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Genetic evaluation for the Australian beef industry - Towards new horizons

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Abstract

This project has added significantly to the profitability of the Australian beef industry by assisting it to increase the national rate of genetic progress by 30% over the past five years with a number of breeds doubling their rates of gain (e.g. Santa Gertrudis, Brahman and Limousin). Research and development of improved genetic evaluation systems for Australian beef cattle from this project will assist to further improve these gains in future years. Specifically the project has developed the first DNA marker assisted breeding values in beef cattle which provides the industry with the opportunity to capitalise on the advancements been made in DNA technology. The expansion of multiple trait selection indexes across all major breeds, the development of new traits and the launch of data quality assurance software are all significant developments that will increase the ability of cattle producer to use genetics to breed more profitable cattle.

Executive Summary

This project assisted in increasing the rate of genetic gain in the Australian seedstock sector by building on the achievements of previous projects and through research, development and adoption on improved or new genetic evaluation procedures from this project, particularly the ability to capture benefits from the expanding power of DNA technologies.

Over the past five years the industry wide rate of genetic gain increased by 30%. Several groups of breeds achieved substantially higher rates of improvement, of particular note were the northern tropical breeds (+170%) and European breeds (+120). The British breeds on average were steady in their rate of progress maintaining their rate of $2.30/cow/yr. Whilst on average these lifts in the rate of gain were an important milestone it is recognised they are less than the overall goal of 100% (i.e. double the rate) however some breeds achieved rates well above this (e.g. Santa Gertrudis, Brahman, Limousin). Within all breeds there were individual breeders making more than three times the average and demonstrates the level of gain that is possible and the goal that should be aimed for as an industry as a whole in the future.

The project has delivered the first DNA marker assisted EBVs computed using a new procedure and represents a major development for beef genetic evaluation. The new procedure was applied to a meat quality trait, also a first, where marker assisted EBVs were computed for shear force in Brahman cattle. This was a significant milestone for that breed, and the methodology developed has the capacity to be expanded to other DNA markers, breeds and traits.

A major new product from the project was the DataAudit software, a data quality assurance program that will identify improved quality data for genetic evaluation and highlights areas of improvement at both the breed and individual herd level. This new software will also serve to boost industry confidence in the quality of the genetic products. Further evidence of quality assurance was provided by the project through several analyses that demonstrated that EBVs predicted the differences in progeny phenotypes for a range of traits and breeds.

Research into new and improved methods for prediction and genetic parameter estimation have ensured the systems are computationally efficient and allow for increasingly more complex models and size of analyses. New procedures for solving the set of equations have lead to greater levels of convergence of the system of equations resulting in more accurate EBVs, particularly of animals compared over time. This development has also greatly assisted the commercialiser moving to monthly evaluations. This is a very significant development for beef genetic evaluation in this country and will allow timely assessment of new data and the most up to date EBVs for a breed. This will be particularly beneficial for the evaluation of ultrasound scan traits and will remove the need for costly and sub-optimal interim analyses.

The project undertook major research into reassessing the role of IGF-I as genetic indicator trait for the feed efficiency trait called net feed intake (NFI). Results from this work led to the need to consider NFI as two separate, but correlated, traits. This impacted the genetic evaluation of NFI and importantly the genetic correlations with IGF-I. As a result IGF-I is now considered a less useful trait for genetic

evaluation thus resulting in a reduced ability of the industry to select for improved NFI. Therefore improving feed efficiency remains a difficult trait complex for genetic evaluation (and improvement) due to difficulties in recording individual feed intake on candidates for selection. Targeted recording on the progeny of future elite sires may be a viable future strategy to allow genetic improvement of this trait.

Over the five years of the project it has contributed significantly to the growth and development of the BREEDPLAN and BreedObject systems across an increasing number of breeds. This has mainly been in the estimation of breed specific adjustment factors, genetic parameters and the development of new EBVs and $Indexes. Of particular note were developments in the Brahman and Belmont Red BREEDPLAN resulting from the large amount of data contributed through the Beef CRCs northern breeding projects. The outcomes were improved accuracy of EBVs of over a 100 sires in each breed, increased level of across herd genetic linkage, complete re-estimated genetic parameters across all traits and the development of new traits.

Multi-trait selection continues to be adopted by the Australian beef industry and is reflected in the growth of the number of breeds with $Indexes and the increase in genetic trends for the majority of the $Indexes. During the project the breeding objectives software was improved significantly with enhanced capacity to deliver products to the industry that assist both seedstock and commercial breeders to focus selection decisions for profit. Among the new features was the ability to rank animals on overseas objectives, providing the capacity for growth in semen exports and improved identification of potential imports. The equivalence of $Index rankings to the $ per ha was demonstrated; and research included extending feed cost modeling to allow for separate feedlot and pasture phases.

The TakeStock software provides seedstock herds with a genetics report card that allows each herd to benchmark its performance against a set of key performance indicators and with the breed average. Whilst the reports are technically challenging, which has currently limited its widespread release, the vast majority of the feedback is that is it provides invaluable information to those herds that are focused on making rapid genetic improvement.

Progressively more genetic improvement research is focused on traits that affect costs of production. In beef production a major contributor to costs is the running of the breeding cow. Therefore it is important we have suitable genetic evaluation of cow traits, and the ability of producers to match the genetics of the cow herd to their production environment. Research in this project evaluated genetic variability in existing cow traits (e.g. fertility, cow weight, milk, calving ease) and also in new traits e.g. cow longevity. It is likely that improving genetic evaluation and selection support systems for cow traits will increase in importance in the future as pressures on the beef industry from environmental constraints multiply.

Interaction with both the beef industry and scientific communities were important contributors to the success of this project. Regular meetings ensured the research was relevant and results were disseminated as quickly as possible to reduce the lag time. Importantly, results were scientifically peer reviewed in a total of 32 refereed publications and 37 conference papers. This ensures our research is of high scientific standard and therefore is of maximum benefit to beef producers.

Table of Contents

1 Acknowledgements

BFGEN100B has been the work of a team of scientists, research assistants, technical staff, support staff and students. Principal investigators were H-U Graser, D. Johnston, B. Tier, K. Meyer and S. Barwick. Other scientists included W. Upton, G. Jeyaruban, M. Wolcott, K. Donoghue and C. Iker. Computer programmers, software and database specialists included C. Girard, T. Henzell, A. McCann, J. Cook and A. Fitzpatrick. Students included K. Moore, C. Worsnop, C. Iker, M. Wolcott, and M. White. Support staff included M. Youman and K. Dobos. Contributions from other AGBU colleagues and outside scientists, particularly UNE and Beef CRC network are acknowledged. Acknowledged is the access to both research data from the Beef CRC and industry data from breed Societies and their members. The close working collaboration with ABRI staff is recognised and finally the financial contributions and support of MLA and the parent organisations of AGBU (Innovation and Investment NSW and the University of New England) are acknowledged.

2 Background

2.1 Background - Previous R&D

This projected aimed to build on previous R&D in genetic improvement for the Australian beef industry to deliver to the Australian beef industry world's best genetic evaluation systems to allow the selection of genetically improved beef cattle with higher weaning rates, increased carcass weights and better meat quality combined with higher efficiency of feed utilisation. Key funding support for this R&D over the past two decades has been provided by MLA (and its predecessor organisations). Intellectual property and associated software is owned by MLA and I&I NSW and UNE as described in Analytical Software Ownership Agreement (1992) and genetic evaluation software (and associated products) is exclusively licensed to Agricultural Business Research Institute.

3 Project Objectives

The project had 5 objectives aimed at providing the beef industry with a state-of-the-art genetic evaluation system that facilitates increasing rates of genetic gains with a major contribution to beef industry objectives to double of the genetic trend in profitability through improvements in within and across-breed selection, increased accuracy of selection and reduced generation interval for all breeds and market production systems. This will be achieved through improved analytical methods and increased quality of performance recording, combined with greater focus within the seedstock sector towards quantifiable breeding objectives and higher selection intensities.

3.1 Objective 1

Increasing industry genetic gain through new-generation genetic evaluation

3.2 Objective 2

Utilising DNA/gene-based information in beef breeding

3.3 Objective 3

Genetic evaluation that can be applied across breeds

3.4 Objective 4

Genetic evaluation for cow performance traits

3.5 Objective 5

Advances in industry recording and greater adoption of genetic technology

4 Approach/Methodology

4.1 Methodology

To achieve these objectives AGBU will maintain a core group of scientists whose dedication and experience in the development of genetic evaluation systems for beef cattle is unmatched world-wide. This team will use a range of approaches and methodologies (and develop new ones) to solve each of the objectives through a series of defined strategies and tasks. Many of the tasks employed to meet the objectives will require data to develop procedures and to estimate parameters. Commonly these data (performance and pedigree) will be provided courtesy of the Breed Societies and their members. Key research data sets will also be used from the Beef CRC and Industry progeny test programs.

4.1.1 Methodology - increasing gains through new generation genetic evaluation.

The project will deliver to industry versions 5.0 of BREEDPLAN and BreedObject that will include many of the research achievements of the previous MLA contract. The program will undertake strategic research into the utility of advanced statistical procedures measures and will examine which have the potential to greatly increase the computational efficiency of genetic evaluations, make evaluations more relevant to industry and lift accuracies. Included will be new computing strategies that will enable faster evaluations and the capacity to undertake analyses currently impossible or commercially infeasible.

The seedstock industry has during the last few years has developed a scoring system for structural traits based on research undertaken in connection with the Validation project in the mid 90s and with input of AGBU. A number of industry technicians have been accredited and have commenced commercial data collection. Sufficient data is now becoming available to estimate heritabilities and genetic correlations and to develop the module, which calculates EBVs in a multi-trait model.

The operational integrity of the BREEDPLAN and BreedObject systems is critical to future adoption and genetic gain in the Australian beef industry. R&D to ensure the BREEDPLAN system is used effectively by all users and that changes are made to meet the needs of breeds as they develop over time.

4.1.2 Methodology - utilising DNA information.

The industry is starting to use gene tests for two meat tenderness genes commercialised by Genetic Solutions. The accumulated phenotypic data in the CRC (e.g. including shear force), plus temperament data (e.g. flight time) recorded by seedstock producers and research projects, will be used together with the gene marker information to develop a tenderness EBV.

AGBU has developed a procedure for incorporating the GeneSTAR marbling gene into BREEDPLAN. Over the next 12 months it is anticipated that the number of genotype records on breed Society databases will be sufficient to allow this procedure to be tested. The size of the effect in industry data has to be confirmed and procedures have to be developed for including the effect in $Indexes.

New methods will be developed for combining, in one evaluation system, traditional performance and pedigree information with an increasing amount of genotypic data that is related to economically important traits. The availability of potentially important genotypic data has been made more likely by recent work to sequence the bovine genome.

4.1.3 Methodology - genetic evaluation across breed.

Data will be utilized from previous research projects that have been designed for some breeds and traits. However for ongoing multi-breed evaluations data is required across all breeds wishing to participate and eventually across all traits. This will eventually make multi-breed $Indexes possible. While some information will come from research herds there is another source that is currently untapped. Some seedstock breeders are known to performance record more than one breed. This is potentially extremely valuable data. It will require careful scrutiny to assess its usefulness. Recommendations will be made to improve future data.

4.1.4 Methodology - genetic evaluation across breed.

The work addresses a concern in industry that selection on EBVs can favour cows that are not always suited to their environment. It will provide important information on whether accuracies of cow genetic evaluations are being affected by the environment faced by cows and whether there is a need to separately provide for situations where resources are more limiting to cow performance.

4.1.5 Methodology - advances in industry recording and great adoption

We will use field data and research data (e.g. CRC and Durham) to demonstrate that parent EBVs and $Indexes translate into phenotypic differences of the next generation across a range of breeds, traits and market production systems.

5 Results and Discussion

The project has been successful in achieving its milestones especially when recognising that the research environment changed over the five year period and certain task were given higher priorities whilst others were delayed. In particular, additional major tasks were undertaken in the area of DNA technologies and genomic selection. Listed below are the major achievements of each objective and supporting material is provided in the series of appendices: refereed scientific journal papers (Appendix J); a list of refereed conference papers (Appendix C); and internal research reports (Appendix I).

5.1 Objective 1 - Increasing gain through new generation genetic evaluation

5.1.1 Deliver BREEDPLAN and BreedObject Versions 5.0

Various additional features were added to the BREEDPLAN and BreedObject software in Version 5.0. However prior to delivery to ABRI further modifications were required to the modeling of the net feed intake (NFI) trait and the new precondition conjugate gradient (PCG) solver. During the final testing phase of the new software several issues were revealed regarding the genetic correlation of NFI with IGF-I (further supported by research [J26] in CRC2 northern data). This led to substantial additional research and resulted in the reconfiguration of NFI into two separate, but correlated, traits [C24]. Further, the genetic correlations with IGF-I were significantly lower (and in opposite directions) with the NFI traits and therefore IGF-I became a less useful as a genetic indicator trait of NFI as previously reported [J10]. Therefore the traits NFI and IGF-I were not included in Version 5.0 and the proposed developments in BreedObject were also affected. However, trial NFI EBVs continued to be regularly computed for Angus and Hereford in a separate bivarate analysis and new test EBVs were computed for Shorthorn [I4] using data recorded in the Durham R&D project.

Commercial implementation of the new PCG solver required considerable additional research to achieve consistent and reliable stopping criterion across all breeds which was required to avoid operational issues with the commercialiser. The modified solver was implemented at ABRI however it has taken them considerable time to move all breeds across to the new solver (and a new ABRI computer) but this has now been completed. The new solver allows far greater levels of convergence of the system of equations and thus more accurate EBVs of animals, particularly those compared across years. The solver also added to ABRI's ability to move to monthly BREEDPLAN evaluations which is a very significant development for beef genetic evaluation in this country. It ensures the industry has the most up to date prediction of genetic merit. Importantly it also removes data quality issues of ultrasound scanning data that often required scanning at inopportune times to meet the infrequent (often only annual) runs. Monthly breed run also removes the need for costly, and sub-optimal, interim analyses.

New procedures were implemented in Version 5.0 that altered the contributions of overseas EPDs to the computation of EBVs on imported animals and their progeny. This particularly affected the Angus breed where levels of importation information were high. The change directly affected the EBVs of high usage overseas sires (and their offspring) and is a likely contributor to the slowing of the annual genetic trend of Angus in the past 5 years as some of the heavily used sires dropped for their IMF EBV.

5.1.2 More advanced procedures

5.1.2.1 Underpinning science

Strategic research was undertaken throughout the project, and while it may not have had immediate application, it is essential in anticipation of future requirements and improvement in the areas of prediction and estimation. In the future we will have to use alternative methods of estimation and prediction as we progress to more complex analyses for inclusion of additional genetic effects (e.g. DNA markers and dominance [C16]), or much larger analyses e.g. international and multi-breed evaluations. Research in both these areas was successful and this represents large potential benefits in terms of allowing more sophisticated future analyses. Research has shown the increasing size of the number of equations in our analyses (e.g. multi-breed, MBVs, international) can be addressed with alternative methods of analyses [P1, P4, P5, P9, C15]. Techniques such as principal components [P6, P8] and factor-analytic models [P15, C14] will help in the future to reduce computational requirements of our evaluations. International evaluations were used as an example where fitting each country as a different trait (i.e. G x E) greatly increases the dimensions of the equations to be solved and the results of using factor analytic models for the analyses showed a large computation advantage [P22, C26].

Estimation of genetic parameters is an important ongoing task in any genetic evaluation systems and the ability to use larger dataset and more complex models increases the accuracy of the estimates. Research into improved methods and development of estimation software has been a key objective of this project [P16, P17, P18, P19, P20, C3]. Recent research also showed advantages of alternative methods to increase the accuracy of parameter estimation by the joint modeling of the genetic and environmental covariance matrices [C28] and this research will be expanded.

5.1.2.2 New traits

Research and development of new traits for genetic evaluation resulted in a trial EBVs for shear force (measure of meat tenderness), flight time (measure of temperament) and for structural soundness traits (see section 4.1.3). The shear force EBVs were part of the R&D into the incorporation of tenderness DNA markers (see section 4.2.1). Early research showed the benefits of flight time as a measure of temperament and a genetic predictor of meat tenderness [J14] and as a result flight time EBV were developed as part of this project for Shorthorn, Santa Gertrudis and Brahmans using a mix of research and industry records. Brahman released trial FT EBVs in October 2008 using data mainly recorded in the various northern Beef CRC projects and recently were re-computed and available via the BREEDPLAN web site [I1]. Santa Gertrudis trial FT EBVs were first computed in 2007 and again in November 2009 using data recorded in 7 herds, however very low levels of across herd genetic linkage of the herds recording the trait has meant the EBVs are currently only comparable within herd [I2]. It is expected with increased levels of recording that linkage will improve and across herd EBVs will be possible in the future. Shorthorn produced a test set of FT EBVs from sires whose progeny were recorded for flight time in their Durham R&D project [I3].

Basic research into the application of proportional hazard models to the genetic prediction of cow survival was undertaken to assess the suitability of the methods using data from two beef breeds [C27]. The models were implemented using the Survival Kit software (Ducrocq and Solkner 1998) and applied to records for length of cow productive life derived from standard BREEDPLAN data input files. Results showed a piece-wise Weibull model (Weibull models are well suited for live-time data) with a time dependent stage effect modeled the annual culling pattern reasonably well and there was clear evidence of genetic variation and definable risk factors. However irregularities in the variance component estimates suggested issues with data quality and this needs to be addressed in the data recording system if these kinds of analyses are to be progressed.

5.1.3 BreedObject R, D and E

The research and development of the technology behind breeding objectives and multiple trait index selection achieved many milestones during the five years of the project. Most importantly, the beef industry is shifting its focus from selection on single or a few traits to multiple trait selection for total merit or profit and this is largely the result of increased adoption of BreedObject $Indexes. At the conclusion of the project there are 31 breed standard Indexes publicly available for across all of the major breeds in Australia.

5.1.3.1 Index developments

Existing indexes were revised or new ones developed for nine breeds, as follows: Angus, Hereford, Murray Grey, Brahman, Simmental, Charolais, Shorthorn, and Limousin. Importantly, three breeds (viz: Santa Gertrudis, Belmont red and Red Angus [I9]) had new indexes developed and released to their breeders. The BreedObject web site continued to expand in usage. With over 1400 registered users worldwide the site is providing a critical role for users to develop customised $Indexes [I7: figure g]. The site is fully integrated with breed databases, providing access to sale and semen catalogues, EBVs and Indexes for animals of all breeds. The system was greatly enhanced in 2007 to allow indexes of other countries of the same breed to be displayed for animals (or semen). This can be done from the perspective of either an Australian or an overseas user. This development has the potential to increase semen exports of superior Australian genetics and to improve the identification of potential imports.

5.1.3.2 Research outcomes

Research and developments in breeding objectives and indexes included ensuring alignment with developments and changes in BREEDPLAN evaluation, in particular updating the genetic variance and covariance matrices for all breeds. This occurs both because parameters are routinely updated and because breeds are at different stages with respect to their level of performance recording and the development of EBVs. Breed specific matrices that were updated for developing $Indexes included those for Angus, Belmont Red, Brahman, Charolais and Hereford.

Fundamental research was undertaken in several areas and many of these research outcomes will be delivered through version6.0 of BreedObject software due for release in 2010. The equivalence of rankings on $Index with rankings of animals on $ per hectare was demonstrated. Other developments included new methods for the non-linear valuing of traits, expanded feed costing, more accurate separation of the assessment of feed requirements for different phases of production (e.g. pasture versus feedlot), and procedures for new traits and for varying trait variances across systems. New trait developments included those in line with developments in BREEDPLAN (e.g. NFI, temperament, tenderness) and provision for possible future requirements for measures of methane and for genes of large effect.

5.1.3.3 Genetic trends

Estimated breeding values (EBVs) are the basic industry measures of genetic differences among seedstock. Over time, EBVs available through BREEDPLAN have come to encompass the growth, carcass, fertility and calving ease trait complexes [P3] and in some breeds trial EBVs for net feed intake, docility, structural soundness and very recently a DNA marker-based EBV for meat tenderness [c25]. Over the past decade, $Indexes have become the accepted measure of genetic differences in overall breeding value for multiple trait merit [P2].

5.1.3.3.1 Example of favourable change across multiple traits

EBVs from a BREEDPLAN analysis are derived not only for currently active animals but also for all earlier-born and related animals in the database of the breed involved. Because the EBVs are directly comparable across all animals in the analysis, the breed's genetic trend can be determined from the means for animals born over different years. Trait genetic trends calculated for Angus, expressed in absolute units, are shown in [I7: figures a-d]. The graphs show simultaneous favourable genetic changes across multiple traits in Angus since the first introduction of BREEDPLAN in 1985 and particularly since the early-to-mid 1990s when genetic evaluation started to include traits other than growth. At the same time as growth (e.g. 600d live weight) has increased by more than 65 kg in Angus, intramuscular fat % (in a 300 kg carcass) has increased by about 1.5%, eye muscle area by about 3 cm^2, and days from bull-in to calving (reflecting both improved calving rate and earliness of calving) has decreased by about 3 days There have also been other favourable changes. Calving ease, for example, initially declined as growth potential increased, but it has since also improved despite further increases in growth.

Also of interest is the rate of genetic change in a trait (the slope of the trend curve) at a particular time, or over an interval. To facilitate comparison across traits and breeds, and possibly across species, the rate of change may be expressed in standard units (I7: figure e]. A suitable standard unit is the trait genetic standard deviation, as that allows comparisons on an equal basis with respect to the amount of genetic change that was possible. The graph shows rates of genetic gain in the same Angus traits using time intervals that correspond to developments in BREEDPLAN. Rates of gain have generally increased over time and in line with the availability of the different EBVs and $Indexes. Rates of gain have been higher in growth traits than in other traits, and have noticeably slowed for birth weight and mature cow weight over the last two time intervals. Rates of gain in IMF% and EMA have been greater over the last two time intervals; and rates of gain in calving ease have increased despite birth weight still increasing to some extent with other growth traits.

5.1.3.3.2 Breed trends

Plots of genetic trends for each breed for each of their $Indexes are presented in Appendix I8 and also in genetic standard deviation units for the major breeds [I7; figure f]. The average annual rates of gain for the 2008 minus 2006 born animals differed greatly across the breeds with an average gain of $1.80/cow/yr and a range across breeds of $0.00 to +$3.75. As a group of breeds the tropical breeds had a remarkable increase, albeit from a low base. The increase on average was 175% greater than that between 2004 minus 2002 born animals, with Santa Gertrudis and Brahman showing large gains. The Belmont Red made no gain, this might reflect the fact that they were the most recent breed to have Indexes developed. The European breeds on average also showed a more than doubling of their gains (+120%), with Limousin having a +167% increase. The British breeds had the highest average rate of gain in the 2006/8 period (2.51/cow/yr) but they did not increase their rate of gain compared to the 2002/4 period. This was mainly due to a slowing of the rate of gain in both Angus and Murray Grey, whereas Shorthorn and Hereford both showed modest rates of increase of between +20 and +51%. While the gains on average are low, particularly in some breeds, the rates of gains differ greatly across herds within a breed. Within a breed some breeders were achieving rates of gain 3-4 times the average.

When the annual rates of gain were compared on a genetic standard deviation basis there were also large differences between the breeds. Breeds commonly are at different stages in their performance recording, EBV availability, and introduction or revision of the breeding objectives underlying their $Indexes. Angus clearly has the largest trends on a standard deviation basis (approaching 0.12) reflecting their level of performance recording and longer term focus on selection. Herefords are moving towards 0.06 of a standard deviation and Santa Gertrudis doubled their rate. Whilst current gains are encouraging they are considerably lower than what is theoretically possible. Gains of 0.15 genetic standard deviations are achievable but will require greater levels of performance recording across the full range of traits in the breeding objective and a greater focus on selection using $Indexes.

5.1.4 Structural soundness EBVs

Research into a genetic evaluation of structural soundness (i.e. linear type) traits resulted in a new analytical model being developed and the release to industry of new structural soundness EBVs. Initial research revealed difficulties with the computation of EBVs from existing methods/models records scored on an intermediate optimal scale [C27]. The subsequent research developed a modification of the threshold model to include a double threshold for expressing the EBVs. Over 5000 records were available on Angus seedstock cattle scored at around 18 months of age and these were used to compute trial Angus EBV. The EBVs for five feet and legs traits were released to over 30 herds in March 2008 and updated in July 2008 [I5] and February and December 2009. Future research will be required to develop EBVs for structural traits scores on breeding females, including scores for teats and udders. Importantly, the estimation of genetic correlations with earlier scores will be critical to assess the utility of the earlier scores.

5.1.5 BREEDPLAN and BreedObject operating effectively for all users.

Considerable time was spent throughout the project ensuring the operational integrity of the systems and timely response to issues raised by the commercialiser. These included issues with running the software on a range of commercial platforms, addressing problems, and performing upgrades for new breeds and expanding traits. Periodically research was undertaken to check underlying methods and traits. For example research was undertaken to investigate benefits of alternative slicing interval [c12] and a study was done to investigate the effect of the addition of data from new herds on the genetic parameter estimates in Brahmans [C8]).

Research was undertaken in to the development of a BREEDPLAN analysis for the Wagyu breed. The work included parameter estimation for growth traits and development of appropriate controller files for the breed given their data. The majority of the work was examining a small carcase dataset in an attempt to use the data for developing carcase EBVs.

Other significant development work for existing EBVs for new breeds included research into an EBV for days to calving for Belmont Reds. Although significant additional data (of high quality) was added from the CRC 2 northern breeding project there were still data quality issues with existing data and that is being resolved by ABRI and the breed Society. Trial EBVs were also produced for NFI_F for Brahman and Belmont Red sires (as part of CRC projects [P26]) and recently trial Angus docility EBVs have been computed.

BREEDPLAN evaluations rely on accurate estimates of the underlying genetic variance and covariance structures for the multi-trait evaluations. Therefore re-estimation of parameters is an important ongoing job for the maintenance of high quality EBVs. As part of this project genetic parameters and adjustment factors were updated on a breed basis and implemented into the BREEDPLAN evaluations (e.g. Brahman, Hereford, Angus, Limousin). Research was also required to upgrade the procedures and re-estimation of the adjustment factors for carcase traits to a 300kg carcase weight basis for heavy weight (i.e. greater than 400kg) carcases in Angus. This was necessary due the increased numbers of heavy weight carcases from industry progeny test programs. The new procedures and adjustments were implemented at the end of 2008. Also periodically the input files for the importation of overseas EPDs have to be updated as changes occur in the overseas analyses or when new breeds or trait become available.

5.2 Objective 2- Incorporation of DNA information

Significant developments in the field of DNA genotyping, and the emergence of companies selling DNA tests to the Australian breeding sector, increased the priority (and resources) given to the research and for the development of procedures for the incorporation of DNA results into EBV computations. Initially there was a need for AGBU to act as an independent service provider for the validation of commercially available marker tests. This then led to the development of analyses for the validation of company products (with additional funding outside this project) and progressed into methodologies to calibrate panels of markers for their use in genetic evaluation.

5.2.1 Tenderness EBV

The project delivered the first marker assisted EBVs using shear force and GeneSTAR tenderness markers as a prototype for this work [C25]. This represented a first for beef genetic evaluation in Australia. The research found proposed methods for incorporating marker effects were generally not suitable given the heterogeneity of the data and genetic parameters in a genetic evaluation including marker genotypes. Therefore a new approach was developed using a modification to the multiple trait methodology. The effects of the DNA markers on the target trait are summed in a prediction equation and this 'phenotype' is used as a separate trait (with a heritability close to one) in a multiple trait model with other traits. This method allows the marker information on those with genotypes to contribute through the genetic correlation with other traits.

An international workshop was held in Armidale as part of the SmartGene for Beef Project and one of the aims was to present and receive comments on AGBU's method for incorporating marker data into BREEDPLAN. The workshop was very productive with a great deal of interaction and exchange of ideas. The group generally endorsed the procedure proposed (also a similar procedure was proposed independently by US scientists) however it was recognised as a first step and will need modifications as we move towards genomic selection rather than individual markers. There was also discussion of post BLUP selection index approaches that are alternative methods. Following the workshop, AGBU scientists have been analysing the predictive power of MBVs (developed by companies) on key carcase and feed efficiency traits. This work has also investigated additional ways of assessing their value to genetic evaluation (e.g. amount of variance explained). As a direct result of this validation role the results have been posted on a Beef CRC web site. Collaboration between AGBU scientists and US continued to ensure consistence of procedures across countries. The US has now also adopted the preferred method of evaluation and reporting the effects of marker panel predictions.

The new methodology developed in the project to incorporate marker information was applied to Brahman data and new trial Brahman BREEDPLAN tenderness EBVs were produced and represented a new era in genetic evaluation. The analysis used records on shear force, flight time and DNA marker phenotypes from the four commercialised GeneSTAR tenderness markers. Variances and covariances were estimated using the Brahman data and trial shear force EBV^{M} were released to Industry in October 2008 and updated in July 2009 [I6] and published on the Brahman BREEDPLAN web site [I1]. The initial work into the quantitative genetics of shear force trait occurred in conjunction with the Beef CRC [C32, C20] and these outcomes were built on to produce the marker assisted EBVs using information from the SmartGene for beef project. These were the first marker assisted EBVs in Australia and the methods and procedures are now coded into the BREEDPLAN Version 6.0 thus allowing other markers and breeds to compute marker assisted EBVs in the future when sufficient data exists to estimate the required genetic correlation estimates between the markers and all traits in the BREEDPLAN analysis.

5.2.2 Use GeneSTAR marbling markers

Results of SmartGene for Beef analysis showed no significant effects of the four GeneSTAR marbling markers on IMF or marbling score in any breed. Therefore specific inclusion of these markers in to BREEDPLAN was not warranted. However the procedures developed in Version 6. 0 (mentioned above) will allow any future panel of marker effects to contribute to the IMF EBV provided estimates of the genetic correlations with marbling and IMF can be estimated.

5.2.3 New methods long term

The development of the DNA technology has far exceeded our predictions at the commencement of the project. Currently the ability to genotype approximately 50,0000 SNP in cattle is routine and is predicted to increase to 600K within the next 6 months. This certainly creates opportunities previously not imagined but also requires fundamental research to methods of determining associations [P35, C29] and understanding the mechanisms of linkage disequilibrium [C13, C30, C31] has been critical. Strategic research in these areas has been important to further our knowledge regarding this technology and to allow its application to beef cattle selection.

5.3 Objective 3 -Across breed evaluations

5.3.1 Industry herd linkage

The first component of this work identified over 90 herds that were performance recording more than one breed. Angus was the breed that was run with the most other breeds (N=11) but Hereford/Poll Hereford (N=8) and Charolais (N=8) also form good links between herds/breeds. Of these approximately 60 herds were contacted and surveyed on their recording practices and the contemporary rearing of the breeds. The 16 respondents allowed us to establish that it may be possible to re-assemble data from different breed society databases but would require the breeder to confirm joint contemporary groups. If this was to become a reliable source of future ongoing data for across breed comparisons it was identified that direct consultation with each individual breed would be required to ensure the quality of data.

5.3.2 Prototype analysis

Software has been written to allow the implementation of regular across breed EBV runs and this required modifications to the data input software (i.e. allow more than 1 breed) and to the code for setting up the appropriate breed specific genetic parameter files. A test run was conducted using three European breeds (Charolais, Limousin and Simmental). While successful in producing a single set of EBVs issues still exist around the required level of accuracy of the across breed comparisons, particularly for Charolais and also for the non-growth traits. This research highlighted the need for good head-to-head breed comparison data and the issues regarding mechanisms for its ongoing future collection. For northern tropical breeds the collection of data in the Beef CRC II northern breeding project has contributed greatly to the data on the direct comparison of Brahman and Belmont Red. The data from Belmont Research station has head-to-head comparison of all animals from birth. Estimates of breed differences for steers included all growth and feed intake (P26), and carcase and meat quality traits (P32). For heifers breed differences have been estimated for early growth (P27), age at puberty (P28) and early in life adaptive measures (P30). Data collection on cows continues and with join mating groups in the future estimates will be available for cow weights, condition, reproduction (e.g. days to calving) and cow survival. It is anticipated that comparisons will be generated between Santa Gertrudis and Droughtmaster in the future.

5.4 Objective 4 - Genetic evaluation of cow traits

This objective has not shown as much progress as planned mainly due to re-allocation of time to work in the area of incorporation of DNA markers. Also milestones were delayed or cancelled due to the lack of availability of data. Mention has already been made of the basic research towards analyses of potentially new trait cow productive life. In addition to this our involvement in data collection in seedstock herds and through CRC projects is ensuring that quality datasets are being accumulated for future work.

5.4.1 Cow evaluations under limited resources

Data analyses were carried out to develop a measure of the environment experienced by animals for use in defining production situations generally. This focussed on indirect measures of energy balance as these also have potential to be indicators of cow residual feed intake. This research has not yet yielded useful results. Testing of ideas has been restricted by a lack of available data, particularly on animals that have records for both feed intake and mature cow weight.

There is a concern in industry that the superiority of high $Index cows might not apply when stocking rates are high. In this project we were able to demonstrate, from theory, that rankings on $Index align with rankings on $ per ha (and with $ per DSE or $ per feed unit) irrespective of stocking rate. This is because feed requirement (expected feed intake less residual feed intake) is always accounted for in $Index calculations. The calculations assume herd size is adjusted (or additional feed provided) if feed requirement per cow increases, so that total herd feed requirement is unaltered. This is a usual assumption for valuing the $ per ha impact of technologies. Feed requirement per cow does generally increase as overall genetic merit increases, so there is an ongoing need for industry to revise stocking rates as genetic merit increases. The research in this project highlighted that an EBV for expected feed requirement could be of benefit to industry to assist in the needed ongoing revision of stocking rates.

5.4.2 More advanced procedures for evaluation of cow traits

The heritabilities and genetic correlations for the range of existing female traits (milk, cow weight, and days to calving) have been re-estimated through a series of complete trait genetic parameter estimations conducted for several breeds during the project. These new estimates have been included in the updated parameter files and continue to show that large amounts of genetic variation exists for the maternal traits however levels of data recording still remain low relative to the growth traits. Increasing the levels of recording particularly for mature cow weight and days to calving will need to be a focus of future work, including encouraging several breeds currently without days to calving to initiate recording to allow the development of this important EBV.

In conjunction with the Beef CRC, two important datasets (Northern lifetime fertility project and Southern Maternal productivity project) are being developed that will assist in the future to investigate a range of cow traits. To date, research into genetic differences in heifer age at puberty in Brahmans and Tropical Composites has revealed heritabilities of 50% [P28] and illustrate the genetic variation that exists in these breeds. Further research into the genetics of lactation anoestrous and lifetime reproductive performance in these genotypes, coupled with body composition data, will greatly assist in developing improved genetic evaluations for cow reproduction traits. The cow longevity data from the northern project will also be critical in testing developments made in this project in use of survival analyses.

The project identified that to further enhance female fertility EBVs (e.g. days to calving) in breeds with high levels of AI (e.g. Angus) there is the need to collect additional joining details from the AI programs. Unfortunately delays at ABRI in implementing these requirements meant that they were not release until November this year and therefore data were not available to progress this work during the project. Data should start accumulating over the next 12 months. Another emerging issue regarding the genetic evaluation of cow traits is the expected influence of early weaning strategies on the genetic evaluation of maternal weight traits (i.e. milk). The increasing use of early weaning as a routine management practice potentially increase greatly the number of calf weight records from these practices and thus influence our ability to partition the direct and maternal components of calf weight. However it was identified that to do any research in this area firstly required the alteration to the data recording systems to record actual weaning date that has previously not been captured by the NBRS databases.

5.5 Objective 5 - Advances in recording and greater adoption

5.5.1 EBVs studies

A range of studies were undertaken that showed EBVs were predicting phenotypic differences as expected. In general the results were extremely good and showed in most cases the EBVs were working as expected. However there was the odd occurrence where this was not the case. Notably, data issues with regard to the abattoir processing (i.e. fat trimming) of the carcases led to problems with inaccurate phenotypes in the Angus progeny test. Also, in CRCII Brahman IMF scan data the correlation with the carcase IMF was very low and therefore the decision was made to turn off the scan IMF trait in Brahman BREEDPLAN until such time as the ultrasound prediction algorithm could be improved.

Results from phenotypic data from 2001 and 2001 drop Herefords regressed on their sires EBVs showed regression coefficients very close to the expected 0.5 for the weight traits and slightly less than 0.5 for the scan traits. Overall conclusions from this study were the results showed the EBVs were predicting the expected differences in progeny performance on average across the breed in seedstock herds.

Analyses of three years of data from the MLA donor company Trangie Angus progeny test project were performed across a range of traits to investigate the ability of pre-progeny test EBVs of the sires (i.e. many were young unproven bulls) to predict phenotypic performance of their progeny. This work was done on a sub-contract basis with Angus Australia. The results in general were sound but unfortunately data issues, particularly from the abattoir, have hampered this work and the outcomes.

The EBVs, on approximately 50 Brahman bulls from the CRCII northern breeding project, were used in a series of analyses where the phenotypes in the CRC progeny were regressed on the sire's BREEDPLAN EBVs and the significance of the regression coefficient, and its difference from expectation of 0.5, were assessed. In general, the coefficients were significant (except IMF EBV) and most were close to 0.5 with some exceptions for traits measured in heifers where their levels of trait expression in the CRC herds were expected to be general lower than average seedstock herd.

Results from research determining the magnitude of genotype by environment interactions (GxE) for BREEDPLAN traits in Angus seedstock herds across Queensland and Victorian herds showed all the correlations were very high (not significantly different from 1.0) thus showing little evidence of GxE for weight, carcase and fertility traits [J21]. The only exception was for bull scan IMF but editing to remove possible data anomalies resulted in higher correlations.

Results from analyses of Beef CRCII Regional Combinations project data on the regressions of three measures of marbling recorded on the progeny out of Hereford dams of 25 Angus sire's BREEDPLAN IMF EBV showed the regression were highly significant for all three measures of marbling and was not affected by growth path treatments used in that study [P29, C23]. The regression coefficient for IMF was 0.36 (0.08) and was not significantly different from its expectation of 0.5 even though the actual level of IMF% (progeny out of Hereford cows) was lower than the average Angus phenotype in their BREEDPLAN analysis. Results clearly show selecting on Angus BREEDPLAN IMF EBV will change marbling (both marbling score and IMF%).

5.5.2 Quality assurance and new recording methods

5.5.2.1 DataAudit software

Development of a new software product called DataAudit is a major achievement of this project. DataAudit checks the quality of the input data of BREEDPLAN analyses and is written in Fortran 90 and is compatible with the BREEDPLAN suite of software and uses standard BREEDPLAN input files. The software computes an array of statistics on an individual herd or an entire breed across a nominated set of years and summaries results for each year and an average. The software performs a series of calculations to generate statistics that describes the basic features of the herd (e.g. numbers born, pedigree known, sex ratios, date of birth statistics), the level of performance recording (i.e. completeness) and finally the quality of the records across all BREEDPLAN traits. The results are able to be weighted and summed to give scores for a trait across years. The output results identify herds and breeds with exceptional performance recording practices and also those herds or traits where the recording is below average. This software is a tool that will be extremely useful in increasing data quality in future evaluations by removing poor quality data and also assisting breeds and individual breeders to target particular traits where data quality is found to be an issue. The software also provides a mechanism for rating herds and this may be used by breeds to differentiate between members in their level of performance recording. Finally, this new software is an important development to increase the consumer's confidence in the quality of the BREEDPLAN system and increasing the trust in BREEDPLAN EBVs. The software was delivered to ABRI for testing in March 2009 and will require input from AGBU to assist with its implementation (planned for early 2010).

5.5.2.2 New methods of recording

Over the past five years there has not seen any major technological development in new recording methods applied to beef performance recording. However, potential new measures may emerge from genetics research conducted in the Beef CRC2&3 northern projects in female [P28] and male reproductive [C35] and adaptive traits [P30, C34]. Developments in performance recording could include possibilities in the redefinition of the days to calving of traits and the use of ovarian scanning and IGF-I. Recording of heifer and cow body composition (hip height, eye muscle, fats and condition score [P27]) may emerge as additional new measures.

In the area of ultrasound scanning the project has been involved in the ongoing evaluation of enhanced ultrasound scanning algorithms for IMF. The software offered by the CUP laboratory in the US may prove more useful in predicting IMF% at lower levels than existing systems and would therefore be a major benefit for recording bulls in seedstock herds.

6 Success in Achieving Objectives

6.1 Success in Achieving Objective 1- Increasing industry genetic gain through new-generation genetic evaluation

All scheduled tasks regarding this objective have been achieved where the developments to the BREEDPLAN and BreedObject systems will assist industry in the future to enhance rates of genetic gain.

- Version 5.0 of BREEPLAN and BreedObject implemented, including new solver for all breeds
- Developed new tenderness and structural soundness EBVs
- Regular re-estimation of breed specific adjustment factors and genetic parameters for all traits
- New and updated $Indexes
- Developed new techniques for estimating genetic parameters
- Monitored rates of genetic progress
- Maintained operational integrity of BREEDPLAN and BreedObject systems

6.2 Success in Achieving Objective 2 - Utilising DNA/gene-based information in beef breeding

All tasks for this objective were achieved to incorporated DNA based information into EBVs and additional tasks were also achieved in this area of independent validation of DNA marker information into EBVs.

- Released first marker assisted EBV in Australian livestock
- Established methods for validation of commercial markers (and panels)
- Analysed properties of whole genome scan data from 50K chip
- Provided additional analytical work to evaluate claim on DNA markers

6.3 Success in Achieving Objective 3 - Genetic evaluation that can be applied across breeds

Most of the scheduled tasks were partially completed and this was because of a reallocation of resources during the project.

- Established possible industry sources of multi-breed data
- Developed software for multi-breed evaluations, including new genetic grouping strategies
- Tested prototype software with three European breeds

6.4 Success in Achieving Objective 4 – Genetic evaluation for cow performance traits

Many of the research tasks are still incomplete mainly due to the unavailability of suitable sized datasets but this is being addressed and datasets will become available over the next 12 months to allow this work to proceed.

- Re-estimated genetic parameters for maternal traits, including genetic correlations
- Assessed suitability of methods for conducting cow longevity evaluations
- Data collection for future maternal and reproductive trait genetic analyses
- Redefined NFI to be two traits for postweaning and finishing tests

6.5 Success in Achieving Objective 5 - Advances in industry recording and greater adoption of genetic technology

All tasks for this objective were achieved with the noted achievement of the development of the data audit software.

- Delivered new data audit software
- Provided numerous analyses of proof of EBVs
- New EBVs provided incentive to record additional traits

7 Impact on Meat and Livestock Industry – now & in five years time

7.1 Impact on Meat and Livestock Industry – now

The project is already having a direct input on the beef industry through implementation of the research through:

* enhanced EBVs for selection of seedstock and commercial bulls across an increased number of breeds, traits and selection indexes.

* provided the industry with the ability to incorporate gene markers into EBV thus optimising the two difference sources of genetic information when making selection decisions

7.2 Impact on Meat and Livestock Industry – 5 years

The project will have impacts for years beyond its completion as many of the research output have only been recently implemented and some are yet to be released, these include:

* improved EBVs through enhancements to procedures and parameters will allow future increased rates of genetic progress

* enhanced and expanding breeding objectives ensures future focus of selection based on total merit

* new traits allowing selection for traits previously not able to be changed easily by selection and allowing a better matching of genetics required to meet requirements of difference production systems and markets

* DataAudit software will increase the quality of data used thus increasing the accuracy of EBVs

* Application of outputs from TakeStock reports will greatly assist seedstock breeders to examine and compare their genetic progress against breed KPIs.

8 Conclusions and Recommendations

8.1 Conclusions

The Project has been very successful providing the Australian beef industry with improved genetic evaluation systems. This will have immediate and long term benefits on the industry through increased rates of genetic gain in seedstock herds and improved ability for commercial cattle producers to produce beef targeted for particular market production systems.

8.2 Recommendations

The project outputs have been routinely implemented throughout the course of the project however some new developments still remain to be delivered or in some cases the research is yet to be finalised. These areas should be completed as soon as possible. The project has demonstrated that genetic progress is being achieved in the Australian beef industry however large differences exist between breeds and also between herds within a breed. There is a clear opportunity for the industry to increase significantly the current rates of gain but this will require further R&D to increase the accuracy of selection and targeted extension to increase the level of adoption.

9 Bibliography

V. Ducrocq and J. Sölkner (1998) 'The survival kit - v3.0' a package for large analyses of survival data. In Proc. 6th World Congress on Genetics Applied to Livestock Production 27:447-448

10 Appendices

10.1 Appendix P

10.2 Appendix C

10.3 Appendix I

APPENDIX P (refereed scientific papers)

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Genetic Evaluation for the Australian Beef Industry - Towards New Horizons

In submitting this report, we agree that Meat & Livestock Australia Limited may publish the report in whole or in part as it considers appropriate.

APPENDIX P: refereed journal papers

P1 Albuquerque, L G and **Meyer, K** (2005). "Estimates of covariance functions for growth of Nelore cattle applying a parametric correlation structure to model within-animal correlations." *Livestock Production Science* 95: 213-222.

P2 **Barwick, S A** and **Henzell, A L** (2005). "Development successes and issues for the future in deriving and applying selection indexes for beef breeding." *Aust J of Experimental Agriculture* 45:923-933.

P3 **Graser, H-U; Tier, B; Johnston, D J and Barwick, S A** (2005). "Genetic evaluation for the beef industry in Australia." *Aust J of Experimental Agriculture* 45:913-921.

P4 **Meyer, K** (2005). "Advances in methodology for random regression analyses". *Aust J of Experimental Agriculture* 45:847-858.

P5 **Meyer, K** (2005). "Estimates of genetic covariance functions for growth of Angus cattle." *J Anim Breed Genet* 122(2): 73-85.

P6 **Meyer, K** (2005). "Genetic principal components for live ultrasound scan traits of Angus cattle." *Animal Science* 81(3):337-345.

P7 **Meyer, K** (2005). "Random regression analysis using B-splines to model growth of Australian Angus cattle." *Genetics Selection Evolution* 37(5):473-500.

P8 **Meyer, K** and Kirkpatrick, M (2005). "Restricted maximum likelihood estimation of genetic principal components and smoothed covariance matrices." *Genetics Selection Evolution* 37(1): 1-30.

P9 **Meyer, K** and Kirkpatrick, M (2005). "Up hill, down dale: quantitative genetics of curvaceous traits." *Proc. Roy. Soc B.* 360(1459):1443-1455.

P10 **Moore, K L; Johnston, D J; Graser H-U** and Herd, R (2005). "Genetic and phenotypic relationships between insulin-like growth factor-I (IGF-I) and net feed intake, fat, and growth traits in Angus beef cattle." *Aust J Agric Research* 56(3): 211-218.

P11 **Phocas, F; Donoghue, K and Graser H-U** (2005). "Investigation of three strategies for an international genetic evaluation of beef cattle weaning weight." *Genetics Selection Evolution* 37:361-380.

P12 **Robinson, D L** (2005). "Accounting for bias in regression coefficients with example from feed efficiency." *Livestock Production Science* 95(1-2):155-161.

P13 **Robinson, D L** (2005). "Assessing the accuracy of modeling weight gain of cattle using feed efficiency data." *Livestock Production Science* 95(3):187-200.

P14 **Kadel, M J; Johnston, D J**; Burrow, H M; **Graser, H-U** and Ferguson, D M (2006). "Genetics of flight time and other measures of temperament and their value as selection criteria for improving meat quality traits in tropically adapted breeds of beef cattle." Aust. J Agric Research 57(9): 1029-1035.

P15 **Meyer, K** (2007). "Multivariate analyses of carcass traits for Angus cattle fitting reduced rank and factor-analytic models." *J Anim Breed Genet* 124 (2):50-64.

P16 **Meyer, K** (2007). "WOMBAT – a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML)." *J Zhejiang University Science B* 8 (11):815-821.

P17 **Meyer, K** (2008). "Likelihood calculations to evaluate experimental designs to estimate genetic variances." *Heredity* 101 (3):212-221.

P18 **Meyer, K** (2008). "Estimation of genetic parameters: it takes three to tango." *Journal of Animal Breeding and Genetics*125 (6):361-362.

P19 **Meyer, K** (2008). "Parameter expansion for estimation of reduced rank covariance matrices." *Genetics Selection Evolution* 40 (1):3-24.

P20 **Meyer, K** and Kirkpatrick, M (2008). "Perils of parsimony: Properties of reduced-rank estimates of genetic covariance matrices." *Genetics* 180 (2):1153-1166.

P21 **Jeyaruban, M G; Johnston, D J and Graser, H-U** (2009). "Estimation of genotype x environment interactions for growth, fatness and reproductive traits in Australian Angus cattle." *Animal Production Science* 49:1-8.

P22 **Meyer, K** (2009). "Factor-analytic models for genotype x environment type problems and structured covariance matrices." *Genetics Selection Evolution* 41:21.

Associated published papers (no reprint provided)

P23 McKiernan, W A; Wilkins, J F; **Barwick, S A**; Tudor, G D; McIntyre, B L; Graham, J F; Deland, M P B and Davies, L (2005). "CRC 'Regional Combinations' project – effects of genetics and growth paths on beef production and meat quality; experimental design, methods and measurements." *Aust J of Experimental Agriculture* 45:959-969.

P24 Thompson JM; Perry, D, Daly, B, Gardner, G E, **Johnston D.J.** and Pethick, D W. (2006) "Genetic and environmental effects on muscle structure response post-mortem". *Meat Sci.* 74:59-65.

P25 Intaratham, W; Koonawootrittriron, S; Sopannarath, P; **Graser, H-U** and Tumwasorn, S (2008). "Genetic parameters and annual trends for birth and weaning weights of a Northeastern Thai indigenous cattle line." *Asian-Australasian Journal of Animal Sciences* 21(4):478-483.

P26 **Barwick, S A; Wolcott, M L; Johnston, D J**; Burrow, H M and Sullivan, M T (2009). "Genetics of steer daily and residual feed intake in two tropical beef genotypes, and relationships among intake, body composition, growth and other post-weaning measures." *Animal Production Science* 49:351-366.

P27 **Barwick, S A; Johnston, D J**; Burrow, H M; Holroyd, R G; Fordyce, G; **Wolcott, M L**; Sim, W D and Sullivan, M T (2009). "Genetics of heifer performance in 'wet' and 'dry' seasons and their relationships with steer performance in two tropical beef genotypes." *Animal Production Science* 49:367-382.

P28 **Johnston, D J; Barwick, S A**; Corbet, N J; Fordyce, G; Holroyd, R G; Williams, P J and Burrow, H M (2009). "Genetics of heifer puberty in two tropical beef cattle genotypes in northern Australia and associations with heifer and steer production traits." *Animal Production Science* 49:399-412.

P29 McKiernan, W A; Wilkins, J F; Irwin, J; Orchard, B and **Barwick, S A** (2009). "Performance of steer progeny of sires differing in genetic potential for fatness and meat yield following post-weaning growth at different rates: 2. Carcass traits." *Animal Production Science* 49:525-534.

P30 Prayaga, K C; Corbet, N J; **Johnston, D J; Wolcott, M L**; Fordyce, G and Burrow, H M (2009). "Genetic analyses of heifer adaptive traits and their relation to growth, pubertal and carcass traits in two tropical beef cattle genotypes." *Animal Production Science* 49:413-425.

P31 Wilkins, J F; McKiernan, W A; Irwin, J; Orchard, B and **Barwick, S A** (2009). "Performance of steer progeny of sires differing in genetic potential for fatness and meat yield following post-weaning growth at different rates: 1. Growth and live animal composition." *Animal Production Science* 49:515-524.

P32 **Wolcott, M L; Johnston, D J; Barwick, S A; Iker, C L**; Thompson, J M and Burrow, H M (2009). "The genetics of meat quality and carcass traits in two tropical beef genotypes and the impact of tenderstretch on genetic and phenotypic tenderness." *Animal Production Science.* 49:383-398.

Books and Theses

P33 van der Werf, J. Graser, H-U, Frankham, R and Condro, C (eds) 2008 "Adaptation and Fitness in Animal Populations. Evolutionary and Breeding perspectives on Genetic Resource Management." Springer

P34 Worsnop, C (2008) Estimation of breeding values for animals selectively slaughtered. Masters Thesis, UNE

P35 Moore, K. (2009) Methods and modles for the accurate estimation of the effects of single nucleotide polymorphisms (SNP) in beef cattle. PhD Thesis, UNE.

APPENDIX C (refereed conference papers)

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APPENDIX C: Refereed Conference Papers

C1 **Johnston, D J** and **Moore, K L** (2005). " 'Stocktake' - genetic audit software for Australian seedstock beef producers." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.161-164.

C2 **Meyer, K** (2005). "Estimates of covariance functions for growth of Angus cattle from random regression analyses fitting B-spline functions." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.52-55.

C3 **Meyer, K** (2005). "Ordering strategies to reduce computational requirements in variance component estimation." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.282-285.

C4 **Meyer, K** (2005). "Reduced rank estimates of the genetic covariance matrix for live ultra-sound scan traits." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.56-59.

C5 **Meyer, K** (2005). "Sampling behaviour of reduced rank estimates of genetic covariance functions." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.286-289.

C6 **Moore, K L; Johnston, D J** and Burrow, H M (2005). "Sire breed differences for net feed intake in feedlot finished beef cattle." In Proceedings of the 16th Conference of the Association for the Advancement of Animal Breeding and Genetics. Noosa, Australia. September 25-28. pp.76-79.

C7 **Barwick, S A; Henzell, A L** and **McCann, A R** (2007). "Evaluating Australian bulls on indexes of other countries and international bulls on Australian indexes." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.521-524.

C8 **Donoghue, K A; Johnston, D J** and **Graser, H-U** (2007). "Impact of addition of new herds on genetic parameter estimates in the Australian Brahman population." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.352-355.

C9 Gubbins, T and **Upton, W H** (2007). "Breeding Program Design Initiatives." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.16-21.

C10 **Jeyaruban, M G; Johnston, D J** and **Graser, H-U** (2007). "Development of a genetic evaluation system for structural soundness traits in Angus cattle." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.391-394.

C11 **Johnston, D J** (2007). "Genetic trends in Australian beef cattle – Making real progress." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.8-15.

C12 **Johnston, D J; Brown, D J** and **Graser, H-U** (2007). "The effect of age slicing interval on the variance components and data effectiveness for birth and 200day weights in Angus cattle." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.344-347.

C13 Khatkar, M S; Zenger, K R; Cavanagh, J A L; Hawken, R J; Hobbs, M; Barris, W; Thomson, P C; Nicholas, F W; **Tier, B** and Raadsma, H W (2007). "Extent of linkage disequilibrium and haplotype blocks in bovine genome using high density SNP markers." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.215-218.

C14 **Meyer, K** (2007). "Performance of REML algorithms in multivariate analyses fitting reduced rank and factor-analytic models." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.280-283.

C15 **Meyer, K** (2007). "Covariance structures for quantitative genetic analyses." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.142-149.

C16 **Meyer, K** (2007). "Scope for estimation of variances due to sex-linked, maternal and dominance effects in mixed model analyses." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.407-410.

C17 **Meyer, K** and Kirkpatrick, M (2007). "A note on bias in reduced rank estimates of covariance matrices." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.154-157.

C18 Nicol, D C and **Upton W H** (2007). "Breedleader™ – advanced breeding and genetics short course for beef seedstock producers." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.175-178.

C19 **Upton, W H**; Nicol, D C and Freer, R E (2007). "Overcoming barriers to adoption of genetic technologies in the beef industry." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.158-166.

C20 **Wolcott, M L; Johnston, D J; Barwick, S A** and Thompson, J M (2007). "Genetics of meat quality traits in two tropically adapted genotypes of beef cattle 1. Genetic parameters and correlations." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.356-359.

C21 **Worsnop, C D; Johnston, D J** and **Graser, H-U** (2007). "Accounting for selective slaughter over time when estimating breeding values for carcase traits – a simulation study." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.364-367.

C22 Banks, R G; Burrow, H and **Graser, H-U** (2009). "Progress in development and implementation of a strategy for commercialisation of DNA marker technology for the Australian beef industry."

Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.22-25.

C23 **Barwick, S A; Johnston, D J; Wolcott, M L**; Wilkins, J F and McKiernan, W A (2009). "Evaluation of the Angus BREEDPLAN IMF% EBV in 100d-fed Angus x Hereford steer progeny." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.484-487.

C24 **Jeyaruban, M G; Johnston, D J and Graser, H-G** (2009). "Factor-I, growth and ultrasound scanned traits in Angus cattle." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.584-587.

C25 **Johnston, D J; Tier, B and Graser, H-U** (2009). "Integration of DNA markers into BREEDPLAN EBVs." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.30-33.

C26 **Meyer, K** (2009). "Factor-analytic models to reduce computational requirements in international genetic evaluation for beef cattle." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.442-445.

C27 **Meyer, K** (2009). "Survival analyses for length of productive life on Angus cows." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.608-611.

C28 **Meyer, K** and Kirkpatrick, M (2009). "Cheverud revisited: Scope for joint modelling of genetic and environmental covariance matrices." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.438-441.

C29 **Moore, K L**; Gibson, J and **Johnston, D J** (2009). "The effect of linkage disequilibrium on the estimates of Single Nucleotinde Polymorphic effects." Proceedings of the British Society of Animal Science. Southport, UK. March 30 – 1 April 2009. p044

C30 **Zhang, Y D and Tier, B** (2009). "Population stratification, not genotype error, causes some SNPs to depart from Hardy-Weinberg Equilibrium." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.243-246.

C31 **Zhang, Y D and Tier, B** (2009). "Cattle residual feed intake candidate genes." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.664-667.

Associated

C32 **Iker, C; Wolcott, M L; Johnston, D J** and Thompson, J M (2007). "Genetics of meat quality traits in two tropically adapted genotypes of beef cattle 2. Influence of tenderstretching." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.360-363.

C33 **Khusro, M; Brown, D J; Graser, H-U** and **Tier, B** (2007). "The effect of linkage and flock size on the accuracy of estimated genetic group effects." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.545-548.

C34 Corbet, N J; Prayaga, K C; **Johnston, D J** and Burrow, H M (2007). "Genetic variation in adaptive traits of cattle in north Australia." Proceedings of the 17th Conference of the Association for the Advancement of Animal Breeding and Genetics. Armidale, Australia. September 24-26. pp.348-351.

C35 Corbet, N J; Burns, B M; Corbet, D H; **Johnston, D J**; Crisp, J M; McGowan, M R; Prayaga, K C; Venus, B K and Holroyd, R G (2009). "Genetic variation in growth, hormonal and seminal traits of young tropically adapted bulls." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.121-124.

C36 Prayaga, K C; Mariasegaram, M; Harrison, B; **Tier, B**; Henshall, J M and Barendse, W (2009). "Genetic markers for polled condition in cattle – the current status and the future plans." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.92-95.

C37 **Wolcott, M L and Johnston, D J** (2009). "The impact of genetic markers for tenderness on steer carcass and feedlot exit and heifer puberty traits in Brahman cattle." Proceedings of the 18th Conference of the Association for the Advancement of Animal Breeding and Genetics. Barossa Valley, South Australia. September 28-October 1. pp.159-162.

APPENDIX I (Internal research documents)

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