					

Table A12. Partial and model R-square for variables entered or removed to predict leg weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Leg weight	ALeg		0.291	0.291	<.0001	ALeg		0.291	0.291	<.0001
	AMiddle		0.073	0.364	<.0001	Live weight		0.093	0.384	<.0001
	AShoulder		0.049	0.413	<.0001	LShoulder		0.031	0.414	<.0001
	WMiddle1		0.014	0.426	<.0001	AMiddle		0.021	0.436	<.0001
	WShoulder2		0.009	0.435	<.0001	AShoulder		0.011	0.446	<.0001
	WLeg2		0.003	0.438	0.0046	WMiddle1		0.007	0.454	<.0001
	LShoulder		0.004	0.442	0.004	WShoulder2		0.004	0.458	0.0012
	LLeg		0.003	0.445	0.01	WLeg2		0.004	0.462	0.0013
	WMiddle3		0.002	0.447	0.0244	LLeg		0.002	0.465	0.0199

Table A13. Partial and model R-square for variables entered or removed to predict middle weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Middle weight	WMiddle1		0.227	0.227	<.0001	Live weight		0.278	0.278	<.0001
	LPig		0.092	0.319	<.0001	AMiddle		0.056	0.335	<.0001
	WMiddle3		0.030	0.349	<.0001	LShoulder		0.043	0.378	<.0001
	LShoulder		0.019	0.367	<.0001	WMiddle1		0.027	0.405	<.0001
	ALeg		0.011	0.378	<.0001	ALeg		0.012	0.416	<.0001
	AMiddle		0.014	0.392	<.0001	WShoulder2		0.009	0.426	<.0001
		LPig	0.000	0.392	0.8723	WMiddle3		0.012	0.438	<.0001
	WShoulder2		0.013	0.405	<.0001					
	AShoulder		0.004	0.410	0.0025					
	WLeg1		0.002	0.411	0.0457					

Table A14. Partial and model R-square for variables entered or removed to predict shoulder weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Shoulder weight	WMiddleI		0.234	0.234	<.0001	Live weight		0.263	0.263	<.0001
	LPig		0.106	0.339	<.0001	LShoulder		0.091	0.353	<.0001
	AShoulder		0.038	0.377	<.0001	WLoinI		0.054	0.407	<.0001
	LShoulder		0.014	0.390	<.0001	ALeg		0.019	0.426	<.0001
	AMiddle		0.019	0.409	<.0001	AMiddle		0.017	0.442	<.0001
		LPig	0.000	0.409	0.7843	WLegI		0.011	0.453	<.0001
	ALeg		0.021	0.429	<.0001	AShoulder		0.012	0.465	<.0001
	WLegI		0.016	0.445	<.0001	LPig		0.005	0.469	0.0009
	LPig		0.004	0.448	0.0042	WShoulder2		0.002	0.471	0.0301
	WShoulderI		0.002	0.450	0.0399	LMiddle		0.002	0.473	0.0488
	WShoulder2		0.003	0.453	0.0052	WShoulderI		0.002	0.475	0.0469

Table A15. Partial and model R-square for variables entered or removed to predict loin weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Loin weight	WMiddle3		0.149	0.149	<.0001	Live weight		0.195	0.195	<.0001
	ALeg		0.055	0.204	<.0001	ALeg		0.035	0.229	<.0001
	LPig		0.026	0.230	<.0001	WMiddle3		0.021	0.250	<.0001
	WMiddle1		0.011	0.240	<.0001	LShoulder		0.014	0.264	<.0001
	WShoulder2		0.006	0.246	0.0013	AMiddle		0.007	0.271	0.0003
	AMiddle		0.004	0.251	0.0054	WShoulder2		0.007	0.278	0.0006
	AShoulder		0.003	0.254	0.0152					
		LPig	0.001	0.253	0.1897					

Table A16. Partial and model R-square for variables entered or removed to predict belly weight omitting or fitting live weight.

	Live weight not fitted					Live weight fitted				
	Variable	Variable	Partial	Model	P-value	Variable	Variable	Partial	Model	P-value
	Entered	Removed	R-Square	R-Square		Entered	Removed	R-Square	R-Square	
Belly weight	WMiddle1		0.178	0.178	<.0001	Live weight		0.190	0.190	<.0001
	LShoulder		0.071	0.249	<.0001	LShoulder		0.065	0.255	<.0001
	AMiddle		0.043	0.292	<.0001	WMiddle2		0.044	0.299	<.0001
	WMiddle3		0.011	0.303	<.0001	AMiddle		0.021	0.320	<.0001
	WShoulder2		0.012	0.315	<.0001	WShoulder2		0.007	0.327	0.0002
	ALeg		0.008	0.323	0.0002	WMiddlew1		0.007	0.334	0.0004
	LPig		0.004	0.326	0.0072	WMiddle3		0.004	0.338	0.0048
	AShoulder		0.005	0.331	0.0014		WMiddle2	0.001	0.337	0.1215
	WLeg1		0.004	0.335	0.006	ALeg		0.003	0.340	0.0111
	LLeg		0.003	0.338	0.015	LPig		0.007	0.346	0.0003
	WLeg2		0.002	0.341	0.0361	WLeg2		0.004	0.350	0.0079
						AShoulder		0.003	0.353	0.0122
						LLeg		0.002	0.355	0.034

Genetic parameters for primal cut weights

Significant fixed effects

The p-values of significant effects and the coefficients of determination of each model are outlined in Table A17 and Table A18 for all traits. A number of characteristics of the birth litter affected growth due to the specific management procedures on farm. Weight of the pig at recording was significant as a linear and quadratic covariable for fat and muscle depth recorded on the live pig. The quadratic term of hot carcass weight was only significant for loin depth.

The fixed effect model explained over 80% of the variation for the three primal cuts of forequarter, leg and middle which was mainly due to fitting hot carcass weight (Table A18). In comparison, the coefficient of determination was lower for loin and belly weight with values of 0.654 and 0.743. These high coefficients of variation have implications for genetic improvement of these traits as they limit the amount of variability available for selection. Fixed effect models explained only 12 to 41% of the variation for the alternative trait definitions based on the percentage of each primal cut relative to hot carcass weight. Although the trait definition included already an indirect adjustment for hot carcass weight, this factor was still significant for all primal cut percentage traits except loin percentage accounting for approximately 3 to 6% of the variation.

Fitting cold carcass weight instead of hot carcass weight increased the coefficient of determination by 2% for forequarter weight and by 3% for leg weight. Middle weight was not affected by this substitution of hot carcass weight with cold weight indicating that weight loss occurred mainly on the hind and fore quarters.

Table A17. Coefficients of determinations (R²) and p-values of significant fixed effects for average daily gain (ADG), backfat (BF), muscle depth (MD), carcass fat depth (FD) and carcass loin depth (CLD).

Trait	R ²	CG ¹	Genotype	BPar	BNBA	BLacL	BPar*BNBA	BWlin	BWq
Average daily gain	0.142	***	0.0004	***	***	***	0.0022	-	-
Backfat	0.294	***	0.0002					***	0.0008
Muscle depth	0.261	***						***	***
Trait	R ²	CG	Genotype					HCWlin	HCWq
Carcass fat depth	0.365	***	***					***	
Carcass loin depth	0.342	***	0.0024					0.0022	0.0159

¹ Abbreviations of fixed effects: CG: contemporary group, BPar: Parity of birth litter, BNBA: number born alive of birth litter, BLacL: lactation length of birth litter; BPar*BNBA: interaction of BPar and BNBA, BWlin: linear covariable of body weight, BWq: quadratic covariable of body weight, BWc: cubic covariable of body weight, HCWlin: linear covariable of hot carcass weight, HCWq: quadratic covariable of hot carcass weight, HCWc: cubic covariable of hot carcass weight.

Table A18. Coefficients of determinations (R²) and p-values of significant fixed effects for primal cut weights and primal cut percentages

Trait	R ²	CG	Genotype	CWlin	CWq	Agelin
Forequarter weight	0.842	***		***		
Middle weight	0.852	***		***		
Leg weight	0.863	***		***		
Loin weight	0.654	***	***	***	***	
Belly weight	0.743	***	***	***		
Forequarter percentage	0.172	***		0.0005	0.0045	0.0455
Forequarter percentage	0.143	***				
Middle percentage	0.186	***		***		
Middle percentage	0.138	***				
Leg percentage	0.170	***		***		
Leg percentage	0.119	***				
Loin percentage	0.307	***	0.0008			
Belly percentage	0.409	***	***	0.0001	***	
Belly percentage	0.350	***	***			

Abbreviations: CG: contemporary group; CWlin: linear covariable for cold carcass weight; CWq: quadratic covariable for cold carcass weight; Agelin: linear covariable of age;

Heritability estimates

Estimates of the heritability and the common litter effect for growth rate corresponded to previous estimates (Table 19). The litter effect was not significant for any trait describing characteristics of the carcass as previously found (e.g. Hermes and Jones, 2011).

Both backfat and muscle depth recorded on the live animal had no significant heritability estimates while carcass fat and loin depth were highly heritable with estimates of 0.57 ± 0.06 and 0.29 ± 0.11 , respectively. Higher heritabilities for PorkScan™ measures in comparison to live-animal measures were also reported by Hermes and Jones (2011) for an independent data set, although differences were not as large as was found in the current study. The live-animal measures had smaller means and variability due to the younger age at recording which is expected to have contributed to these non-significant heritabilities for backfat and muscle depth recorded on the live pig.

Heritability estimates for primal cut weights varied from 0.16 ± 0.04 for loin weight to 0.24 ± 0.05 for leg weight (Table 20). The range of heritabilities was effectively the same for primal cut percentages varying from 0.14 ± 0.04 for loin percentage to 0.26 ± 0.06 for belly percentage. Adjusting primal cut percentage traits for cold weight did not affect heritability estimates significantly, because the weight adjustment reduced both the phenotypic and additive genetic variance. The reduction in additive genetic variation resulting from this adjustment for age supports the simpler model for primal cut percentages.

Table A19. Estimates of heritabilities (h^2) and common litter effects (c^2) estimates both with standard errors (SE) along with variance components for growth and fat or muscle depth measurements.

Trait	h^2	se	c^2	se	V_A^1	V_C^1	V_E^1	V_P^1
Average daily gain	0.39	0.02			1831		2876	4707
	0.18	0.02	0.08	0.01	817	348	3253	4418
Backfat	0.05	0.02			0.054		1.043	1.098
	0.04	0.02	0.02	0.02	0.047	0.018	1.034	1.098
Muscle depth	0.01	0.02			0.144		9.167	9.311
	0.003	0.02	0.04	0.02	0.038	0.365	8.921	9.324
Carcass fat depth	0.57	0.06			2.438		1.830	4.268
	0.52	0.08	0.04	0.03	2.191	0.150	1.880	4.221
Carcass loin depth	0.29	0.11			7.340		17.65	24.99
	0.19	0.12	0.09	0.07	4.649	2.223	17.89	24.76

¹Abbreviations: V_A : additive genetic variance; V_C : Variance due to common litter effect; V_E : Residual variance; V_P : phenotypic variance.

Table A20. Estimates of heritabilities (h^2) and common litter effects (c^2) estimates both with standard errors (se) along with variance components for primal cut weights and percentages.

Trait	h^2	se	c^2	se	V_A^1	V_C^1	V_E^1	V_P^1
Forequarter weight	0.20	0.05			0.200		0.819	1.02
Leg weight	0.24	0.05			0.187		0.604	0.791
	0.23	0.05	0.01	0.03	0.179	0.010	0.600	0.790
Middle weight	0.23	0.05			0.293		0.982	1.276
Loin weight	0.16	0.04			0.174		0.944	1.119
Belly weight	0.23	0.06			0.191		0.638	0.830
	0.18	0.06	0.06	0.04	0.148	0.049	0.627	0.825
Forequarter percentage	0.20	0.05			0.441		1.802	2.243
Forequarter percentage - adjusted for CW ¹	0.20	0.05			0.432		1.741	2.173
Leg percentage	0.22	0.05			0.400		1.390	1.790
	0.21	0.05	0.01	0.03	0.383	0.023	1.381	1.788
Leg percentage - adjusted for CW	0.23	0.05			0.389		1.294	1.683
	0.23	0.05	0.01	0.03	0.380	0.012	1.290	1.682
Middle percentage	0.22	0.05			0.639		2.208	2.847
Middle percentage - adjusted for CW	0.23	0.05			0.624		2.060	2.684
Loin percentage	0.14	0.04			0.336		2.003	2.340
Belly percentage	0.26	0.06			0.493		1.370	1.863
	0.21	0.06	0.05	0.04	0.396	0.101	1.354	1.851
Belly percentage adjusted for WT	0.25	0.06			0.415		1.277	1.692
	0.19	0.06	0.06	0.04	0.323	0.095	1.262	1.680

¹Abbreviations: CW: cold carcase weight; V_A : additive genetic variance; V_C : Variance due to common litter effect; V_E : Residual variance; V_P : phenotypic variance.

Genetic correlations between primal cut weights

Both fat measurements on the live animal (backfat) and the carcase (fat depth) had a high genetic correlation of 0.83 ± 0.16 (Table A21). Although this genetic correlation was not significantly different from unity, a genetic correlation of 0.8 is usually considered as the biological threshold to treat two traits as separate traits in genetic evaluations. In comparison, both muscle depth measurements were genetically different traits as indicated by the estimate of genetic correlation between muscle depth and loin depth of -0.27 ± 0.54 . The high standard error reflects the uncertainty of this estimate which is due to the low heritability for muscle depth and the low number of records for loin depth.

A high carcase loin depth was genetically associated with slow growth (-0.50 ± 0.19) and low fatness levels recorded on the carcase (carcase fat depth -0.42 ± 0.20) and live pig (backfat -0.22 ± 0.36). These genetic associations were not found between muscle depth recorded on the live pig and measures of lean meat growth.

Please note, genetic parameters from the bivariate analyses of growth and backfat converged only when the quadratic weight adjustment for backfat was omitted from the model. This change in model for backfat did not affect the heritability estimate and led to a non-significant increase in the genetic correlation with growth of 0.05 in comparison to the full model with convergence problems.

Table A21. Estimates of genetic correlations (above diagonal) and residual and phenotypic correlations (first and second row below diagonal) between growth and fat or muscle depth measurements

Trait		Average gain	daily	Backfat	Muscle depth	Carcase fat depth	Carcase loin depth
Average gain	daily			0.27(0.19)	0.28(0.33)	0.08(0.10)	-0.50(0.19)
Backfat		-0.05(0.03) -0.01(0.02)			0.82(0.48)	0.83(0.16)	-0.22(0.36)
Muscle depth		-0.03(0.03) -0.01(0.02)		0.25(0.02) 0.27(0.01)		0.41(0.33)	-0.27(0.54)
Carcase depth	fat	-0.28(0.05) -0.14(0.03)		0.15(0.09) 0.25(0.06)	0.05(0.10) 0.08(0.06)		-0.42(0.20)
Carcase depth	loin	-0.10(0.08) -0.20(0.05)		-0.06(0.12) -0.08(0.09)	-0.04(0.11) -0.05(0.09)	0.11(0.011) -0.10(0.04)	

The alternative trait definitions and models for primal cut weights or percentages had a minimal and non-significant effect on estimates of genetic correlations between these traits (Tables A22, A23, A24). Therefore, genetic associations are outlined for primal cut weights only (Table A19). The trait definition for primal cut weights included an adjustment for cold weight which implied negative associations between individual primal cuts. Forequarter had moderate negative genetic correlations

with leg (-0.39 ± 0.15) and middle (-0.30 ± 0.15). In comparison, leg and middle had a strong negative genetic correlation (-0.74 ± 0.09) which corresponded to a strong negative genetic correlation between leg and belly (-0.65 ± 0.12). Genetic correlations between loin and other primal cut weights were weaker in comparison to genetic correlations between belly and primal cuts. The high genetic correlations between middle and loin or belly are due to the part-whole associations between these traits.

Table A22. Estimates of genetic correlations between primal cut weights

	Forequarter	Leg	Middle	Loin	Belly
Forequarter		-0.39(0.15)	-0.30(0.15)	-0.16(0.19)	-0.29(0.17)
Leg	-0.05(0.04) -0.13(0.02)		-0.74(0.09)	-0.31(0.17)	-0.65(0.12)
Middle	-0.46(0.03) -0.43(0.02)	-0.23(0.04) -0.35(0.02)		0.61(0.12)	0.71(0.10)
Loin	-0.35(0.04) -0.32(0.02)	-0.14(0.04) -0.17(0.02)	0.68(0.02) 0.66(0.01)		-0.10(0.19)
Belly	-0.13(0.04) -0.16(0.02)	-0.12(0.04) -0.24(0.02)	0.40(0.04) 0.48(0.02)	-0.40(0.04) -0.34(0.02)	

Table A23. Estimates of genetic correlations between primal cut percentages – no weight adjustments

	Forequarter	Leg	Middle	Loin	Belly
Forequarter		-0.38(0.16)	-0.30(0.16)	-0.10(0.19)	-0.34(0.16)
Leg	-0.01(0.04) -0.09(0.02)		-0.76(0.09)	-0.29(0.18)	-0.69(0.11)
Middle	-0.49(0.03) -0.45(0.02)	-0.27(0.04) -0.38(0.02)		0.54(0.13)	0.74(0.08)
Loin	-0.37(0.04) -0.32(0.02)	-0.13(0.04) -0.16(0.02)	0.67(0.02) 0.64(0.01)		-0.15(0.18)
Belly	-0.15(0.05) -0.20(0.02)	-0.16(0.05) -0.30(0.02)	0.44(0.04) 0.52(0.02)	-0.37(0.04) -0.32(0.02)	

Table A24. Estimates of genetic correlations between primal cut percentages – weight adjustments

	Forequarter	Leg	Middle	Loin	Belly
Forequarter		-0.42(0.15)	-0.28(0.16)	-0.16(0.19)	-0.27(0.17)
Leg	-0.06(0.04) -0.14(0.02)		*	-0.34(0.17)	-0.68(0.11)
Middle	-0.46(0.03) -0.42(0.02)			0.62(0.12)	0.71(0.09)
Loin	-0.36(0.04) -0.32(0.02)	-0.12(0.04) -0.16(0.02)	0.68(0.02) 0.66(0.01)		-0.10(0.19)
Belly	-0.13(0.04) -0.16(0.02)	-0.11(0.05) -0.25(0.02)	0.41(0.04) 0.48(0.02)	-0.39(0.04) -0.33(0.02)	

Genetic correlations between growth and fat or muscle depth and primal cut weights

Selection for increased growth will lead to a proportionally larger middle weight (rg: 0.30 ± 0.12) mainly due to a higher belly weight (0.46 ± 0.46 , Table A25). Genetic correlations between both fat depth measures and primal cut weights were in the same direction, although estimates were considerably larger for backfat recorded on the live animal. In particular, the high genetic correlation between backfat and belly weight of 0.96 ± 0.22 is noteworthy. In comparison, fat depth recorded on the carcass had a genetic correlation of 0.44 ± 0.12 with belly weight. It should be explored whether the time of measuring fat depth may have contributed to these differences in genetic correlations.

Selection for reduced backfat is expected to lead to more weight in the hind leg of pigs as indicated by a strong genetic correlation of -0.62 ± 0.25 between backfat and leg weight. The corresponding genetic correlation between fat depth and leg weight recorded on the carcass was lower in magnitude (-0.22 ± 0.13).

Both measurements of loin depth recorded on the live animal or the carcass had no significant genetic associations with primal cut weights. The direction of genetic correlations between loin depth and primal cut weights followed expectations with a higher loin weight being (lowly) associated with a higher leg and loin weight and lower belly and forequarter weights. In comparison, Mérour and Hermes (2009) found genetic correlations between loin weight and muscle depth recorded on the carcass or live animal of 0.55 and 0.23, respectively. No genetic associations were found between leg weight and muscle depth in the study by Mérour and Hermes (2009) who did find negative genetic correlations of -0.30 and -0.25 between belly weight and muscle depth measure as was found in the current study. Overall, this brief comparison illustrates differences in genetic correlations between studies which may be due to differences in trait definitions between the French and Australian data sets.

Table A25. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut weights and growth, fat or muscle measurements

		Average daily gain	Live backfat	Live muscle depth	Carcase fat depth	Carcase loin depth
Forequarter	rg	-0.04(0.15)	-0.19(0.25)	0.27(0.41)	-0.20(0.13)	-0.15(0.25)
	re	0.05(0.04)	0.21(0.08)	-0.14(0.07)	-0.24(0.06)	-0.13(0.08)
	rp	0.04(0.03)	0.16(0.06)	-0.11(0.06)	-0.21(0.02)	-0.13(0.04)
Leg	rg	-0.23(0.13)	-0.62(0.25)	-0.18(0.38)	-0.22(0.13)	0.15(0.25)
	re	0.10(0.04)	-0.05(0.08)	0.06(0.08)	-0.17(0.06)	0.00(0.08)
	rp	0.02(0.03)	-0.11(0.07)	0.04(0.07)	-0.18(0.02)	0.04(0.04)
Middle	rg	0.30(0.12)	0.53(0.22)	0.05(0.37)	0.29(0.12)	-0.11(0.25)
	re	-0.07(0.04)	-0.20(0.08)	-0.08(0.08)	0.25(0.06)	0.11(0.08)
	rp	0.01(0.03)	-0.11(0.07)	-0.07(0.07)	0.25(0.02)	0.06(0.04)
Loin	rg	0.03(0.16)	-0.17(0.28)	-0.09(0.41)	-0.05(0.15)	0.08(0.26)
	re	0.00(0.04)	-0.09(0.08)	0.00(0.08)	0.17(0.06)	0.14(0.07)
	rp	0.01(0.03)	-0.09(0.07)	0.00(0.07)	0.09(0.02)	0.12(0.04)
Belly	rg	0.46(0.12)	0.96(0.22)	0.20(0.39)	0.44(0.12)	-0.36(0.25)
	re	-0.06(0.04)	-0.16(0.08)	-0.09(0.08)	0.09(0.07)	0.00(0.09)
	rp	0.06(0.03)	-0.03(0.07)	-0.07(0.06)	0.21(0.02)	-0.09(0.04)

Table A26. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut percentages (unadjusted for weight) and growth, fat or muscle measurements

		Average daily gain	Live backfat	Live muscle depth	Carcase vat depth	Carcase loin depth
Forequarter	rg	-0.30(0.14)	-0.25(0.24)	0.26(0.42)	-0.20(0.13)	-0.11(0.26)
	re	-0.07(0.04)	0.24(0.08)	-0.17(0.07)	-0.23(0.06)	-0.16(0.08)
	rp	-0.12(0.03)	0.18(0.06)	-0.13(0.06)	-0.20(0.02)	-0.15(0.04)
Leg	rg	-0.50(0.10)	-0.73(0.25)	-0.18(0.39)	-0.25(0.13)	0.21(0.25)
	re	-0.09(0.04)	-0.01(0.08)	0.03(0.08)	-0.16(0.6)	-0.02(0.08)
	rp	-0.19(0.03)	-0.08(0.07)	0.01(0.07)	-0.18(0.02)	0.04(0.04)
Middle	rg	0.55(0.10)	0.61(0.21)	0.07(0.38)	0.31(0.12)	-0.18(0.26)
	re	0.10(0.04)	-0.26(0.08)	-0.06(0.08)	0.24(0.06)	0.15(0.08)
	rp	0.21(0.03)	-0.15(0.07)	-0.05(0.07)	0.25(0.02)	0.07(0.05)
Loin	rg	-0.03(0.16)	-0.17(0.29)	-0.12(0.42)	-0.03(0.15)	0.07(0.27)
	re	-0.01(0.04)	-0.10(0.08)	0.00(0.08)	0.16(0.06)	0.15(0.07)
	rp	-0.01(0.03)	-0.11(0.07)	-0.01(0.07)	0.09(0.02)	0.13(0.04)
Belly	rg	0.68(0.09)	0.96(0.20)	0.20(0.38)	0.42(0.11)	-0.41(0.24)
	re	0.13(0.04)	-0.21(0.08)	-0.07(0.08)	0.09(0.07)	0.03(0.09)

rp	0.27(0.02)	-0.07(0.07)	-0.05(0.07)	0.22(0.02)	-0.09(0.05)
----	------------	-------------	-------------	------------	-------------

Estimates of correlations between primal cut percentages, which were not adjusted for cold carcase weight, and growth, fat or muscle depth measures (Table A26) corresponded well with estimates of corresponding genetic correlations between primal cut weights and growth, fat or muscle depth traits. The additional adjustment of primal cut percentages for weight reduced estimates of genetic correlations with growth rate (Table A27). Other estimates of genetic correlations did not change significantly due to the weight adjustment.

Table A27. Genetic (rg), residual (re) and phenotypic (rp) correlations between primal cut percentages (adjusted for weight) and growth, fat or muscle measurements

		Average daily gain	Live backfat	Live muscle depth	Carcase fat depth	Carcase loin depth
Forequarter	rg	-0.01(0.15)	-0.19(0.25)	0.25(0.41)	-0.18(0.13)	-0.16(0.25)
	re	0.08(0.04)	0.23(0.08)	-0.16(0.07)	-0.23(0.06)	-0.14(0.08)
	rp	0.06(0.03)	0.18(0.06)	-0.13(0.06)	-0.20(0.02)	-0.15(0.04)
Leg	rg	-0.19(0.13)	-0.60(0.25)	-0.14(0.38)	-0.22(0.13)	0.15(0.25)
	re	0.10(0.04)	-0.05(0.08)	0.06(0.08)	-0.17(0.06)	0.00(0.08)
	rp	0.03(0.03)	-0.11(0.07)	0.05(0.07)	-0.18(0.02)	0.04(0.04)
Middle	rg	0.28(0.13)	0.53(0.22)	0.04(0.37)	0.28(0.12)	-0.11(0.25)
	re	-0.08(0.04)	-0.23(0.08)	-0.09(0.08)	0.24(0.06)	0.12(0.08)
	rp	0.00(0.03)	-0.14(0.07)	-0.08(0.07)	0.24(0.02)	0.06(0.05)
Belly	rg	0.37(.13)	0.95(0.22)	-0.12(0.42)	0.42(0.12)	-0.28(0.26)
	re	-0.10(0.04)	-0.18(0.08)	0.00(0.08)	0.09(0.07)	-0.01(0.08)
	rp	0.01(0.03)	-0.05(0.07)	-0.01(0.07)	0.21(0.02)	-0.08(0.04)

Options for incorporating primal cut weight traits into breeding objectives

Rationale

Current pig breeding objectives focus on productivity traits that increase revenues and reduce costs at farm level, with little consideration of yields of primal cut regions with different market values. Currently in Australia, there are significant premiums in wholesale markets for belly and loin primal regions (see Eyes and Ears, APL), and genetic parameters reported earlier indicate that genetic variation exists in the amounts of cuts present in the carcass.

In this section, two approaches to incorporate primal cut breeding values into the breeding objective are outlined and discussed. Firstly, a detailed calculation dealing with each cut specifically by using its own economic value is considered. With this approach, it is assumed that estimated breeding values for primal cut weights are adjusted to a constant carcass weight. Secondly, a much more simple approach is presented based on placing economic emphasis on the most value primal cut, the middle section of the carcass which is also adjusted to a constant carcass weight.

Economic values for the four main primal cuts of forequarter, leg, belly and loin

To estimate the economic values of primal cut components of the carcass, we assume that the weighted average values of the primal cuts used in the economic value calculation equals the total farmer value of the carcass. This places a conservative value on changes in primal cut proportions, in that it assumes that farmers get paid a similar proportion of the extra value of heavier primal cuts as the proportion of final carcass value that they capture at the farm gate.

Since it is most appropriate to assume that pigs are slaughtered at a target weight in pig production, a constant carcass weight adjustment is most sensible for estimated breeding values of these traits.

For conservatively estimated farmer economic values, we calculate the economic value of each primal for forequarter (EV_CFQW), leg (EV_CLegW), belly (EV_CBW) and loin (EV_CLW) as follows;

$$EV_CFQW = PC_{FQ} \cdot \kappa,$$

$$EV_CLegW = PC_{Leg} \cdot \kappa$$

$$EV_CBW = PC_B \cdot \kappa$$

$$EV_CLW = PC_L \cdot \kappa$$

where κ is used to translate relative prices (PC_{FQ} , PC_{Leg} , PC_B and PC_L) for forequarter, leg, belly and loin respectively into prices for each primal cut that result in the same carcass value as derived from the typical carcass weight price received by farmers (P_p). The value κ is derived as:

$$\kappa = \frac{P_p}{PC_S \cdot \rho Cwt_S + PC_H \cdot \rho Cwt_H + PC_B \cdot \rho Cwt_B + PC_L \cdot \rho Cwt_L}$$

The relative prices for primal cuts represent their relative economic importance at the farm gate level, which is lower than the whole-sale or retail level. Therefore, this mechanism allows information about prices for individual primal cuts at each stage of the supply chain to be converted to prices relevant at the farmer gate level. However, any other level (whole-sale or retail) could be

applied if benefits of higher carcase yield should be evaluated for the full supply chain which is relevant for integrated systems.

With primal cut estimated breeding values adjusted to a constant carcase weight, it would be appropriate to directly work out economic values for primal cut weights for a vertically integrated breeding and production system based on final values received for primal cuts at sale from the vertically integrated business. For example, if the retail price of the meat generated from the loin primal cut is worth A\$ 8 per kg of loin primal cut weight, then EV_CLW could be taken directly as A\$ 8.00. This would give a substantially higher value than the conservative farmer based values described using the equations above. However, in the absence of vertical integration, it is unlikely that the farmer would receive the full reward for delivering more of the valuable primal cut weights via a carcase payment system.

It should be noted that the economic values calculated in this way do not depend on whether the estimated breeding values for primal cut weights are expressed on an adjusted age, or an adjusted carcase weight, basis. They are the same for either form of adjustment. However, with constant age adjustment, it is not appropriate to have carcase weight in the breeding objective, and the economic values for primal cuts translate directly into an effect of faster growth rate leading to a heavier more valuable carcase.

Please note, it is assumed that economic values for primal cut weights are independent of the pricing grid based on fat depth. If this assumption is not met, then the economic value of subcutaneous fat may have to be adjusted to be less negative because the carcase pricing grids for penalties against carcase fatness is partly based on the fact that primal cut yields are likely to be lower when carcase P2 fat is higher.

Results

Economic values

The above method was applied using carcase proportions derived from data collected for this study. Relative values for primal cuts were based on what was reported in Eyes and Ears issue number 534 from May 2013. A slaughter carcase weight of 80kg and a carcase weight price of 3.05 were assumed. Results are presented in Table A28 below.

Table A28. Primal specific assumptions used in the calculations and resulting economic values derived for specific cuts.

	Forequarter	Leg	Belly	Loin
Proportion of carcase	0.33	0.33	0.15	0.19
Price relative to forequarter	1.00	1.03	2.34	2.00
Economic value	2.18	2.24	5.11	4.37

It should be noted in Table A28 that the economic values for primal cuts are all positive. However, at a constant carcase weight, it is intuitive that it would be desirable to reduce the proportions of lower value cuts in the carcase. This will be achieved through the underlying negative genetic

correlations between some primal cut weights. In order to understand how an index with the above economic values could achieve the intuitive outcome, it is necessary to consider the genetic relationships among traits to quantify the expected genetic changes in other primal cut weights when a single primary cut weight is increased while holding carcass weight constant. These effects were computed using the concept of partial genetic regressions. The partial genetic regressions were derived based on genetic standard deviations and genetic covariances obtained in this study.

Genetic response

Genetic regressions quantify the expected genetic changes in other (carcass weight adjusted) primal cut breeding values when each change trait is increased by one kg (Table A29). It should be noted that the expectations for the column for the sum of genetic regressions is minus one. That is because, at a constant carcass weight, if one primal cut weight of the carcass is increased by one kg, all of the other primal cut weights should collectively decrease by one kg. The sums of genetic regressions differed from one, particularly for the leg and loin (column 6 of Table A29). This anomaly is a direct reflection of sampling errors in the estimates of the genetic correlations and heritabilities used to derive the genetic regressions. However, the general trend of expected changes based on selection using the economic values derived is as expected as indicated by the net changes in carcass values which arise from a change in each primal cut weight by one kg assuming a constant carcass weight. Loin and belly are the most valuable primal cuts and an increase in these primals will lead to a higher market value of the carcass of \$2.80 and \$2.60 at the farm gate level. An increase in leg weight has larger negative economic consequences for the overall carcass value because it has a strong negative genetic correlation with belly weight.

In practice then, the economic values as calculated in Table A28 could be applied directly to estimated breeding values. Animals with high breeding values for low-value primal cut weights (leg and forequarter) should have correspondingly negative breeding values for high value cuts (loin and belly), and therefore be penalised by the index accordingly.

Table A29. Genetic regressions (b_{gen}), economic values (EV) and the net change in carcass value for a one-kg change in each primal cut on the value of the carcass at farm gate after accounting for correlated changes in other primal cut weights (Net-change).

Change trait	Response trait b_{gen} on change trait				Sum of b_{gen}	EV	Net change ¹
	Leg	Loin	Belly	Forequarter			
Leg		-0.30	-0.65	-0.40	-1.36	2.52	-3.29
Loin	-0.32		-0.10	-0.17	-0.59	3.87	2.76
Belly	-0.65	-0.10		-0.30	-1.04	4.93	2.58
Forequarter	-0.38	-0.15	-0.28		-0.81	2.27	-0.75

¹Calculated as the sum of products of each response cut change with its economic value; please note the genetic regression of a trait on its own value is 1.0.

An economic value for middle weight at a constant carcass weight

While theoretically correct, understanding the above approach depends on a complex set of inter-relationships among a set of traits with part-whole relationships, and positive economic values for

primal cuts with lower market value are somewhat counter-intuitive. There are also risks of over and under emphasis for the different cuts because of sampling errors in the genetic parameters that would be required to derive the estimated breeding values. The part- whole relationships could also complicate the breeding value estimation process because of non-positive definiteness in the parameter matrices. For this reason, a more simple but efficient alternative to the above approach would be beneficial.

An alternative approach is to combine belly and loin primal components into a single breeding value as long as these two traits have similar market prices as well as similar market prices for leg and forequarter. An economic value would then be defined for middle weight adjusted to a constant carcass weight based on the difference in weighted (by carcass proportion) average return from the middle (belly and loin combined) versus the weighted average return from the forequarter and leg. This results in an economic value of \$2.48 for weight of middle cuts at a constant carcass weight in our example. No other primal cut weight would be part of the breeding objective.

Comparison of approaches

It is possible to test whether re-ranking of animals would occur from the two alternative approaches described above using genetic parameters calculated as part of this study. The variance of each breeding objective is computed as $\mathbf{a}'\mathbf{G}\mathbf{a}$ where $\mathbf{a}$ is a vector of economic weights, and $\mathbf{G}$ is a genetic variance covariance matrix among traits. Using the parameters described earlier for primal cut weights including the weight of the middle as a trait), and the economic values derived here, the standard deviation of the two breeding objectives was 1.71 for the full specification approach described for the first approach above, and 1.34 for the second approach. The variance of the simpler breeding objective depends only on the economic value and phenotypic variance for the middle, which is only slightly lower than the phenotypic variance of the loin. The higher variance with the more detailed approach likely reflects the fact that the net impact as computed from the genetic regressions of a change in loin (a higher value middle cut) appears to be biased upwards significantly, because an increase in loin of one kg is accompanied by a reduction in the other primal cuts of 0.59 kg only.

It is also possible to estimate the loss of efficiency that would occur from using the simple approach under the assumption that the more detailed approach is the correct one. This can be calculated as the correlation between breeding objectives as $\mathbf{a}_1'\mathbf{G}\mathbf{a}_2/\sqrt{(\mathbf{a}_1'\mathbf{G}\mathbf{a}_1 \times \mathbf{a}_2'\mathbf{G}\mathbf{a}_2)}$ which resulted in a value of 0.988. The vectors $\mathbf{a}_1$ and $\mathbf{a}_2$ represent the vectors of economic weights for both approaches and $\mathbf{G}$ is the additive genetic co-variance matrix of breeding objective traits. Thus, the simple approach has the advantage of being more straight forward to derive and explain, while resulting in an equivalent ranking of animals in our example and with less risk of upward bias due to sampling errors in the large number of correlations required for the more detailed approach.

The more-detail approach, however, is superior if loin weight has a higher economic weight than belly weight as it makes better use of the less stringent genetic correlations between loin and leg. On the other hand, the simple approach is superior if a weaker negative genetic correlation between middle weight and leg is assumed. The negative genetic correlation of -0.74 between middle weight and leg has a higher magnitude than genetic correlations of -0.31 and -0.65 between loin and belly with leg weight. It is not known which genetic correlation is biased and all estimates of genetic correlations have a level of uncertainty as quantified by their standard errors.

Potential contribution to the overall breeding objective

The above calculations compute economic values for alternative primal cut traits. These can be converted into economic weights that could be incorporated with economic weights for other traits in a terminal line breeding objective. To do this, the economic value needs to be multiplied by a corresponding discounted genetic expressions (DGE) coefficient. The relevant DGE coefficient to facilitate comparison with economic values calculated using the recently developed Pig EV model is 9.24 (Hermesch et al., 2013; Pork CRC Project 2B-102). Thus the standard deviation of the simple breeding objective for primal cuts (equivalent to the genetic standard deviation for middle cut weight at a constant carcass weight x the economic value of \$2.48) gives $2.48 \times 9.24 = 22.9$. This is a similar contribution to the breeding objective than the current main carcass trait of P2 fat depth (see Table A30 below) demonstrating the importance of extending the breeding objective to include this additional carcass trait.

In the instance of a fully vertically integrated pig production system from breeder through to wholesaler or beyond, the economic value of the middle cut trait could be approximately three fold higher (Mérour and Hermesch, 2008). In this instance, the full benefit of the extra carcass value arising from the heavier middle cuts can be accounted for in the breeding objective. In this instance, the relative importance of middle cut weights in the breeding objective would be more comparable to the relative importance of feed conversion ratio.

Table A30. Percent contribution of individual breeding goal traits to a terminal sire line breeding objective including weight of the middle.

Breeding objective traits -terminal line	EW	% contribution to breeding objective
Weight of the middle	22.9	9
Feed conversion ratio	-253	26
Average daily gain	0.816	17
Post weaning survival	1402	37
P2 fat depth	-15.7	11

Implications & Recommendations

Improving selection for carcass quality

The current payment system for pigs is based on fat depth at a given carcass weight in Australia. By increasing the weight of the more valuable primal cuts in carcasses with the same fatness and weight levels, additional returns can be achieved per carcass. These additional returns possible per carcass are currently underutilised in the Australian pig industry. This project provides information about variation in primal cut weights, methodology to predict weights of individual primal cuts and outlines genetic parameters and selection strategies to increase the weight of the middle, which is the most valuable primal cut in the Australian market.

Considerable variation has been observed in primal pork cuts recorded in Australian pigs. Hot carcass weight explained forty to eighty percent of the variability in individual primal cut weights. Fat depth, loin depth and weight loss explained an additional one to six percent of the variation in primal cut weights. Primal cut weights varied by four (shoulder or leg weight) and three (belly or loin weight) kilograms per carcass for carcasses with a hot carcass weight of 78.0 to 80.0 kg only.

The economic value of a trait represents the change in profit if a trait is increased by one unit. A higher weight of the middle for a fixed carcass weight improves profit of a slaughter pig at the farm gate level by \$2.48 per kg of the middle based on market prices relevant in 2013. This project found that the weight of the middle may vary up to six kg between pigs with the same carcass weight. This variation in weight of middle results in a potential difference in the return per carcass of \$15 which is not captured by the current payment system in Australia.

Economic values are required to include economically important traits in the breeding objective, which is the overall index used to select pigs. Often economic values are multiplied by genetic standard deviations of traits to make a comparison of the economic importance of traits included in the breeding objective possible. The economic value for weight of the middle at a constant carcass weight contributed 9% to the breeding objective derived for terminal sire lines in Australia. This economic emphasis is similar to the economic importance of fat depth at the P2 site highlighting the need to include primal cut weights in Australian pig breeding programs.

Two approaches to include weight of primal cuts in breeding objectives were outlined. The simple approach of using the price difference between the weight of the middle and other primal cuts (forequarter and leg) is recommended for the current Australian payment system that places similar prices on the components of the middle, loin and belly and also uses similar prices for forequarter and leg. The more detailed approach is recommended when prices are higher for the loin than the belly because it allows for making better use of the less negative genetic correlation between loin and leg. Similarly, this approach is recommended when prices for leg and forequarter are more diverse than current price structures.

Breeders should evaluate the accuracy of ultrasound measurements from time to time by taking repeated measures on a sample of at least 50 pigs to ensure consistency of measurements over time. This quality control of measurement techniques is particularly important for new operators. Further, selection has resulted in a considerable shift in the mean of fat and muscle depth which affects variance components used in BLUP-based genetic evaluation systems. It is therefore recommended to re-estimate variance components every few years.

The higher heritability estimates for fat and muscle depth measures of the PorkScan™ system in comparison to measures on the live animal found previously have been confirmed in this independent data set. The reliability of the PorkScan™ system should be improved to ensure that the Australian pig industry can make better use of this superior technology.

A simple procedure was outlined to obtain image-analysis measures of live pigs that describe conformation of pigs using a free software package. These image-analysis measurements had predictive power for the weight of pigs or carcasses and the weight of primal cuts demonstrating the usefulness of image analysis for prediction and possibly selection of carcass market value. The first width measurement of the middle at the tail end was the most important conformation trait on the live pig to predict weight in primal cuts. Further image-analysis traits with superior predictive ability for primal cut weights were area of the leg or middle and length of the pig or shoulder. These results should be used in any further developments of the prediction equations of the PorkScan™ light-striping system. Further, established technologies like the highly-awarded German device optiSCAN (www.hl-agrar.de) should be evaluated for collection of image-analysis measures that are useful for prediction and selection of primal cut weights.

Selection strategies for improved carcass market value that involve measurements on the live animal will be outlined to industry through the established technology-transfer pathways of AGBU to ensure that results from this project are adopted by Australian breeders.

Technical summary

Introduction

Primal cut weights in pigs are heritable (Newcom *et al.*, 2002; van Wijk *et al.*, 2005; Gilbert *et al.*, 2007; Mérour *et al.*, 2010). However, heritability estimates were variable between studies indicating that differences in populations and cutting procedures may have affected these estimates. The weight in individual primal cuts reflects the shape of an animal. Genetic parameters for linear measurements on the live pig were not found. However, high heritability estimates have been found for carcass length (Engellandt *et al.*, 1997; Gilbert *et al.*, 2007; Mérour *et al.*, 2009) indicating that linear shape measures will respond to selection and may be used as selection criteria for primal cut weights in pigs. So far, adoption of new selection criteria to improve saleable meat yield has been hindered by the lack of data available in Australia. It was the aim of this study to record primal cut weights and to develop selection strategies for improved carcass market value.

Data

The data included primal cut weights recorded on 2,311 carcasses from castrates that belonged to four different genotypes. Pigs were born in one farm and raised in five different grow-out facilities. Lifetime growth rate, backfat depth at the P2 site and muscle depth between the third and fourth last ribs were recorded on pigs at 143.5 ± 3.84 days of age. Backfat and muscle depth were recorded using real time ultrasound. A photo of the pig standing in the weighing crate was taken four days later along with an additional weight measure for a proportion of pigs. Genetic analyses of growth, backfat and muscle depth included information from contemporaries of project animals recorded in 2012. Version ImageJ 1.46r was used for the analyses of images of boars standing in a weighing crate. A total of 14 linear or area measurements were used to describe conformation of pigs. A total of 36,312 records were collected from the images of 2,283 pigs that had information about primal cut weights available.

Variation in primal cut weights for a fixed carcass weight

There was considerable variation in the four primal cut weights for a fixed carcass weight. Data were limited to 201 carcasses with a hot standard carcass weight of 78.0 to 80.0 kg only. Shoulder weight and leg weight varied by about four kg per carcass ignoring the tails of each distribution. The variations in belly and loin weights were only slightly smaller with a range of three kilograms.

Prediction of primal cut weights

Correlations

The proportion of variation explained by hot standard carcass weight alone was considerably higher for shoulder weight and leg weight in comparison to weight of belly and loin. Hot standard carcass weight explained only 41 and 43% of the variation observed in weight of the loin. Fat depth, loin depth and weight loss explained an additional three to six percent of the variation in primal cut weights observed in the subset of data graded by the PorkScan™ system. In comparison, the additional variation explained by these three factors varied from one to four percent in the subset of data graded by the Hennessy Chong system. The additional variation explained by adding fat depth to the model was largest for weight of shoulder and belly, while fat depth was not significant for loin weight. Loin depth explained an additional 1.9% of the variation for loin weight and was of less importance for the other primal cut weights. Weight loss was a significant factor for all four primal cut weights. However, the proportion of additional variation explained by this factor was variable between data sets for individual primal cut weights.

Numerous image-analyses measures had high Pearson correlations ranging from 0.42 to 0.54 with cold carcass weight. In comparison, fat and muscle depth recorded on the carcass at slaughter had correlations of 0.51 and 0.43, respectively. It should be noted though, that image analyses measures were taken three weeks prior to slaughter which is expected to have led to lower associations. Fat and muscle depth recorded at the same time on the live animal had lower correlations of 0.13 and 0.24, respectively. The image-analyses measures used in this study were very simple measures based on limited research and development. Overall, these results demonstrate that live-animal measures based on image analyses describing conformation of animals are useful predictors of the weight of pigs.

The length of the pig had highest correlations with the main primal cut weights varying from 0.42 to 0.45. The length of the leg and shoulder had higher predictive power than the length of the middle for the main primal cut weights. Length and width measurements had lower associations indicating that these measures complement each other for the predication of primal cut weights.

In summary, a number of image analyses measures had associations with primal cut weights that corresponded to the magnitude of correlations found between carcass fat or muscle depth and primal cut weights (range: 0.34 to 0.55). These correlations were higher than Pearson correlations observed between fat or muscle depth recorded on the live pig and primal cut weights, which ranged from 0.09 to 0.25.

Prediction equations

Image-analysis measures alone accounted for 51% of the variation in cold weight and 41 to 45% of the variation in weight of the leg, middle and forequarter. A lower proportion of the variation was explained by image-analysis traits for weight of the loin (25%) and the belly (34%). When live weight

was included in the model, the models accounted for an additional 2 to 3% of the variation in cold weight or primal cut weights.

Image-analysis measures differed in their predictive ability for individual primal cut weights. The first width measurement of the middle (WMiddle1) had a partial R-Square of above 1% for all primal cut weights and cold weight. This image-analysis measure explained considerable variation for cold weight (28%), forequarter (23%), middle (23%) and belly (17%) weight. Therefore, this is the most important conformation trait on the live pig to predict weight in primal cuts.

Regression analyses showed that of the 14 image-analysis traits investigated, width of the middle at the tail, area of the leg or middle and length of the pig or shoulder were the five image-analysis traits with the highest predictive ability for cold or primal cut weights.

Association between primal cut percentages and image-analysis traits

A long pig has a lower leg percentage and a higher middle percentage while a short pig has a higher leg percentage and a lower middle percentage. These associations reflect the conformation of Landrace-type pigs (maternal lines) versus Pietrain-type pigs (terminal lines). Maternal lines are generally longer and have a less-pronounced leg while selection for lean meat in terminal sire lines has resulted in shorter, more muscular type of pigs. These associations are reflected in a positive Pearson correlation between carcass fat depth and middle percentage due to positive association of carcass fat depth with belly percentage and negative Pearson correlations between carcass fat depth and leg or forequarter percentage. In Australia, the middle is more valuable than the leg and the full market value of the carcass should be evaluated for different types of pigs in regard to conformation and primal cut weights.

Heritability estimates

Both backfat and muscle depth recorded on the live animal had no significant heritability estimates while carcass fat and loin depth were highly heritable with estimates of 0.57 ± 0.06 and 0.29 ± 0.11 , respectively. Higher heritabilities for PorkScan™ measures in comparison to live-animal measures had been reported earlier for an independent data set, although differences were not as large as was found in the current study. The live-animal measures had smaller means and variability due to the younger age at recording which is expected to have contributed to these non-significant heritabilities for backfat and muscle depth recorded on the live pig.

Heritability estimates for primal cut weights varied from 0.16 ± 0.04 for loin weight to 0.24 ± 0.05 for leg weight (Table A20). The range of heritabilities was effectively the same for primal cut percentages varying from 0.14 ± 0.04 for loin percentage to 0.26 ± 0.06 for belly percentage. Adjusting primal cut percentage traits for cold weight did not affect heritability estimates significantly, because the weight adjustment reduced both the phenotypic and additive genetic variance. The reduction in additive genetic variation resulting from this adjustment for age supports the simpler model for primal cut percentages.

Genetic correlations

Alternative trait definitions and models for primal cut weights or percentages had a minimal and non-significant effect on estimates of genetic correlations between these traits. The trait definition for primal cut weights included an adjustment for cold weight which implied negative associations between individual primal cuts. Forequarter had moderate negative genetic correlations with leg (-0.39 ± 0.15) and middle (-0.30 ± 0.15). In comparison, leg and middle had a strong negative genetic correlation (-0.74 ± 0.09) which corresponded to a strong negative genetic correlation between leg

and belly (-0.65 ± 0.12). Genetic correlations between loin and other primal cut weights were weaker in comparison to genetic correlations between belly and primal cuts. The high genetic correlations between middle and loin or belly are due to the part-whole associations between these traits.

Selection for increased growth will lead to a proportionally larger middle weight ($rg: 0.30 \pm 0.12$) mainly due to a higher belly weight (0.46 ± 0.46 , Table A25). Genetic correlations between both fat depth measures and primal cut weights were in the same direction, although estimates were considerably larger for backfat recorded on the live animal. In particular, the high genetic correlation between backfat and belly weight of 0.96 ± 0.22 is noteworthy. In comparison, fat depth recorded on the carcass had a genetic correlation of 0.44 ± 0.12 with belly weight. It should be explored whether the time of measuring fat depth may have contributed to these differences in genetic correlations.

Selection for reduced backfat is expected to lead to more weight in the hind leg of pigs as indicated by a strong genetic correlation of -0.62 ± 0.25 between backfat and leg weight. The corresponding genetic correlation between fat depth and leg weight recorded on the carcass was lower in magnitude (-0.22 ± 0.13).

Both measurements of loin depth recorded on the live animal or the carcass had no significant genetic associations with primal cut weights. The direction of genetic correlations between loin depth and primal cut weights followed expectations with a higher loin weight being (lowly) associated with a higher leg and loin weight and lower belly and forequarter weights.

Selection strategies

Two approaches to incorporate primal cut breeding values into the breeding objective are outlined and discussed. Firstly, a detailed calculation dealing with each cut specifically by using its own economic value is considered. With this approach, it is assumed that estimated breeding values for primal cut weights are adjusted to a constant carcass weight. Secondly, a much more simple approach is presented based on placing economic emphasis on the most value primal cut, the middle section of the carcass which is also adjusted to a constant carcass weight.

It is also possible to estimate the loss of efficiency that would occur from using the simple approach under the assumption that the more detailed approach is the correct one. This can be calculated as the correlation between breeding objectives as $\mathbf{a}_1' \mathbf{G} \mathbf{a}_2 / \sqrt{(\mathbf{a}_1' \mathbf{G} \mathbf{a}_1 \times \mathbf{a}_2' \mathbf{G} \mathbf{a}_2)}$ which resulted in a value of 0.988. The vectors $\mathbf{a}_1$ and $\mathbf{a}_2$ represent the vectors of economic weights for both approaches and $\mathbf{G}$ is the additive genetic co-variance matrix of breeding objective traits. Thus, the simple approach has the advantage of being more straight forward to derive and explain, while resulting in an equivalent ranking of animals in our example and with less risk of upward bias due to sampling errors in the large number of correlations required for the more detailed approach.

The more detailed approach, however, is superior if loin weight has a higher economic weight than belly weight as it makes better use of the less stringent genetic correlations between loin and leg. On the other hand, the simple approach is superior if a weaker negative genetic correlation between middle weight and leg is assumed.

At the farm gate level, including weight of the middle in selection decisions has a similar contribution to the breeding objective than the current main carcass trait of P2 fat depth demonstrating the importance of extending the breeding objective to include this additional carcass trait.

In the instance of a fully vertically integrated pig production system from breeder through to wholesaler or beyond, the economic value of the middle cut trait could be approximately three fold higher. In this instance, the full benefit of the extra carcase value arising from the heavier middle cuts can be accounted for in the breeding objective. In this instance, the relative importance of middle cut weights in the breeding objective would be more comparable to the relative importance of feed conversion ratio.

References

- Doeschl-Wilson, A. B., D. M. Green, A. V. Fisher, S. M. Carroll, C. P. Schofield, and C. T. Whittemore. 2005. The relationship between body dimensions of living pigs and their carcass composition. *Meat Science* 70:229-240.
- Engellandt, T., N. Reinsch, S. Reinecke, and E. Kalm. 1997. Schätzung genetischer parameter für die vaterlinien Pietrain und Belgische Landrasse der Schweineherdbuchzucht Schleswig-Holstein. *Züchtungskunde* 69(1):39-53.
- Fisher, A. V., D. M. Green, C. T. Whittemore, J. D. Wood, and C. P. Schofield. 2003. Growth of carcass components and its relation with conformation in pigs of three types. *Meat Science* 65:639-650.
- Gilbert, H., T. D. Bidner, J. Gruand, J.-C. Caritez, Y. Billon, P. Guillouet, H. Lagant, J. Noblet, and P. Sellier. 2007. Genetic parameters for residual feed intake in growing pigs, with emphasis on genetic relationships with carcass and meat quality traits. *Journal of Animal Science* 85(12):3182-3188.
- Green, P. 2008. Carcase measurement. Page 22 in Proc. Pan Pacific Pork Expo incorporating Uptake, Gold Coast, QLD, Australia.
- Hermesch, S. and R. M. Jones. 2011. Higher heritability estimates for fat and muscle depth obtained using the Porkscan TM system. Page 57 in Proc. Manipulating pig production XIII. Proceedings of the Thirteenth Biennial Conference of the Australasian Pig Science Association.
- Merour, I. and S. Hermesch. 2008. Variation and trends for weight of individual carcase cuts. Pages 83-92 in AGBU Pig Genetics Workshop. S. Hermesch and K. Dobos, ed. Animal Genetics and Breeding Unit, Armidale.
- Merour, I., S. Hermesch, R. M. Jones, and T. Tribout. 2009. Genetic correlations between carcase length, fat and muscle depths and primal cut weights in the French Large White sire line. Matching genetics and environment: a new look at an old topic. Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics, Barossa Valley, South Australia, Australia, 28 September-1 October, 2009.
- Merour, I., T. Tribout, and S. Hermesch. 2010. Between-breed variability of primal cuts weight and genetic correlations with pork quality traits. Pages 161-165 in Journées de la Recherche Porcine en France. Vol. 42.
- Newcom, D. W., T. J. Baas, J. W. Mabry, and R. N. Goodwin. 2002. Genetic parameters for pork carcass components. *Journal of Animal Science* 80:3099-3106.
- van Wijk, H. J., D. J. G. Arts, J. O. Matthews, M. Webster, B. J. Ducro, and E. F. Knol. 2005. Genetic parameters for carcass composition and pork quality estimated in a commercial production chain. *Journal of Animal Science* 83:324-333.

Use of haemoglobin levels in sows and piglets to improve piglet survival, performance and pork quality

Introductory Technical Information

Using haemoglobin levels in blood as a selection criterion for iron content in pork was proposed at the previous AGBU Pig Genetics Workshop (Jones and Hermes, 2010). Since then, a project has been completed demonstrating that haemoglobin levels recorded on farm using the HemoCue Hb 201+ analyser can indeed be used as a selection criterion for iron content in pork and other pork quality traits. Haemoglobin levels in growing pigs had moderate genetic correlations with iron content in pork, redness of pork and pH 24 hours *post mortem* (Hermes, 2012). However, it was also noted that the recording procedures used on farm during the project should be modified to improve the accuracy of on-farm measures of haemoglobin levels.

Haemoglobin levels above 100 g/l are considered adequate, whereas haemoglobin levels of 80 or 70 g/l are generally considered borderline anaemic, respectively (National Research Council, 1998). Piglets raised in intensive production systems do not have access to soil, a natural source of iron, and require supplementation of iron to prevent piglet iron deficiency anaemia. This requirement was first described in the 1920s as outlined by Payne (2009) who provided a comprehensive review of the numerous studies conducted over the last 90 years to evaluate alternative husbandry practices and their effects on iron status in piglets. Payne (2009) found an unexpected rate of iron deficiency in an Australian study and reported mean haemoglobin levels of pigs kept indoors were 80 g/L and 87 g/L for piglets either receiving creep or not receiving supplementary feed. Piglets were derived from older sows with an average parity number of 6.1, which may have contributed to this unexpected iron deficiency in piglets since a decline in iron levels with increasing parities have been reported recently (Auvigne *et al.*, 2010; Gannon *et al.* 2011). In addition, Auvigne *et al.* (2010) found that higher fatness levels in sows were associated with higher haemoglobin levels. Finally, Payne (2009) pointed out that the greater bone size and bone weight of outdoor pigs may have been due to increased bone mineralisation resulting from enhanced mineral uptake, in particular iron uptake, of the outdoor-fed pigs.

The condition of sows prior to farrowing affects their performance during lactation and has genetic associations with sow survival (Bunter *et al.* 2010). These sow characteristics may also be associated with blood haemoglobin levels in sows, which have been shown to affect iron levels in piglets (e.g. Wange *et al.*, 2009). Using information about body condition and haemoglobin levels in sows is expected to have beneficial effects on sow and piglet survival in regard to performance levels and genetic improvement of sow and piglet survival. In addition, maternal influences during gestation on muscle fibre development have been demonstrated (Dwyer *et al.* 1993, Dwyer *et al.* 1994), which ultimately may affect meat quality characteristics including iron content which was genetically associated with muscle fibre characteristics in the study by Larzul *et al.* (1997). Therefore, haemoglobin levels in sows may have carry-over effects on performance of growing pig and pork quality.

This is further demonstrated by the effect of the common litter on haemoglobin levels at five weeks of age as found (Hermes, 2011). The common litter effect is confounded with the sow effect. The review by Bunter (2009) showed that piglet traits are predominantly affected by the sow, genetically and environmentally, rather than at the piglet level. Therefore, sow traits are often used to improve pre-weaning piglet performance.

A recent study found that piglets with higher haemoglobin levels at birth had higher survival rates prior to weaning (Rootwelt *et al.* 2012). The mean haemoglobin levels of piglets surviving or dying until weaning were 105 g/L versus 99 g/L. In sows, a gradual reduction in mean haemoglobin levels with increasing parities was found in a survey of herds conducted in Western Australia (Gannon *et al.*, 2011). The authors concluded that progeny of sows with marginal haemoglobin levels of below 100 g/L were at greater risk of iron deficiency. Based on a review of the literature, Capozzalo *et al.* (2009) hypothesised that iron deficiency in older sows is expected to be mirrored in their progeny. However, the review also showed that supplementation of sows with iron during gestation did not raise iron levels in piglets.

There is a paucity of studies investigating the genetic configuration of haemoglobin and its genetic associations with other traits. A small selection experiment for high haemoglobin levels in piglets was initiated in the early 1960s based on eight Yorkshire sows (Fahmy and Bernard, 1978). Information from this selection experiment is very limited and 'the experiment was terminated abruptly after the fourth generation because of an unexpected reproductive problem.' The information available indicated differences in haemoglobin levels in piglets between the selection line for higher haemoglobin levels in piglets and a control line. The authors concluded that 'the problem is worthy of further investigations'.

A series of experiments were conducted in mink to evaluate genetic differences of haemoglobin levels between breeds and between selection lines within breed (Geddes-Dahl and Helgebostad, 1971). The experiments showed that fecundity and haemoglobin levels were interdependent traits and had to be considered simultaneously. The comparison of breeds showed lower fecundity for the breed with lower haemoglobin levels. Progeny from sires with high haemoglobin breeding values tended to be more viable and fecundity was far superior for the within-breed selection line for higher haemoglobin levels. Overall, these early results indicate that genetic associations between haemoglobin levels and viability or fecundity exist.

Research Methodology

Developing recording procedures for haemoglobin levels

Development of reliable procedures to record haemoglobin levels in sows, piglets and growing pigs was the first aim of this research. An initial trial was designed with Kristy Tickle at Rivalea following discussions with Prof Tore Framstad from Norwegian School of Veterinary Science, Oslo, Norway at the APSA meeting in 2011. He has researched aspects of haemoglobin and other blood parameters extensively and provided valuable advice for recording haemoglobin in young piglets, which was invaluable for the design of the subsequent trial of this Project to evaluate alternative recording procedures for haemoglobin in young piglets. Further, Tore Framstad provided a number of research papers relevant to the topic and invited Susanne Hermesch as an external collaborator to a new research project on the use of haemoglobin levels in pig veterinary research.

Analyses of the first haemoglobin data

The first haemoglobin data available were analysed to quantify sources of variation. These analyses showed that the sow affected haemoglobin levels in piglets which was outlined to breeders to initiate recording of haemoglobin levels in sows and piglets along with other sow traits on farm.

Analysis of haemoglobin levels and sow or piglet traits recorded by breeders

Following the completion of the initial trial to evaluate recording procedures for haemoglobin levels in sows and piglets, breeders were contacted to express their interest to record haemoglobin levels on farm. Initially, five breeding companies expressed an interest to participate and two further breeding companies requested additional information. Eventually, three breeders agreed to record haemoglobin levels on farm. However, one breeder had staff changes and could not obtain on-farm measurements during the period of this project. Two breeders have agreed to continue recording haemoglobin levels in sows and piglets on farm until December 2013. Data available until May 2013 were used to characterise initial traits and evaluate phenotypic associations between sow and piglet traits.

Discussion of Results

Recording haemoglobin levels in sows

Evaluation of recording procedures for haemoglobin levels in sows prior to farrowing and one-day old piglets were based on 47 sows from two maternal lines. These sows represented first (15 sows), second (15 sows) and third (17 sows) parity sows. Sows were ear pricked on entry to the farrowing house to collect drops of blood for two replicates of measuring haemoglobin levels in blood. The time was recorded when each sow was measured for haemoglobin levels indicating that it took on average about two minutes to record each sow for both haemoglobin measures.

Haemoglobin levels in sows were 106.2 to 107.9 g/L for the duplicate measures (Table B1). The coefficient of variation was low with values around 8%. In comparison, the coefficients of variation were considerably higher for sow weight and fatness depth in sows. Larger variation in sow weight is expected due to the large parity effects for sow weight. Fat depth recorded in sows has been found to be more variable in Australian data sets in comparison to European data sets (Gilbert *et al.*, 2012).

A maximum difference between two replicates of a specific measure of 10% of the mean is often used as a criterion to evaluate the accuracy of a measurement. Only measurements from one sow exceeded this threshold value, haemoglobin measures in all other sows achieved this criterion. The correlation between both haemoglobin measurements was 0.89 and the close association between both measurements is further illustrated in Figure B1.

Table B31. Data statistics for sow traits.

Variable	N	Mean	SD	CV	Min	Max
Sow weight (kg)	47	249.4	42.32	17.0	180	316
Sow fat depth (mm)	47	21.6	5.127	23.7	13.5	39.2
Haemoglobin - 1st measure (g/L)	47	106.2	9.95	9.37	79	128
Haemoglobin - 2nd measure (g/L)	47	107.9	8.48	7.86	85	122
Average haemoglobin level (g/L)	47	107.1	8.96	8.36	82.5	123

SD, standard deviation; CV, coefficient of variation; Min and Max, minimum and maximum.

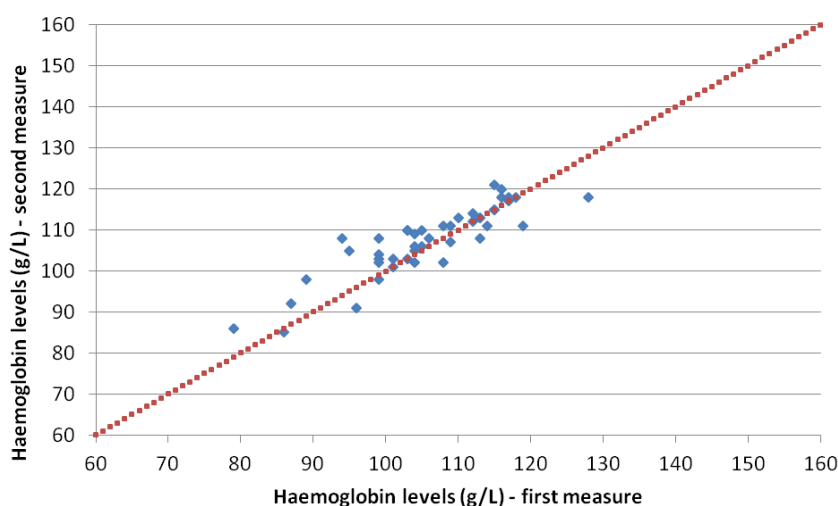


Figure B6. Plot of first versus second measure of haemoglobin levels recorded in sows

Recording haemoglobin levels in piglets

Shortly after farrowing, two male and two female piglets were chosen based on their birth weight. Each litter was represented by a light, two medium and one heavy piglet. Two blood samples were collected from the ear and two blood samples from the cut-off tail of one-day old piglets. The design was fully cross-classified within each litter in regard to the order of haemoglobin measurements from each blood-collection site on the piglet. These piglets had not received any iron injection prior to recording haemoglobin levels. On average it took about four minutes to record all four haemoglobin measures on each piglet.

Duplicate haemoglobin levels in piglets were recorded at two locations using either the ear or the cut-off tail to collect droplets of blood. Mean haemoglobin levels were higher for measurements taken at the ear in comparison to the measurement based on the tail (Table B2). The average haemoglobin level based on the first two ear measurements was 88.6 g/L in comparison to 83.6 g/L for the equivalent measurement taken at the tail. Analysis of variance using a generalised linear model showed that location was the only significant effect for haemoglobin levels in piglets in these data.

The coefficients of variation varied from 16 to 18% for measures taken on the ear in comparison to coefficients of variation ranging from 21 to 23% for measures based on the tail. The higher coefficients of variation for haemoglobin measures taken from the tail indicate a larger measurement error for this site to collect blood droplets.

Measurements taken a few minutes later on the pig increased the mean haemoglobin levels from 88.6 g/L to 92.7 g/L for measurements taken at the ear of the piglet. An increase of 5.1 g/L may be of biological importance although this increase was statistically not significant ($P: 0.55$) since it was only observed at the ear. The order of measurements did not increase the mean tail measurement, which may be expected given that the tail has been removed from the animal.

Handling piglets including cutting the tail poses a certain level of stress to the animal, which has been shown to increase haemoglobin levels (Dubreuil *et al.* 1993). However, the increase in haemoglobin levels observed in the current study of about 5 g/L was lower than the increase in haemoglobin levels of about 20 g/L observed by Dubreuil *et al.* (1993) following a five-minute snare.

Table B32. Data statistics for haemoglobin levels in piglets.

Variable	N	Mean	Std Dev	CV	Min	Max
<i>Ear was first location to collect blood</i>						
Piglet birth weight	89	1.61	0.32	0.20	0.53	2.40
1st haemoglobin measure - ear	94	88.5	15.5	0.17	50.0	130.0
2nd haemoglobin measure - ear	94	88.7	15.9	0.18	54.0	127.0
3rd haemoglobin measure - tail	94	81.6	19.1	0.23	39.0	134.0
4th haemoglobin measure - tail	94	83.5	18.0	0.22	43.0	132.0
Average haemoglobin level - ear	94	88.6	15.4	0.17	52.0	128.5
Average haemoglobin level- tail	94	82.6	17.7	0.21	41.5	133.0
<i>Tail was first location to collect blood</i>						
Piglet birth weight	88	1.60	0.34	0.21	0.55	2.38
1st haemoglobin measure - tail	92	82.3	19.0	0.23	27.0	126.0
2nd haemoglobin measure - tail	92	85.0	17.6	0.21	28.0	125.0
3rd haemoglobin measure - ear	92	93.5	16.8	0.18	53.0	146.0
4th haemoglobin measure - ear	92	91.9	15.2	0.16	54.0	138.0
Average haemoglobin level - tail	92	83.6	17.6	0.21	27.5	125.5
Average haemoglobin level - ear	92	92.7	15.4	0.17	53.5	138.0

SD, standard deviation; Min and Max, minimum and maximum; CV, coefficient of variation

The Pearson correlation between duplicate measurements was highest (0.92) for haemoglobin levels based on the two first measures of the ear. This correlation dropped to 0.86 when the two measurements at the ear were taken after the tail had been cut off. The correlations between duplicate measures based on blood droplets collected from the tail were 0.85 and 0.83 for the first and second pair of duplicates recorded on the tail. The higher repeatability of measurements based on the ear versus the tail is illustrated in Figure B2 and Figure B3.

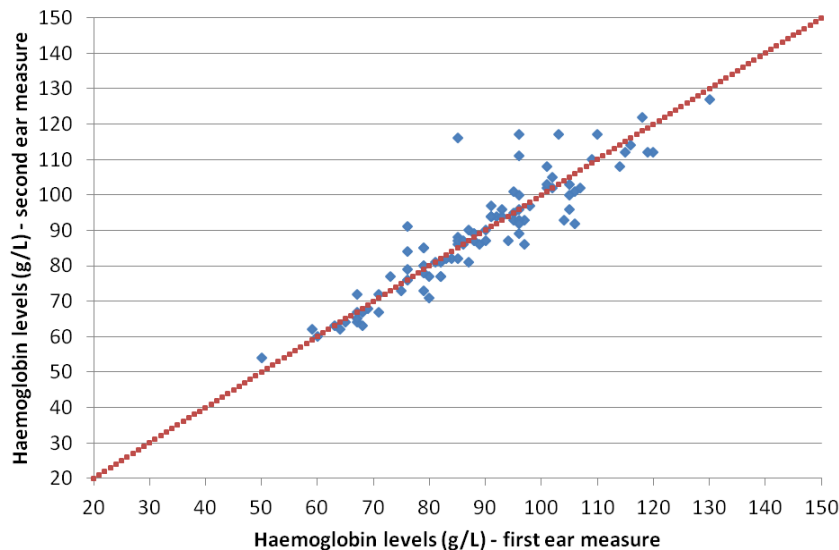


Figure B7. Plot of first versus second ear measure of haemoglobin levels recorded in piglets.

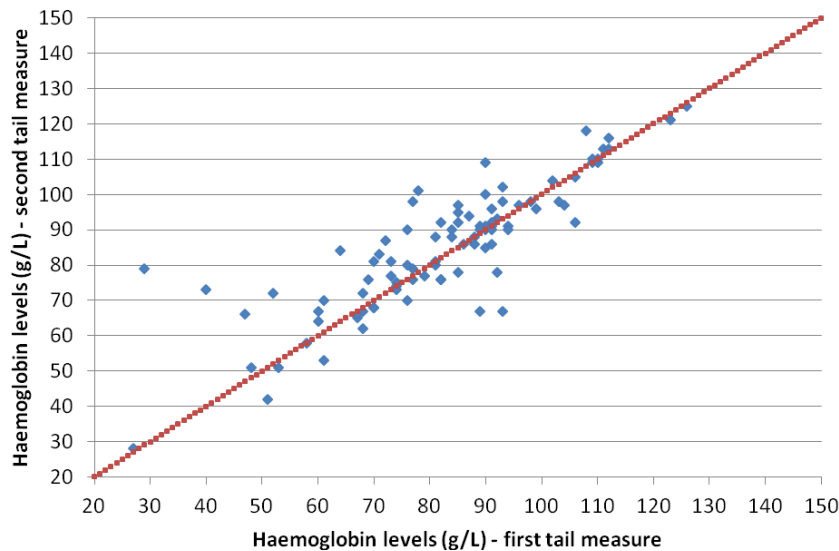


Figure B8. Plot of first versus second tail measure of haemoglobin recorded in piglets.

Recording haemoglobin levels in growing pigs

Haemoglobin measurements were also evaluated on 50 male and 48 female growing pigs from one maternal line. Most pigs were recorded on one day (N=84), while the remaining pigs were recorded on the subsequent day. The recording time of haemoglobin levels was much more variable for growing pigs recorded at 20 weeks of age shortly before slaughter as the larger animal had to be secured for the collection of blood droplets from the ear.

The mean haemoglobin level of these pigs was 109 g/L based on the average of both measurements (Table B3). Using a replicate value reduced the variation slightly in comparison to the single measurements. The mean difference between both haemoglobin measures was small with 2.25 g/L although there was considerable variation in the difference between both haemoglobin measures observed for individual pigs.

Table B33. Data statistics for haemoglobin levels in growing pigs

Variable	N	Mean	SD	CV	Min	Max
Live weight (kg)	98	74.21	9.29	12.5	50	103
1 st haemoglobin measure (g/L)	98	109.8	11.7	10.6	70	153
2 nd haemoglobin measure (g/L)	97	107.9	11.5	10.7	71	137
Average haemoglobin level (g/L)	97	109.0	10.4	9.55	83	136

SD, standard deviation; Min and Max, minimum and maximum; CV, coefficient of variation

A maximum difference between two replicates of a specific measure of 10% was not achieved for 13% of pigs for which the difference between both haemoglobin measures exceeded 11 g/L. The Pearson correlation between these two measures was 0.68. This comparably low correlation between the two measurements was due to some extreme outliers for one measurement as indicated in Figure B4.

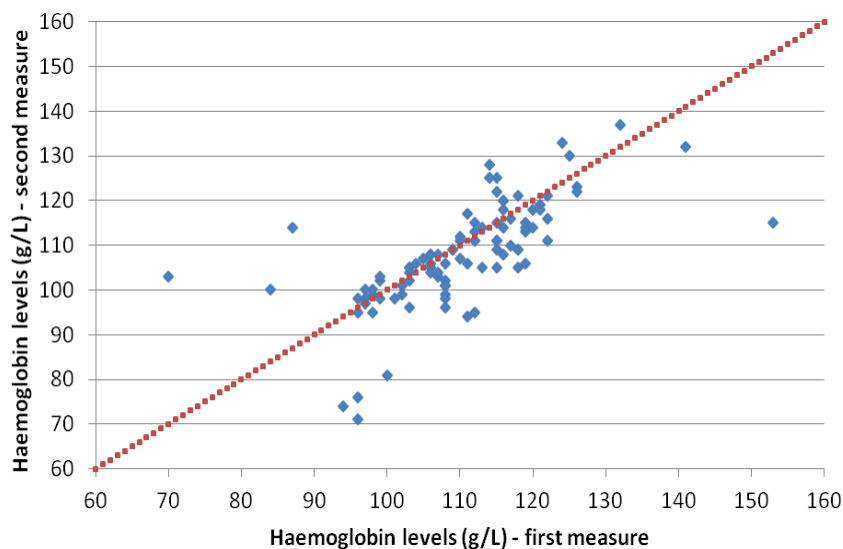


Figure B9. Plot of first versus second measure of haemoglobin levels recorded in growing pigs.

A sampling comparison between the ear and the tail for testing of haemoglobin levels in piglets

Haemoglobin (Hb) testing on farm is a new technology within the pig industry that can be used for improving survivability in piglets (Rootwelt *et al.*, 2012) and as a selection criterion for iron content in pork (Hermesch and Jones, 2012). The testing requires a 10µL sample of blood to be collected from the young piglet. The most logical time to collect this sample is at litter processing when piglets are already being handled, thereby minimising stress on the piglet. The aims of the study were to determine whether the location from which the blood sample was collected from the piglet (ear versus tail) influenced Hb measurement and whether the order of collection (ear or tail first) had any impact on Hb measurement.

Haemoglobin levels were measured on 186 twelve-hour old piglets (Large White and Landrace, PrimeGro™ Genetics, Corowa, NSW) prior to iron injection. Litters were represented by two males and two females (one light, two medium and one large piglet). Each piglet had four blood samples taken, two ear samples and two tail samples. Piglets were alternated as to which measurement was to be taken first. A HemoCue® Hb201+ was used to measure Hb concentration in the four samples immediately after collection. This machine has been previously tested to show accurate results on farm in sows when compared to laboratory analysis (Gannon *et al.*, 2011). Small droplets of blood collected using curettes were taken from both the ear of the piglet and the piglet's tail area, after the tail had been cut and were inserted into the HemoCue® for measurement: both tests were done twice. This process took four minutes per piglet. Data was analysed by analysis of variance for the main effects of location, order and their interactions using GenStat (VSN International, Oxford UK). A Pearson's correlation was also acquired to obtain repeatability of the two samples taken at each location.

Table B34. Influence of blood sample collection location and order of sampling on Hb concentrations

	Ear		Tail		Significance		
	1st (n=94)	2 nd (n=92)	1st (n=92)	2 nd (n=94)	Location	Order	Location x Order
Hb (g/L)	88.6	92.7	83.6	82.6	<0.001	0.40	0.13
SD	15.4	15.4	17.7	17.6			
CV	0.17	0.17	0.21	0.21			
SED					1.72	1.72	2.43

SED, standard error of difference, SD, standard deviation, CV, coefficient of variation

Haemoglobin concentration was significantly higher in blood collected from the ear (90.7g/L) compared to the tail (83.1 g/L). The coefficients of variation were higher in the tail (21%) than the ear (17%) indicating larger measurement errors (Table B5). The order of sample collection did not significantly influence Hb concentration although the interaction of location and order showed a trend towards significance due to the increase in Hb levels at the ear from the first to second sample. The second Hb sample collected at the ear was taken after the tail was cut. The stress imposed by cutting the tail may have increased Hb levels for the second ear sample. The Pearson's correlations showed that the duplicate samples collected from the ear were highly correlated,

regardless of order of sampling (ear sampled first – correlation of 0.92, ear sample second – correlation of 0.86). In comparison, lower correlations between duplicates were found for tail samples (tail sampled first – correlation of 0.83, tail sampled second – correlation of 0.84).

Blood sampling from the ear of the piglet resulted in higher mean Hb concentrations and more consistent results when compared to samples obtained from the tail. Using the ear of the piglet to obtain a blood sample for Hb testing could be easily implemented by industry. This would allow Hb levels to be used as a trait for selection and management to increase survivability in piglets and iron content in pork.

Within-litter variability in haemoglobin levels of piglets

Four haemoglobin measures were taken per piglet with two measurements at either the ear or the tail of the piglet. Four piglets were recorded per litter. The data included 47 sows from two maternal lines with 186 piglets.

Pedigree and other performance data available from the herd recording system at Rivalea were used to evaluate fixed effects for haemoglobin levels in piglets using the SAS procedures GLM and MIXED. Each of the four individual haemoglobin measures was treated as a separate dependent variable. Sex of the piglet was the only significant fixed effects. Other effects evaluated included parity of the sow, breed of the piglet (3 levels) or the sow (2 levels) and location of recording (ear, tail).

A number of linear covariables were evaluated as well and weight of the sow prior to farrowing was approaching significance at the 5% level. This covariable is partly confounded with parity of the sow, which was not significant. Fat depth of the sow prior to farrowing, litter size of the birth litter, piglet birth weight and haemoglobin levels in sows fitted as linear covariables were not significant.

In addition, piglet birth weight was analysed in order to compare results between this well-known trait and haemoglobin levels. Breed of the sow (P value: 0.03) and parity (P value: 0.01) were significant fixed effects for piglet weight at birth. These effects have previously been identified as significant effects for piglet weight at birth.

The random effect of sow was evaluated with the SAS procedure MIXED fitting significant fixed effects outlined above. The variance due to sow along with the residual variances are shown for each trait in Table B6. The random effect of the sow accounted for 34 to 39 % of the total variation for haemoglobin measures. In comparison, sow explained 27% of the variation for piglet weight at birth in these data. The sow effect represents permanent environmental effects of the sow and genetic effects which cannot be distinguished in these data. These analyses showed that the sow affected haemoglobin levels in piglets significantly.

Table B35. Variance components along with proportion of total variance due to sow.

Trait	Sow	Residual variance	Total variance	Sow variance/ Total variance
1 st haemoglobin measure	104.4	205.5	309.5	0.34
2 nd haemoglobin measure	112.9	173.0	285.9	0.39
3 rd haemoglobin measure	112.0	212.1	324.1	0.35
4 th haemoglobin measure	102.8	157.7	260.5	0.39
Piglet birth weight	0.027	0.072	0.099	0.27

Phenotypic analyses of haemoglobin levels in sows and piglets as well as traits describing sow performance and condition

Description of data

Haemoglobin levels in sows were 110.9 and 114.5 g/L in two herds (Table B7). The haemoglobin levels in sows were both higher in comparison to the pilot study of this project which had a mean haemoglobin level of 107.1 (Table B1). A haemoglobin level of 100 g/L has been recommended as the minimum level for haemoglobin levels in sows in a Danish study (Polsen, 2006 cited in Gannon et al. 2011; APSA 2011). A significant proportion of sows had a haemoglobin level below the recommended level of 100 g/L in all herds and haemoglobin levels should be increased.

Haemoglobin levels in piglets were slightly lower than sow levels for both herds with values of 102.3 and 107.2 g/L. These values were both higher than haemoglobin levels of around 90 g/L in the pilot study of this project (Table B2). There were some extreme haemoglobin levels for some sows or piglets. These extreme values were confirmed by taking repeated measures of the animal.

These results show that haemoglobin levels in sows and piglets differ between herds. Herds with higher haemoglobin levels in sows also had higher haemoglobin levels in piglets. Further, haemoglobin levels in sows and their piglets were positively associated within both herds. Pearson correlations between haemoglobin levels in sows and the average haemoglobin level of the litter based on the three individual piglet measures were consistent between both herds with correlations of 0.13 and 0.14. Higher haemoglobin levels in sows were associated with higher haemoglobin levels in piglets. This finding offers opportunities to target intervention strategies to maintain adequate haemoglobin levels in sows with beneficial effects on haemoglobin levels in piglets.

The weight and fat depth of sows was recorded in Herd B for sows from different parities. The low fat depth of 18.7 mm was unexpected and low values for fat depth were often measured repeatedly to confirm low values. It was noted by the breeder that a subjective conformation score was not a good indicator of actual fat depth measures for the majority of sows.

Table B36. Data statistics for variables recorded on sows and piglets including haemoglobin levels (Hb, g/L) (SD: Standard deviation; CV: Coefficient of variation)

Variable	N	Mean	SD	CV	Min	Max
<i>Herd A</i>						
Hb-S – sows prior to farrowing	185	110.9	16.93	15.3	73.0	170.0
Hb-iP – individual piglets at birth	495	102.3	20.76	20.3	11.0	250.0
Hb-aP – average of 3 piglet measures	165	102.3	13.76	13.5	67.7	148.0
Number born alive (NBA)	191	11.04	2.89	26.2	4.0	20.0
Stillborn (SB)	191	0.99	1.44	145.5	0.0	7.0
Average piglet birth weight (ABW)	135	1.51	0.24	15.8	0.9	2.3
<i>Herd B</i>						
Hb-S – sows prior to farrowing	287	114.5	12.80	11.18	70.0	150.0
Hb-iP – individual piglets at birth	831	107.1	22.36	20.89	45.0	196.0
Hb-aP – average of 3 piglet measures	277	107.1	15.40	14.38	61	163
Sow weight prior to farrowing (SWt)	288	258.7	37.20	14.38	128	348
Sow fat depth prior to farrowing (SFD)	269	18.72	3.64	19.43	11.0	33.0
Number born alive (NBA)	277	10.84	2.70	24.89	3.00	17.00
Stillborn (SB)	277	0.63	0.90	142.74	0.00	5.00
Average piglet birth weight (ABW)	277	1.53	0.286	18.66	0.00	2.37
Individual piglet birth weight (IBW)	831	1.54	0.40	25.84	0.45	2.60

Associations between haemoglobin levels and sow reproductive performance

Associations between traits were evaluated using Pearson correlations which are shown for both herds in Table B8. Correlations between traits which were consistent between herds or between trait groups are highlighted in bold. These associations have a greater certainty despite the low number of records available so far for these highly variable traits which were not adjusted for systematic effects.

Haemoglobin levels in sows and piglets were positively correlated which is further reflected in corresponding associations with other traits. Haemoglobin levels in sows and piglets were negatively correlated with a number of weight traits of the sow and the litter. Selection and production emphasis on higher average birth weight to improve survival and performance of piglets is therefore associated with lower haemoglobin levels in sows and piglets. Further, larger litter size was associated with lower haemoglobin levels in piglets in both herds. Again, indicating that higher productivity is associated with lower haemoglobin levels in piglets which have been shown to be associated with reduced survival (Rootwelt et al., 2012). Associations between numbers of still born piglets were predominantly negative for trait combinations observed in both herds supporting the hypothesis that higher haemoglobin levels in sows and piglets favour survival of piglets.

These associations will be further investigated and extended to genetic analyses once more data have become available from both herds.

Table B37. Pearson correlations between haemoglobin levels and sow reproductive traits for herd B (above diagonal) and herd A (below diagonal).

	Hb-S	Hb-aP	SWt	SFD	BA	SB	ABW
Hb-S		0.14	-0.29	0.04	-0.23	-0.10	-0.13
Hb-aP	0.09		-0.06	-0.07	-0.16	-0.11	0.00
SWt				0.42	0.11	0.28	0.21
SFD					-0.04	0.09	0.01
NBA	0.18	-0.08				-0.05	-0.28
SB	-0.07	0.00			-0.08		-0.01
ABW	-0.17	-0.19			-0.58	-0.14	

* for abbreviations of traits see Table B7.

The effect of parity and breed on haemoglobin levels in sows

The effects of parity and breed were investigated in first analyses using the GLM procedure (SAS, 2011). There were no statistically and biologically significant differences between Large White and Landrace sows for all three traits. Sows from parity 1 to 9 were present in the current data and parities of 6 and above were grouped together due to the low number of records in the higher parities. Parity was highly significant (P-value < 0.001) for all three traits and least squares means are shown in Table B9. The model only included parity in these first analyses.

The weight of sows shortly prior to farrowing increased continuously from 226 kg in gilts to 333 kg for older sows with 6 or more parities. Backfat was lowest in second parity sows with 17.3 mm and increased in older sows. In contrast, haemoglobin levels decreased continuously with higher parities indicating that iron levels in blood getting depleted as sows mature. The effect of parity explained 68, 19 and 9% of the variation in sow weight, sow fat depth and sow haemoglobin levels, respectively.

Fat depth of sows was as significant linear covariable for sow weight and sow haemoglobin levels. These two traits increased by 1.91 kg per mm and by 1.07 g/L per mm fat depth in sows.

Table B38. The effect of parity on sow traits (se: standard error)

Parity	Sow weight (se)	Sow fat depth (se)	Sow haemoglobin level (se)
1	226 (2.5)	18.3 (0.40)	121 (1.85)
2	256 (4.0)	17.3 (0.71)	113 (2.89)
3	274 (4.9)	19.9 (0.78)	116 (3.63)
4	293 (7.1)	20.1 (1.13)	114 (5.28)
5	308 (12.3)	24.0 (1.96)	108 (9.13)
6 and above	333 (8.1)	23.4 (1.28)	104 (5.98)

Implications & Recommendations

The collection of droplets of blood of sows staying in farrowing crates has worked well and can be recommended. The procedure can easily be done in the shed when sows are placed in the farrowing crate. The high repeatability indicates that one measure is sufficient once the recording procedure has been established on farm for each operator by taking repeated measures initially.

Haemoglobin levels can be recorded in one-day old piglets using drops of blood from the ear. Measurements were highly repeatable in the current study and one measure should be sufficient once an operator has become familiar with the testing procedure on farm.

It is possible to use ear pricking as a methodology to collect drops of blood for measuring haemoglobin levels. However, growing pigs will have to be secured by a snout rope during the collection process to ensure the safety of the operator. The correlation between repeated haemoglobin measurements was lower than corresponding correlations between haemoglobin measures obtained in sows and piglets. It is recommended to use two replicates for the measurement of haemoglobin levels in growing pigs with the HemoCue Hb201⁺ system on farm.

Herds with higher mean haemoglobin levels in sows also had higher mean haemoglobin levels in piglets. Within herds, higher haemoglobin levels in sows were associated with higher haemoglobin levels in piglets. Further, the random effect of sow was an important effect for haemoglobin levels in piglets. These results offer opportunities to target selection and intervention strategies to maintain adequate haemoglobin levels in sows with beneficial effects on haemoglobin levels in piglets. The simple measurement procedure developed in this study should be used by breeders and producers to record and monitor haemoglobin levels in sows and piglets on farm regularly.

Fat depth levels of sows were low demonstrating the changed physiology of modern sows. It was noted by the breeder that a subjective conformation score was not a good indicator of actual fat depth measures for the majority of sows. Therefore, fat depth and weight measurements of sows should be monitored on farms.

Technical summary

Introduction

Survival of piglets is an important welfare trait with significant economic importance. Higher haemoglobin levels have been shown to be phenotypically associated with improved survival. However, there is a paucity of studies investigating genetic associations between haemoglobin levels and survival of piglets and fecundity of sows. Reliable on-farm records of haemoglobin levels in sows and piglets are required to investigate phenotypic and genetic associations between haemoglobin levels and piglet survival and sow reproductive performance.

Recording haemoglobin levels in sows, piglets and growing pigs

Evaluation of recording procedures for haemoglobin levels in sows prior to farrowing and one-day old piglets were based on 47 sows from two maternal lines. These sows represented first (15 sows), second (15 sows) and third (17 sows) parity sows. Sows were ear pricked on entry to the farrowing house to collect drops of blood for two replicates of measuring haemoglobin levels in blood. The time was recorded when each sow was measured for haemoglobin levels indicating that it took on average about two minutes to record each sow for both haemoglobin measures.

Haemoglobin levels in sows were 106.2 to 107.9 g/L for the duplicate measures. The correlation between both haemoglobin measurements was 0.89. Shortly after farrowing, two male and two female piglets were chosen based on their birth weight. Each litter was represented by a light, two medium and one heavy piglet. Two blood samples were collected from the ear and two blood samples from the cut-off tail of one-day old piglets. The design was fully cross-classified within each litter in regard to the order of haemoglobin measurements from each blood-collection site on the piglet. These piglets had not received any iron injection prior to recording haemoglobin levels. On average it took about four minutes to record all four haemoglobin measures on each piglet.

Duplicate haemoglobin levels in piglets were recorded at two locations using either the ear or the cut-off tail to collect droplets of blood. Mean haemoglobin levels were higher for measurements taken at the ear in comparison to the measurement based on the tail (Table B2). The average haemoglobin level based on the first two ear measurements was 88.6 g/L in comparison to 83.6 g/L for the equivalent measurement taken at the tail.

Measurements taken later on the pig increased the mean haemoglobin levels from 88.6 g/L to 92.7 g/L for measurements taken at the ear of the piglet. An increase of 5.1 g/L may be of biological importance although this increase was statistically not significant ($P=0.55$) since it was only observed at the ear. The order of measurements did not increase the mean tail measurement, which may be expected given that the tail has been removed from the animal. Handling piglets including cutting the tail poses a certain level of stress to the animal, which has been shown previously to increase haemoglobin levels. It should be evaluated whether this on-farm measure of haemoglobin could be used as a measure of acute stress.

The Pearson correlation between duplicate measurements was highest (0.92) for haemoglobin levels based on the two first measures of the ear. This correlation dropped to 0.86 when the two measurements at the ear were taken after the tail had been cut off. The correlations between duplicate measures based on blood droplets collected from the tail were 0.85 and 0.83 for the first and second pair of duplicates recorded on the tail.

Haemoglobin measurements were also evaluated on 50 male and 48 female growing pigs from one maternal line. Most pigs were recorded on one day ($N=84$), while the remaining pigs were recorded on the subsequent day. The recording time of haemoglobin levels was much more variable for growing pigs as the larger animal had to be secured for the collection of blood droplets from the ear.

Haemoglobin levels in piglets are affected by the sow effect

Pedigree and other performance data were used to evaluate fixed effects for haemoglobin levels in piglets using the SAS procedures GLM and MIXED. Each of the four individual haemoglobin measures was treated as a separate dependent variable. Sex of the piglet was the only significant fixed effects. Other effects evaluated included parity of the sow, breed of the piglet (3 levels) or the sow (2 levels) and location of recording (ear, tail).

The random effect of sow was evaluated with the SAS procedure MIXED fitting significant fixed effects outlined above. The variance due to sow along with the residual variances are shown for each trait in Table B6. The random effect of the sow accounted for 34 to 39 % of the total variation for haemoglobin measures. In comparison, sow explained 27% of the variation for piglet weight at birth in these data. The sow effect represents permanent environmental effects of the sow and genetic effects which cannot be distinguished in these data. These analyses showed that the sow affected haemoglobin levels in piglets significantly.

Analyses of haemoglobin levels in sows and piglets and traits describing sow condition and fecundity

Haemoglobin levels in sows were 110.9 and 114.5 g/L in two herds. A haemoglobin level of 100 g/L has been recommended as the minimum level for haemoglobin levels in sows in a Danish study. A significant proportion of sows had a haemoglobin level below the recommended level of 100 g/L in all herds and haemoglobin levels should be increased.

Haemoglobin levels in piglets were slightly lower than sow levels for both herds with values of 102.3 and 107.2 g/L. These values were both higher than haemoglobin levels of around 90 g/L in the pilot study of this project.

These results show that haemoglobin levels in sows and piglets differ between herds. Herds with higher haemoglobin levels in sows also had higher haemoglobin levels in piglets. Further, haemoglobin levels in sows and their piglets were positively associated within both herds. Pearson correlations between haemoglobin levels in sows and the average haemoglobin level of the litter based on the three individual piglet measures were consistent between both herds with correlations of 0.13 and 0.14. Higher haemoglobin levels in sows were associated with higher haemoglobin levels in piglets. This finding offers opportunities to target intervention strategies to maintain adequate haemoglobin levels in sows with beneficial effects on haemoglobin levels in piglets.

The weight and fat depth of sows was recorded in Herd B for sows from different parities. The low fat depth of 18.7 mm was unexpected and low values for fat depth were often measured repeatedly to confirm low values. It was noted by the breeder that a subjective conformation score was not a good indicator of actual fat depth measures for the majority of sows.

Haemoglobin levels in sows and piglets were positively correlated which is further reflected in corresponding associations with other traits. Haemoglobin levels in sows and piglets were negatively correlated with a number of weight traits of the sow and the litter. Selection and production emphasis on higher average birth weight to improve survival and performance of piglets is therefore associated with lower haemoglobin levels in sows and piglets. Further, larger litter size was associated with lower haemoglobin levels in piglets in both herds indicating that higher productivity is associated with lower haemoglobin levels in piglets. Associations between numbers of still born piglets were predominantly negative for trait combinations observed in both herds supporting the hypothesis that higher haemoglobin levels in sows and piglets favour survival of piglets.

Effect of parity and breed on haemoglobin levels in sows

The effects of parity and breed were investigated in first analyses using the GLM procedure. There were no statistically and biologically significant differences between Large White and Landrace sows for all three traits. Sows from parity 1 to 9 were present in the current data and parities of 6 and above were grouped together due to the low number of records in the higher parities. Parity was highly significant (P -value < 0.001) for all three traits.

The weight of sows shortly prior to farrowing increased continuously from 226 kg in gilts to 333 kg for older sows with 6 or more parities. Backfat was lowest in second parity sows with 17.3 mm and increased in older sows. In contrast, haemoglobin levels decreased continuously with higher parities indicating that iron levels in blood getting depleted as sows mature. The effect of parity explained 68, 19 and 9% of the variation in sow weight, sow fat depth and sow haemoglobin levels, respectively.

Fat depth of sows was as significant linear covariable for sow weight and sow haemoglobin levels. These two traits increased by 1.91 kg per mm and by 1.07 g/L per mm fat depth in sows.

References

- Auvigne, V., H. Perrin, A. Laval, B. Bertucat, and V. Normand. 2010. Anaemia in the hyperprolific sow: Effect of injectable iron administration and relation with fattening score. Page 213 in 21st IPVS Congress. Vancouver, Canada.
- Bunter, K. L., C. R. G. Lewis, S. Hermes, R. Smits, and B. G. Luxford. 2010. Maternal capacity, feed intake and body development in sows. in Proc. WCGALP, Leipzig, Germany.
- Capozzalo, M., I. Williams, H. Payne, and B. Frey. 2009. Second 200 mg doses of iron dextran at two weeks does not improve growth or haemoglobin level of piglets regardless of parity. Page 28 in School of Animal Biology, Faculty of Natural and Agricultural Sciences. Vol. Honours. University of Western Australia, Perth.
- Dubreuil, P., C. Farmer, Y. Couture, and D. Petitclerc. 1993. Hematological and biochemical changes following an acute stress in control and somatostatin immunized pigs. *Can. J. Anim. Sci.* 73(2):241-252.
- Dwyer, C. M., J. M. Fletcher, and N. C. Stickland. 1993. Muscle cellularity and postnatal growth in the pig. *Journal of Animal Science* 71:3339-3343.
- Dwyer, C. M., N. C. Stickland, and J. M. Fletcher. 1994. The influence of maternal nutrition on muscle fiber number development in the porcine fetus and on subsequent postnatal growth. *Journal of Animal Science* 72:911-917.
- Fahmy, M. and C. Bernard. 1978. Selection for high haemoglobin level in piglets to develop an anemic-resistant line of swine. *Livestock Production Science* 5:225-230.
- Gannon, K. M., B. Frey, H. G. Payne, and B. P. Mullan. 2011. A survey of sow blood haemoglobin by parity in Western Australia. Manipulating pig production XIII. Proceedings of the Thirteenth Biennial Conference of the Australasian Pig Science Association. Australian Pig Science Association (Inc).
- Gedde-Dahl, T. and A. Helgebostad. 1971. Genetic aspects of resistance to anaemia in mink red raw fish. *Acta Agriculturae Scandinavica* 21:284-292.
- Gilbert, H., J. P. Bidanel, Y. Billon, H. Lagant, P. Guillouet, P. Sellier, J. Noblet, and S. Hermes. 2012. Correlated responses in sow appetite, residual feed intake, body composition, and reproduction after divergent selection for residual feed intake in the growing pig. *Journal of Animal Science* 90(4):1097-1108.
- Hermes, S. and R. M. Jones. 2012. Genetic parameters for haemoglobin levels in pigs and iron content in pork. *Animal* 6(12):1904-1912.
- Jones, R. M. and S. Hermes. 2010. First genetic analysis of blood haemoglobin levels and iron content in pork. Pages 17-24 in 2010 AGBU Pig Genetics Workshop Notes. S. Hermes and K. Dobos, ed. AGBU, Armidale.
- Larzul, C., L. Lefaucheur, P. Ecolan, J. Gogué, A. Talmant, P. Sellier, P. Le Roy, and G. Monin. 1997. Phenotypic and genetic parameters for longissimus muscle fiber characteristics in relation to growth carcass, and meat quality traits in Large White pigs. *Journal of Animal Science* 75:3126-3127.
- Payne, H. G. 2009. How does the pre-weaning environment affect gut structure and function, and lifetime performance of the pig? Page 181 in Faculty of Health Sciences, School of Veterinary and Biomedical Sciences. Vol. Mather of Philosophy of Murdoch University. Murdoch University.
- Rootwelt, V., O. Reksen, W. Farstad, and T. Framstad. 2012. Blood variables and body weight gain on the first day of life in crossbred pigs and importance for survival. *Journal of Animal Science* 90(4):1134-1139.

Fostering adoption of research results in the Australian pig industry

Fostering adoption of research results has always been an integral part of R&D conducted in pig genetics at AGBU. The AGBU pig genetics workshops held every two years in Armidale are the main event to discuss research results with representatives of the main pig breeding companies in Australia. In total, 12 papers were presented at the workshop as shown below, which are available on the AGBU web pages at: http://agbu.une.edu.au/pig_genetics/workshop2012.html. The publicity around the workshop led to an increase in the number of visits to site in September and October 2012 (Figure1).

Pig Genetics Workshop, October 24-25, 2012

Table of Contents

H-U. Graser, **Looking back into the future**, AGBU, pp1-6. ([View](#)).

C. Moran, **Looking back to move forward – a personal perspective on pig molecular genetics from RFLPs to nextgen sequencing**, University of Sydney, pp 7-12. ([View](#))

A.A. Swan, **Genomic selection in the Australian sheep industry**, AGBU, pp 13-18. ([View](#))

S. Hermesch ¹, K.M. Tickle ² and A.K. Lealiifano ², **Variation in weights of primal pork cuts**, ¹ AGBU, ² Rivalea (Australia), 19-22. ([View](#))

P. Tabuaciri, K.L. Bunter and H-U. Graser, **Thermal imaging as a potential tool for identifying piglets at risk**, AGBU, 23-30. ([View](#))

S. Hermesch ¹ and K.M. Tickle ², **Recording haemoglobin levels in sows, piglets and growing pigs on farm**, ¹ AGBU, ² Rivalea (Australia), 31-38. ([View](#))

K.L. Bunter, **Breeding sows better suited to group housing**, AGBU, 39-44. ([View](#))

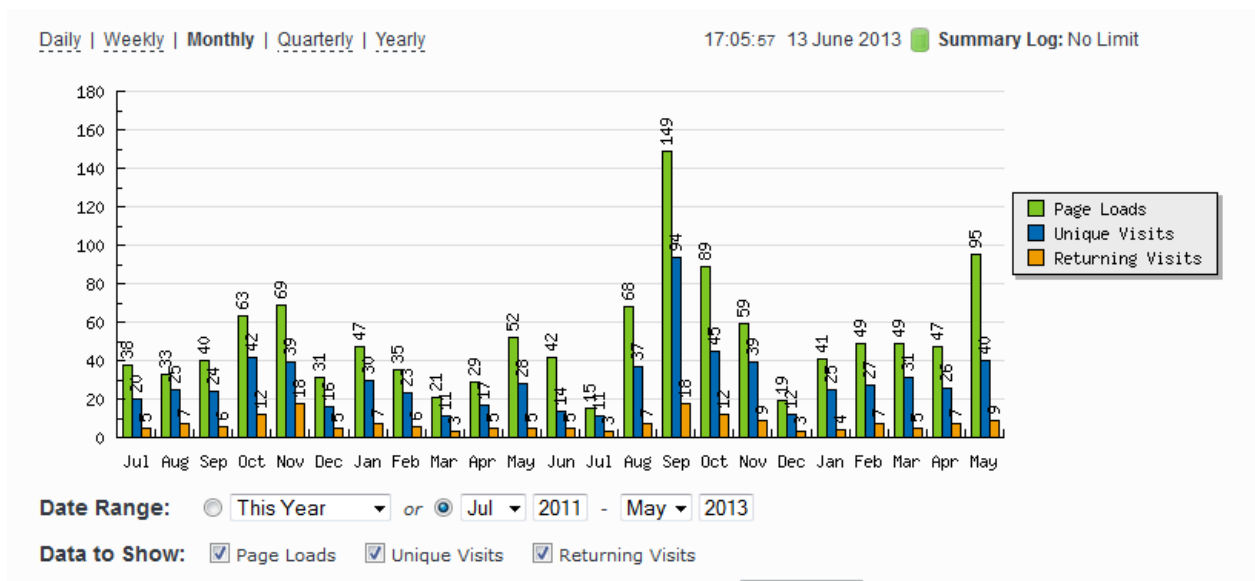
S. Hermesch C.I. Ludemann ² and P.R. Amer ², **PigEV – a new tool to derive economic values for pigs**, ¹ AGBU, ² AbacusBio Ltd, 45-52. ([View](#))

L. Li and S. Hermesch, **Genotypes differ in their response to variation in environments experienced by pigs on farm**, AGBU, 53-60. ([View](#))

S.Z.Y. Guy ¹, P.C. Thomson ¹ and S. Hermesch ², **Breeding tolerant pigs for health and productivity**,¹ University of Sydney, ² AGBU, 61-68. ([View](#))

S. Hermesch, **Breeding pigs with improved disease resilience**, AGBU, 69-72. ([View](#))

J.R. Walters, **Genetic analyses of traditional breeds – the UK experience**, UPB Genetic World, 73-87. ([View](#))



Visits to AGBU pig genetics workshop web pages from July 2011 until May 2013.

Publications arising

Industry publications and presentations

Book

Hermesch, S. & Dobos, K. 2012. 2012 AGBU Pig Genetics Workshop notes, October 24-25, 2012. Animal Genetics and Breeding Unit, Armidale, NSW, pp. 87.

Book chapters and Newsletter articles

Hermesch, S. & Tickle, K. M. 2012. Recording haemoglobin levels in sows, piglets and growing pigs on farm. In: Hermesch, S. & Dobos, K. (eds.) 2012 AGBU Pig Genetics Workshop Notes. Armidale: AGBU, p. 31-38.

Hermesch, S., Tickle, K. M. & Lealiifano, A. K. 2012. Variation in weights of primal pork cuts. In: Hermesch, S. & Dobos, K. (eds.) 2012 AGBU Pig Genetics Workshop Notes. Armidale: AGBU, p. 19-22.

Morgan, J & S. Hermesch. 2013. Recording haemoglobin levels on farm is simple. *PigBytes* is a newsletter from the pig industry teams at NSW DPI, Victorian DEPI and Queensland DAFF. Editor: J. Morgan, Issue 18, July 2013.

Web-supported seminar

Hermesch, S. & Jones R. M. 2012. Genetic analyses of haemoglobin levels in pigs and iron content in pork. AGBU web-supported seminar, 15 February 2012, available at http://agbu.une.edu.au/pig_genetics/pdf/Presentations/Hermesch-Jones-Iron-Pork-2012.pdf

Journal paper

Lewis, C. R. G. & Hermesch, S. 2013. Genetic parameters and phenotypic trends in the mean and variability of number of stillborn piglets and changes in their relationships with litter size and gestation length. *Animal Production Science*, 53, 395-402.

Refereed conference paper

Lewis, C. R. G., Bunter, K. L. & Hermesch S. 2012. Effect of within-year variation on growth performance and subsequent reproductive performance in gilts. Presented at ADSA-AMPA-ASAS-CSAS-WSAS Joint Annual Meeting, July 15-19 2012, Phoenix Arizona.

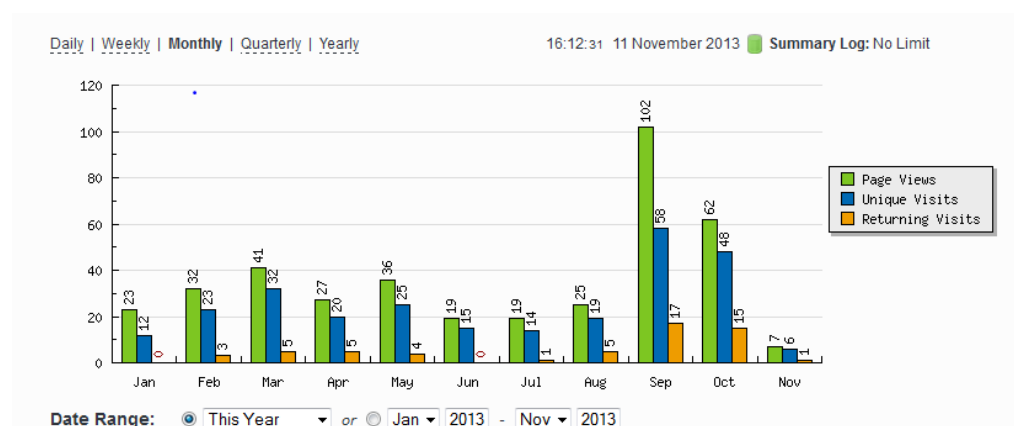
Tickle, K. M., Collins, C. L. & Hermesch, S. 2013. A sampling comparison between the ear and the tail for testing of haemoglobin levels in piglets. Australasian Pig Science Association, November 2013, submitted.

Appendix I: Industry presentations in September and October 2013

Webinars on piglet survival and osteochondrosis in pigs

Following the completion of the project in June 2013, industry presentations continue as indicated in the main report. A webinar on piglet survival, outlining implications of selection strategies for piglet viability, was presented in September 2013 by Susanne Hermesch three times to industry due to the high interest in this topic by industry. This webinar has been placed on the AGBU web pages (http://agbu.une.edu.au/pig_genetics/presentations.html) and has been downloaded 47 times since the 16th of September following announcements to industry. The increased interest in the web page containing the presentation is demonstrated below.

A further webinar was held by Ilse van Grevenhof, a visiting scientist from University of Wageningen to the University of New England.



Number of page view and visits of AGBU web page listing presentations for pigs.

Identification of risk factors determining the prevalence
of osteochondrosis (OC) in pigs

Ilse van Grevenhof

Animal Breeding and Genomics Centre - WUR

In collaboration with:
Veterinary Faculty (UU)
Adaptation physiology (WUR)
Topigs bv
Product board animal feed



Title page of webinar presented by Ilse van Grevenhof to industry on 3 October 2013.