



Final report

Wagyu Collaborative Genetics Research Project – Stage 2

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Abstract

In 2015 the Wagyu breed didn't have Estimated Breeding Values (EBVs) for carcass traits using genetic parameters which were calculated from Wagyu data. Furthermore, only a limited number of sires had carcass EBVs published. The traditional beef industry model where seedstock breeders bred and then collected performance data on their animals wasn't feasible for Wagyu.

It was essential to facilitate the genotyping and recording of large volumes of carcass data from commercial enterprises. To enable this there needed to be significant changes made to the Wagyu recording system. A Single Nucleotide Polymorphism (SNP) genotype database had to be developed and a register for Wagyu content animals had to be approved by the AWA board and implemented.

This project made a very significant contribution to the implementation of Single-Step Wagyu BREEDPLAN which produce carcass EBVs for Marble Score and Marbling Fineness, and enhanced Carcass Weight and Eye Muscle Area EBVs using actual carcass data, Japanese Carcass Camera records and genomic information. The new Wagyu carcass EBVs also made it possible to develop four BreedObject Indexes.

Each month the Wagyu pedigree, performance and genomic data are extracted for analysis and the EBVs and Indexes loaded into the Wagyu database for publication on the AWA website Animal Search database. A comprehensive Wagyu Breeding Guide lists high accuracy Wagyu sires and dams ranked in carcass EBV and Index order with complete explanations.

Executive summary

Background

Research results from P.PSH.0646 showed that AUS-MEAT and Japanese Carcase Camera records have high genetic correlations and that carcase EBV traits Marble Score, Marble Fineness and Eye Muscle Area have moderately-high heritabilities.

This project was initiated to facilitate the collection of 5,000 carcase records and genotypes to help establish a genomic analysis and assist with the calculation of Wagyu specific variance components and genetic parameters to enable the calculation of highly accurate Single Step Wagyu EBVs. These EBVs would in turn allow the development and calculation of Wagyu specific BreedObject Indexes.

The whole Wagyu industry would benefit from highly accurate EBVs and Indexes by improving the accuracy of selection of parents and the genetic improvement of breeding and feeder animals. The benefit of identifying genetically superior parents and increasing their use in the Wagyu supply chain will reduce the proportion of animals with unacceptable carcase quality. The cost of feeding Wagyu and Wagyu cross animals for 400 to 600 days is very high and if the number of animals with low marbling and/or carcase weight can be reduced, it will have a positive effect on the profitability of the Wagyu industry.

Objectives

The genomically enhanced EBVs and the single step genomic BREEDPLAN analysis produced in P.PSH.0646 will be incorporated in the production Wagyu GROUP BREEDPLAN analysis. Predictive genomic performance tests will be developed and commercialised for breeding and commercial feedlot slaughter animals. A new business model will be developed to enable collection of large numbers of genomic and phenotypic records needed to build and maintain the accuracy of the genomically enhanced EBVs. Promising young sires will be identified and their widespread use encouraged across Wagyu breeding herds supplying performance data, reducing genetic interval and further increasing genetic gain.

This project will increase the rate of genetic gain of Australian Fullblood/Purebred Wagyu at a faster rate than any other Australian beef breed over the next ten years, by developing a low-cost, whole of Wagyu industry genetic advancement model.

Methodology

This project used a novel approach to the Beef Information Nucleus concept. It utilised the Australian Wagyu industry's unique commercially focused structure, combining its large volumes of phenotypic production data from the vertically integrated commercial producer base, and the latest advances in genomic technology to rapidly increase the breed's rate of genetic gain.

Genomic information combined with the phenotypic information collected through this project helped with the estimation of genetic parameters and was used in Wagyu BREEDPLAN analysis when Single Step was implemented for the Wagyu breed in April 2018.

Results/key findings

All the objectives of this project have been successfully achieved through the completion of the activities described below.

The development and implementation of a Wagyu specific SNP Database and the loading of all available Wagyu genotypes into this database was an important first step to facilitate a genomic analysis. The subsequent capture and recording of large volumes of commercial progeny performance records from birth to carcass supplied critical information for the implementation of a genomic analysis for the Wagyu breed. The use of the digital carcass camera and the incorporation of AUS-MEAT data assisted to obtain large volumes of carcass data which assisted with the development of Wagyu specific EBVs for carcass quality traits.

The availability of the above data made it possible to implement Single-Step BREEDPLAN for Wagyu in April 2018 which delivered genomic EBVs to the Wagyu industry. The genomic EBVs made it possible to then develop four additional BreedObject Indexes which focus on Wagyu specific production systems and markets.

The development and validation of a genomic test to determine the percentage Wagyu content of an animal was necessary to facilitate the registration and performance recording of “unknown” Purebred animals with no pedigree as “base” animals in a performance register. This helped to establish a SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals.

A Matesel service was established using the genomically enhanced EBV and BreedObject Indexes to help members optimise matings to increase genetic progress while reducing inbreeding at the same time. This Matesel service also assisted several members to establish their own progeny test programs to identify promising young sires.

Benefits to industry

This project contributed very significantly in making the implementation of Single-Step BREEDPLAN for Wagyu possible. It also facilitated the development of Wagyu specific carcass EBVs to improve the carcass quality of commercial slaughter animals. Once genomic EBVs were implemented it assisted with the development of four BreedObject Indexes. These EBVs and Index values makes it possible for Wagyu breeders to now accurately select superior breeding animals and to make rapid genetic progress in the highly valuable Wagyu carcass traits. These developments fast tracked the genetic development of the Wagyu breed and will, for many years to come, greatly benefit all segments of the Australian Beef industry which use Wagyu genetics and depend on animals with superior genetics to increase their profitability.

Future research and recommendations

The AWA regards the collection of performance data from genotyped Wagyu animals as a very high priority. To build on the achievements of this project and further expand the existing reference population, the AWA designed and implemented a progeny test program. The first round of progeny test matings, using 38 bulls, have already been completed.

Table of contents

Executive summary.....	3
1. Background.....	7
2. Objectives.....	9
3. Methodology.....	9
3.1 Implement a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcase and Weight traits – COMPLETED.....	9
3.2 Develop and validate a genomic test to determine the percentage Wagyu content of an animal – COMPLETED.....	10
3.3 Design a Project Plan for Stage 2 to achieve the best technical and business outcomes for the Wagyu breed’s genetic improvement – COMPLETED.	11
3.4 Stage 2 - A new business model for AWA which involves:.....	11
3.4.1 Capture and record large volumes of commercial progeny performance records from birth to carcase – COMPLETED.....	11
3.4.2 Register and performance record “unknown” Purebred animals with no pedigree as “base” animals in a performance register – COMPLETED.....	12
3.4.3 Use the Japanese carcase camera to obtain large volumes of carcase data for research purposes – COMPLETED.	12
3.4.4 Establish SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals – COMPLETED.....	12
3.4.5 Establish a MateSel service using SNP based relationships and genomically enhanced EBV performance prediction – COMPLETED.	13
3.4.6 Establish a Young Sire Program – COMPLETED.....	13
3.5 Wagyu Group BREEDPLAN tailored to best meet the needs of Australian Wagyu production:.....	14
3.5.1 Incorporate AUS-MEAT and camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry – COMPLETED.....	14
3.5.2 Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis – COMPLETED.....	14
3.5.3 Develop additional BreedObject Indexes which include the new carcass EBVs – COMPLETED.....	14
3.6 Increase the accuracy of Wagyu genomic EBVs – COMPLETED.	15

4.	Results	15
4.1	Implemented a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcase and Weight traits.	15
4.2	Developed and validated a genomic test to determine the percentage Wagyu content of an animal.....	16
4.3	Designed a Project Plan to achieve the best technical and business outcomes for the Wagyu breed’s genetic improvement which involved the following:.....	16
4.3.1	Captured and recorded large volumes of commercial progeny performance records from birth to carcase.	16
4.4	Wagyu Group BREEDPLAN tailored to best meet the needs of Australian Wagyu production:.....	17
4.4.1	Incorporate AUS-MEAT and Japanese carcase camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry.....	17
4.4.2	Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis.....	17
4.4.3	Develop additional BreedObject Indexes which include the new carcass EBVs.	17
5.	Conclusion	22
5.1	Key findings	23
5.2	Benefits to industry.....	23

1. Background

The Australian Wagyu industry has rapidly emerged over the past 20 years to be a very significant component of the Australian beef industry. High marbling (MSA Marble Score 6 through to 9+) has differentiated Wagyu from all other breeds, creating very significant domestic and international demand in retail sectors where highest quality is the hallmark. Very high meat value is accelerating both Wagyu Fullblood and Crossbred Wagyu production.

Revered in Japan, highest quality Wagyu in Japan sells for over \$1000/kg. Wagyu has developed world-wide recognition in a few short years as the elite beef product. The Wagyu brand is recognised world-wide by the top chefs as the most desirable beef product to use, with that reputation translating to customers and their desire for the product in their own cooking. This is due to Wagyu's excellent eating quality and food health status. High levels of marbling (intramuscular fat) comprising high proportions of unsaturated fatty acids are the key to these claims.

As marbling and meat texture were the primary considerations in Japanese breeding, little consideration was given for other production traits. In addition, the Japanese animals were mostly small, with the cattle being individually hand-fed in close confines. Wagyu live cattle, semen and embryos were exported from Japan through the USA to Australia during a brief four year window in the 1990's before the Japanese government closed the trade through breeder pressure, on the basis of Wagyu being a "National Treasure". As a result, the breed outside Japan has a very limited gene pool, with virtually no prospect of further genetic exports from Japan.

Australian beef production requires a more holistic trait balance including fertility, maternal, growth and feed efficiency while maintaining elite carcass quality and genetic diversity. Continuous genetic improvement of the limited Wagyu gene pool is vital.

The Australian Wagyu Association (AWA) in association with the MLA Donor Company have undertaken the Wagyu Collaborative Genetics Research (WCGR) Project Stage 1 (P.PSH.0646) and Stage 2 (P.PSH.0715).

Stage 1 was started in 2012 to identify, determine and establish EBVs relevant to the Wagyu breed. It involved collection of performance and pedigree data on up to 3,920 Wagyu animals, including data collected using the Japanese Digital Camera Image Analysis methodology. Genotypes were collected on 2,147 Wagyu animals.

The analysis of the above-mentioned collected performance, pedigree and genotype data was done in two phases. The first phase of the data analysis used traditional pedigrees and a univariate analysis for each recorded trait (univariate meaning that trait is analysed on its own). Subsequent to univariate analysis, a series of bivariate analyses (2 traits at a time) to estimate the genetic relationship or correlation between the pairs of traits.

Some important results from Phase 1 were:

- Carcass marbling, whether measured using the carcass camera (CCMP) or via AUS-MEAT score (CMAU), is moderately to highly heritable (current estimate for heritability is 0.52 for CMAU and 0.35 for CCMP)
- Carcass Marbling Fineness Index is moderately to highly heritable (0.50)
- The two measures of carcass marbling (CCMP and CMAU) are genetically essentially the same trait (genetic correlation = 1.00).

- Carcase Eye Muscle Area and Camera Rib Eye Area are both moderately-highly heritable (heritability of 0.56 and 0.62 respectively), and strongly correlated genetically (correlation = 0.83)
- The distribution of Carcase AUS-MEAT Marble Scores suggests that actual marbling extends well past AUS-MEAT Score 9 – the overall mean is 7.4, and if the trait is normally distributed, there would be approximately 17% of the total sample > score 9, 6% >10, 2% >11 and 1% >12.
- There is considerable variation in estimated marbling % within a Carcase AUS-MEAT Marble Score, and the variation appears to increase as marble score increases.
- There was still some suggestion of data harvesting impacting the results. The analysis found a subset of animals with low Carcase and Camera EMA, suggesting these animals may have been killed much lighter – either as an identified separate cohort, or possibly simply lighter weight and possibly “condition” animals culled out from cohorts earlier.

At the completion of Phase 1, Sire Research Breeding Values were available from these univariate analyses which used traditional pedigree information.

Phase 2 of P.PSH.0646’s data analysis involved the use of a genomic relationship matrix analysis. This second phase essentially repeated Phase 1, except it replaced, where an animal had a genotype, the pedigree relationship between animals with the more precise genomic relationship. The results from GBLUP showed the carcase traits (most were measured using camera images) were highly heritable. For most traits the heritability estimates from GBLUP were higher than or similar to those from the pedigree based BLUP using the bigger dataset, eg CWT, CCRA. For marbling traits (CCMP and CMAU) the GBLUP results were higher than those from the traditional pedigree Phase 1 analyses. The genetic correlations between the carcase marbling measures (CCMP vs CMAU) and between values for eye muscle area measured by camera images and by the traditional method were the same as the results from BLUP analyses. The Carcase marbling fineness (CCFI) were also highly correlated with marbling measures (CCMP and CMAU).

The GEBVs of 22 sires whose progeny had genotypes and carcase weights were highly correlated with their BLUP EBVs. The correlations between GEBV and EBV were all around 0.6 to 0.9, with slightly greater spread in all cases (reflecting the increased heritability estimates for the traits).

Key points from Phase 2 were:

- The dataset has proved amenable to use genomic information in estimating genetic parameters and hence estimating breeding values.
- The results from the genomic analysis confirmed and in general slightly improved those from a pedigree analysis.
- The key messages about the genetics of key traits remained:
 - There was substantial genetic variation for all the traits of interest, indicating that if the breed wished to make genetic improvement of marbling, carcase weight at constant age, muscling etc, there is plenty of scope to do so.
 - Selection for combinations of traits is possible.
- The dataset and research established the concept that genotyping can be a useful tool for the Wagyu breeder and producer – both in use in selection, and for use in sorting animals for production.

2. Objectives

This project has been designed to achieve the best technical and business outcomes for the Wagyu breed's genetic improvement. It aims at building on the platform created in Stage 1 (P.PSH.0646) and moving to full implementation and commercialisation of Single-Step BREEDPLAN EBVs for the Wagyu breed.

To enable a Single-Step BREEDPLAN analysis for the Wagyu breed it was necessary to complete the following:

- Develop and implement a SNP database to store all available Wagyu genotypes.
- Implement a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcase and Weight traits.
- Incorporate AUS-MEAT and camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry.
- Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis.
- Develop additional BreedObject Indexes which include the new carcass EBVs.
- Develop and validate a genomic test to determine the percentage Wagyu content of an animal.
- Capture and record large volumes of commercial progeny performance records from birth to carcase and where possible genotype these animals.
- Register and performance record “unknown” Purebred animals with no pedigree as “base” animals in a performance register.
- Use the digital carcase camera to obtain large volumes of carcase data for research purposes.
- Establish a SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals.
- Establish a MateSel service using SNP based relationships and genomically enhanced EBV performance prediction.
- Establish a Young Sire Program.

3. Methodology

3.1 Implement a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcase and Weight traits – COMPLETED.

P.PSH.0646 collected data from large cohorts of predominantly Fullblood/Purebred Wagyu progeny from large commercial Wagyu producer operations. This delivered 3,920 performance recorded animals (which included data collected using the Japanese Carcase Camera) and just over 2,147 genotypes. Analysis of the carcase camera records, AUS-MEAT kill sheet data and MSA grading data have delivered new research Estimated Breeding Values (EBVs) for Rib Eye Area, Marbling Percentage and Fineness of Marbling from the imaging and Carcase weight, Marbling Score and P8 Fat from the AUS-MEAT and MSA data.

The data captured as part of P.PSH.0646 was analysed as two distinctive phases. Phase 1 comprised of traditional pedigree analysis which demonstrated that it is possible to collect and genetically

analyse detailed carcass information on commercial Wagyu animals. The results obtained from the phase 1 analysis showed that:

- Carcass marbling, whether measured using the camera or via AUS-MEAT score, is moderately to highly heritable (current estimate for heritability is 0.52 for CMAU and 0.35 for CCMP);
- Carcass Marbling Fineness Index is moderately-highly heritable (0.50);
- The two measures of carcass marbling (CCMP and CMAU) are genetically essentially the same trait (genetic correlation = 1.00) and
- Carcass Eye Muscle Area and Camera Rib Eye Area are both moderately-highly heritable (heritability of 0.56 and 0.62 respectively) with a strong genetic correlation (0.83).

Phase 2 comprised a Genomic relationship matrix G analysis (GBLUP) and found the carcass traits are highly heritable and for most traits the heritability estimates from GBLUP are higher than or similar to those from the pedigree based BLUP. The genetic correlations between the carcass marbling measures (CCMP vs CMAU) and between values for eye muscle area measured by camera images and by the traditional method were unity, as in the BLUP analyses (phase1). The Carcass marbling fineness or coarseness indices (CCFI and CCCI) are also highly correlated with marbling measures (CCMP and CMAU). The GEBVs were highly correlated with their BLUP EBVs.

This project identified the need for several developments and the importance of the registration, collection of data and genotyping of large numbers of commercial animals to enable the implementation of Single-Step Wagyu Breedplan. These prerequisites for a genomic BREEDPLAN analysis were addressed in the following ways:

- In November 2015 the Australian Business Research Institute (ABRI) was requested to develop a SNP database for the AWA and this was implemented in July 2016. All available genotypes were loaded into this database.
- The AWA board approved the development and implementation of a Slaughter Register to enable the recording of commercial Wagyu animals and the ability to link performance data and genotypes to those animals.
- Large volumes of commercial progeny performance records from birth to carcass and genotypes were collected and loaded into the Wagyu system.
- The Japanese carcass camera was used to obtain large volumes of carcass data.

In April 2018 Single-Step Wagyu BREEDPLAN was implemented which, in addition to standard BREEDPLAN EBVs, produce carcass EBVs for Marble Score and Marbling Fineness using actual carcass data, Japanese carcass camera records and genomic information stored in the Wagyu system.

3.2 Develop and validate a genomic test to determine the percentage Wagyu content of an animal – COMPLETED.

The Animal Genetic and Breeding Unit (AGBU) have completed breed composition analysis software which analyse SNP genotypes and provides the percentage breed composition from the genotype. The test was validated using 1100 known Wagyu content Fullblood and crossbred genotypes.

This genomic test is also used in Single-Step BREEDPLAN to determine the genomic relationship of a genotype to the breed's allele frequencies and serve as an important quality assurance check to determine if the genotype should be used in the analysis.

The AGBU developed algorithm calculate an animal's Breed Percentage through the following steps:

- The allele frequencies for the different breeds included in the reference dataset are calculated
- the allele frequencies for the specific animal is calculated
- the correlation between the breed and animal's allele frequencies are calculated - this represents the animal's Breed percentages.

AWA have used this solution to develop a Wagyu Content Test with the results enabling the registration of animals with identified Wagyu content into the Wagyu Content Register. This enables many animals with Wagyu content to be identified, registered and performance recorded to further increase EBV accuracy and for the first time describe the Wagyu-type herd performance more accurately.

3.3 Design a Project Plan for Stage 2 to achieve the best technical and business outcomes for the Wagyu breed's genetic improvement – COMPLETED.

A project plan was designed by involving AGBU and ABRI technical staff to consider weaknesses and future opportunities for the Wagyu breed. The planning sessions identified several areas which needed urgent action to ensure the breed is appropriated positioned to remain relevant in a rapidly changing beef industry. The following were identified as the most urgent actions to be taken:

- Capture and record large volumes of commercial progeny performance records from birth to carcass.
- Register and performance record "unknown" Purebred animals with no pedigree as "base" animals in a performance register.
- Use the digital carcass camera to obtain large volumes of carcass data for research purposes.
- Establish SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals.
- Establish a MateSel service using genomically enhanced EBVs.
- Establish a Young Sire Program

3.4 Stage 2 - A new business model for AWA which involves:

3.4.1 Capture and record large volumes of commercial progeny performance records from birth to carcass – COMPLETED.

In 2015 there was still a large number of Wagyu members who were very sceptical of the ability of BREEDPLAN to accurately predict the genetic merit of Wagyu animals. This situation had the potential to severely impede the future genetic improvement of the breed and had to be addressed as a matter of urgency.

The one way to increase confidence in BREEDPLAN was to facilitate the loading of large volumes of performance records and then to ensure the appropriate genetic parameters are used to calculate Wagyu EBVs.

The necessary registration and performance recording processes were approved by the AWA board and implemented to allow registration of commercial (performance tested) animals at no cost to the member.

Several technical workshops were conducted across Australia to educate Wagyu members regarding BREEDPLAN and the importance of recording accurate performance information in as large as possible contemporary groups. The same workshops were also used to introduce members to future opportunities to use genomic information for the estimation of genetic merit of animals.

3.4.2 Register and performance record “unknown” Purebred animals with no pedigree as “base” animals in a performance register – COMPLETED.

In January 2016 the AWA board approved the development of the Wagyu Content Register which made it possible to register and performance record Wagyu animals with limited pedigree in the AWA registration system. These animals then allowed their progeny to be parent verified, registered and performance recorded to increase the number of performance records available for the BREEDPLAN analysis.

Most animals in this register are now in their third and fourth generation, parent verified and genotyped through high density SNP testing and an important source of pedigree and performance data for the BREEDPLAN analysis.

3.4.3 Use the Japanese carcass camera to obtain large volumes of carcass data for research purposes – COMPLETED.

The Japanese Digital Carcass Camera is operation in most abattoirs processing large numbers of Wagyu or Wagyu influenced animals with results loaded into the Wagyu database.

The Japanese digital carcass camera and analysis have been extremely valuable to Wagyu, providing accurate Marbling Percentage, Marbling Fineness and Eye Muscle Area analysed traits.

In November 2015 a new BREEDPLAN model was implemented for Wagyu which calculated carcass EBVs for Marble Score and Marbling Fineness, and enhanced Carcass Weight and Eye Muscle Area EBVs using actual carcass data as well as Japanese Carcass Camera records.

3.4.4 Establish SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals – COMPLETED.

Single-Step BREEDPLAN was trialled by AGBU in Stage 1 and found to be very promising and was necessary to allow the calculation of breeding values for un-phenotyped by including their SNP genotypes in the analysis.

To make SNP genotypes available to the BREEDPLAN analysis all the genotypes need to be stored in a database which is accessible.

At the request of AWA, ABRI developed and implemented a SNP database for Wagyu. AWA loaded historic SNPs which were previously stored at AGBU and the University of Queensland into the AWA SNP database.

Since the implementation of Single-Step Wagyu BREEDPLAN in April 2018, EBVs are calculated and published for un-phenotyped Wagyu animals which are genotyped. This allowed members to more accurately do initial selection of young breeding animals (mainly male calves) based on genomically enhanced carcass EBVs, including newly developed carcass quality traits, rather than only growth EBVs and visual appearance.

3.4.5 Establish a MateSel service using SNP based relationships and genomically enhanced EBV performance prediction – COMPLETED.

Wagyu live cattle, semen and embryos were exported from Japan through the USA to Australia during a brief four year window in the 1990's before the Japanese government closed the trade through breeder pressure, on the basis of Wagyu being a "National Treasure". As a result, the breed outside Japan has a very limited gene pool, with virtually no prospect of further genetic exports from Japan. In 2004 it was estimated the American Wagyu population had an effective population size of only 15 animals, placing Wagyu well below the threshold recommended for an "endangered" species.

The Australian Wagyu population originated from a relatively small number of animals which were exported from Japan. This limited founder genetic pool increases the risk of inbreeding which could lead to inbreeding depression in production traits, increased homozygosity of recessive genetic conditions and a reduction in genetic diversity.

To address this risk the AWA implemented a MateSel service to help members optimise their matings by reducing co-ancestry while increasing genetic merit of resultant progeny. The MateSel service is available to all AWA members and an analysis can be requested on an individual basis by contacting the AWA.

3.4.6 Establish a Young Sire Program – COMPLETED.

In 2015 Wagyu carcass EBVs expanded to the whole AWA database population and EBVs with 30% or higher accuracy (standard threshold for EBVs reportability) reported in website Animal Search displaying EBVs for over 80,000 registered animals. This development enabled members to search most of the registered Wagyu population on a range of EBVs.

For the first time, young Wagyu animals were reporting with up to 50% accuracy and the use of young bulls were encouraged at the November 2015 Wagyu Genetics workshop with 60 major breeder attendees. Many Wagyu breeders now also use the AWA MateSel service to identify promising young bulls and incorporate them in their own progeny test programs.

A Wagyu Sire Progeny Test Program emphasising young sire use and performance recording and NFI testing has been established. Program rules were developed and agreement reached with Kerwee Feedlot to provide Net Feed Intake testing through their GrowSafe bin feeders.

3.5 Wagyu Group BREEDPLAN tailored to best meet the needs of Australian Wagyu production:

3.5.1 Incorporate AUS-MEAT and camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry – COMPLETED.

Aus-Meat and carcass camera data have been incorporated in the November 2015 Wagyu BREEDPLAN analysis with this data used in the calculation of carcass EBVs. This development enabled Wagyu to, for the first time, open the Web Search Facility to include all animals and all traits. Before November 2015 Carcass EBVs were not available on the Wagyu Web Search Facility

Due to the substantial increase in the number of carcass records, variance components and genetic parameters were re-calculated for Wagyu and used when Single-Step BREEDPLAN was implemented for Wagyu in April 2018.

3.5.2 Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis – COMPLETED.

The AWA implemented Single-Step Wagyu BREEDPLAN in April 2018, utilising refined analysis and software improvements drawing solely on Wagyu performance data to deliver the world's first public Wagyu-specific genomic and pedigree analysis platform.

Significant improvements in EBVs that more closely reflected genetic relationships in Wagyu data was evident. As an example, 'high accuracy' sires with previous EBV accuracies of more than 75%, the EBV for Marble Score has decreased in range by approximately 1 EBV Marble Score unit. The previous top Marble Score sire had an MS EBV value of + 3.4. This is now + 2.6, but the same sire remains an industry leader for Marble Score.

The decrease in range for Marble Score is primarily due to the addition of genomic information in Single-Step Wagyu BREEDPLAN which has detected a higher genomic relationship between popular sires than was previously estimated by pedigree within standard Wagyu BREEDPLAN.

For high accuracy sires, the range in EBV for Carcass Weight has increased in range by 35 kgs. Previously, the highest Carcass Weight EBV among this group of sires was + 58.1 kg: the highest CWT EBV in this group of sires is now 75.0 kg. This increase in EBV range is largely due to the improved estimate of the heritability of Carcass Weight enabled by the substantially expanded Wagyu-only dataset.

These changes have been applied to the April 2018 Wagyu GROUP BREEDPLAN analysis and to all subsequent monthly analyses. The new Single-Step Wagyu BREEDPLAN model is based solely on Wagyu data and Wagyu EBVs are directly derived from Wagyu performance data. This means that Single-Step Wagyu BREEDPLAN is a World-first Wagyu specific genomic and pedigree analysis platform.

3.5.3 Develop additional BreedObject Indexes which include the new carcass EBVs – COMPLETED.

A Feedlot Terminal Index was the first Wagyu index which have been developed. It wasn't a BreedObject Index and only utilised the Carcass Weight EBV and the Marble Score EBV, being the traits which determine the price of Wagyu carcasses. The assumptions for this index was a 420kg carcass, a base price of \$8.50/kg carcass weight and an increase/decrease in value of the carcass of

\$1 per kilogram per marbling score. It is assumed that only half of the difference in EBVs will be passed on to the progeny because only half the genes come from the sire.

Following implementation of Single-Step Wagyu BREEDPLAN in April 2018, the AWA has worked intensively with AGBU to develop and deliver four new Wagyu BreedObject \$Indexes.

The four profitability \$Indexes are designed to optimise profit outcomes from commercial breeder, self-replacing, Fullblood terminal and F1 terminal production systems. The indexes are:

- Wagyu Breeder \$Index (WBI)
- Self-replacing Breeding \$Index (SRI)
- Wagyu Fullblood Terminal \$Index (FTI)
- Wagyu F1 Terminal \$Index (F1 Index)

Each of these \$Indexes are targeted specifically for a defined production and market scenario and that members can identify and use the index that best suits their situation.

The Wagyu Breeder Index aims to select bulls to produce profitable females for the production of steer progeny, while the Self-replacing Breeding Index can be used to select bulls that will produce more profitable females for retention in Fullblood or Purebred herds. The Fullblood Terminal and F1 Terminal Indexes can be used to select bulls that will produce more profitable slaughter progeny

3.6 Increase the accuracy of Wagyu genomic EBVs – COMPLETED.

Commercial Fullblood Wagyu slaughter animals were registered in the Wagyu Slaughter register and SNP genotyped using commercially available genomic (>24K) SNP chips. These genotypes and the carcass data collected on these animals were stored on the Wagyu system.

There were 4,963 commercial animals (the progeny of 474 bulls) which had carcass data recorded and had DNA samples available for genotyping. The sires of the commercial animals are from several of the major Wagyu seedstock herds and represented some animals and bloodlines which, previously, had very little carcass information recorded.

For the past five years a thousand commercial slaughter animals per year were registered. These animals were genotyped and also had carcass data collected.

The addition of this data, as well as high level of member interest and investment in data collection, made it necessary to re-calculate the Wagyu genetic parameters in 2018 and it is in the process of being re-estimated again as more data has continued to be added.

4. Results

4.1 Implemented a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcass and Weight traits.

Single-Step Wagyu BREEDPLAN was implemented for Wagyu in April 2018 and it included new Wagyu specific carcass quality EBVs for Marble Score and Marbling Fineness Index.

4.2 Developed and validated a genomic test to determine the percentage Wagyu content of an animal.

A genomic test was developed and implemented for Wagyu. The AWA board approved the use of the Crossbred Wagyu Test to permit the registration of commercial Wagyu animals.

4.3 Designed a Project Plan to achieve the best technical and business outcomes for the Wagyu breed's genetic improvement which involved the following:

4.3.1 Captured and recorded large volumes of commercial progeny performance records from birth to carcass.

The AWA board approved the implementation of a Slaughter Register to record commercial Wagyu slaughter animals at no cost to the breeder. This development encouraged the registration and submission of carcass data for large numbers of commercial animals which was previously not registered due to the cost involved.

4.3.2 Registered and performance recorded "unknown" Purebred animals with no pedigree as "base" animals in a performance register.

The implementation of the Crossbred Wagyu Test and Slaughter Register facilitated the recording and capture of performance data and genotypes of "unknown" Wagyu animals. The availability of genotypes for these animals made it possible to include their performance data into the Single-Step Wagyu BREEDPLAN analysis.

4.3.3 Use the Japanese carcass camera to obtain large volumes of carcass data.

The Japanese carcass camera is used in the major Wagyu processing abattoirs to assess Wagyu specific carcass quality traits.

4.3.4 Establish SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals.

The implementation of Single-Step Wagyu BREEDPLAN enabled the use of genomic information to improve the estimation of the genetic merit of un-phenotyped Wagyu animals.

4.3.5 Establish a MateSel service using SNP based relationships and genomically enhanced EBV performance prediction.

Once the EBVs for carcass quality traits were published and BreedObject Indexes were developed, a MateSel service was established by the AWA. This service helps members to effectively manage inbreeding levels in their herds while increasing the genetic merit of the next generation.

4.3.6 Establish a Young Sire Program.

A young Sire Program was established to encourage the use of promising young bulls and the assist in the genotyping, collection of Net Feed Intake and carcass data. There are significant additional costs involved with Net Feed Intake testing and this is a factor limiting the support for this program. Many Wagyu breeders are now using genomically enhanced EBVs to select young bulls and use

these young bulls in their own progeny test programs. Therefore, the objectives of the Young Sire Program have been achieved by promoting the importance of identifying and using young bulls to find the next generation of high genetic merit sires.

4.4 Wagyu Group BREEDPLAN tailored to best meet the needs of Australian Wagyu production:

4.4.1 Incorporate AUS-MEAT and Japanese carcass camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry.

AUS-MEAT and Japanese carcass camera records are included in the Single-Step Wagyu BREEDPLAN analysis to calculate Wagyu specific EBVs for carcass quality traits (Marble Score and Marble Fineness Index).

4.4.2 Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis.

Single-Step Wagyu BREEDPLAN was implemented for Wagyu in April 2018 and it included new Wagyu specific carcass quality EBVs for Marble Score and Marbling Fineness Index.

4.4.3 Develop additional BreedObject Indexes which include the new carcass EBVs.

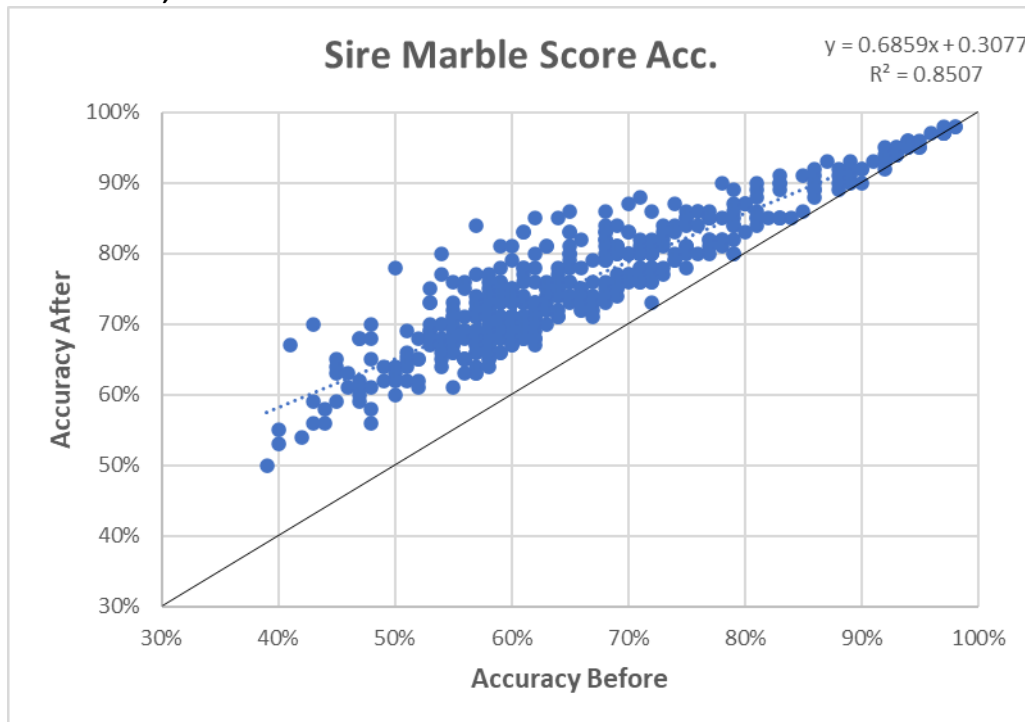
After the implementation of Single-Step Wagyu BREEDPLAN four BreedObject Indexes were developed for Wagyu.

The focus of this project was to register and collect large volumes of data and genotypes to enable the implementation of Single-Step Wagyu BREEDPLAN. To show the advantage of the additional data and genotypes it would be ideal to compare EBVs of sires and dams before and after project animals, performance data and genotypes were added to the analysis. However; the additional animals and information were added to each monthly Single-Step Wagyu BREEDPLAN analysis as it became available. The additional information was added on a very regular basis which made before and after analysis impossible.

Due to the regular addition of information, model and parameter changes, the only way to demonstrate the benefit of the genotypes and carcass records of the 4,963 commercial animals is by comparing the EBVs of their sires before and after the carcass data and genotypes were added to the analysis. To allow the comparison of EBVs and accuracy changes which could be attributed to the addition of the genotypes and carcass data, a special BREEDPLAN analysis was done using the data from the most recent analysis but removing the genotypes and carcass data of the 4,963 commercial animals. The benefits of the additional information, which this project provided to the Single-Step Wagyu BREEDPLAN analysis, is shown in below in Fig. 1. to Fig. 8.

The accuracy of an EBV is a good indication of the quality and quantity of data contributing to that EBV and an increase in the accuracy indicates that additional information was added to the analysis. The increase in the accuracy of the Marble Score EBV of sires is shown in Fig. 1. and this accuracy increase is also observed for the Carcass Weight, Eye Muscle Area and Marbling Fineness EBVs.

Figure 1. Comparison of Marble Score EBV accuracy of sires before and after the addition of the data of the 4,963 commercial animals.



When additional information is added to the Single-Step Wagyu BREEDPLAN analysis, one expects that it will influence the EBVs of all related animals. The additional information from performance recorded progeny will impact the EBVs of their parents in a positive or negative way. The before and after comparison of carcass EBVs of the sires are shown below in Fig. 2. to Fig. 5. The observed differences are remarkable, especially considering the number of other carcass records added by members outside of this project and is a clear indication of the substantial additional value this project added to the Wagyu genetic analysis.

Figure 2. Comparison of Carcase Weight EBV of sires before and after the addition of the data of the 4,963 commercial animals.

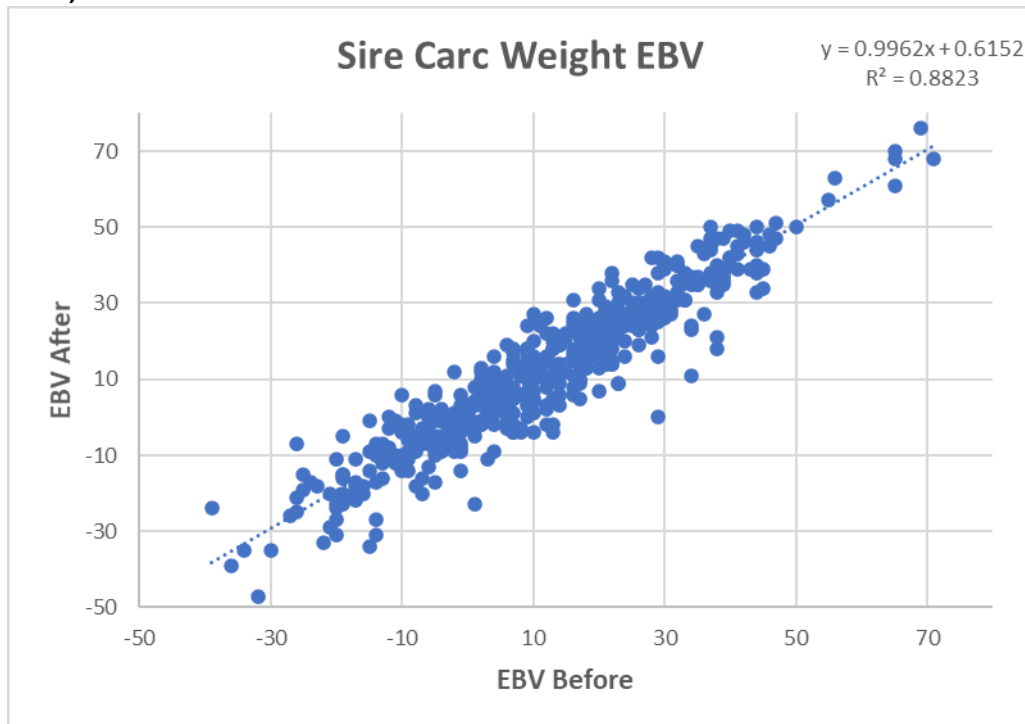


Figure 3. Comparison of Eye Muscle Area EBV of sires before and after the addition of the data of the 4,963 commercial animals.

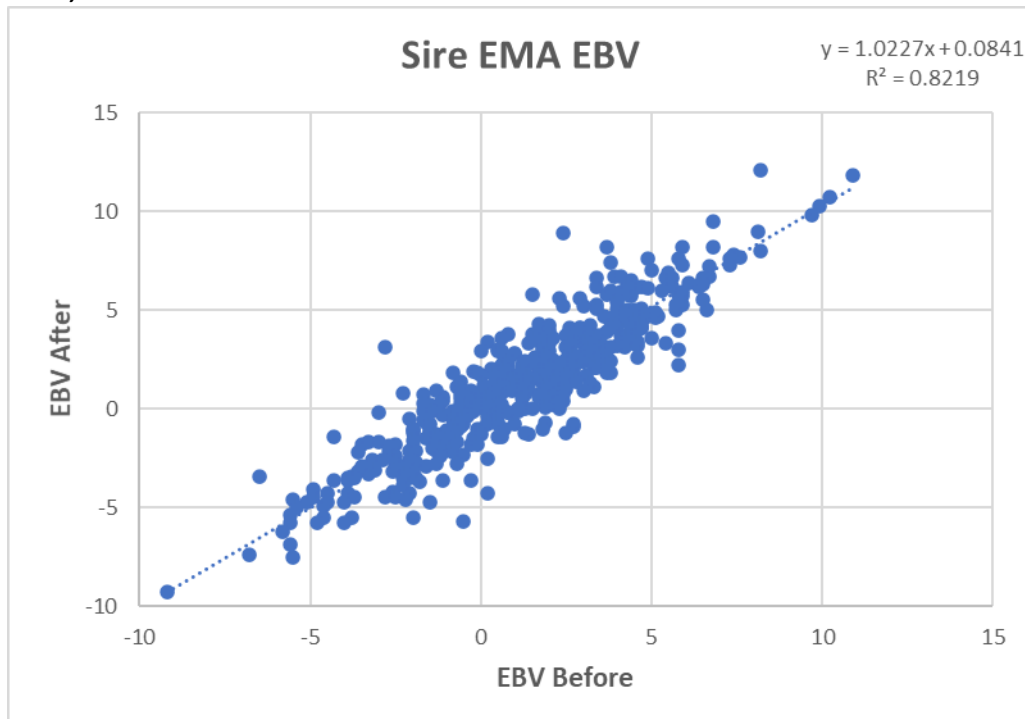


Figure 4. Comparison of Marble Score EBV of sires before and after the addition of the data of the 4,963 commercial animals.

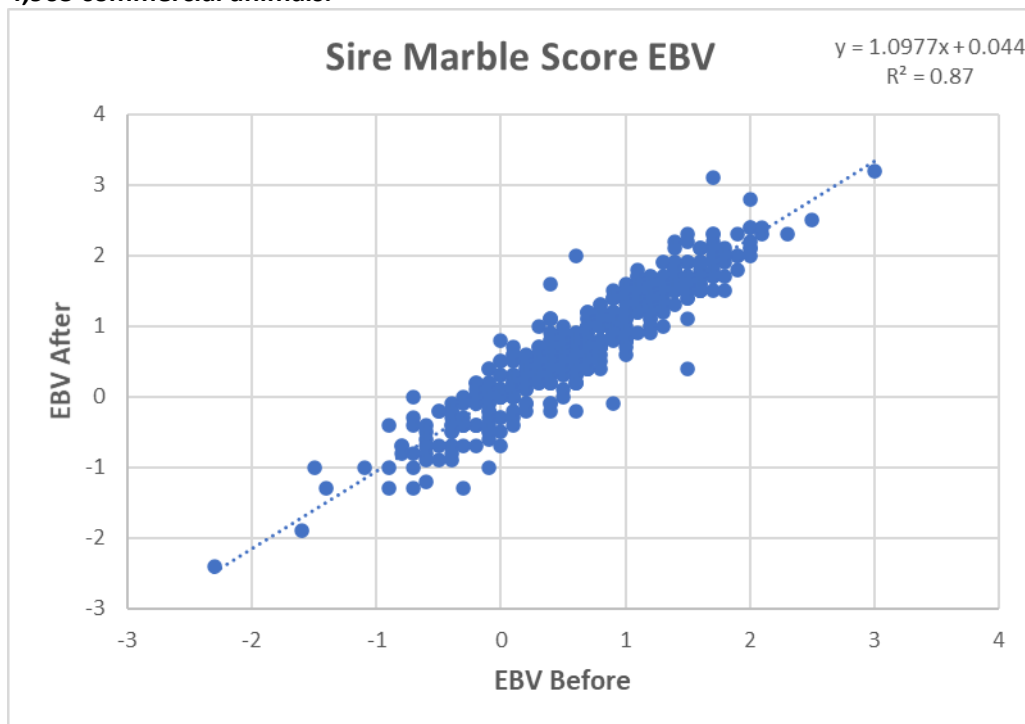
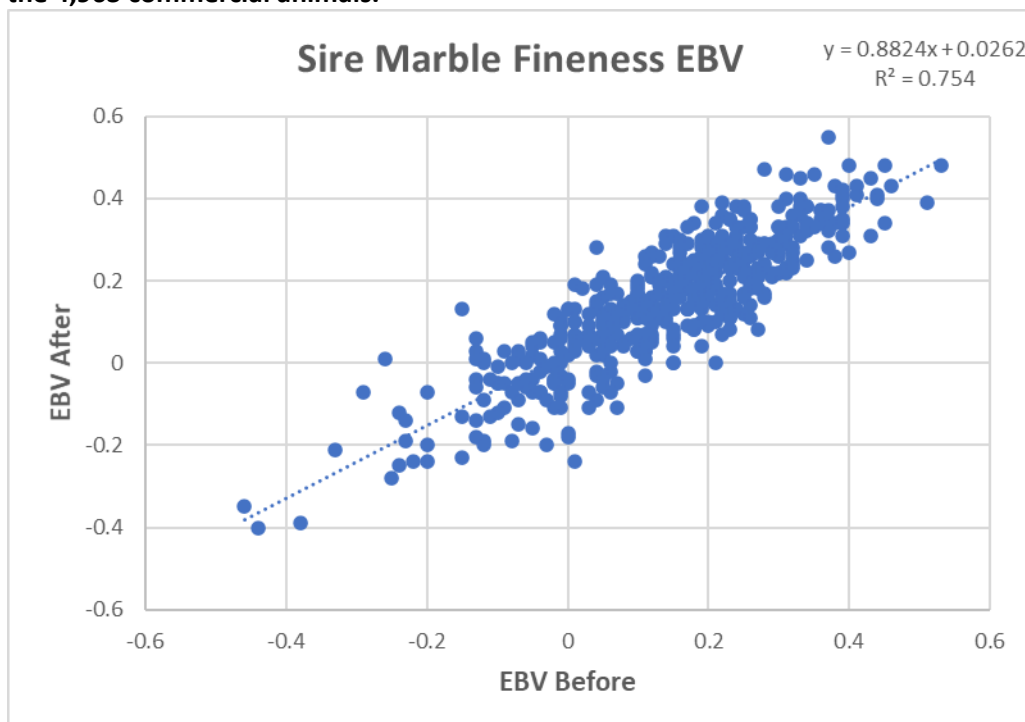


Figure 5. Comparison of Marble Fineness EBV of sires before and after the addition of the data of the 4,963 commercial animals.



When additional information is added to the Single-Step Wagyu BREEDPLAN analysis, one expects it will result in changes to EBVs. These changes in the EBVs will in turn result in changes to the BreedObject Index values of the relevant animals. The before and after comparison of the Self Replacing Index, Fullblood Terminal Index and F1 Terminal Index values of the sires are shown below in Fig. 6., Fig. 7. and Fig. 8. respectively. Some of the sires changed up or down by more than \$50.

The practical implications of these changes are that two animals which had the same Index value before the additional information was added, could differ with \$100 after the information was added. These differences clearly show the momentous commercial benefit of having more accurate EBVs available for the analysis.

Figure 6. Comparison of Self Replacing Index of sires before and after the addition of the data of the 4,963 commercial animals.

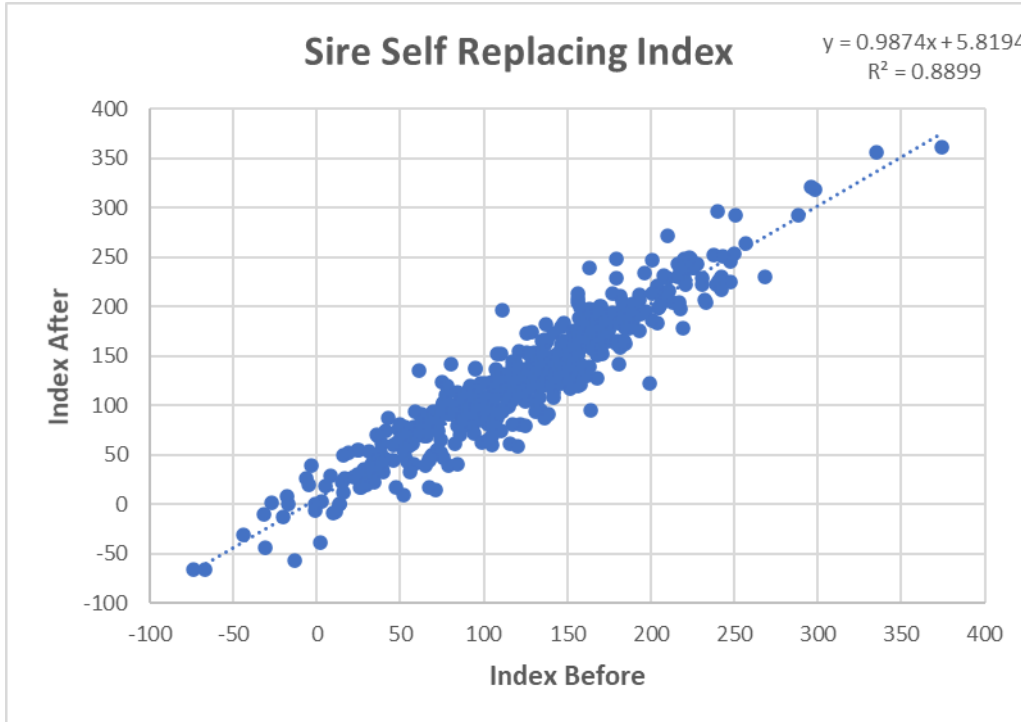


Figure 7. Comparison of Fullblood Terminal Index of sires before and after the addition of the data of the 4,963 commercial animals.

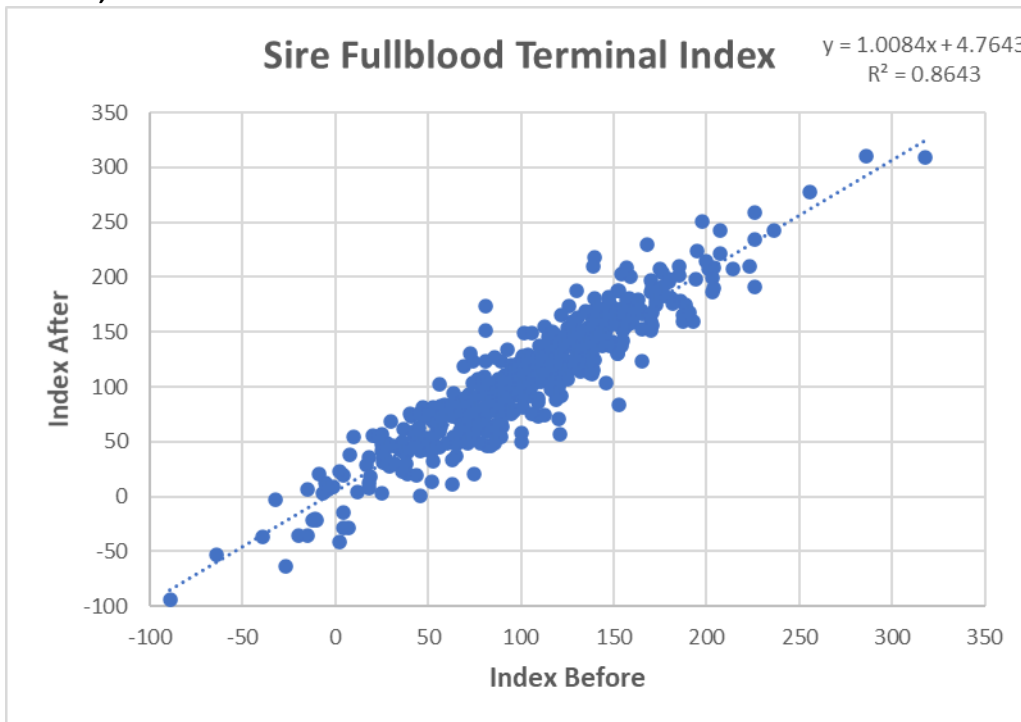
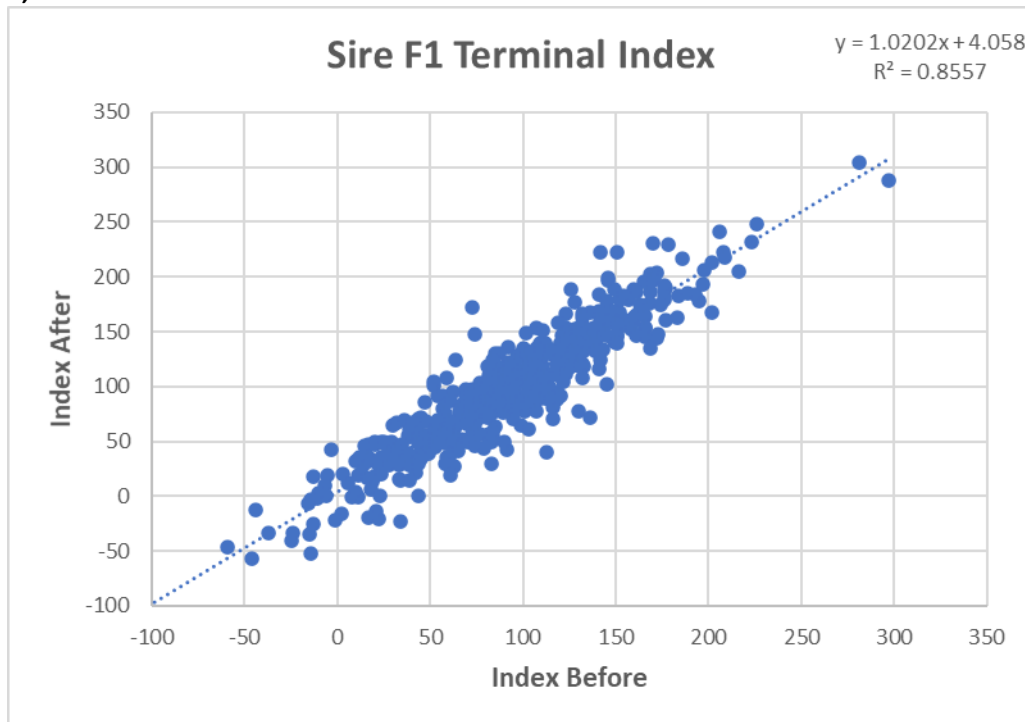


Figure 8. Comparison of F1 Terminal Index of sires before and after the addition of the data of the 4,963 commercial animals.



5. Conclusion

The purpose of this project was to achieve the best technical and business outcomes for the Wagyu breed's genetic improvement.

The implementation of a SNP database to store all available Wagyu genotypes and development of the Slaughter Register to enable the registration and collection of performance data on large numbers of commercial Wagyu animals were critical components to enable the implementation and commercialisation of Single-Step BREEDPLAN EBVs for the Wagyu breed.

The availability of genomically enhanced EBVs permitted the development of BreedObject Indexes which reflects the cost and income components of the major Wagyu production environments and markets.

Highly accurate EBVs and BreedObject Indexes are necessary to enable to use of MateSel. This project therefore also played a major role in allowing the AWA to supply a MateSel service to AWA member to increase genetic diversity while making substantial genetic progress in their herds.

The availability of accurate genetic information assist members to, at a much younger age, decide which animals will be kept as breeding stock and which will become progeny test animals which will be fed and killed to collect carcass data from.

5.1 Key findings

To achieve the best technical and business outcomes for the Wagyu breed's genetic improvement the following developments implemented, data collected and loaded and changes made to the AWA system:

- Develop and implement a SNP database to store all available Wagyu genotypes.
- Implement a genomic analysis representative of the Wagyu breed producing Wagyu EBVs for Carcase and Weight traits.
- Incorporate AUS-MEAT and camera data into the Wagyu BREEDPLAN analysis to produce and then communicate the new carcass EBVs to industry.
- Implement Single-Step BREEDPLAN for Wagyu to deliver genomic EBVs in the production analysis.
- Develop additional BreedObject Indexes which include the new EBVs specific for the improvement of Wagyu carcass quality traits.
- Develop and validate a genomic test to determine the percentage Wagyu content of an animal.
- Capture and record large volumes of commercial progeny performance records from birth to carcass and where possible genotype these animals.
- Register and performance record “unknown” Purebred animals with no pedigree as “base” animals in a performance register.
- Use the Japanese carcass camera to obtain large volumes of carcass data.
- Establish a SNP genomic test service to predict performance of un-phenotyped Fullblood/Purebred Wagyu animals.
- Establish a MateSel service using SNP based relationships and genomically enhanced EBV performance prediction.
- Establish a Young Sire Program.

5.2 Benefits to industry

This project played a pivotal part in revolutionising the Wagyu breed's genetic development by facilitating AWA system and regulatory changes to enable the genotyping, registration, and performance testing of large numbers of commercial Wagyu animals. This additional information underpinned the implementation of Single-Step BREEDPLAN EBVs, including new EBVs for Wagyu specific carcass quality traits, and BreedObject Indexes.

In addition to the substantial benefits of Wagyu breeders having access to these most accurate selection tools to drive genetic progress for a range of economically important traits to Wagyu production systems, it also allows Wagyu breeders access to MateSel to further accelerate genetic progress while managing genetic diversity.

The ability for Wagyu breeders to accurately select superior breeding animals and to make rapid genetic progress will greatly benefit all sectors of the Australian Beef industry which use Wagyu genetics. In addition to the Fullblood Wagyu producers the very substantial number of Wagyu X Angus F1 producers can select genetically superior Wagyu bulls using the F1 Terminal Index.