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IMPLEMENTATION AND DELIVERY OF THE WAGYU FEEDER CHECK

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SUMMARY

Most Wagyu animals were imported into Australia between 1990 and 1997. Since then, the number of Wagyu and Wagyu-influenced animals in feedlots continued to increase to the point where many high-quality beef export brands are now Wagyu or Wagyu-cross animals. Wagyu and Wagyu-cross animals are typically feedlot fed finished for 350 to 450 days. These extended periods in the feedlot makes it valuable to identify non-performers and to remove them from long-fed programs. The Wagyu Feeder Check (WFC) was developed through partnership with Australian Wagyu Association (AWA), Neogen and CSIRO and is a commercially available DNA test, delivered using a web-based information system developed by AWA and The Helical Company. The system provides producers or feedlot operators with the ability to test feeders and rank them on genetic merit for five feedlot and carcase performance traits as well as the Wagyu Feeder Index which combine the five trait scores into a single value. The WFC system also enables the registration and collection of carcase data of Wagyu and Wagyu-cross animals. This significantly increase the Wagyu reference population for further recalibration of the WFC algorithms as well as genetic analysis of registered Fullblood and Purebred animals.

INTRODUCTION

The Wagyu breed in Australia was established from 221 Fullblood foundation animals mostly exported from Japan between 1990 and 1997. In comparison to other breeds Wagyu is a relative recent introduction to the Australian beef industry. In the past decade the number of Wagyu and Wagyu-cross animals on feed increased very significantly to around 300,000 (Australian Wagyu Association annual survey data, unpublished). In 2018 Single-Step BREEDPLAN, which incorporates the use of genomic information in conjunction with all traditional sources of data in the estimation of breeding values, was implemented for high Wagyu content Fullblood and Purebred animals. This development stimulated high density SNP testing of seedstock animals and the collection of carcase data increased sharply for those animals which were not retained for breeding purposes. The Animal Genetics and Breeding Unit (AGBU) developed a genomic data pipeline which incorporates a range of quality assurance (QA) checks to ensure genotype integrity (Connors *et al.* 2017). However, in many cases these QA checks exclude the genotypes of animals with a genomic Wagyu content lower than 80%. Most F1 to F3 Wagyu crosses therefore do not have genomic information used to determine their genetic merit through EBVs.

Wagyu and Wagyu-cross animals are often feedlot fed for 350 to 450 days. Due to these extended periods in the feedlot, it is very beneficial to identify animals that are likely to perform poorly and eliminate them from long-fed programs. The Wagyu Feeder Check (WFC) was developed to address the need of the Wagyu sector for the feedlot assessment of F1, F2 and F3 Wagyu feeder cattle for economically important traits as well as the AWA developed Wagyu Feeder Index.

DEVELOPMENT OF WAGYU FEEDER CHECK

The WFC prediction is based on a commercially available DNA test which was developed through partnership with AWA, Neogen and CSIRO.

The development of the WFC genomic algorithms (Reverter *et al*. 2023) utilised 8,316 genotypes supplied by Neogen and corresponding carcase phenotypes supplied by the AWA. The carcase data supplied by AWA originated from eight independent commercial supply chains with phenotypes for five economically important traits. This reference population consisted of 2,120 Fullblood Wagyu and 6,196 Wagyu crosses, mainly Wagyu-Angus F1 animals.

The WFC provides a score to reflect the genetic merit of Wagyu content animals for five key traits: average daily gain during feedlot finishing (ADG), hot carcase weight (CWT), carcase eye muscle area (CEMA), AUS-MEAT marbling score (MARB), and carcase subcutaneous fat depth at the rump or P8 site (CP8). The genetic merit scores (Molecular Breeding Values; MBVs) range between 1 and 10 (10 being the highest genetic merit). According to Reverter *et al.* (2023) the genomic prediction accuracies were in the range of 55-65% for all traits except CEMA which were in the 40-50% range. They concluded that the use of the WFC will benefit feedlot operators who finish Wagyu breed content animals and who wish to remove poor performers from their long-fed feeding programs.

THE WAGYU FEEDER INDEX - TRAIT WEIGHTED PROFIT RANKING

Based on the relative impact of the WFC traits on feedlot performance and carcase value, the Wagyu Feeder Index (WFI) was developed by the AWA to simplify sorting animals based on a single value reflecting their genetic merit for feedlot profit.

The WFI calculation is highly aligned to the Wagyu F1 $Index published by the AWA as part of its Wagyu BREEDPLAN reported selection indexes. The relative contributions of each of the WFC traits to the Wagyu Feeder Index is 50% for Marble Score, 16.7% for Carcase Weight, 12.5% for Eye Muscle Area and P8 Fat depth and 8.3% for Average Daily Gain.

WAGYU FEEDER CHECK TESTING AND REPORTING OF RESULTS

The results of the WFC are mainly being used to remove low genetic merit animals from long-fed programs, or to identify animals for which feeding periods can be reduced but still achieve required carcase performance. To ensure timely assignment of animals to the most appropriate feeding program, the reporting of results needs to be automated to minimise human intervention which normally slows down the process. It was also very important to simplify the ability to download and interpret results and to graphically present progeny distributions to assist in the comparison of sires.

The AWA in conjunction with The Helical Company developed a web-based information system to collate the WFC test requests, collect, store, process and report the results (Garrick *et al.* 2025). This process is automated and allows the member to log in and complete the test request, invoices the member for the testing, notifies Neogen of the test request, downloads the test results and genotypes from the Neogen server, loads the results into the Helical database, runs a parent discovery analysis and notifies via email and an online dashboard to the member that the results are available. The parent discovery is a key enabler of the overall value proposition by facilitating the linkage of animals with otherwise unknown parentage to their AWA registered sire so that the commercial sire population can also be managed.

In addition to the tabular display and ability to download the results, each animal's results are also displayed graphically in a radar plot. Figure 1 shows how the WFC scores are graphically displayed for animals with low, average and high marbling potential.

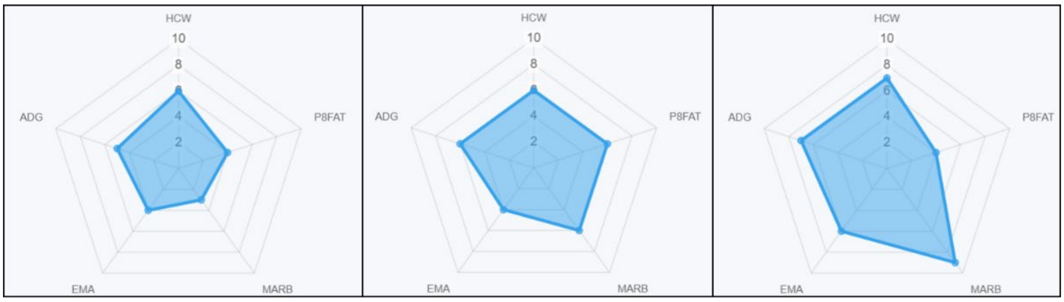

Figure 1. The graphical display showing the trait rankings of an animal with low (left), average (middle) and high (right) marbling WFC scores

The genotypes of WFC tested animals are automatically included in a parent discovery analysis which now includes over 500,000 genotyped animals.

Where sires are identified through the parent verification process, a breeder can evaluate the sires by comparing the WFC score distributions of their respective progeny. Figure 2 shows the proportional progeny trait score distribution graph of two sires and how their trait distributions compare to all animals tested in the specific batch. The average trait ranking distributions of progeny makes it possible to identify and cull a genetically inferior sire well before kill data of progeny is analysed and remove these from impacting future production. Likewise, a breeder may decide to use a high performing bull in an artificial insemination program to increase the number of genetically superior progeny.

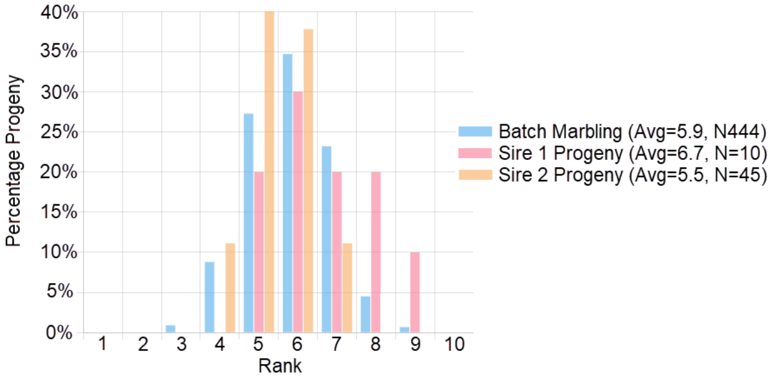

Figure 2. Distribution graph comparing marble trait scores of the progeny of two sires and all animals tested in that batch

USING WAGYU FEEDER CHECK

Development of the WFC delivers a novel approach in optimising management strategies to meet profitability and sustainability targets in the Wagyu industry and is aimed to support supply chain participants who produce export quality Wagyu beef using a feeding period of typically around 350 - 450 days.

The WFC provides the commercial producer or feedlot operator with the ability to test feeders before or at feedlot entry to verify sire parentage and identify low genetic merit carcase performance animals. Animals that are identified as not meeting the performance criteria for a supply chain can be drafted into short-feeding programs or other endpoints, saving on resource use and investment of capital.

The AWA estimates that removing the bottom 10% of crossbred Wagyu feeders to short-fed programs (150 days) would save AUD $22 million in feed costs per year, limiting resource use inefficiencies and reducing financial losses on low performing animals. Removing the bottom 5% of sires and their progeny from future years would save a further $11 million in production losses.

There are a significant number of large northern commercial enterprises which are in the process of introducing Wagyu into their herds to improve fertility and age at first calving. Many of these enterprises are now confronted with the prospect of deciding which of the F1, F2 and F3 females are genetically superior for carcase traits and should be retained as breeding replacements. When these females are WFC tested, the sire discovery and trait scores significantly simplify the process of deciding which females are genetically superior for the feedlot traits.

CARCASE DATA SUBMISSION

The AWA encourages the registration of parent-verified WFC tested animals in the free-of-charge AWA Slaughter Register. A carcase data refund of $5 per WFC tested Slaughter Registered animal is provided when carcase data is submitted and loaded into the AWA database. This has stimulated a significant volume of commercial carcase data submission, with a recent extract for recalibration of the WFC genomic predictions increasing the number of animals in the reference population from 8,000 to close to 18,000.

These additional genotypes and phenotypes constitute a significant increase to the Wagyu reference population and allows the AWA to improve the WFC genomic predictions. It also provides the AWA with large numbers of carcase data and genotypes necessary for improving its genetic estimates of registered cattle within the AWA public genetic evaluation (Wagyu BREEPLAN) for Fullblood and Purebred cattle.

CONCLUSION

The Wagyu Feeder Check is an industry driven tool for the commercial Wagyu sector to determine the genetic merit of F1, F2 and F3 Wagyu animals. The automation of the test request and results delivery pipeline allows for reduced timelines and accuracy due to minimal human intervention. The independent development and delivery of the WFC pipeline demonstrates the maturation of genomic services provision with the Australian beef industry to provide rapid implementation of commercially relevant services.

The cost-free registration of WFC tested animals and rebate for carcase data are innovative ways of stimulating the submission of carcase data for animals which already have a genotype available thereby increasing the Wagyu reference populations. Due to the increase in the number of carcase records available, updated WFC validations are currently under development and promise to deliver even higher levels of accuracy to identify genetically superior animals.

The WFC provides an excellent example of the benefits that can accrue when a Breed Association champions a collective approach to delivering an information system that leverages the activities of a range of stakeholders that span the beef production chain and its supporting industries.

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