**Wagyu Webinar #3: Data to EBVs. Prof Rob Banks, Dr Yuandan Zhang and Dr Matt Wolcott**

## PRESENTED BY PROFESSOR ROB BANKS, DR YUANDAN ZHANG AND DR MATT WOLCOTT

Introduction

Welcome everybody to the Wagyu Webinar, this is the first on the topic of converting performance data to EBVs. I'm Matt McDonagh, CEO of the Australian Wagyu Association. Our speakers will be Mike Buchanan, who is the president of the AWA, who will give a brief background to today's topic and then we will hear from Professor Rob Banks and Dr Yuandan Zhang from Australian Genetic Breeding Unit, which is based at University of New England. Rob and Yuandan will be talking about performance data and collection and calculating EBVs. Dr Matt Wolcott from AGBU, will join us to present information on a Wagyu data audit for breed and data quality.

Before handing over to Mike, I would like to acknowledge Neogen Australasia, as our sponsor for today's webinar. Genomics is a key contributor to our genetic progress, so please watch this short video from Neogen.

[Neogen Promotional Video]

MB:

Welcome everyone and thank you to Neogen for the support of our webinar today.

This is the fourth in our webinar series (sic Webinar #1 was members only) in about 6 weeks, and with this the start of the pointy end of reviewing Wagyu EBVs. It is a subject that has raised a lot of interest and some controversy with Wagyu membership since we announced that it would be undertaken at the start of the year. AWAs Wagyu breed development strategy is built around BREEDPLAN and we are firmly committed to it. But if the key EBVs are not perceived as credible and accurate, even if they are entirely accurate as genetic predictions, then we face a significant barrier.

Coming into this Board last November, the clear message was that some Wagyu EBVs were unclear to some members when compared to raw data. This has been particularly in relation to carcase EBVs. In a typical scenario, a member would visit our website and look up a slaughtered animal, and then see EBV values for that animal that may not correlate to real carcase data.

The Association has produced quite a lot of print material to explain why that may be the case. Phenotype does not equal genotype and in the case of carcase traits this concept can be challenging to grasp. Subsequent misunderstanding erodes confidence in Wagyu BREEDPLAN.

In an effort to communicate more effectively, these webinars provide a more sophisticated method of presentation from experts into plain English. Our webinar program is enabled by AGBU's team of geneticists, led by Professor Rob Banks. In this case, we used the GIC (genetic improvement committee) as guinea pigs for the first trial run of the

webinar. What we share here is built on that trial run. From here on, we plan a series of EBV-focused webinars. These webinars will focus on the construction and deconstruction of EBVs. Moving from the well-accepted phenotype measurements like 400-day growth through to our most sophisticated carcase metrics.

I hope what follows will be of value, and we encourage you to log on to review the material as we build on today's foundation. It is my pleasure to hand over to Professor Rob Banks and Dr Yuandan Zhang.

RB:

Thanks Mike, and to reinforce Mike's point that to understand how data is turned into EBVs is really important and central to Wagyu BREEDPLAN.

I will speak about why data collection is important, what affects its value and a couple of comments around genomics. My colleagues will go into more detail on those.

So the core question we are interested in BREEDPLAN and breeding is to identify which animals, and in this case, bulls, and how can we find out? It is the genes we are interested when assessing with BREEDPLAN, their appearance or phenotype, is a clue. The genes are not the same as visually what you see.

The question of working out the genetic merit, depends on understanding the distinction of the phenotype of what we see such as weight, height. The phenotype is the result of the genes and non-genetic effects such as age, feed, age of its dam). What we are really trying to differentiate the gene of the animal, as that is what is passed on to its progeny and the non-genetic that affect its own performance. So for EBVs we need to distinguish between the two. We can only separate the two factors if we have information that identifies the non-genetic factors.

I will demonstrate by showing the accuracy of breeding values, how well they describe the genes if we don't identify the non-genetic factors compared to when we do. A simple exercise but quite dramatic results. To reinforce the point, in order to get good estimates of the genes, we have to be able to distinguish the non-genetic effects. How we do that is to measure the heritability of the trait, and therefore the accuracy of the EBV.

In this example, the table shows example traits versus actual traits. In each case, we have worked out the heritability of the trait – how well we see the genes, when we don't record the non-genetic factors (under heritability-poor recording column) and we distinguish that with good recording. At 600-day weight, when we don't record the non-genetic factors, the heritability is at 12% compared to 38% with good recording. Which translates the accuracy of how well we are describing when we are not recording goes from 34% to 62% when we are, based on one animal's records.

And you can see as we go down the table, pretty much the same story for P8 fat depth, we go from 53% to 65%, eye muscle area 39% to 51%, condition score 35 to 64% and hip height from 59 to 76%. The accuracy of the EBVs, how well they describe the genes of the animals increases significantly when we take into consideration the non-genetic factors such as which contemporary group the animal was in, the age of the animal, how old its mother was.

You can see the ratios indicate big improvements in accuracy of describing the genes when we properly record and take account of the non-genetic factors, to gain a clearer picture of the animal. To sum up that point, good recording is therefore 20-80% more valuable. Simply putting in just the weight without any other information, is giving very low accuracy. With more data, we get a more accurate picture of the genes.

It applies whether we are using BLUP, which is standard BREEDPLAN, but it is even more important when we start using genomics. Genomics is built on the data that is submitted for animals that have genotypes/DNA and when using genomics, the quality of the data effects all EBVs for everybody to a much greater extent than without. The really impt point is that recording of non-genetic effects - contemporary group, age, etc – is very important.

We are now going to see some validation of BREEDPLAN EBVs which is a continuous process, constantly checked. One way is to produce progeny from sires with known EBVs and compared; the other is predicting performance of animals from earlier data. Yuandan will go through the latter in a moment.

The important point is that recording of non-genetic effects makes a big difference to accuracy of EBVs and how well we describe an animal. So Yuandan will talk about EBVs, their purpose to evaluate an animal, using clues based on an animal's own performance for traits and correlated traits and genomics which is also based on performance records.

We also need to remove the 'noise', which are the non-genetic factors affecting the observed performance, such as contemporary groups, age. We then test predictions against outcomes.

How we go about this, is to first remove any extreme values; generate adjusted records taking account of the non-genetic factors and compare those records with EBVs with animals and/or parents.

YZ:

In the next few slides, I will demonstrate examples of how the EBVs are generated and the steps we use. The example we will use is the 400-day weight. When we receive that 400-day weight, we know that this information, may be affected by non-genetic factors that affect the EBVs.

Non-genetic factors we consider include the contemporary group, which refers to animal's life, age, the mother's age, and whether this is the first calf for the mother. We make a phenotype adjustment to remove the non-genetic factors.

In this table I will show you the step by step process we use to adjust for phenotype.

The raw phenotype is adjusted across 5 steps, the first is the contemporary group (the herd, the season, year born). Step 2 adjusts for age, the third and fourth step is contemporary group, age and mother's age. The final step are the heifer factors. After these adjustments, we will compare how the values are affecting EBVs. If we don't have phenotype information, we can predict from pedigree.

We have two types of values – estimated with those animals that use a phenotype evaluation system, the other type is without a phenotype and these animals will be predicted. (EBVt). Using the BLUP system gives us the PEBVt prediction, or including genomic information is the GEBVt.

In our case, we will show different steps of adjustment for EBVs. In terms of animals we test we use those without phenotypes and those with phenotypes where we can mask those, so they can be the test animal. We have 5722 test animals, and of those 645 had parents with phenotypes.

The correlation coefficients table shows the phenotype adjustments to give GEBV, PEBV, GEBVt and PEBVt. How those parameters correlate for phenotypes goes from 0.3 to 0.5, 0.9 for EBVs. This chart shows the different levels of correlation, from a cloud like scatter at low level, but a higher correlation which is closer to a straight line.

This chart then shows the correlation of phenotype with the different adjustment with the EBVs for the test animals. The phenotype is very low – 0.3, but after we adjust for the 5 steps, the correlation does not vary very much, but may be contemporary group is a major factor. From step 5 to EBVs there is a substantial increase, which reflects the value of genomic or pedigree information to give the EBV prediction.

Using the same concept, we can look at the correlations with predicted EBVs for test animals, where the phenotype is treated as low. The spread of variance for the test animals on EBVs with the 5 step adjustments decreases and reflects the genetic value of the animal. Similar trends occur where the phenotypes of the parents are low.

The next step is the prediction, looking at the mid parent values – the average of the parents' value. For the phenotype 5 step adjustments, we have the mid parent values and EBVs. We use the correlation of the animal's own records compared to the prediction from the mid-parent values. The chart shows that the mid-parent predictions with the 5 step adjustments are very low, but with the EBVs the correlation is very high. With the mid parent values, the prediction can be very useful, but is not as good as the EBV.

In summary, for animals with phenotype adjustment it is important for genetic valuation, the value is closer to the EBV. Using the prediction method, the phenotype predictions is very low, but using genetic system it is useful for EBVs. In most cases it has a higher power prediction, but depends on how much information is available.

RB:

To sum up Yuandan, there is a lot of material to cover.

The really important principle that Yuandan has demonstrated is that when we start with the raw phenotype, in each step, we adjusted for the non-genetic factors (contemporary groups, age, relatives etc). the height of the bars, is a measure of the accuracy of the breeding values. What that means is the breeding values, based on raw phenotype has an accuracy of around 30%. We can take that up to around 60%, by taking account of the non-genetic factors that affect that animal's performance.

We really want to stress the steps in going from raw data to EBVs, in a sense, there is two big processes done – we take account of the non-genetic factors which make a substantial difference – can be dependent on the trait – but it is much better to take account of those non-genetic factors affecting its own performance and then the combined with the adjusted records from related animals to give a high accuracy EBV.

The two things we have tried to convey to you, is that if we want to gain a clear picture of the animal's genes we have to do two things – take account of the non-genetic factors affecting each animal, which can be substantial, and then bring in the knowledge we have of relatives. When we think of raw phenotypes as a guide to animals, on their own without adjustment they are not an effective tool at all. Taking adjustments, we can have high and useful accuracy to describe the genes. The raw phenotypes should not be taken on their own, as a guide to the genetics of the animals.

MM

Thank you, Rob, for walking us through that and making good points at the end. It is now my pleasure to introduce Dr Matt Wolcott, who is a research scientist at AGBU. He has done a Bachelor of Applied Science in Gatton, QLD before doing a Masters in Beef Science at UNE through the Beef CRC and in 2013 finished his PhD at UNE with AGBU looking at improving steer and cow productivity.

MW

This material was presented to the AWA Board, and each breed society is presented with similar material. As a rule we don't pass this on beyond the Board level, but AWA has indicated that it is relevant to the Wagyu breeders.

I will look at the data that is coming in for evaluation – quantity and quality. I hope that we can see this as an opportunity to make improvements to genetic evaluation. It can be perceived as a bit negative, but we encourage you to look at it as an opportunity to improve.

The first step is to look at recording practices, by utilising software developed at AGBU, called Data Audit. It gives us information on data quality and quantity and evaluates the results for animals within a specific breed over a specific time frame. The key information we will look at is data recording by traits and quality scores, which are calculated on some fairly sophisticated analyses that we base loosely on a similar fashion to tax auditing systems.

This analysis is for animals born from 2014 – 2018, a five-year period, looking at traits by category – weight, reproduction, carcase, scanning traits. In instances where traits are sex specific, we have adjusted for that.

We will see a lot of graphs – we have levels of recording relative to the black bar which is 100%, compared to animal traits that came into the evaluation about 12,500 animals per year.

For weights relative to the analysis – birthweight, 200, 400, 600 day weight and mature cow weight. There is no getting around the fact, is that there are relatively low levels of recording against the weight traits. One of the things that is clear is that for breeders have an opportunity to make decisions about moderating mature cow weight, while selectin for early growth traits is pretty limited given the low level of mcwt coming weight.

For reproduction traits, we look at gestation and scrotal circumference. We have about 28% of the calves in the evaluation period come in under AI, and the gestation length is less than half of those. It is opportunity to increase the accuracy around reproduction by including more of that data. Similarly, scrotal has less than 1000 records. In the absence of days to calving, it is a key phenotype driving the reproduction evaluation, and worth increasing the amount of data. I will make the observation that for Wagyu, days to calving is an opportunity that is there to be grabbed to give a better description of reproduction.

For bull scan traits, P8 fat, rib fat and eye muscle scans, we low levels of recordings. It is worth pointing out that for Wagyu, scanned IMF is not giving us good information on how they are performing as carcases after the long finishing process. But it is also true, there is good information on fat and eye muscle from scan traits. And you have the information on young animal fat and eye muscle will contribute to carcase traits directly. The records taken on selection candidate will give you information.

For heifers, the scan rate records are higher, but not a great deal. Heifers do express differences in genetic fat better than bulls, so can gain more information on genetics from heifers than bulls on eventual carcase fat. Wagyu has a favourable relationship between eye muscle and fat and IMF, which is worth exploiting. Increased levels of fat levels in young animals, may boost the accuracy of the eye muscle as well.

Analysis of carcase traits, shows levels are around 10%, but in comparison to other breeds are actually pretty good. Wagyu is actually pretty good at collecting data on these high value traits. As Rob and Yuandan suggested, genomics presents an opportunity to spread the accuracy around to relatives for carcase traits.

In summary, it is clear that there are some pretty good opportunities to improve accuracy of key traits for evaluation. The one that stands out is reproduction, there is not a lot of data at this stage. Increasing scrotal circumference data will help, and introducing the days to calving for the breed would be a really good step to evaluating reproduction more effectively.

I would also like to mention the Southern Multi-breed Project will contribute some really good reproduction data, and what animal breeds go into that experiment, particularly which Wagyu bulls, will give decisions on what information comes out of the experiment.

Data quality of the breed uses complex analysis, using metrics similar to business auditing. It is scored between 0 and 100; anything about 80 is not too much cause for concern.

Examining data at the breed level, it gives an indication of what needs to be addressed at a broad level, but much more useful to look at the individual herd level. Is something AGBU does at the extension level, to help with genetic evaluation.

The first result of data quality for our traits out of 100 for birth, 200, 400, 600 day weight as well as mature cow weight. The results in general are pretty good, sitting at above 80% is good news for the majority. We commonly see mature cow weight that is lower, usually due to precision of recording. Not uncommon for scales to record in 2kg increments for heavier animals, giving a loss in precision, and often why we see mcwt dipping below 80%.

Reproduction traits – scrotal and gestation length, nothing too alarming there. The quantity may be low, but the quality is good.

Quality scores for bull scan rates, common issue is the fat depths. It is a problem that is attributed to a lack of variation. We are scanning animals that are quite young, and in the case of Wagyu in this time period, a value of 4mm of fat, made up almost 30% of all the data. At 5mm was over 30% - when two values make up more than 60% of the data, it makes it difficult to separate the genetic differences. It may also be partly due to the low number of records.

Heifer scan traits: similar sort of pattern, 4mm fat depth is almost 40% of all the records. It is pleasing to see that P8 is over the Score of 80 level. There is plenty of breeds where this is not the case.

Carcase traits: pleasing, every single trait is cwt, P8 ema, IMF, camera traits are all 90% or better. Great news for highly valued, high investment traits – the accuracy extracted for those will be close to maximum.

Generally, data quality is good for Wagyu. The heritability of carcase traits eg IMF, is spreading the accuracy through the evaluation nicely. It is worth pointing out that any animals that have both phenotype and genotype are automatically are part of reference population, making sure the data collected of them is high quality is important. This result is telling us the case.

A couple of take-home key messages, for Wagyu breeders. The first is around scanning. We know that scanning for young animals is not working especially well for Wagyu and that will be the case for the foreseeable future. Scanned EMA and fat of young animals, can still contribute to evaluation. It is a record for selection candidates, something that can be measured in a young bull and get EBVs back on quickly, to make selection decisions.

Around recording reproduction, is of high economic importance, there is no breeding system where this is not the

case. If there is anything that stands out from this evaluation is that more information coming in is going to be useful. Southern multi-breed project will certainly help with that as there will be some useful data coming in for that suite of traits.

The accuracy of the evaluation is dependent on the quality of the data, while we don't have vast amounts of data, the quality is generally very good. If people want some pointers on where to spend your recording resources, the weightings put on traits in the $Indexes is a really good starting point. Which will show that marbling, reproduction, birth and growth weight are the areas driving profitability driving Wagyu.

MM

We have reached the end of the formal part of the webinar, questions can be submitted.

Q1. Ultrasound scanning – is there a way of getting better result through ultrasound for predictions of progeny?

MW: probably better for marbling, as much as we would like for Wagyu, given the long feed time and the variation in marbling from young animals through to slaughter the answer at this stage is probably no, and as a scanner myself, I say that with some regret. It is unlikely that we are able to take scans of IMF in young animals and see how it relates to carcase traits. It probably means that good quality carcase data to predict traits. For EMA I think it already performs pretty well. Differences in EMA in young animals tend to follow through regardless of the finishing phase. Making sure that animals are in good shape when you scan them will go a long way to having quality data.

Q2. What other traits can Wagyu focus on to get better performance data?

RB: Matt W made a strong case for much better data on fertility traits. In particular recording, which cows had calves, and those that did not. I think it is referred to as 'whole of herd' recording. Getting early measures of calf performance, the breed will be in a better place to make sure fertility is good, but also build data to address concerns around early life survival.

MW: I agree, focus on the traits that are available at the moment, as it covers most aspects of productivity for the breed, and I do think that reproduction is a key area for every breed. It's a matter for Wagyu to give yourselves the ability to monitor reproduction as you measure productivity in other directions. There is a clear case for selecting on marbling, but you would want to make sure there is unfavourable correlations to other traits. By having good data coming into the equation for those traits, you can make sure that doesn't happen.

RB: the other one I would like to mention around reproduction for wagyu is to make the cost of feed, which I imagine is not routinely measured, but it would make enormous sense as feed is an important cost factor in the value chain. Recording feed intake, we know with other breeds, is a really powerful tool to address methane in cattle. Gathering data on feed intake on steers would allow you to start making progress managing cost of feed, and set you up reducing methane output, which is likely to be an industry cost in the future. A good level of data can then be leveraged through genomics.