



CROSSBRED WAGYU DATA

GETTING THE MOST OUT OF
THIS PERFORMANCE DATA

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As highlighted in our *Major improvements to AWA Wagyu BREEDPLAN article*, one primary function of the Wagyu BREEDPLAN genetic analysis is to separate the proportion of trait performance that can be attributed to genetics vs trait performance due to environmental influences.

To allow this, Wagyu BREEDPLAN analyses how progeny performance from sires and dams compares within management groups (contemporary groups), so that relative genetic merit can be estimated for each animal. Genomic information further defines the genetic influence and in conjunction with recorded pedigrees the relatedness of animals.

Now that Wagyu BREEDPLAN can accommodate data from crossbred Wagyu animals (F1 and higher content progeny: *crossbred data now used in Wagyu BREEDPLAN article*, it is essential that members plan and manage appropriate groups of animals if they wish to use crossbred data to contribute to the EBVs of their sires.

Unlike fullblood progeny data, which provides information to support sires and dams, using crossbred F1 progeny data only provides performance information to support the Herdbook registered sire of the crossbred progeny. As higher-grade data (F2 and F3) is provided, BREEDPLAN will also attribute genetic information to other known parents and grandparents.

**TIPS FOR PLANNING
AND RECORDING KEY
INFORMATION TO GET
THE MOST OUT OF YOUR
CROSSBRED DATA**



1. ONLY USE REGISTERED SIRES

This seems like an obvious point, but to use crossbred data to prove EBVs for your sire, the sire must be registered with the Australian Wagyu Association. You also need to make sure other sires whose progeny you wish to compare to, are also registered with the AWA so that a valid comparison can be made.

2. USE MORE THAN ONE SIRE

A key purpose of Wagyu BREEDPLAN is to use progeny performance data to determine genetic differences between sires. If you only have data from the progeny of one sire within a group, that data cannot be compared to the progeny of another sire. The use of only one sire is called a single-sire contemporary group and the data is of no value for analysis of genetic differences between sires.

For this reason, BREEDPLAN requires that at least two sires be represented in each contemporary group if the performance of the progeny is to be compared and used to determine the genetic potential of each of the sires and to calculate their EBVs. This can be achieved through mating two sires naturally or using artificial insemination programs with a natural “back-up” sire. Where AI is used, it is recommended that the back-up sire/s are put in with the females shortly after AI (within 21 days) so that all calves are born within a certain period and can be considered in one contemporary group. Calves will only be considered as one contemporary group if they are born within 45 or 60 days of one another.

3. RECORD BIRTH DATE

Age is a key determinant of most traits, particularly weight traits and carcass traits. So that BREEDPLAN can accurately account for age differences between animals within crossbred data sets, birth date must be accurately recorded. Slaughter data for F1 cattle cannot be used without a birth date record as age at slaughter is required.

4. DNA TEST YOUR CALVES

Production of commercial (slaughter) Wagyu F1 and higher content cattle usually occurs in large management groups with multi-sire AI and/or natural joining programs. DNA testing is necessary to accurately ascribe the correct sire to each animal. The AWA will conduct parent verification on all crossbred Wagyu slaughter progeny. Genomic SNP testing for parentage is recommended.

5. KEEP ANIMALS TOGETHER WHOLE-OF-LIFE

Wherever possible, keep all progeny (of the same sex) together and manage them the same. This ensures that all progeny have been given an equal opportunity to perform and can be directly compared within their contemporary groups. This is typical in most commercial production scenarios, where lots of animals are sold from a breeder to a buyer to make ‘pens’ within a feedlot and the whole pen is sent for slaughter on the same day.

6. SLAUGHTER DATE

Only data from animals slaughtered at the same facility on the same day will be compared to each other in BREEDPLAN. There can be large variation in carcass trait performance between slaughter days and between slaughter facilities. Communicate with the feedlot that the animals are for BREEDPLAN analysis and request that they ensure all your animals are slaughtered on the same day in the same facility, where possible.

7. DO NOT HARVEST ANIMALS BASED ON LIVEWEIGHT AT SLAUGHTER

In certain situations, to even out carcass weight within production runs, animals that are closest to the desired finishing weight may be drafted out of multiple pens to create a more even slaughter group. Unfortunately, this practice (Harvesting) invalidates contemporary groups as it removes the variation between progeny performance that would have been used by BREEDPLAN to determine genetic differences between sires. Harvesting of animals out of pens at a target slaughter weight should not be done if you want to use that data in Wagyu BREEDPLAN.



If you require any further information from the AWA to assist you with developing effective crossbred Wagyu contemporary groups, please contact the AWA Technical Service Manager – Mr Carel Teseling, or the MSO team.

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The points provided in this article are to assist AWA members to plan the production of crossbred Wagyu progeny to gain maximum benefit from using performance data in Wagyu BREEDPLAN to inform EBVs of sires.

8. SEND ALL THE SLAUGHTER INFORMATION ON THE PROCESSOR FEEDBACK SHEET TO THE AWA

AWA requires the complete data set for loading data into Wagyu BREEDPLAN. It is important that all carcass data, high and low is submitted so that the maximum amount of variation is available to inform the calculation of EBVs. Without variation in the data, the genetic variation in the sires cannot be determined.

On this last point (8), as an example: If 30 progeny from two different sires are slaughtered in one group with an average marble score of 6, but the top marble score is 9 and the bottom marble score is 1, BREEDPLAN can use this entire range to accurately determine genetic difference between the sires of the calves.

However, if a member only reported data for animals with above average marble score, very limited variation in data would be reported (e.g. only progeny with marble score 6-9). The outcome of this data being used in BREEDPLAN would be that little change in EBVs would be observed, as the number of progeny are limited and the range in the data is limited, thereby reducing the ability of BREEDPLAN to determine genetic variation between sires.

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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