GENOMICS – WHY MORE PERFORMANCE DATA?

THE POWER OF THE AUSTRALIAN WAGYU ASSOCIATION GLOBAL GENETIC ANALYSIS - WAGYU BREEDPLAN AND ESTIMATED BREEDING VALUES - HAS IMPROVED DRAMATICALLY IN THE LAST FIVE YEARS.

The power of the Australian Wagyu Association global genetic analysis – Wagyu BREEDPLAN and Estimated Breeding Values – has improved dramatically in the last five years. Due in part, to the inclusion of a large number of carcase records to calculate new genetic parameters for carcase traits in the Wagyu BREEDPLAN analysis in 2015.

This facilitated more accurate carcase EBVs for a large number of sires with progeny that had carcase data recorded. The improvement was largely a result of the great effort of AWA members to capture thousands of carcase records into the AWA database.

It was further facilitated in 2018 with Wagyu Single-Step BREEDPLAN allowing the use of genomic SNP information within the BREEDPLAN analysis. Genomic SNP data contributes information to the estimation of the genetic merit of animals which have not been or can't be measured for a trait such as the collection of carcase data on a breeding animal.

With the support of the MLA Donor Company and through use of AWA and member funds, most animals for which carcase records were collected were also genotyped on 50K or higher platforms. These animals served as the reference (training) population to assist the Wagyu Single Step BREEDPLAN analysis to associate phenotype of recorded animals with the genotypes of animals in Wagyu BREEDPLAN.

The large number of animals with performance data that was supplied by AWA members, which were subsequently genotyped (50K SNP tested) was the critical hurdle our industry had to clear to enable the implementation of Wagyu Single Step BREEDPLAN.

Having a reference set of animals with performance data and genotypes is necessary to allow BREEDPLAN to create a link between the phenotype (performance trait) and the genotype which then serve as a reference population.

Having a large reference population of data and genotypes makes it possible to calculate an animal's EBVs using pedigree and genomics before any performance information has been collected for that animal. This is especially valuable where young animals are selected for breeding purposes before they have their own or progeny data recorded.

WHAT DATA CONTRIBUTES TO EBVS?

The information used to calculate Estimated Breeding Values (EBVs) can be categorised into three main contributors. As more information from these sources are added, the accuracy (confidence) of the EBVs increase and the EBVs change to reflect the additional data.

1. **Genetic merit of related animals** – initially the EBVs of the parents will determine the "starting point" of the EBVs of the calf and is sometimes called a mid-parent EBV. Other relatives will also, through the parents, influence the EBVs of an animal.

2. **The genotype of the animal** - if an animal is genotyped with a 50K SNP test, this information can be used to contribute to the animal's EBVs by more accurately determining the value of inherited genes from the sire and dam.

3. **Performance data** – the performance data of the animal and all its relatives contribute to the animal's EBVs. If the animal becomes a parent, the performance data of its progeny will also contribute to its EBVs. Progeny performance data is a very powerful source of information as it can be measured on a large number of progeny and will serve as proof of the genetic merit of the parent.
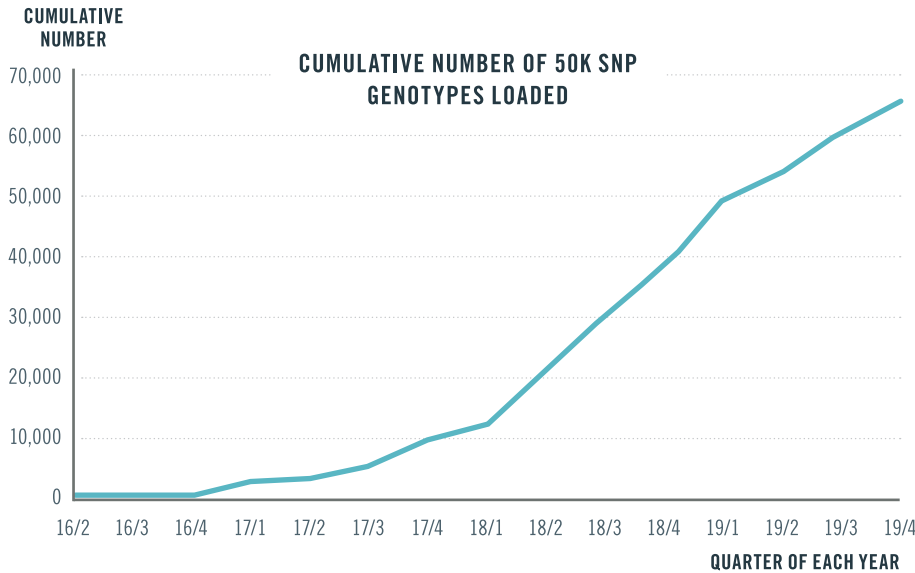
CUMULATIVE
NUMBER

CUMULATIVE NUMBER OF 50K SNP GENOTYPES LOADED

QUARTER OF EACH YEAR

FIGURE 1

Cumulative increase in the number of 50K SNP genotypes loaded into the Australian Wagyu Association database.

PROGRESS IN WAGYU

The accumulation of 50K SNP gentoypes has increased in the Australian Wagyu Association database with a high proportion of Wagyu Herdbook registered animals now have genomic information contributing to their EBVs.

To have an effective genomic Single Step BREEDPLAN analysis, it is important to have large numbers of animals with performance data which are also SNP tested. The number of animals with traits recorded are shown in Figure 2.
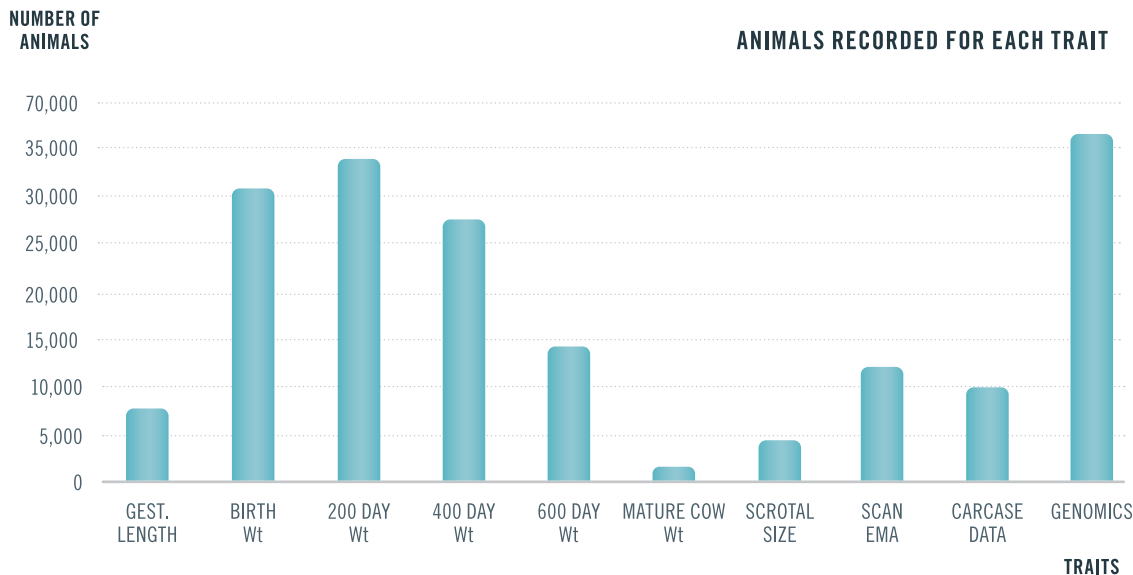
NUMBER OF
ANIMALS

ANIMALS RECORDED FOR EACH TRAIT

TRAITS

FIGURE 2

Number of animals with data recorded for the different traits.

HOW GENOMICS IMPACTS THE ACCURACY OF EBVS:

For breeders using genomics on their herds to improve EBVs, they see changes in the EBVs as well as changes in EBV accuracy for many animals. This is due to more information being available for the calculation of the EBVs. However, genomics does not always have a noticeable impact on the EBVs or EBV accuracies of an animal. It may be that the genomic information confirms the existing pedigree and performance information, meaning that the EBVs of the animal do not change. This is a more likely outcome in high accuracy animals that already have good amounts of performance data.

The following graphs show the changes to EBVs and EBV accuracy that occurred when genomics was added for 1,950 animals between the October BREEDPLAN run and the November BREEDPLAN run. The changes to EBVs and EBV accuracy for these animals is due to the addition of genomic information within the Wagyu BREEDPLAN analysis.

The graph in Figure 3 shows the change in Marble Score EBV accuracy when comparing the October (x axis) to November (y axis) Wagyu BREEDPLAN EBVs for the 1,950 animals which only had genomic information added to the analysis in November. In interpreting this graph, if the EBVs did not change between October to November, they stayed on the black line. If the EBVs changed, they moved away from the black line. You can see that the EBV accuracy for most animals improved, positioned above the black line, meaning that they were higher in November (following genomics being used) than October (when genomics was not used).

In the case of Animal A the addition of genomic information had no impact on its Marble Score EBV accuracy which stayed at 34%. In this case, genomics was unable to add any useable additional information for Animal A. While in the case of Animal B, addition of genomic information increased the accuracy by 17% from 34% to 51%.
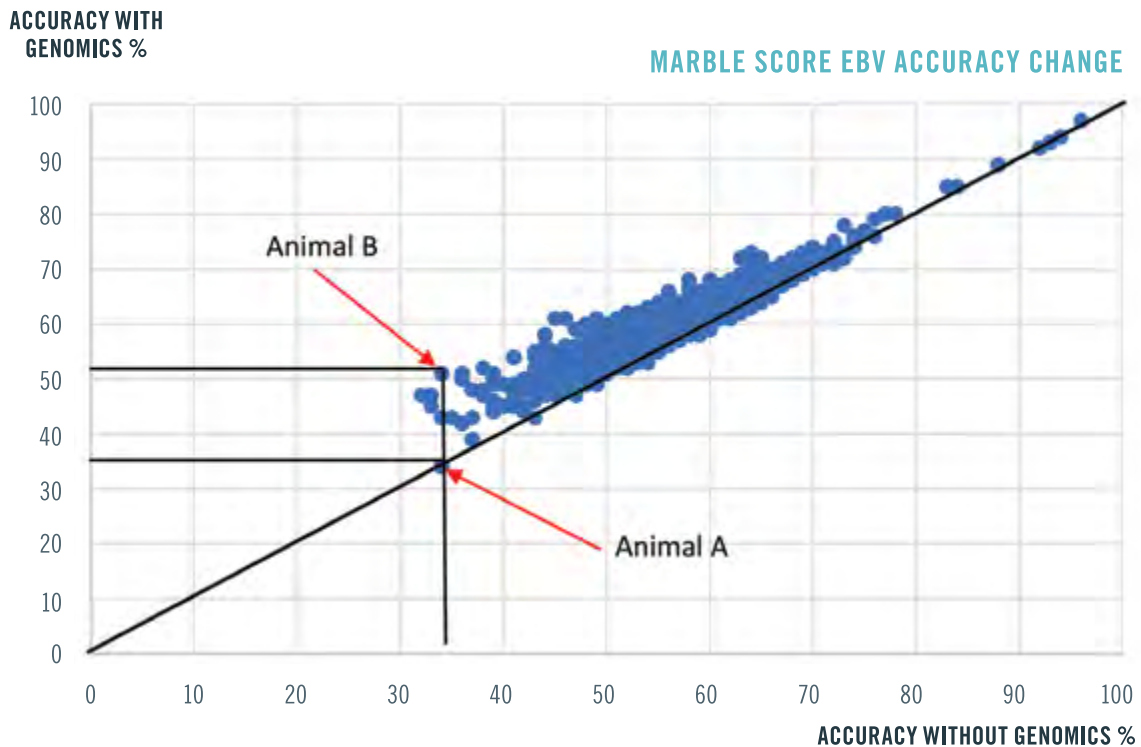

FIGURE 3

Change in Marble Score EBV accuracy when genomic information is added to the BREEDPLAN analysis for 1,950 animals between October and November 2019.

HOW GENOMICS IMPACTS THE EBV FIGURES THEMSELVES

Figure 4 shows the change in the actual Marble Score EBV figures for the 1,950 animals which only had genomic information added to the analysis in November. In this case, you can see that genomics has a large effect on the Marble score EBV figure for many animals. As an example, Animal C and D both had a Marble Score EBV of 0.5 in the October BREEDPLAN analysis (x axis) and with the addition of genomic information in the November analysis, the Marble Score EBV of Animal C increased by 1.1 marble score to 1.6 while the EBV of Animal D decreased by 0.6 of a marble score to –0.1 (y axis).

As described earlier, the EBVs of some animals are not impacted by genomic testing, because the genomics either does not add useable information, or the genomics gives the same answer as the available pedigree and performance data. Figure 5 is very helpful to better understand the proportion of animals and the level of change which could be expected in the example traits of Marble Score and Carcase Weight.

Figure 5 shows that, when genomic information was added to the November 2019 BREEDPLAN analysis for 1,950 animals, the Marble Score EBVs of 26% of these animals didn't change, 26% changed up or down by 0.1, 41% changed up or down by between 0.2 and 0.4 and about 7% changed up or down by 0.5 or more.
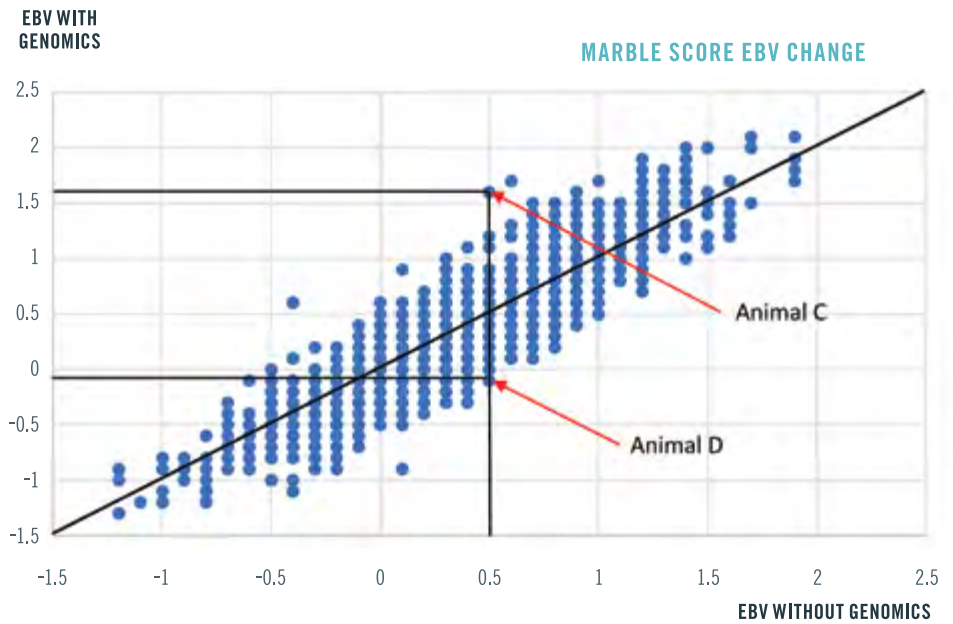

FIGURE 4

Change in Marble Score EBV when genomic information is added to the BREEDPLAN analysis for 1,950 animals between October and November 2019.
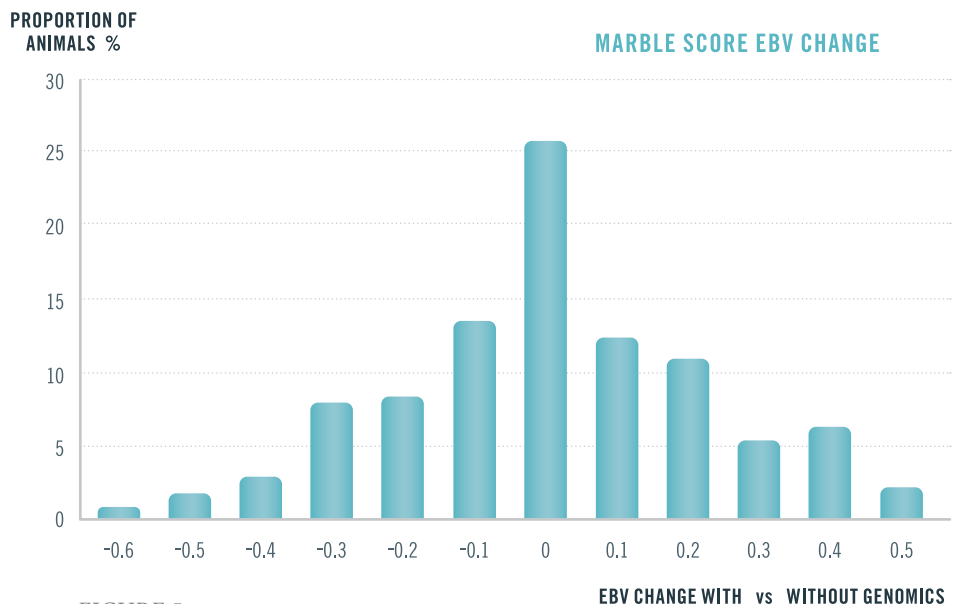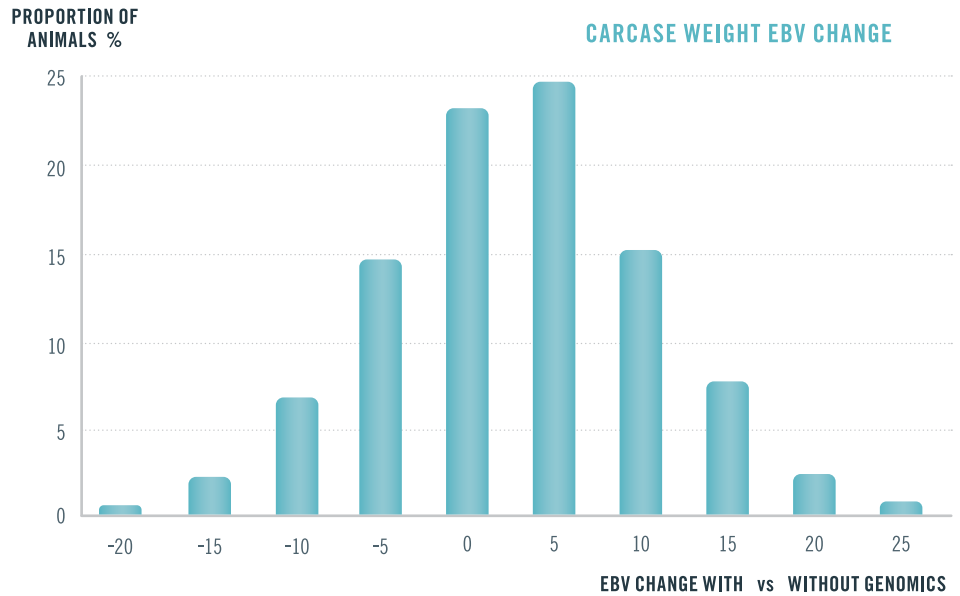

FIGURE 5

Distribution Marble Score EBV change when genomic information is added to the BREEDPLAN analysis.

FIGURE 6

Distribution of Carcase Weight EBV change when genomic information is added to the BREEDPLAN analysis.

Figure 6 shows that when genomic information was added for 1,950 animals for the November 2019 BREEDPLAN analysis, the Carcase Weight EBVs of about 63% of these animals changed up or down by 7.5kg or less and about 37% changed with 7.5kg or more.

PROPORTION OF ANIMALS %

CARCASE WEIGHT EBV CHANGE

EBV CHANGE WITH vs WITHOUT GENOMICS

SUMMARY

The impact of genomics on the accuracy and EBV figures within Wagyu BREEDPLAN is evident. The scale of the changes observed when genomic information is used within Wagyu BREEDPLAN for the example traits provided – Marble Score and Carcase Weights is high. The changes in EBVs s in conjunction with the potential increase in EBV accuracy, represents significant commercial value within breeding decisions. Using genomics within Wagyu BREEDPLAN adds significant information to the genetic analysis and has the potential to dramatically change selection decisions for retained breeding animals and mating decisions.

For the Wagyu industry, using genomic information within Wagyu BREEDPLAN provides far greater insight into the breeding values of registered animals. However, this is all reliant on the continued submission of performance recording that underpins the Wagyu reference population. The importance of continuing to maintain a large and genetically diverse reference population can't be over-emphasised. In general, animals which are more closely related to the reference population benefit more from genomic testing than those that are not closely related to the reference population.

MORE INFORMATION

Contact the Australian Wagyu Association for further information or if you wish to republish any part of this article

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