

BREEDPLAN AND YOU

BENEFITS FOR SMALL, MEDIUM AND LARGE HERDS

There is a misconception that only large herds have the scale to make performance recording for submitting data to Wagyu BREEDPLAN effective. This is not the case.

Whilst there will always be interest in performance recording to prove young sires, half of the genetic improvement comes from the cow base of a herd. The cow base of the herd also remains long after the bull has changed. Performance recording of the cow and its progeny can significantly affect EBVs and increase the accuracy of EBVs for the cow herd. The cow-herd is the foundation of your genetic improvement.

Smaller herds can achieve significant benefits from Wagyu BREEDPLAN, and animal performance data from such herds is useful for all, not just to that herd. This article will address strategies to get the most out of BREEDPLAN regardless of the size of your herd.

PERFORMANCE RECORDING IS THE KEY NEED FOR OUR GENETIC PROGRESS

Registering animals and getting 50K genomic information on them will allow genomic-enhanced EBVs (Estimated Breeding Values) to be reported for your animals through BREEDPLAN. It is linking pedigree and 50K genomic information to performance records of genetically similar animals that is the most important component.

To get the best estimate of the genetic merit of your animals, you need to submit your own performance records that relate to your animals. This will improve the accuracy of the EBVs and can change the EBVs for those animals, their parents and their progeny. The best estimate of the genetic merit of your animal comes when you have submitted performance data on your animal.

Recording and submitting performance data is time consuming and high attention to detail and accuracy is required. It is therefore important if you are going to put in the effort to record performance data on your herd, to make sure it will be effective in BREEDPLAN.

MAKING A CONTEMPORARY GROUP

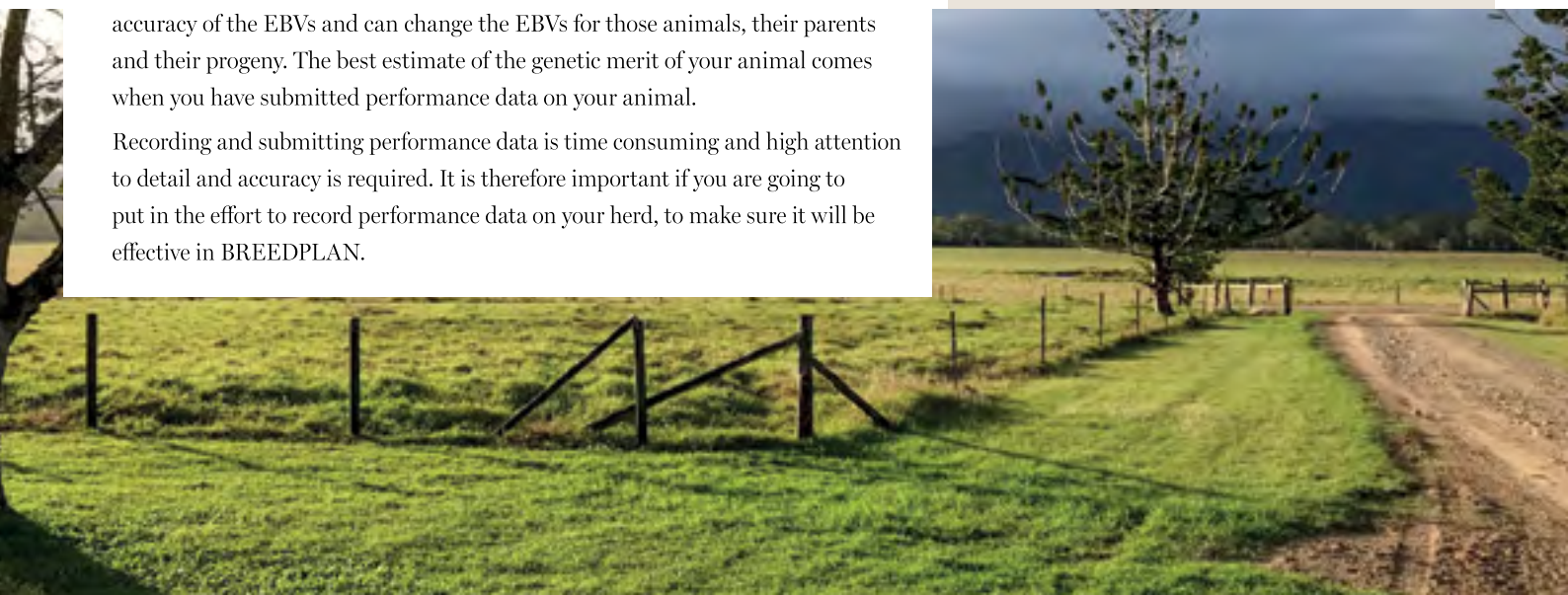
For making a Contemporary Group - the following should be considered... Wagyu BREEDPLAN directly compares the performance of an animal with the performance of other “similar” animals within the same contemporary group. Calves will be analysed in the same contemporary group if they:

- » were bred in the same herd,
- » are of the same sex,
- » are of the same birth number (ie. twins are not compared with single calves),
- » are of the same birth status (ie. ET calves not compared with AI/natural calves),
- » were born in the same calving year,
- » were born within 45 days (for birth and 200 day weight comparisons) or 60 days (for 400 and 600 day weight comparisons) of each other,
- » have been weighed on the same day (and have the same weighing history),
- » have been run under the same conditions.



MORE INFORMATION ON CONTEMPORARY GROUPS

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STRATEGIES FOR GETTING THE MOST BENEFIT OUT OF PERFORMANCE RECORDING

- Using performance recording for the animal's own EBV, e.g. a young heifer or bull:** To compare animals, you need at least two animals in a contemporary group to ensure the performance records for these animals contribute to their own EBVs. As discussed in our September 2018 edition of the Wagyu Update, Volume 69, the more animals in a contemporary group, the more powerful the data is. A group of at least six animals, with more than one sire used, is a useful base for genetic evaluation.
- Using performance recording to improve the females' EBVs:** The EBVs of the cow herd and their accuracy have an equal outcome on the EBVs of the progeny (compared to the bull used). Performance recording progeny within small contemporary groups to improve EBVs for your cow herd can increase EBV accuracy for your young breeding stock, particularly through use of 50K genomics. Once a cow has progeny performance recorded, this data contributes to informing the genetic merit of the cow and future progeny. A minimum of two animals is required in a contemporary group, but again, six animals provides a good level of effective data.
- Using performance recording for proving a sire's EBVs:** In this case, you need a minimum of two sires represented within the contemporary group so that an individual sire is being compared against to at least one other. Each sire needs to have a minimum of two progeny to affect the sires EBV for a trait, but preferably five progeny each to get reasonable improvements in EBV accuracy. In this instance, a minimum contemporary group size of 10 animals – with at least two sires represented – is recommended.
- Using performance recording to obtain high accuracy EBVs early in life:** Taking the best advantage of performance recording for a small herd requires use of all three strategies. This will enable better calculation of EBVs with higher accuracy, sooner. Having higher accuracy EBVs for the sire and dam will provide higher accuracy EBVs in the progeny. 50K SNP genotyping the progeny and recording its performance will likewise impact the progeny's EBVs and improve their accuracy.

CONSIDERATIONS FOR CAPTURING AND USING CARCASE DATA IN PERFORMANCE RECORDING

The Wagyu industry is unique among the performance recorded breeds in that there is a high volume of cattle processed annually for which slaughter data relating to the final carcase outcome is captured by supply chains which in turn, underpins the genomically-enhanced BREEDPLAN EBVs. In many instances, accessing this information for the purposes of submitting it to the AWA for use in Wagyu BREEDPLAN to improve EBVs requires arrangements through the supply-chain back to the original animal breeder to be agreed.

If you are seeking data from supply chain partners for submission to Wagyu BREEDPLAN, in addition to ensuring you can obtain this data, you need to also ensure that the contemporary group structure you have created on-farm is maintained through the supply chain.

For example, if you have 10 animals born in a contemporary group and managed as one group for the purposes of proving two or more young sires, these animals need to be kept in a that group until slaughter. That is, the contemporary group needs to be maintained whole-of-life up to the point of processing in the same facility. It does not matter if the animals are mixed with other animals in a feedlot pen or trucked with other animals to slaughter, as long as the animals are all handled the same way. If the contemporary group is split and slaughtered on two different days, this will reduce the effectiveness of the data. In this situation, it is vital to have recorded that they have been split.

For additional information, see the BREEDPLAN Tip Sheet: Small Herds - Obtaining Effective Results from BREEDPLAN

FREQUENTLY ASKED QUESTIONS

WHY GENETIC EVALUATION SYSTEMS ARE IMPORTANT FOR WAGYU?

WHY IS UNDERSTANDING GENETIC MERIT IMPORTANT FOR MANAGEMENT AND BREEDING DECISIONS?

Genetics usually only accounts for 30 – 50% of the differences in trait performance in beef cattle. Without a genetic evaluation system (Wagyu Single-Step BREEDPLAN), it is impossible to determine if the performance of an animal is due to its genes, or due to its management.

There can be extreme environmental and management differences between Wagyu production systems in Tasmania compared to Queensland's Gulf country, or early weaning and grain backgrounding compared to extensive northern pastoral production systems. These differences have a large effect on the physical performance of an animal. It is impossible to physically compare animals from different production systems and determine their genetic merit without a rigorous genetic evaluation system. Understanding genetic merit requires removing the large effects of environment and management system so that the true value of the genes can be estimated.

WHAT IS BREEDPLAN?

Put simply, BREEDPLAN is the Wagyu industry's publicly available genetic evaluation system. It uses performance records (actual measurements on animals) along with pedigree and genomic information, to estimate the genetic merit of individuals. This allows producers to identify which animals have higher or lower genetic merit for traits they are interested in, and they can use this in their management and breeding decisions. To get the most out of Wagyu BREEDPLAN, you need to:

- » register animals with the AWA so their pedigree information is available;
- » submit performance data on animals in their management groups; and
- » use 50K genomic tests to accurately resolve the merit of the genes provided from the sire and dam in their progeny.

HOW DOES BREEDPLAN ACCOUNT FOR ENVIRONMENT AND MANAGEMENT SYSTEM DIFFERENCES BETWEEN PRODUCERS?

Wagyu BREEDPLAN uses performance records submitted within contemporary groups of animals. By looking at differences within a contemporary group, Wagyu BREEDPLAN can determine performance differences that are due to genes.

The next step is to compare between groups. This depends on the existence of genetic links between groups - a simple example is where a sire has progeny in several different management groups. In each group, the progeny of that sire will be compared with the progeny of other sires, and the common sire essentially provides a base for comparison of the sires used in the various groups. In this case, the common sire provides a genetic link.



breedplan.une.edu.au/tips/

For more information on genetic linkage, see the BREEDPLAN Tip Sheet: Understanding Genetic Linkage

Within Wagyu, we have exceptional genetic linkage between herds due to the common recent ancestry across our industry. There is a high prevalence of use of common sires such as IMUFQTF148 Itoshigenami (5020 progeny), WKSFM0164 World K's Michifuku (4848 progeny) and IMUFQTF147 Itoshigefugi (3907 progeny) as a few examples.

These sires and others that are used across different herds are called 'reference' or 'link' sires by geneticists. Reference or link sires allow the performance data of progeny from mating's in different herds to be benchmarked across herds.

Even having a sire used within one other herd is helpful in creating linkage so your herd can be benchmarked.

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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