Final report

Genetics R&D: crossbred Wagyu data capture and analysis

Abstract

The Australian Wagyu Association's BREEDPLAN analysis historically only used Fullblood Wagyu performance data. With the rapidly growing demand for Fullblood seedstock, Fullblood slaughter animals are becoming more difficult to source.

The purpose of this project was to determine if crossbred Wagyu data can be used in the Wagyu BREEDPLAN analysis. If the data was found to contribute valuable information, it would be included in the Single-Step Wagyu BREEDPLAN analysis to improve the accuracy of the estimation of the genetic potential of a wide range of Wagyu animals.

Relationships were established with several commercial Wagyu producers and feedlots to secure large groups of animals for this project. At feedlot induction tissue samples were collected and submitted to Neogen for 100K genotyping. After the animals were harvested the feedlot supplied feedlot performance and carcase feedback information to the AWA.

 After the commercially produced crossbred Wagyu animals were recorded in the Australian Wagyu Association's (AWA) Slaughter register, the genotypes and carcase data of the 9,500 animals were loaded into the AWA database. These animals, their data and genotypes were supplied to the Animal Genetics and Breeding Unit (AGBU) for analysis to quantify its value to the Wagyu BREEDPLAN analysis.

AGBU analyses determined the genotypes and carcase data of these 9,500 animals contributed significant value to the Wagyu BREEDPLAN analysis. As a result, changes were made to the Wagyu BREEDPLAN model and number of genetic groups, allowing the crossbred data and genotypes to be used to estimate more accurate EBVs.

These higher accuracy Estimated Breeding Values (EBVs) now assist Wagyu breeders to more confidently determine which breeding animals to select and keep in the breeding program.

This project showed that commercial crossbred data can contribute valuable data to the Wagyu Breedplan analysis. It is expected that this finding will stimulate the capture of large numbers of commercial records and when used by the BREEDPLAN analysis, the additional accuracy of the resultant EBVs will greatly benefit all sectors of the Australian Beef industry which use Wagyu genetics.

Executive summary

Background

The Australian Wagyu Association's BREEDPLAN analysis historically only used Fullblood Wagyu performance data and with the rapidly growing demand for Fullblood seedstock, Fullblood slaughter animals are becoming more difficult to source and therefore the value of crossbred Wagyu progeny data needed to be explored.

Objectives

The purpose of this project was to determine the effectiveness of commercial crossbred Wagyu data in the Wagyu BREEDPLAN analysis.

If AGBU determine the commercial crossbred data contributed significant value, it will be included in the Wagyu BREEDPLAN analysis to contribute additional data to their parent's EBVs and thus increasing EBV accuracy.

Methodology

Relationships with large commercial Wagyu producers and feedlots were established to ensure large contemporary groups of commercial animals were available for the project. When the animals were inducted into the feedlots, tissue samples were collected, and the sample numbers associated with the feedlot ID and NLIS number and then submitted to Neogen for SNP testing. After the animals were harvested, the feedlots supplied the carcase feedback as well as feedlot growth and health treatment data to the AWA. A total of 9,500 commercially produced crossbred Wagyu animals were registered in the AWA's Slaughter Register and the genotypes and data loaded into the AWA system. These crossbred Wagyu genotypes and data were supplied to AGBU for analysis to determine its value to the Wagyu BREEDPLAN analysis.

Results/key findings

After their analysis, AGBU recommended that changes were needed to the Wagyu BREEDPLAN model and genetic groups to ensure crossbred Wagyu animal records were handled appropriately in the analysis. These recommended changes have been implemented and the crossbred Wagyu animals and their records are now used to estimate more accurate EBVs for all related animals.

Benefits to industry

Traditionally after a bull is sold to a commercial producer, the collection of progeny performance data stops, causing the EBVs of the bull to be stagnant. The use of commercial data in Wagyu BREEDPLAN will encourage commercial progeny test programs for the collection of carcase data. This additional data will influence the EBVs and increase the accuracy of the EBVs of commercial bulls and their relatives.

Accurate EBVs assist Wagyu breeders to confidently determine which breeding animals to select and keep in the breeding program. The ability to use the data of commercially produced crossbred Wagyu animals in the Wagyu BREEDPLAN analysis will greatly benefit all sectors of the Australian Beef industry which use Wagyu genetics as it will allow non-performing bulls to be removed from breeding programs.

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1. Background

The Wagyu BREEDPLAN analysis historically only used Fullblood Wagyu performance data to contribute to the calculation of EBVs and BreedObject Index Values. With the rapidly growing demand for Fullblood seedstock, Fullblood slaughter animals are becoming more difficult to source and therefore the value of crossbred Wagyu progeny data needed to be explored.

Accurate Wagyu EBVs are of great value to the whole Wagyu supply chain as it assists with the selection of breeding animals to produce profitable progeny which will grow fast and produce carcasses with high marble scores.

This project will determine the effectiveness of crossbred Wagyu data in Wagyu BREEDPLAN. Large quantities of crossbred Wagyu genotypes and data will be captured, loaded, and included in the Wagyu BREEDPLAN analysis. The genotypes will help to determine relationships in the Single Step BREEDPLAN analysis as accurate parentage is virtually unknown in commercial crossbred Wagyu production due to multi-sire joining.

The results from this project will have a direct impact on the Wagyu BREEDPLAN model and ability to use crossbred Wagyu data. If successful, the data and genotypes generated by this project will be included in the Wagyu BREEDPLAN analysis and will then improve the estimation of the genetic potential of a wide range of Wagyu animals.

2. Objectives

The objective of this project was to determine the effectiveness of commercial crossbred Wagyu data in the Wagyu BREEDPLAN analysis.

2.1 Animal recording and data capture

- Enable industry captured commercial crossbred production performance information to be loaded and analysed in the Single Step Wagyu BREEDPLAN analysis.

2.2 BREEDPLAN model change

- Single Step Wagyu BREEDPLAN assessment of the effectiveness of crossbred Wagyu data.

2.3 Inclusion of crossbred data in the Wagyu BREEDPLAN analysis

- Genotypes and phenotypes added to the Single Step Wagyu BREEDPLAN analysis to determine its effect on the EBVs and EBV accuracies for the different breed combinations.
- The data will mainly consist of Wagyu crosses with Angus, Shorthorn, Holstein and Bos indicus/Euro.

3. Methodology

This project was designed to collect carcase data and genotypes on 9,500 crossbred Wagyu animals and to load this data through the normal process into the AWA registration system.

Relationships with large commercial Wagyu producers and feedlots were established to ensure large contemporary groups of commercial animals were available for the project. A contemporary group is a group of animals which were raised in the same environment thus had an equal opportunity to perform. It helps to remove or reduce the impact of environmental effects such as herd management and feeding differences on the animals and allow more accurate calculation of genetic differences between animals.

When the groups of animals were inducted into the feedlots, tissue samples were collected, and the sample number associated with the feedlot ID and NLIS number and then submitted to Neogen for SNP testing. The genotyping has been completed on the Neogen 96K Chip and the genotypes reported and loaded into the AWA system.

To enable the registration of crossbred Wagyu animals in the AWA registration system, the AWA implemented the Content and Slaughter Registers. In preparation for the genotypes of this project to be loaded in the Wagyu system it was also necessary to develop and implement a DNA database in which all AWA genotypes could be stored. The new database ensured genotypes could be extracted and supplied to AGBU for the initial analysis and then subsequently to be available to ABRI for the Wagyu BREEDPLAN analysis.

After their Wagyu breed composition was determined and they were parent verified, the animals were registered. Registration of the crossbred animals require that they are parent verified and that their Wagyu breed composition get recorded. The PV information was very valuable and contributed to the success of this project as the sires of a large proportion of the animals were very accurately identified.

The animals were inducted into feedlots and were harvested to maintain the induction contemporary group structure. Feedlot and carcase records (which include feedlot induction weights, feedlot exit weights, days on feed, carcase weights, eye muscle areas, marble scores and rump fats) have been supplied to the AWA and loaded into the database.
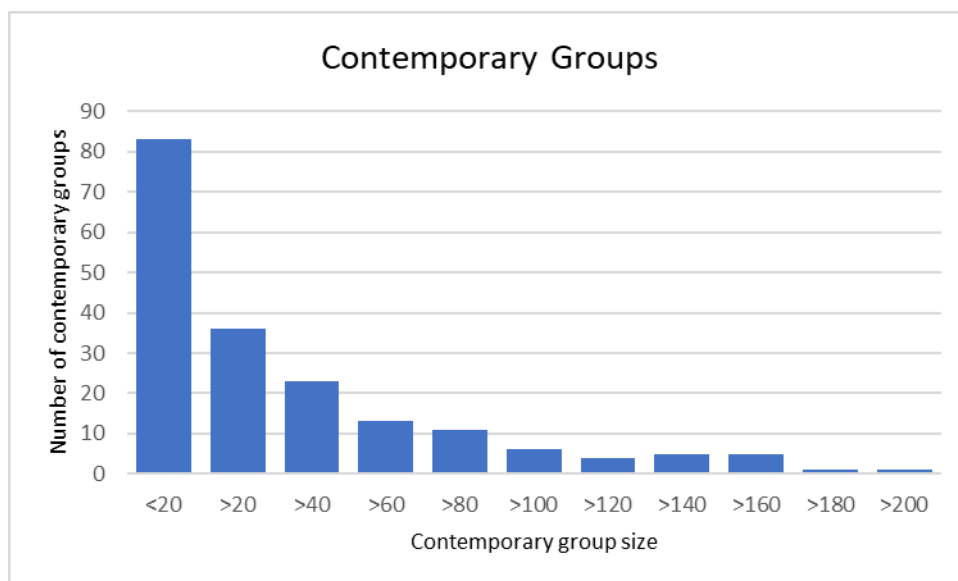
The records of these 9,500 crossbred Wagyu animals were supplied to AGBU in February 2022 and AGBU conducted an analysis to determine the value of crossbred data in the Wagyu BREEDPLAN analysis.

4. Results

4.1 Data Capture

There were 6,352 animals which were able to be SNP parent verified to 310 registered sires. Even though a sire could not be determined for all the crossbred animals, their genomic relationships with other animals were calculated using Single-Step BREEDPLAN as they all had SNP genotypes contributing to the Genomic Relationship Matrix in the analysis.

These project animals represent a range of Wagyu crosses with various levels of Wagyu content in large contemporary groups as shown in Figure 1. There were only 156 animals (less than 2%) in contemporary groups which had less than 10 animals represented. Most of these animals were removed from their contemporary groups due to non-performance or injuries and harvested before the rest of the contemporary group. Contemporary groups consisting of less than 10 animals reduce the opportunity to accurately determine the genetic merit differences of progeny from different sires within the small contemporary group.

Figure 1. Frequency distribution of contemporary group sizes.

4.2 BREEDPLAN model change

After analysis of the Wagyu data, including of the 9,500 crossbred Wagyu animals, and their genotypes and carcase data, AGBU noted that due to the significant increase in crossbred animal data now included in the Wagyu database, changes to the Wagyu BREEDPLAN analysis were necessary. To include Fullblood and crossbred information in the Wagyu BREEDPLAN analysis, the analysis was changed to a type +3 model to account for Fullblood and crossbred information and to account for heterosis of dams and calves. In the type +3 evaluation, breed composition of recipient dams is included in their contemporary group definition.

Further to the above changes, the number of genetic groups and the genetic group structures were modified based on the age and country of origin or breed. The number of genetic groups were therefore increased from 9 to 12.

4.3 Inclusion of crossbred data in the Wagyu BREEDPLAN analysis

In accordance with AGBU's recommendations the BREEDPLAN model was changed to a type 3 model and additional genetic groups were implemented and the crossbred animals and their records were included in the production version of the March 2022 Single-Step Wagyu BREEDPLAN analysis.

There were 310 registered Wagyu sires which had crossbred progeny with carcase data collected through this project. Before the crossbred records were included in the March 2022 Wagyu BREEDPLAN analysis, 145 of these sires had reportable carcase EBVs while 165 of the sires didn't have reportable EBVs. Wagyu animals must have EBV accuracies higher than 30% for the EBV to be reportable.

When the records of the 9,500 crossbred animals were included in the Wagyu BREEDPLAN analysis, the accuracies of the 165 sires increased to above 30% and became reportable. The EBV accuracy distributions for 600Day Weight, Carcase Weight, Eye Muscle Area (EMA) and Marble Score (MS) EBVs of the 165 sires (after the crossbred records were included in the March analysis) are shown in Fig. 2 to Fig. 5. Asall these sires had accuracies lower than 30%, before the crossbred records were added, these results demonstrated in the graphs below are a clear indication of the value of the

crossbred data. In the case of carcase weight, some of these sires had EBV accuracy increases from below 30% to above 90%.

Figure 2. The distribution of 600Day Weight EBV accuracy of the 165 sires after the inclusion of the data of their crossbred progeny.
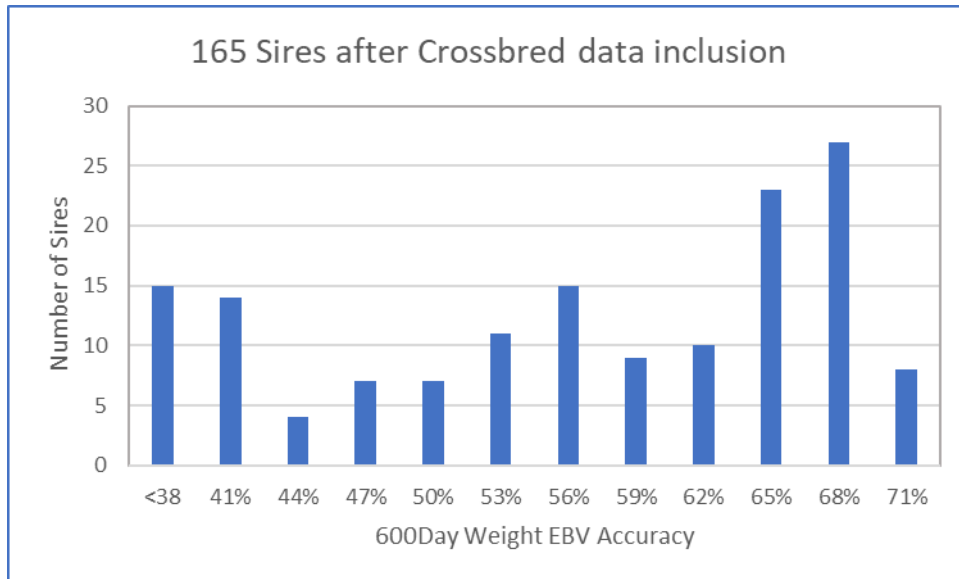

Figure 3. The distribution of Carcase Weight EBV accuracy of the 165 sires after the inclusion of the data of their crossbred progeny.
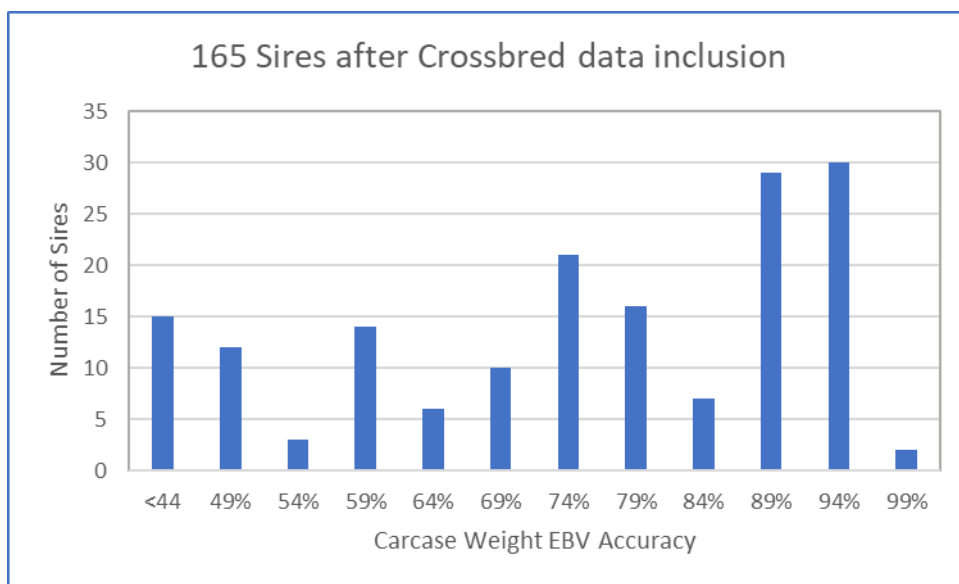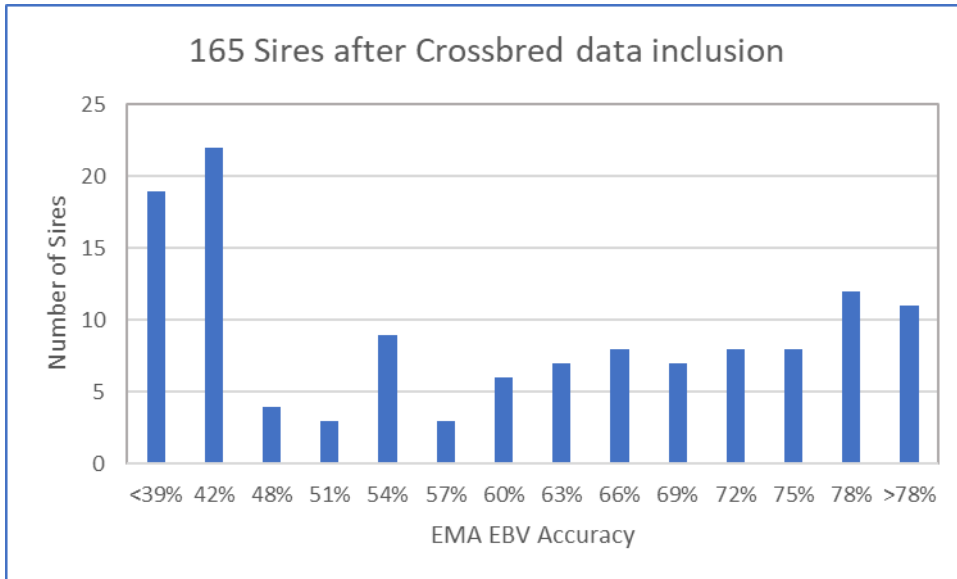
Figure 4. The distribution of Eye Muscle Area EBV accuracy of the 165 sires after the inclusion of the data of their crossbred progeny.
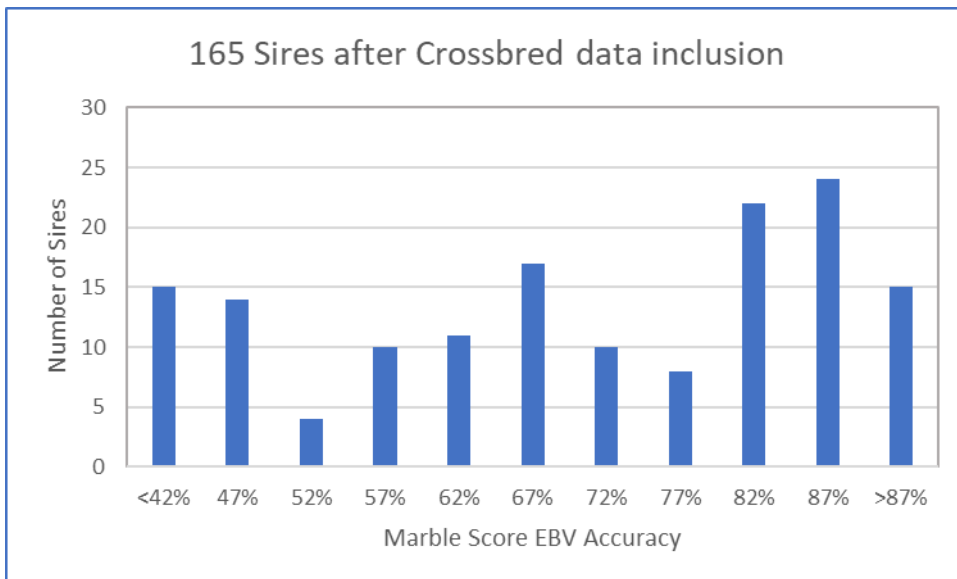

Figure 5. The distribution of Marble Score EBV accuracy of the 165 sires after the inclusion of the data of their crossbred progeny.

The EBVs of the 165 sires are shown in Fig. 6 to Fig. 9. On these graphs the red line represents the EBV average of the 2020 born calves while the two black lines represent the top and bottom 10% values of each trait. It is very encouraging to observe the amount of spread in the EBVs of these sires.

Figure 6. 600Day Weight EBVs of the 165 sires after the inclusion of the data of their crossbred progeny.
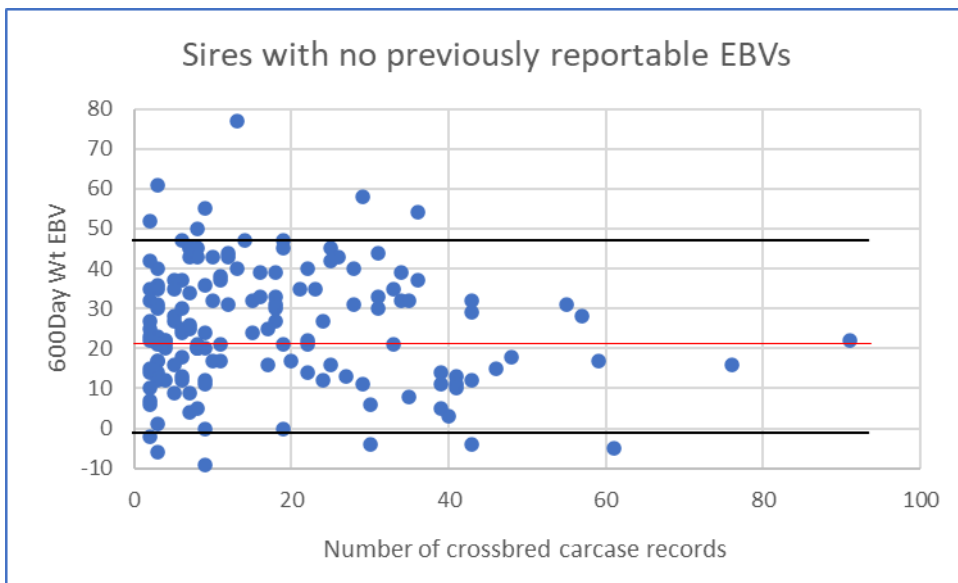

Figure 7. Carcase Weight EBVs of 165 sires after the inclusion of the data of their crossbred progeny.
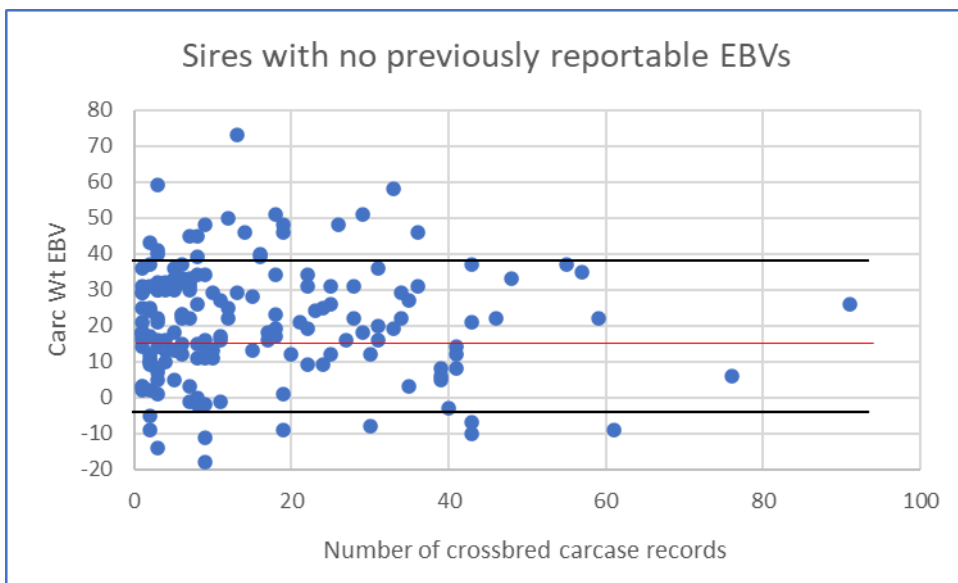
Figure 8. Eye Muscle Area EBVs of the 165 sires after the inclusion of the data of their crossbred progeny.
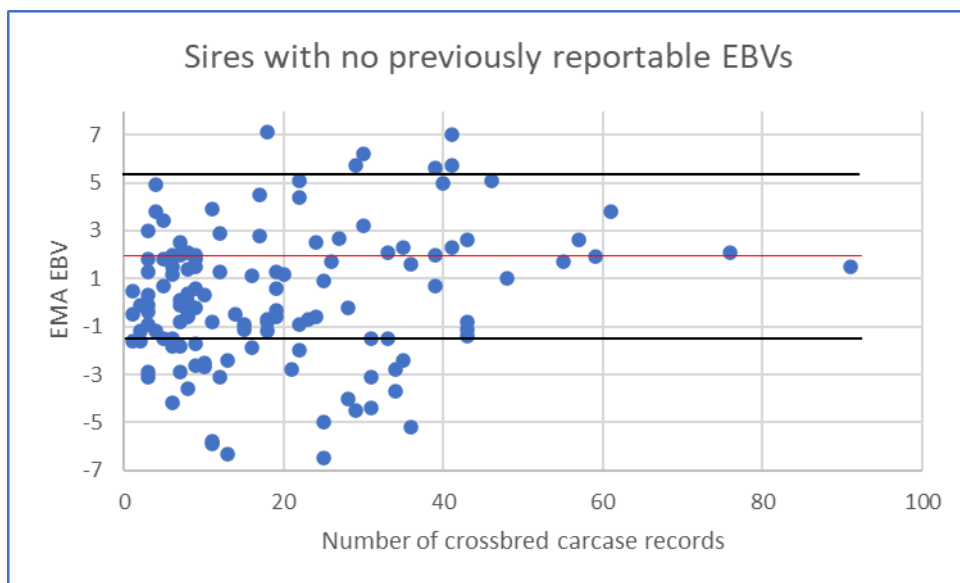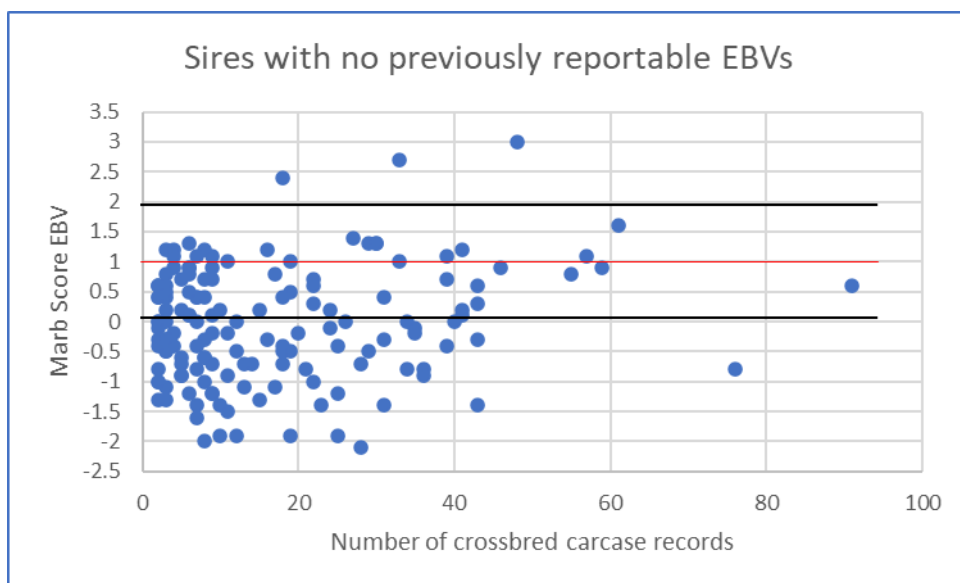

Figure 9. Marble Score EBVs of the 165 sires after the inclusion of the data of their crossbred progeny.

As expected, when the crossbred animals and their data were added to the Wagyu BREEDPLAN analysis, the EBVs and accuracies of the 145 sires which already had reportable EBVs changed. There were 16 of the 145 sires which had Herdbook registered progeny with carcase records in the February 2022 BREEDPLAN analysis (before crossbred records were added). Three of these 16 bulls had between 376 to 535 Herdbook progeny in the February 2022 BREEDPLAN analysis and then another 160 to 420 crossbred progeny added in the March analysis. These Herdbook and crossbred progeny numbers helped to strengthen the analysis as they served as very effective reference sires in the crossbred data. The comparisons of the EBV and accuracy changes of these 16 sires from the February 2022 BREEDPLAN analysis (Fullblood EBVs) and the March 2022 BREEDPLAN analysis which included the crossbred data (Crossbred EBVs) are shown in Fig. 10 and Fig. 11. The Crossbred EBVs are displayed on the primary Y axis (Left) while the accuracy differences between the two analysis are displayed on the secondary Y axis (Right). There are seven sires which had very little or no

change in their EBV accuracies when the crossbred progeny records were added which reflects their very high accuracies obtained through the analysis of their previously registered Herdbook progeny.

Figure 10. Comparison of Carcase Weight EBVs and accuracies of the Fullblood (February 2022) and Crossbred (March 2022) Breedplan analysis results of the 16 sires which already had Herdbook progeny carcase data loaded in the AWA database.
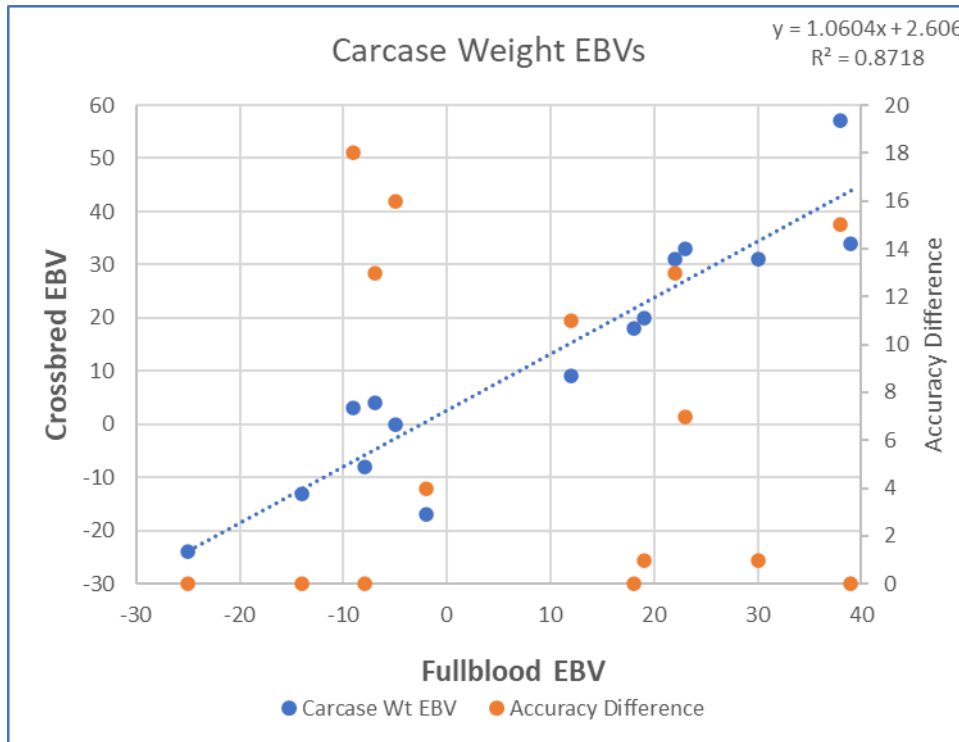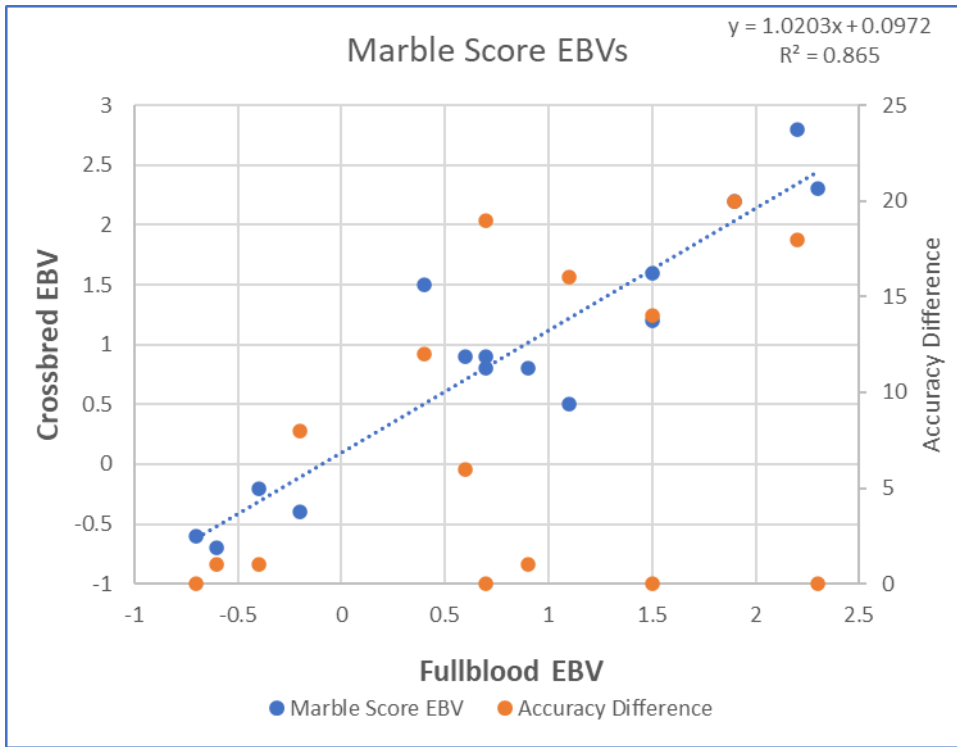
Figure 11. Comparison of Marble Score EBVs and accuracies of the Fullblood (February 2022) and Crossbred (March 2022) Breedplan analysis results of the 16 sires which already had Herdbook progeny carcase data loaded in the AWA database.

Any changes in EBVs will influence the BreedObject $Index values of animals. The changes in the Self Replacing Index of these 16 sires are displayed in Fig. 12 and is a good indication of the significant impact the crossbred data had on some of the sires for this important indicator of profitability.

Figure 12. Comparison of the Self Replacing Index values of the Fullblood and Crossbred Breedplan analysis results of the 16 sires which already had Herdbook progeny carcase data loaded in the AWA database.
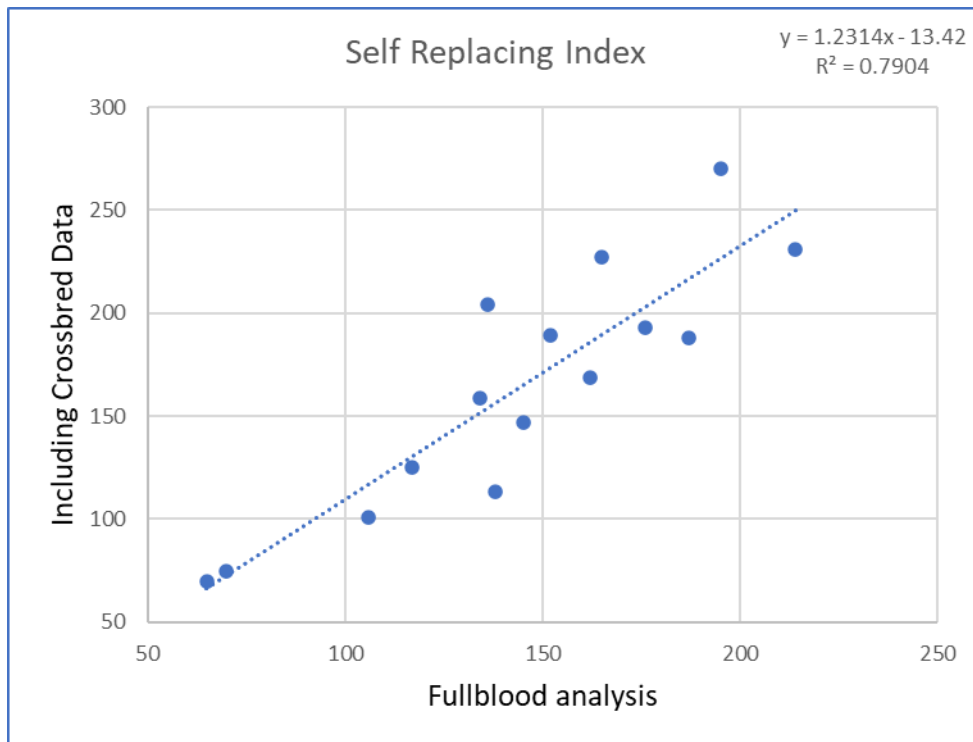
The changes to the EBV and accuracy of the 145 sires which already had reportable EBVs before the data of the crossbred progeny were included in the March analysis are shown in Fig. 13 to Fig. 16. The change in accuracy between the two analysis is a strong indication of the value of the crossbred data. As expected, sires with relatively low accuracies in the February 2022 analysis benefited more from the addition of the crossbred data.

Figure 13. February 2022 (Fullblood) and March 2022 (Crossbred) comparison of the Carcase Weight EBVs of the 145 sires which had reportable EBVs prior to the crossbred data being used.
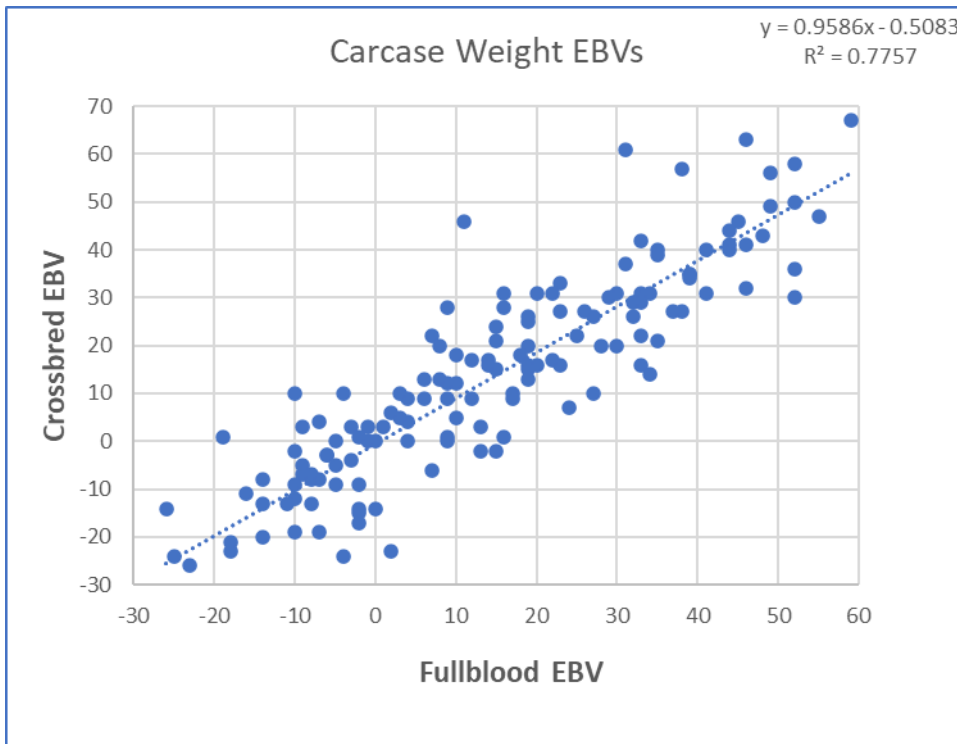

Figure 14. Change in the Carcase Weight EBV Accuracies of the 145 sires from the February 2022 (Fullblood) analysis compared to the March 2022 (Crossbred) analysis.
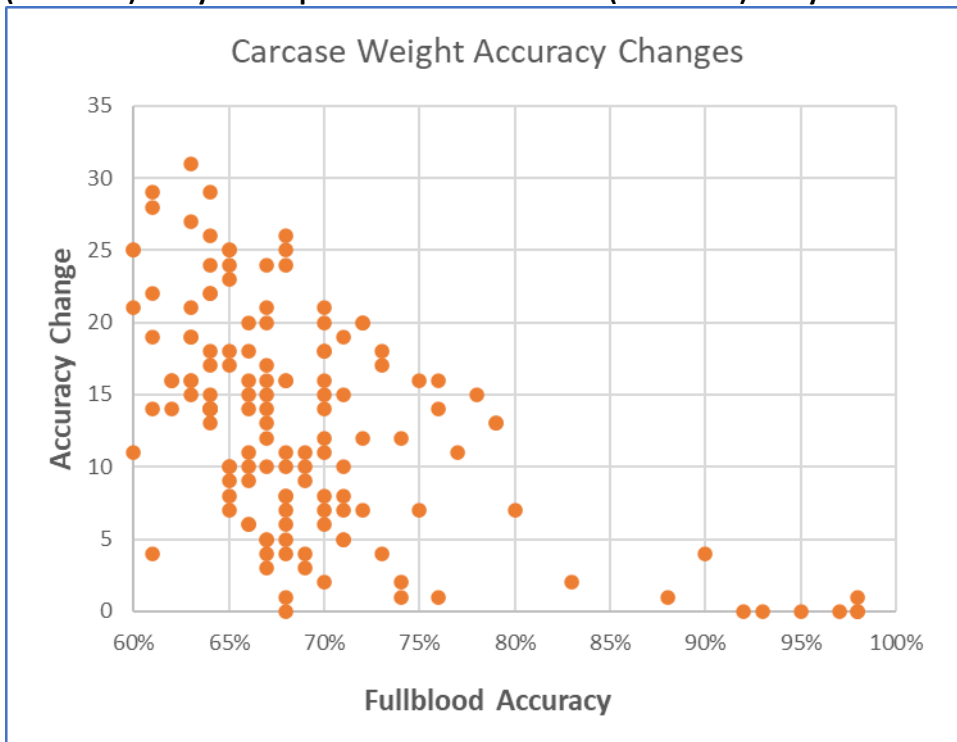
Figure 15. February 2022 (Fullblood) and March 2022 (Crossbred) comparison of the Marble Score EBVs of the 145 sires which had reportable EBVs prior to the crossbred data being used.
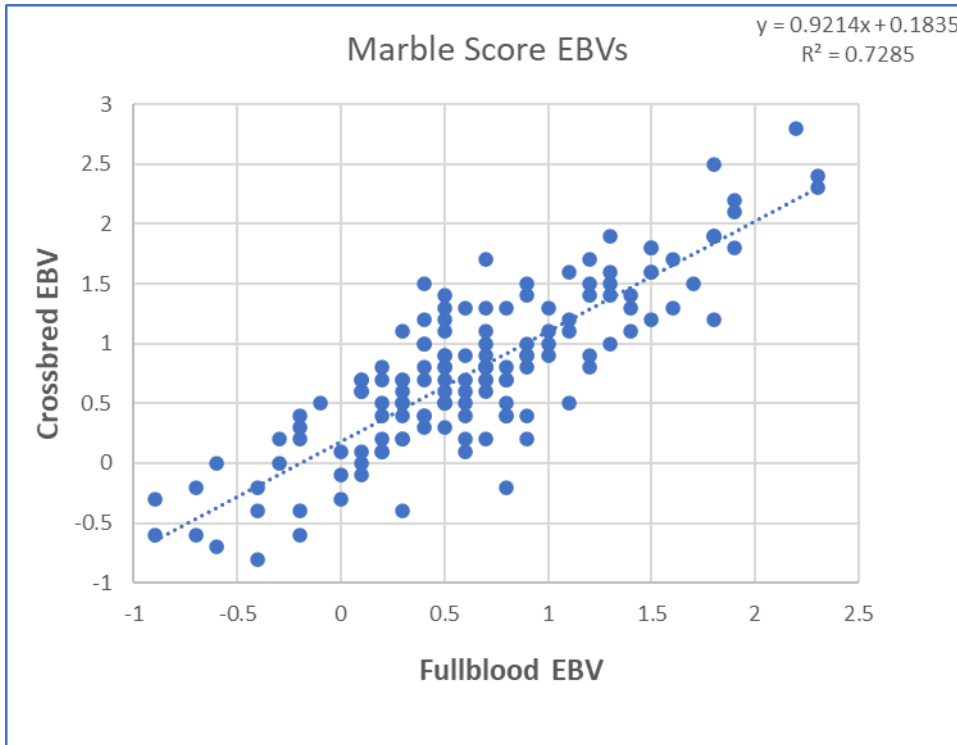

Figure 16. Change in the Marble Score EBV Accuracies of the 145 sires from the February 2022 (Fullblood) analysis compared to the March 2022 (Crossbred) analysis.
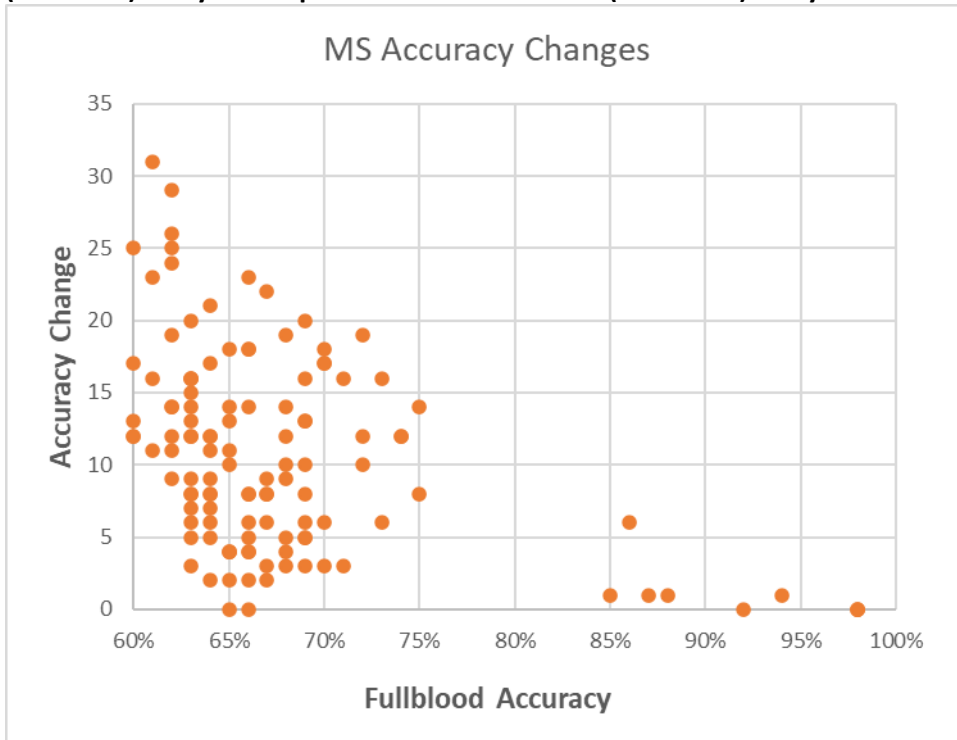
Fig. 17 shows the comparison of the Self Replacing Index values of the 145 sires before and after the crossbred records were added to the analysis. With the addition of the crossbred data the Self Replacing Index values of some of the 145 sires change with more than $50 up or down.

Figure 17. February 2022 (Fullblood) and March 2022 (Crossbred) comparison of Self Replacing Index values of the 145 sires which had reportable EBVs prior to the crossbred data being used.
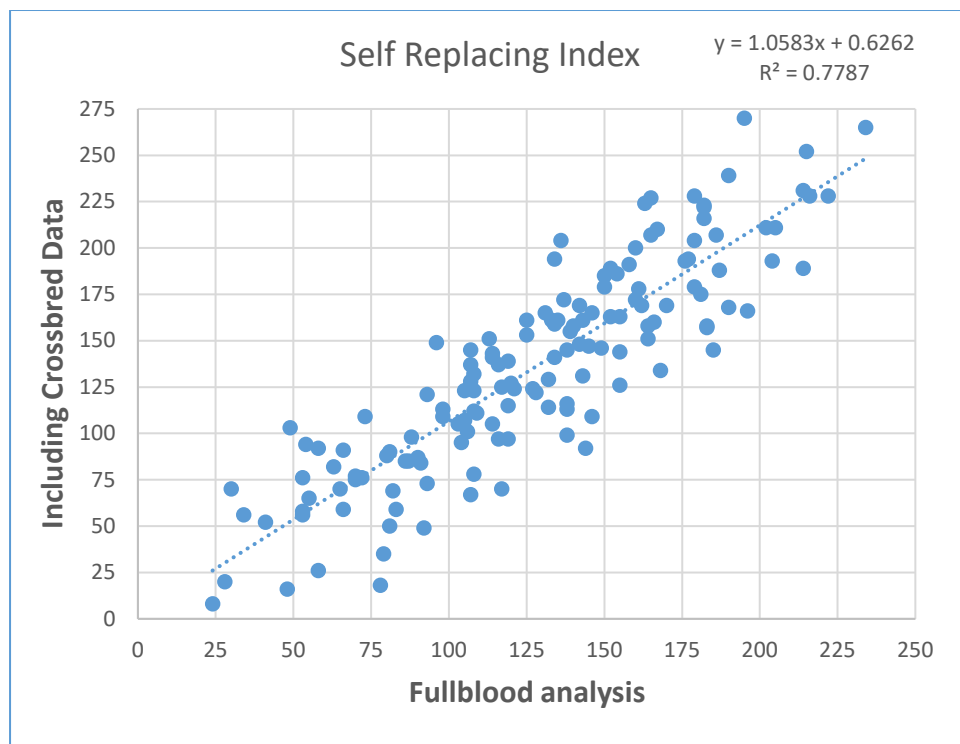
5. Conclusion

This project contributed to record a large number of crossbred Wagyu animals with genotypes and carcase data and enabled AGBU to determine the appropriate model and number of genetic groups for the Wagyu BREEDPLAN analysis. AGBU recommended a model change and increase in genetic groups to be implemented in the production version of the Single-Step Wagyu BREEDPLAN analysis to facilitate the use of crossbred data.

The new model and increased number of genetic groups have been implemented in the March 2022 Wagyu BREEDPLAN analysis. Crossbred Wagyu animals can now be registered with the AWA and their performance data recorded. The loaded performance data will be used by the Wagyu BREEDPLAN analysis to estimate the genetic potential of those animals and their parents and other relatives.

5.1 Key findings

- Crossbred Wagyu data can be used in the Single Step Wagyu BREEDPLAN analysis.
- SNP Parent Verification analysis identified the sires of 67% of the crossbred animals. This is a very encouraging proportion indicating the exceptional coverage of the WAGYU population with SNP genotypes loaded in the Wagyu genotype database.

- Genomic relationships between animals which could not be verified to registered sires were still contributing valuable information to the BREEDPLAN analysis.
- Inclusion of the crossbred Wagyu data in the Single Step Wagyu BREEDPLAN analysis significantly increased the accuracy of many sires.
- As expected, there were relatively little average increase in the EBV accuracy of the 16 sires which had Herdbook progeny with carcase data in the February 2022 analysis. The accuracies increased on average by 1.7%, 6.2%, 7.2% and 7.3% for 600Day Weight, Carcase Weight, EMA and Marble Score EBVs respectively.
- The EBV accuracy of the 145 sires increased on average by 4.2%, 13%, 10.7% and 11.9% for 600Day Weight, Carcase Weight, EMA and Marble Score EBVs respectively.
- Once crossbred data was added in the March 2022 analysis, 165 sires obtained reportable EBVS with average EBV accuracy of 54%, 71%, 56% and 67% for 600Day Weight, Carcase Weight, EMA and Marble Score EBVs respectively
- The observed increases in EBV accuracy are very valuable, especially in the 165 sires where it contributed sufficient data to increase the accuracy to above 30%, which resulted in the EBVs of these sires to become reportable.

5.2 Benefits to industry

This project was instrumental in facilitating the collection of sufficient crossbred Wagyu genotypes and carcase records to enable crossbred data to be included in the Wagyu BREEDPLAN analysis.

As a result of this project, all Wagyu animals will require a SNP parent/sire verification or a SNP genotype (50K to 100K SNPs) before they can be recorded and performance information loaded in the Wagyu database. The parent verification will assist with the accurate recording of parentage which is critical in a genetic analysis. The availability of 50K or 100K genotypes will ensure that Wagyu breed composition can be determined and, even in the absence of parent verifications, the genomic relationships between crossbred animals can be utilised by the BREEDPLAN analysis.

The model changes have now been implemented by Wagyu and are being used in the Wagyu BREEDPLAN analysis routinely. The inclusion of the crossbred data resulted in significant EBV changes and increased accuracy for almost all sires with crossbred progeny. This is a clear indication that crossbred data is valuable and its collection can broaden the base to commercial animals being able to be used for progeny testing.

Where commercial crossbred data gets collected and included in the Wagyu database it will assist those commercial breeders to obtain an estimation of the genetic merit of their bulls which previously may have been unable to be reported. The ability of commercial Wagyu breeders to accurately determine which breeding animals to select and keep in the breeding program will greatly benefit all sectors of the Australian Beef industry which use Wagyu genetics.