

Final Report

Project code: P.PSH.0646
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Date published: October 2014
ISBN: [Request through Publications
Database]

PUBLISHED BY
Meat & Livestock Australia Limited
Locked Bag 991
NORTH SYDNEY NSW 2059

Wagyu Collaborative Genetics Research Project

Stage 1

Meat & Livestock Australia acknowledges the matching funds provided by the Australian Government to support the research and development detailed in this publication.

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Abstract

Performance, pedigree and genotype data on approximately 2-3,000 Wagyu predominantly Fullblood animals was collected, including data collected using the Japanese Digital Camera Image Analysis methodology. The lack of a universal ID system added significant project coordination costs, and will if not rectified, add costs in any project seeking to use detailed carcass data in genetic evaluation. Traditional pedigree analysis has demonstrated that it is possible to collect and genetically analyse detailed carcass information on commercial Wagyu animals, with results showing: carcass marbling, whether measured using the camera or via Ausmeat score, is moderately to highly heritable (current estimate for heritability is 0.52 for CMAU and 0.35 for CCMP); Carcass Marbling Fineness Index is moderately-highly heritable (0.50); the two measures of carcass marbling (CCMP and CMAU) are genetically essentially the same trait (genetic correlation = 1.00); and Carcass Eye Muscle Area and Camera Rib Eye Area are both moderately-highly heritable (heritability of 0.56 and 0.62 respectively), and strongly correlated genetically (correlation = 0.83). The distribution of Carcass Ausmeat Marble Scores suggests that actual marbling extends well past Ausmeat Score 9 – the overall mean is 7.4, and if the trait is normally distributed, there would be approximately 17% of the total sample > score 9, 6% >10, 2% >11 and 1% >12. There is considerable variation in estimated marbling percent within a Carcass Ausmeat Marble Score, and the variation appears to increase as marble score increases. This suggests the Ausmeat Marble Score assessment methodology needs to be extended and its accuracy improved. Genomic relationship matrix **G** analysis (GBLUP) showed the carcass traits are highly heritable and for most traits the heritability estimates from GBLUP are higher than or similar to those from the pedigree based BLUP. The genetic correlations between the carcass marbling measures (CCMP vs CMAU) and between values for eye muscle area measured by camera images and by the traditional method were unity, as in the BLUP analyses. The Carcass marbling fineness or coarseness indices (CCFI and CCCI) are also highly correlated with marbling measures (CCMP and CMAU). The GEBVs were highly correlated with their BLUP EBVs. This dataset and research establish the concept that genotyping can be a useful tool for the Wagyu breeder and producer – both in use in selection, and for use in sorting animals for production.

Executive summary

This project was initiated to research several basic questions:

- Is it possible to collect and analyse detailed carcass information on commercial Wagyu animals, including using genotype to estimate genomic relationship to provide or augment pedigree data?
- Is there genetic variation in the traits so collected and analysed?
- Does use of genomic information enhance the genetic evaluation (if such is possible) either through improving accuracy of parameter estimates and hence EBVs and/or making possible the evaluation of animals with only genotype collected?
- If there is genetic variation for the recorded traits, which of them should be considered for inclusion in ongoing enhanced genetic evaluation of Wagyu cattle?
- What further R&D is worthwhile; including if appropriate research into modified carcass assessment?

Stage 1 of the project involved collection of performance, pedigree and genotype data on approximately 2-3,000 Wagyu animals, including data collected using the Japanese Digital Camera Image Analysis methodology.

The project has highlighted challenges imposed by the lack of a universal ID system, or the limited ability (or willingness) to use that system across interfaces in the value chain. This added significant project coordination costs, and will if not rectified, add costs in any project seeking to use detailed carcass data in genetic evaluation.

Since the first results from this Australian Wagyu Association R&D project were reported in late 2013, an amount of additional performance and genotype data has been added. For example, for the calculation of the genetic correlation between Camera Carcass Marbling % and Carcass Ausmeat Marble Score, the correlation was previously estimated with approximately 1500 animals with records, and now there are over 2,000 animals with records for both traits.

This additional data is underpinning two general results:

- The standard errors of essentially all parameter estimates are now smaller, typically by 2-3% but in some cases considerably more. This means that we can be more confident in the estimates, which in turn means that we can be more confident in the estimated breeding values being generated.
- The estimates themselves have in many cases changed. In most cases changes in the heritabilities and genetic correlations are not large.

The first Phase of the project's data analysis used traditional pedigree, involving a first stage conducting a univariate analysis for each recorded trait (univariate meaning that trait is analysed on its own). The second stage was to conduct a series of bivariate analyses (2 traits at a time) to estimate the genetic relationship or correlation between the pairs of traits.

Some important results to note are:

- Carcass marbling, whether measured using the camera or via Ausmeat score, is moderately to highly heritable (current estimate for heritability is 0.52 for CMAU and 0.35 for CCMP)
- Carcass Marbling Fineness Index is moderately-highly heritable (0.50)
- The two measures of carcass marbling (CCMP and CMAU) are genetically essentially the same trait (genetic correlation = 1.00).
- Carcass Eye Muscle Area and Camera Rib Eye Area are both moderately-highly heritable (heritability of 0.56 and 0.62 respectively), and strongly correlated genetically (correlation = 0.83)
- The distribution of Carcass Ausmeat Marble Scores (Fig. 3) suggests that actual marbling extends well past Ausmeat Score 9 – the overall mean is 7.4, and if the trait is normally distributed, there would be approximately 17% of the total sample > score 9, 6% >10, 2% >11 and 1% >12.
- There is considerable variation in estimated marbling % within a Carcass Ausmeat Marble Score, and the variation appears to increase as marble score increases (Fig. 3 CMAU vs CCMP).
- There is still some suggestion of data harvesting impacting the results. For example, Fig 2 shows a subset of animals with low Carcass and Camera EMA, suggesting these animals may have been killed much lighter – either as an identified separate cohort, or possibly simply lighter weight and possibly “condition” animals culled out from cohorts earlier.

Sire Research Breeding Values are available from the univariate analyses using traditional pedigree.

The second Phase of the data analysis involved the genomic relationship matrix **G** analysis. This Phase essentially repeats Phase 1, except it replaces the pedigree relationship between animals with the more precise genomic relationship, where an animal has a genotype. The Results from GBLUP showed the carcass traits (most were measured using camera images) are highly heritable. For most traits the heritability estimates from GBLUP are higher than or similar to those from the pedigree based BLUP using the bigger dataset, eg CWT, CCRA. For marbling traits (CCMP and CMAU) the GBLUP results are higher than those from the traditional pedigree Phase 1 analyses. The genetic correlations between the carcass marbling measures (CCMP vs CMAU) and between values for eye muscle area measured by camera images and by the traditional method were unity. This is the same as the results from BLUP analyses. The Carcass marbling fineness or coarseness indices (CCFI and CCFI) are also highly correlated with marbling measures (CCMP and CMAU). The GEBVs of 22 sires whose progeny had genotypes and carcass weights were highly correlated with their BLUP EBVs. The correlations between GEBV and EBV are all around 0.6 to 0.9, with slightly greater spread in all cases (reflecting the increased heritability estimates for the traits).

Key points to note are:

- The dataset has proved amenable to use of genomic information in estimating genetic parameters and hence estimating breeding values.
- The results from the genomic analysis confirm and in general slightly improve those from a pedigree analysis.

- The key messages about the genetics of key traits remain:
 - There is substantial genetic variation for all the traits of interest, indicating that if the breed wishes to make genetic improvement of marbling, carcass weight at constant age, muscling etc, there is plenty of scope to do so.
 - Selection for combinations of traits is possible.
- This dataset and research establish the concept that genotyping can be a useful tool for the Wagyu breeder and producer – both in use in selection, and for use in sorting animals for production.

Stage 2 of the project has been designed to achieve the best technical and business outcomes for the Wagyu breed's genetic improvement. It aims at building on this platform and moving to full implementation.

This research is world leading and as such it is likely that other Wagyu producing countries will wish to use the resulting Wagyu Genetic Analysis, providing the opportunity to for the Australian Wagyu Association to deliver a universal international Wagyu analysis.

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