



BLOODLINES vs PEDIGREES & EBVs vs GENOMICS

WHAT'S THE DIFFERENCE?

There is high interest within Wagyu breeders in paying homage to traditional Wagyu bloodlines that trace back to the foundation genetics originating from Japan. From these genetics, more than 250,000 individuals have been registered with the AWA.

BLOODLINE vs PEDIGREES

Bloodlines are defined as an animal's set of ancestors or pedigree. In cattle breeding this concept is particularly associated to desirable characteristics attributed to these ancestors.

So, bloodline = pedigree, or components/blocks of a pedigree. Some breeders like to look at maternal lines, some look at sire lines, some look at both. As there are fewer Bloodlines in the population than individual animals, Bloodline information can be regarded as a simplified version of the pedigree of an animal.

Wagyu breeders analyse bloodlines, sometimes back five or six generations (by looking at the pedigree) in trying to understand the genetic value of their stock based on known or perceived performance of individuals in the pedigree.

Translating this to Wagyu breeding, if you are looking at a five-generation pedigree, there are eight great great grandsires and eight great great granddams. Accounting for their genetic influence and contribution through a pedigree is a significant statistical challenge. The father of Genetics, Gregor Mendel, developed the

principles of inheritance that describe the transmission of genetic traits across generations. He did this in 1865 before anybody even knew that genes existed.

These principles of inheritance can be determined statistically through the analysis of pedigrees, so that estimation of genetic merit can be quantified across very long and complex pedigrees spanning multiple generations.

Quantitative Genetics is the field of science that was born in 1865 from Gregor Mendel's work. It studies the genetic or inherited basis of variation in phenotypes across generations, using analysis of pedigree and trait records. Using quantitative genetics, breeders can determine the inheritance patterns through large and complex pedigree trees to assist prediction of genetic merit in their herds.

In the Wagyu Update Volume 78, pp 34 – 40, we used an example sire SMOFF0278 to show how carcass records contribute to predicting the genetic merit of an animal across generations.

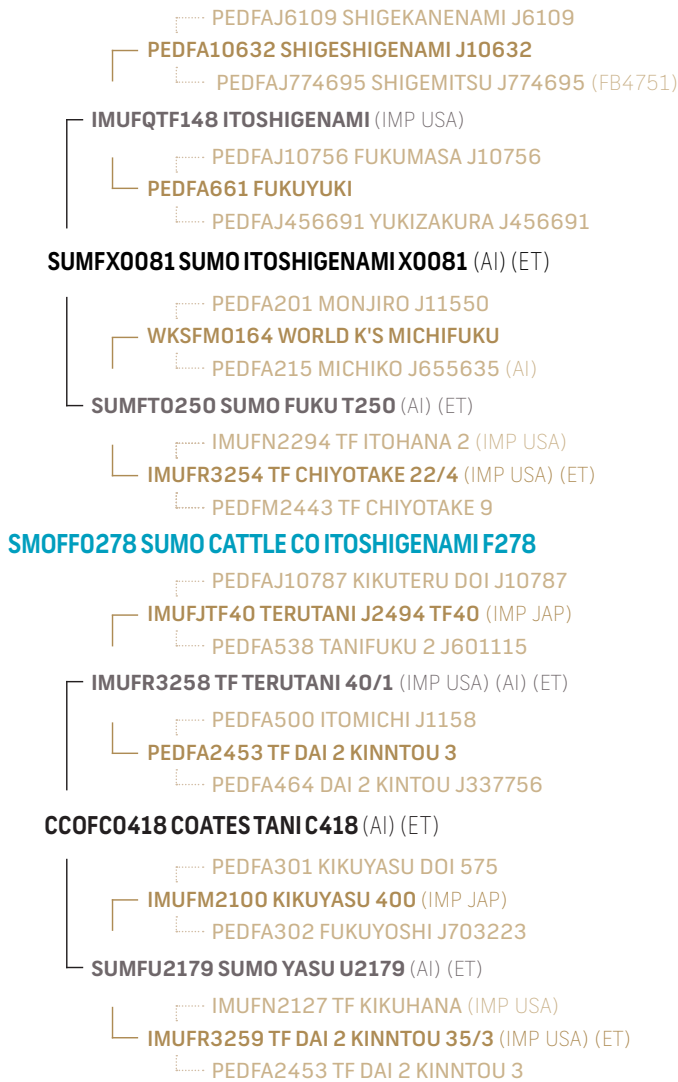


FIGURE 1

Five generation pedigree of the SMOFF0278 showing relative genetic contribution of each generation.

Using this sire again as our example, his five generation pedigree, with eight great great grandsires and eight great great granddams is shown in Figure 1.

Each one of these 16 great great ancestors (theoretically) provides 6.25% of the genetic makeup of the current animal.

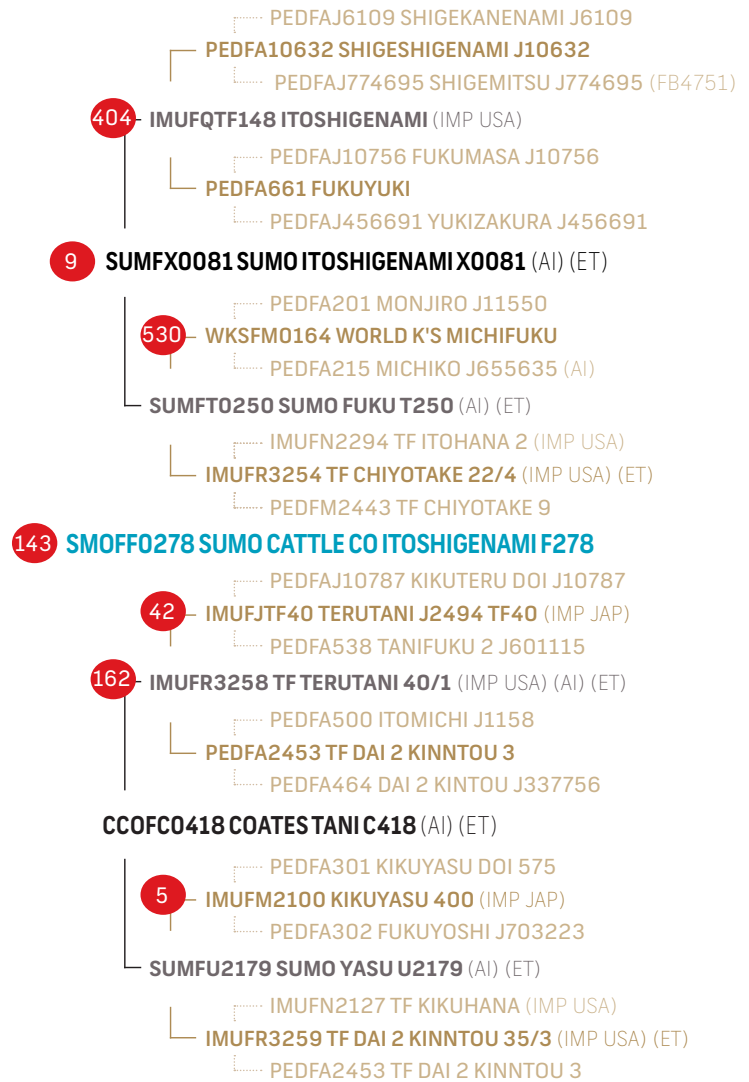
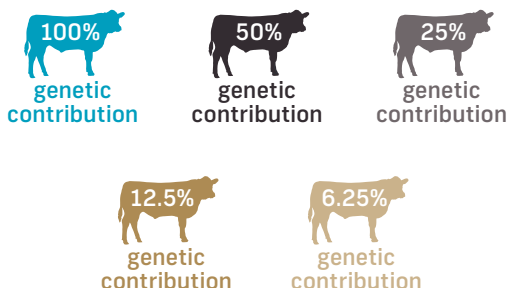


FIGURE 2

Five generation pedigree of the SMOFF0278 showing the 1,295 carcass data records across the generations within his pedigree.

If we overlay SMOFF0278's pedigree with his carcass progeny record numbers and those of animals in his pedigree (Figure 2), we can see that using quantitative genetics, we can obtain far greater information on how SMOFF0278's performance as a carcass sire compares and relates to other animals in his pedigree.

In using the phenotypic carcass data from animals sired by SMOFF0278 and those from across the generations of pedigree for SMOFF0278, we can accurately determine the relative genetic merit of SMOFF0278 and calculate the merit of ancestors in his pedigree for those traits.

AWA BREEDPLAN does this job by calculating the Estimate Breeding Values (EBVs) considering all available pedigree and phenotypic data provided by all AWA members. EBVs account for pedigree (bloodline) and performance data.

● carcass data records

EBVS vs GENOMICS

After Gregor Mendel discovered inheritance, the first DNA sequences were obtained over 100 years later in the late 1970's. The first full mammalian genome sequence (the mouse) was not completed until 2002. In the 20 years since this achievement, our modern understanding of the complexity of the mammalian genome has grown immensely.

The bovine genome was first completed in 2004. This enabled a new ability to look for genetic differences (different mutations) across the whole genome, by comparing the DNA sequence of different individuals and determining where there was DNA sequence variation.

Genomics is the field of science that studies the genes, gene sequences, their inheritance and function. In quantitative genetics, our use of genomics now includes studying the variation in genes between individual animals and determining how these variations relate to performance differences (phenotype differences) between animals.

These genetic variations occur naturally through mutations in DNA that accumulate over time. You can compare the phenotypes of animals with a mutation, to those without a mutation and see if there is any statistical difference. You can do this with a single mutation, or thousands of mutations across the whole genome.

Genomic SNP chips are tools that allow us to screen an individual animal's DNA for differences between many thousands of genetic mutations that occur naturally across the whole genome of an animal. We currently use 'high-density' chips that contain between 50,000 to 100,000 different mutations (SNPs) spanning the whole genome.

Using genomics (the data from the SNP chips), we can determine which SNPs are positively or negatively associated with different traits across the whole Wagyu population. We can then determine if those SNP are present in the DNA of an individual and use this information to improve the genetic prediction (the EBV) for that animal.

SIMPLE DEFINITIONS

BLOODLINE ANALYSIS

Looking at a pedigree information

QUANTITATIVE GENETICS

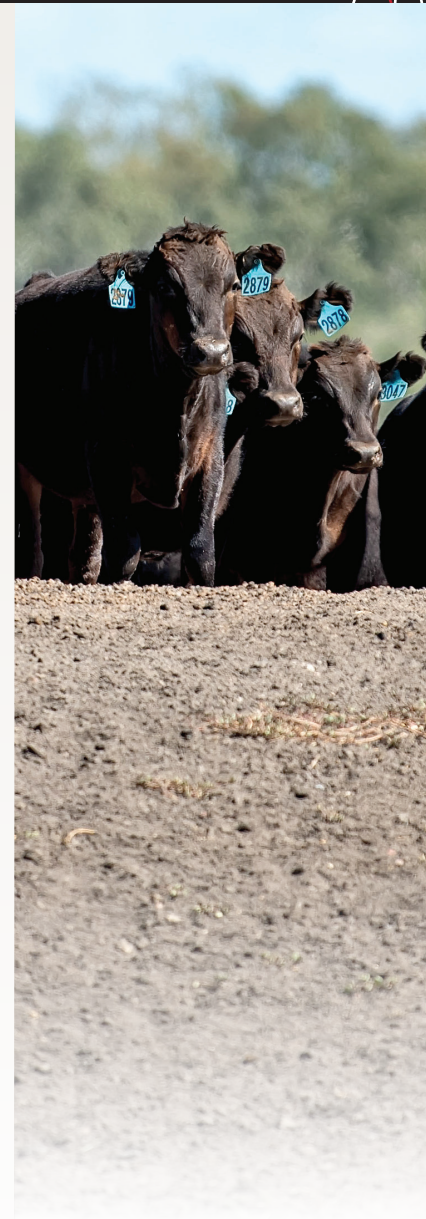
Analysing trait data with pedigree information to quantify genetic merit

GENOMICS

Analysing trait data with genome data to quantify genetic merit

SINGLE-STEP

Analysing trait data with pedigree data and genomic data to quantify genetic merit



So, for AWA members doing genomic testing (50K or 100K SNPs), that information allows BREEDPLAN to account for the individual mutations inherited by an animal and how these are estimated to affect trait performance, in addition to using all pedigree and trait information that is recorded.

Combining genomic information with pedigree and performance data is what we call the generation of Single-Step EBVs. These are reported as the AWA published EBVs for registered animals. Single-Step EBVs are not genomic EBVs, they use genomics, pedigree and trait performance information in one calculation to estimate genetic merit. This gives the best estimate of genetic merit that can be determined.

Genomic EBVs are estimates of genetic merit that only use genomic information and its relationship to a set of trait performance data.

Figure 3 shows the relationship between 400 Day Weight measurements (yearling weight) and EBVs calculated using different levels of information. Within Figure 3, the strength of the relationship is shown on the Y axis, with a strength of 0 equal to no relationship and a strength of 1 equal to a 100% relationship—i.e., they are the same.

Looking at the bars on the left-hand side of the graph (raw phenotype), we can see that the relationship between raw phenotype data and predicted EBVs from genomics alone (GEBV) or from using the mid-parent value alone (PEBV) are both quite low (less than 30%).

The middle bars on the graph show the relationship between the GEBVs and mid-parent PEBV with the phenotype data once management factors including management group, birth date, sex, the cow, the season etc., are taken into account. We can see that the ability of genomics and pedigree to predict the phenotype are much better.

The bars on the right-hand side of the graph are the BREEDPLAN EBVs using genomics, pedigree and trait data (light blue = Single-Step EBVs), vs pedigree and trait data alone (no genomics: teal). You can see that both EBVs have a very strong relationship with the phenotype data, but the addition of genomic information in the light blue Single-Step EBV calculation improves the prediction.

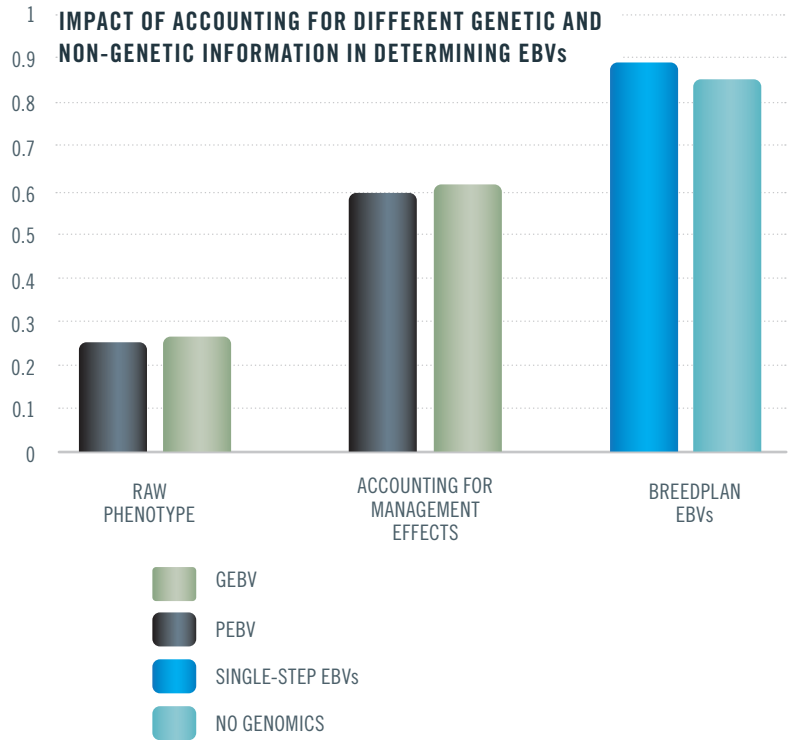


FIGURE 3
The impact of accounting for different genetic and non-genetic information in determining EBVs using genomic information, parent information, or all information (BREEDPLAN EBVs) for the 400 Day weight trait (yearling weight).

Courtesy Dr Yuandan Zhang (AGBU)

SUMMARY

The pedigree of Wagyu animals can span many generations. Mining these pedigrees for useful information is very complex and is the reason why the scientific field of Quantitative Genetics exists. Through AWA BREEDPLAN, we publish EBVs for a large number of traits. These EBVs include pedigree, trait performance data and genomic information to derive the most reliable genetic estimate for individual animals.

AUTHOR

Dr. Matthew McDonagh
Australian Wagyu Association

MORE INFORMATION

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

✉ Communications@wagyu.org.au or ☎ +61 2 8880 7700