AUSTRALIAN WAGYU ASSOCIATION™

WAGYU TECHNICAL
UPDATE

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CROSSBRED DATA NOW USED IN WAGYU BREEDPLAN

CROSSBREEDING - A MAJOR COMPONENT OF AUSTRALIAN WAGYU SECTOR PRODUCTION

The Australian Wagyu Association estimates that historically, up to 80% of Australian Wagyu-content branded production has been derived from F1 animals, although recent production trends have seen a shift towards increased slaughter numbers of fullblood, purebred and high Wagyu content (F2 and F3) cattle.

The Australian Wagyu Sector has emerged over the past 20 years to be a very significant component of the Australian beef industry. Unique high marbling (Marble Score 6 through to 9+) along with marbling fineness, high unsaturated fats and exceptional eating quality, has differentiated Wagyu beef from that of other breeds. Many of these attributes also have very significant benefits for crossbred Wagyu carcase production.

The remarkable quality difference between Wagyu beef and that of other breeds is exemplified in F1 Wagyu beef, where fullblood Wagyu sires are crossed with females of other breeds (primarily Angus). F1 Wagyu product gains significant quality improvements from fullblood Wagyu sire genetics when used across appropriate maternal breeds, with marble score averages for F1 Wagyu (approximately MB 5.5) sitting halfway between fullblood averages and long-fed averages of other breeds.

Crossbreeding with Wagyu genetics provides an instant mechanism to increase the volume of production of high-grade carcases, with fullblood Wagyu sires used in terminal crossing to generate large numbers of slaughter cattle to meet expanding domestic and international markets for high-value Wagyu content product.

One of the ways the AWA supports the Wagyu Sector, is by combining large volumes of pedigree, genomic and performance data into the Wagyu BREEDPLAN genetic analysis to enable estimation of breeding values for Wagyu sires and dams.

As shown in Figure 1, of the article ***Major improvements to AWA Wagyu BREEDPLAN on page 31***, AWA has seen rapid increases in the volume of fullblood carcase data submitted to support Wagyu BREEDPLAN over the last 5 years. This data is vital to improving the EBV accuracy of production traits across the whole registered Wagyu population.

To date, Wagyu BREEDPLAN has only used data from fullblood and purebred progeny to determine the genetic merit of sires and dams for several growth and carcase production traits. The number of crossbred Wagyu progeny of fullblood sires that are slaughtered each year exceeds the total volume of fullblood and purebred production by many folds. This data is a potential source of new information to improve Wagyu BREEDPLAN, particularly the large volumes of F1 and higher content carcase data that can be accessed by members through their supply chain relationships.

WAGYU CROSSBRED BREEPLAN GENETIC ANALYSIS RESEARCH PROJECT

The AWA has now completed a five-year project co-funded by Meat and Livestock Australia to evaluate the impact of using data from crossbred (F1 Wagyu and higher content) in Wagyu BREEDPLAN.

Researchers at the Animal Genetics and Breeding Unit (AGBU) have completed evaluating the inclusion of crossbred carcase data from this project in the Wagyu BREEDPLAN analysis. Data from approximately 8,000 individual crossbred animals was included in trial runs of the Wagyu BREEDPLAN analysis to assess the impacts of using crossbred data along with fullblood data on the calculation of EBVs.

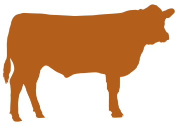
To include crossbred information in the routine Wagyu BREEDPLAN evaluation, the analysis model was expanded to account for heterosis effects of varied maternal breeds and calves. In addition, breed composition of recipient dams was included in the model to better estimate recipient dam impacts on performance of embryo calves.

In the February 2022 Wagyu BREEDPLAN evaluation, 18,000 fullblood and purebred Carcase Weight and Marble Score records were used in the estimation of EBVs. In the evaluation of the crossbred Wagyu BREEDLPAN model, an additional 8,000 crossbred carcase records were used in the estimation of EBVs.

IMPACTS ON FULLBLOOD SIRES WHERE CROSSBRED DATA WAS LOADED FOR THESE SIRES

The following figures show the impact on the EBVs for 300 fullblood Wagyu sires for which 8,000 crossbred progeny carcase records were loaded into Wagyu BREEDPLAN. The figures will describe the Old EBVs (no crossbred carcase data added – extracted February 2022) and compare these to New EBVs (crossbred data included in the March 2022 BREEDPLAN run).

The crossbred progeny records included were Carcase Weight (CWt), Marble Score (MS) and Eye Muscle Area (EMA) data from the 8,000 crossbred carcase records that were parent verified to 300 fullblood sires within the crossbred BREEDPLAN Genetic Analysis Research Project. It is important to note that a high proportion of these 300 sires had no prior carcase data recorded on their progeny and had low EBV accuracies (40% - 50%) prior to the new crossbred analysis.



POSITIVE OUTCOME 1

LARGE CHANGES IN EBV RANGE FOR CARCASE TRAITS

Figure 1 shows that the relationship between the old EBV and the New EBV for the Carcase Weight (CWt) trait is >67%. The New EBVs (on the Y axis) show a far greater variation in CWt EBVs with a 112 kg difference from minimum (-46kg) to maximum (+66kg).

This is a 35% increase in EBV range compared to the Old EBVs, which showed an old CWt EBV range of 83kg difference from minimum (-23) to maximum (+60kg).

This increase in EBV variation for the new CWt EBVs allows much greater ability to select for differences between animals and is a very positive outcome for breeders.

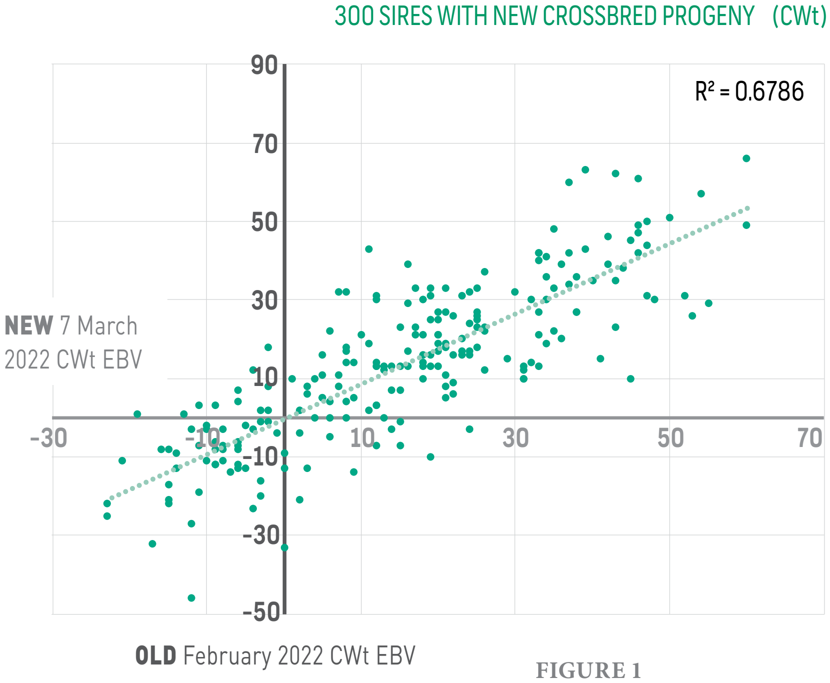


FIGURE 1
Old vs New CWt EBV - 300 sires with new crossbred progeny

Figure 2 shows that the most significant changes seen between the Old and New EBVs upon addition of crossbred progeny carcase data were to the MS EBVs of the fullblood sires of these progeny.

The relationship between the Old EBV and the New EBV for the Marble Score (MS) trait was 46%. Like the EBV range for the CWt trait, the addition of crossbred progeny data increased the variation of EBVs for Marble Score for these sires, from -1.1 to +2.3 MS (3.4 MS range) with the Old BEVs, up to -1.7 to + 2.9 MS (4.6 MS range) with the New EBVs.

This increase in EBV variation for the new MS EBVs allows much greater ability to select for differences between animals and is a very positive outcome for breeders.

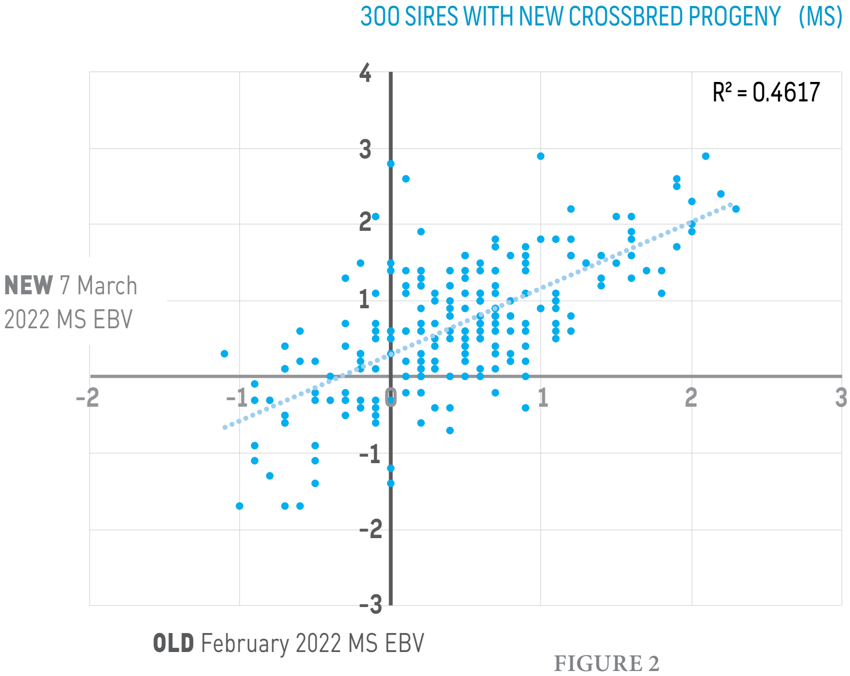


FIGURE 2
Old vs New MS EBV - 300 sires with new crossbred progeny

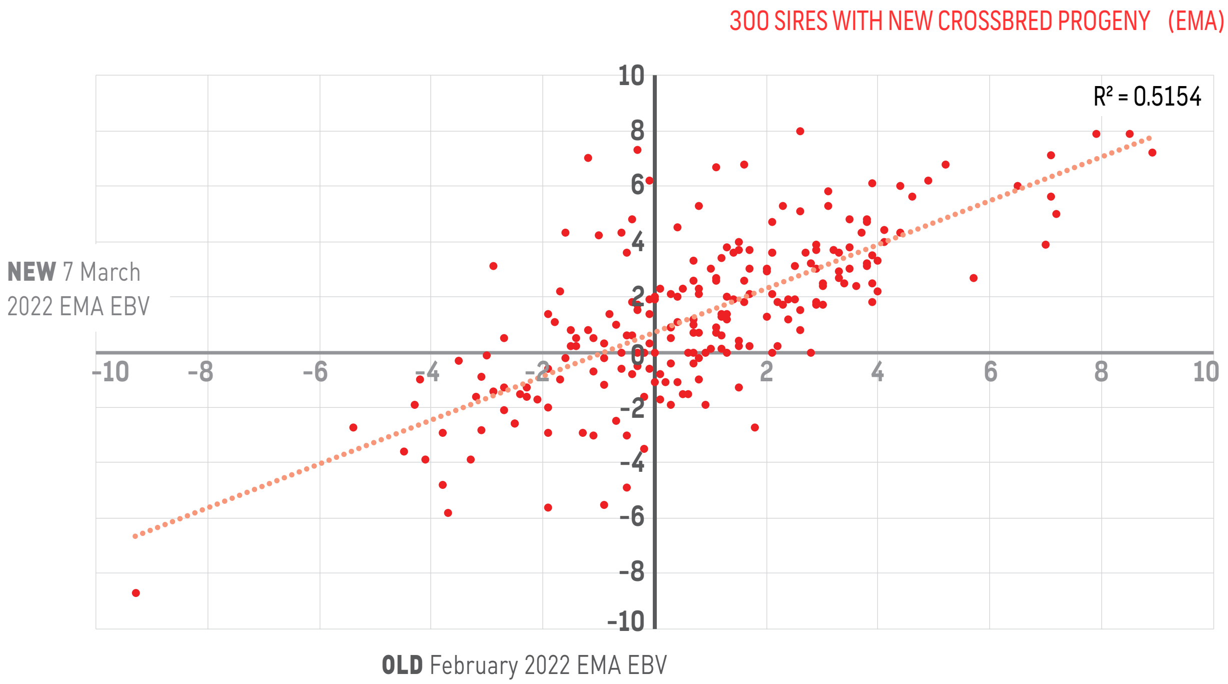
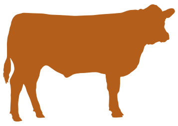


FIGURE 3
Old vs New EMA EBV - 300 sires with new crossbred progeny

Figure 3 shows that the relationship between the Old EBV and the New EBV for the Eye Muscle Area (EMA) trait was 51%. Significant changes occur in these sires, primarily as a result of the large amount of crossbred progeny data being entered and the new Wagyu Genetic Parameters.

Unlike CWt and MS EBV range, the EBV range for the EMA traits is similar for Old and New EBVs.



POSITIVE OUTCOME 2

LARGE CHANGES IN EBV ACCURACY FOR CARCASE TRAITS

When we compared the EBV accuracy (confidence) for the Old EBVs prior to the addition of crossbred data, to the New EBVs after the addition of crossbred data, the average accuracy for the CWt EBV increased markedly from 63% to 78% for these sires (Table 1.).

The average EBV accuracy for the MS EBV increased significantly from 60% to 79% and the average EMA EBV accuracies increased significantly from 54% to 68% for these sires.

CARCASE EBV	OLD ACCURACY average	NEW ACCURACY (average)	OLD EBV RANGE	NEW EBV RANGE
Carcase weight	63%	78%	-23 to +60kg	-46 to +66kg
Marble score	60%	79%	-1.1 to +2.3MS	-1.7 to +2.9MS
Eye muscle area	54%	68%	-8.7 to +8.0cm²	-9.3 to +8.0cm²

TABLE 1
Change in EBV accuracy for Carcase Traits with addition of 8,000 new crossbred progeny records for 300 fullblood sires.

These large increases in average EBV accuracy for these sires reflects that many sires had very low accuracy EBVs prior to addition of the new crossbred carcase progeny data (some were well below 50% accuracy). The large change in accuracy reflects that significant new progeny records for these sires have benefited the ability to estimate the EBVs for these sires.

HOW DOES INCLUDING CROSSBRED DATA IMPACT THE EBVs OF WELL KNOWN (FOUNDATION) SIRES?

In analysing the data to evaluate the impacts of crossbred Wagyu data in Wagyu BREEDPLAN, we identified key Foundation Sires for which significant amounts of fullblood data was already used in BREEDPLAN, but for which good amounts of new crossbred data was also provided (Table 2).

Using these sires, along with 12 other well recorded fullblood sires, we can assess the relative changes in EBVs and accuracies of well-known and used sires.

TABLE 2
Total Carcase progeny numbers for four Foundation sires.

WAGYU FOUNDATION SIRE NAME	FULLBLOOD CARCASE PROGENY pre-existing	CROSSBRED CARCASE PROGENY new	TOTAL CARCASE PROGENY current total
Itoshigefuji (TF-147)	376	426	**802**
World K's Michifuku (M0164)	535	318	**853**
Itoshigenami (TF-148)	412	164	**576**
World K's Haruki 2 (M0139)	80	20	**100**
TOTAL	**1,403**	**928**	**2,331**

Figure 4 shows that for the CWt EBV, the relative ranking of the four Foundation sires based on CWt EBV is very consistent between the Old and New EBVs. Itoshigefuji and Haruki 2 are high ranking growth and CWt sires and their EBVs are high for the CWt trait in both the Old and New EBVs. Of note is Itoshigefuji, who had 426 new crossbred progeny added in the New EBV analysis, more than doubling his recorded progeny number for carcase traits. His CWt EBV did not change and the accuracy of his EBV increased by 1% (he was already 98% accuracy for this trait and moved to 99% accuracy).

The EBVs for Itoshigenami and Michifuku, relatively low-ranking sires for CWt compared to Itoshigefuji and Haruki 2, also changed very little with the addition of significant crossbred progeny data.

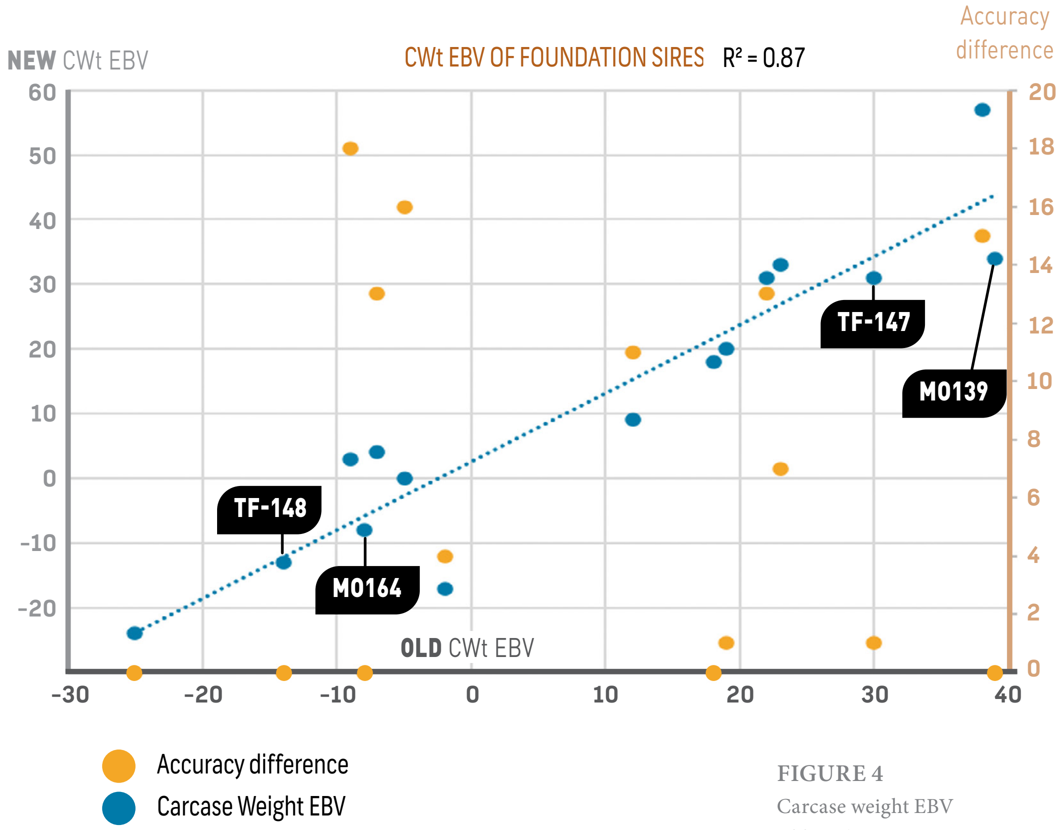


FIGURE 4
Carcase weight EBV
of foundation sires

Figure 5 shows that for the MS EBV, again, the relative ranking of the four Foundation sires based on the MS EBV is very consistent between the Old and New EBVs. Itoshigefuji and Haruki 2 are low ranking marbling sires (compared to the sires in this Figure) and their EBVs are low for the MS trait in both the Old and New EBVs.

The EBVs for Itoshigenami and Michifuku, relatively high-ranking sires for MS EBV compared to toshigefuji and Haruki 2, also changed very little with the addition of significant crossbred progeny data.

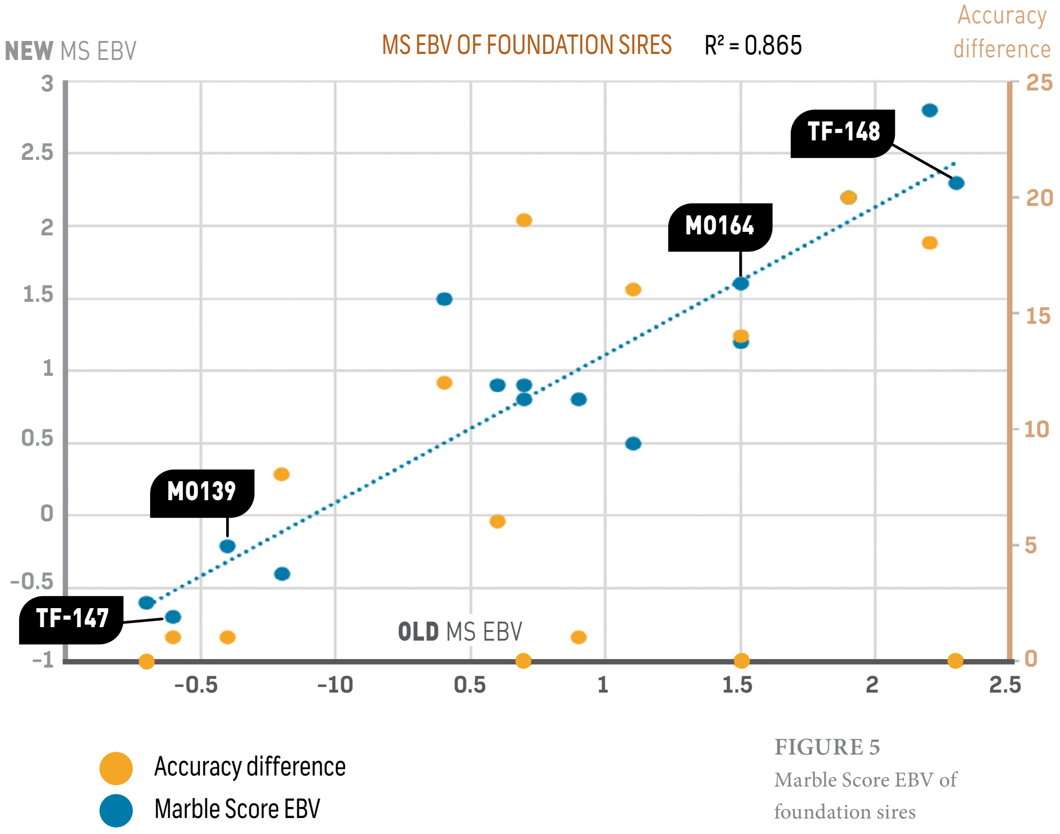


FIGURE 5
Marble Score EBV of
foundation sires

> “... the use of large numbers of crossbred Wagyu progeny data for the four example Foundation sires provides a very consistent and reliable outcome for the CWt and MS EBVs.

The simple comparison between the old and new EBVs for the Foundation sires in Figures 4 and 5 demonstrates that the use of large numbers of crossbred Wagyu progeny data for the four example Foundation sires (926 new records in total), provides a very consistent and reliable outcome for the CWt and MS EBVs. Using crossbred data in Wagyu BREEDPLAN resulted in no significant changes in the CWt and MS EBVs of these Foundation sires. This is a result of both the EBVs for these sires already being highly accurate, and the input of crossbred Wagyu carcase progeny data behaving the same as the fullblood progeny data within the new crossbred BREEDPLAN model.

The ranking of animals for CWt in fullblood EBVs based on fullblood progeny data, is largely the same as in the crossbred data. The ranking of animals for MS in fullblood EBVs based on fullblood progeny data, is largely the same as in the crossbred data. This means that sires can be selected for crossbred F1 Wagyu production based on their fullblood EBVs.

SUMMARY AND FINDINGS

The Wagyu BREEDPLAN genetic analysis model was last updated in 2018 by the independent research group – the Animal Genetics and Breeding Unit (AGBU) based at the University of New England. This update enabled inclusion of crossbred genomic DNA data for the Wagyu BREEDPLAN analysis.

The AGBU have now completed an update of the Wagyu BREEDPLAN genetic analysis model so that data from crossbred animals can now be used to support the calculation of EBVs. This will enable thousands of carcase progeny records from crossbred Wagyu to be used in Wagyu BREEDPLAN to improve EBVs of registered sires.

Inclusion of crossbred carcase data into Wagyu BREEPLDAN significantly increased the variation in EBVs for sires that had progeny data added. These changes are advantageous for Wagyu breeders to make genetic progress when using EBVs in their herds.

The ranking of animals for MS and CWt in fullblood EBVs based on fullblood progeny data, is largely the same as in the crossbred data. This means that sires can be selected for crossbred F1 Wagyu carcase production based on their fullblood EBVs.

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MORE INFORMATION

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