WHAT DO PREFECTURES TELL US ABOUT THE GENETICS OF WAGYU CATTLE IN AUSTRALIA?

BACKGROUND

Wagyu and Wagyu-derived cattle in Australia originate from Japan, and within Japan, from a breeding population originally structured around prefectures.

Prefectures are basically regions of Japan which had breeding programs for the cattle. Those programs included infusing exotic (non-Japanese) cattle genetics into the native cattle (themselves imported from a range of countries in earlier times), and then involving some mix of local focus coupled with infusions from other prefectures. The result being what might be considered "strains" of Wagyu – sub-populations that could all interbreed. These shared genes in common, but at the same time had some degree of differentiation in performance traits.

When Wagyu cattle were imported to Australia, animals were sourced from at least 7 prefectures (as well as "unknown" – meaning the prefectural origin could not be determined).

There had certainly been some progeny testing in Japan – within prefectures – and that had identified some sires with superior genetic merit for carcase traits, including such as Tajiri (Founder of the Tajima line, from Hyogo prefecture), Dai 7 Itozakura (a nationally influential sire in Japan) and Kedaka (an influential sire himself from Tottori prefecture). These "bloodlines" represent the majority of Japanese Black Wagyu genetic background in the registered AWA population. Other minor influences are from the Okayama, Shimane, and Hiroshima prefectures.

Note that when breeders refer to an animal as a founder, it usually implies that the animal has been heavily used within the population over a period of time, and that usually means some amount of inbreeding, whether deliberate or not.
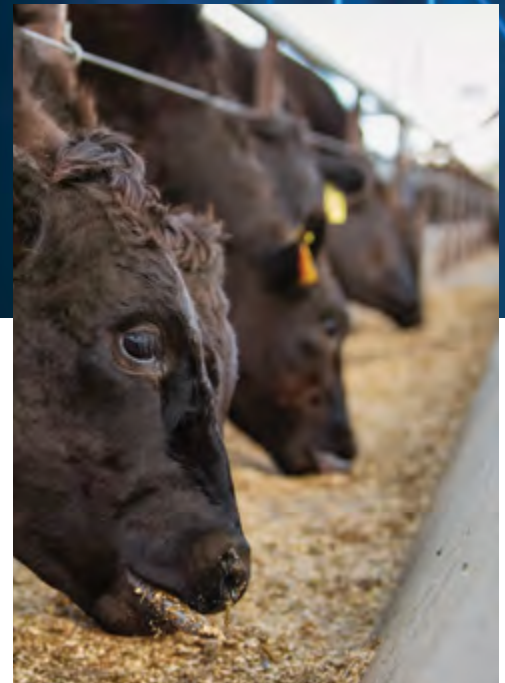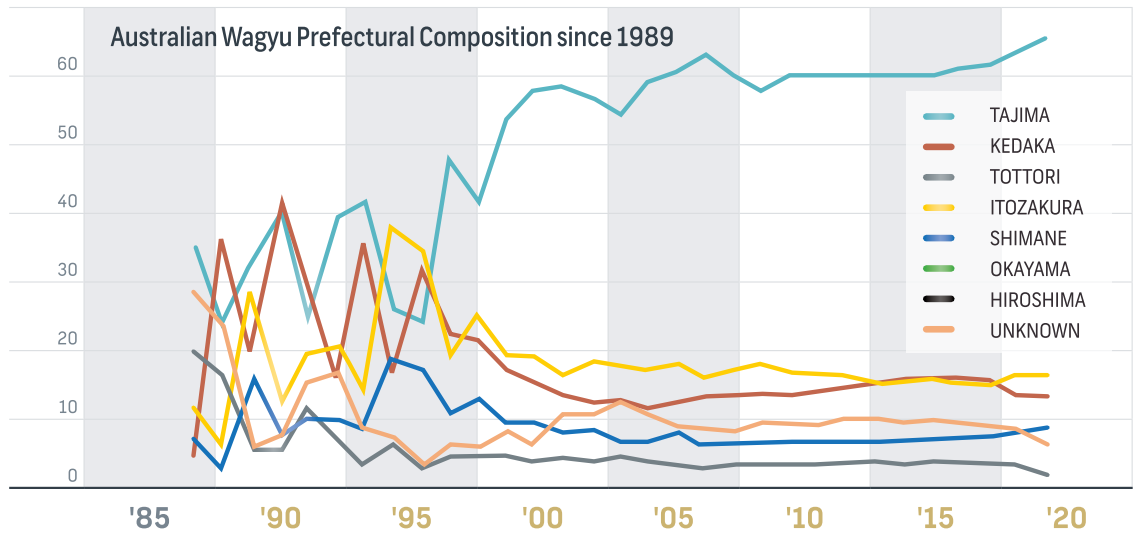
AWA FULLBLOOD JAPANESE BLACK FOUNDATION ANIMALS = 364 INDIVIDUALS

Although it is estimated that genetics from approximately 220 individuals were actually exported from Japan, the pedigree analysis undertaken has demonstrated that these animals trace back to 364 individual animals registered with the Japanese Wagyu Registry. We therefore have the genetic information contained within these 364 foundation animals represented in the AWA Japanese Black Fullblood herd.

Prefectural
composition (%)

Australian Wagyu Prefectural Composition since 1989

TAJIMA
KEDAKA
TOTTORI
ITOZAKURA
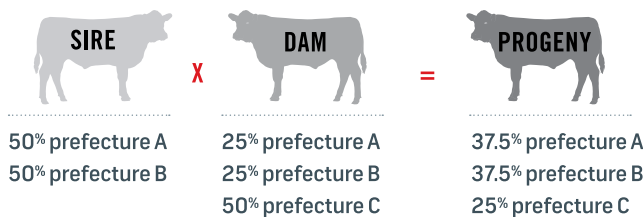SHIMANE
OKAYAMA
HIROSHIMA
UNKNOWN

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... Reducing the available diversity from the 364 individuals down to 7 prefectures or bloodlines results in a significant loss of useful pedigree information that is beneficial for managing genetic gain and maintaining genetic diversity. Prefectural analysis ignores the genetic diversity between individuals of given prefectural composition.

In our work relating to prefectural analysis, we have focussed on two questions:

1. Can we determine the prefectural makeup of each animal, given that we have been provided with prefectural composition data on foundation animals in Australia?

2. Can we analyse performance data to assess how useful knowing the prefectural composition is in describing genetic merit of an animal?

To address the first question, Dr Zhang took the data on prefectural origin for the foundation 364 animals, and spread that information down through the entire pedigree. The principle is simple – assume we have two parents and we know their prefectural origin:

SIRE	X	DAM	=	PROGENY
50% prefecture A		25% prefecture A		37.5% prefecture A
50% prefecture B		25% prefecture B		37.5% prefecture B
		50% prefecture C		25% prefecture C

Starting with the original imported animals, this allows us to determine prefectural makeup for all animals with pedigree. The most interesting outcome of this work is the patterns in prefectural composition over time in the AWA Herdbook – the largest Herdbook

registry outside of Japan (Figure 1).

The picture is clear: the animals identified in the Australian database did not change proportions of different prefectures in any consistent way until about 1997, and from then on there has been a clear increase in % Tajima, to around 50%, with the % across the population for other prefectures being relatively stable since then.

The second question is perhaps the key question – can we use prefectural composition to help us determine or predict genetic merit? We examined this question in a number of ways:

» Observing trends in phenotypic performance to see whether there is any relationship with prefecture

» Analysing the entire performance database to see how well prefecture explains variation, and compare that with how well EBVs explain variation (EBVs based on pedigree relationships)

In terms of trends in phenotypic performance, we found weak associations between Prefecture % and observed carcase weight and observed carcase marbling. Weak means there was an overall pattern, but there is lots of spread around that pattern: the relationship between prefectural composition and the trait is not a very good explanation of what we see.
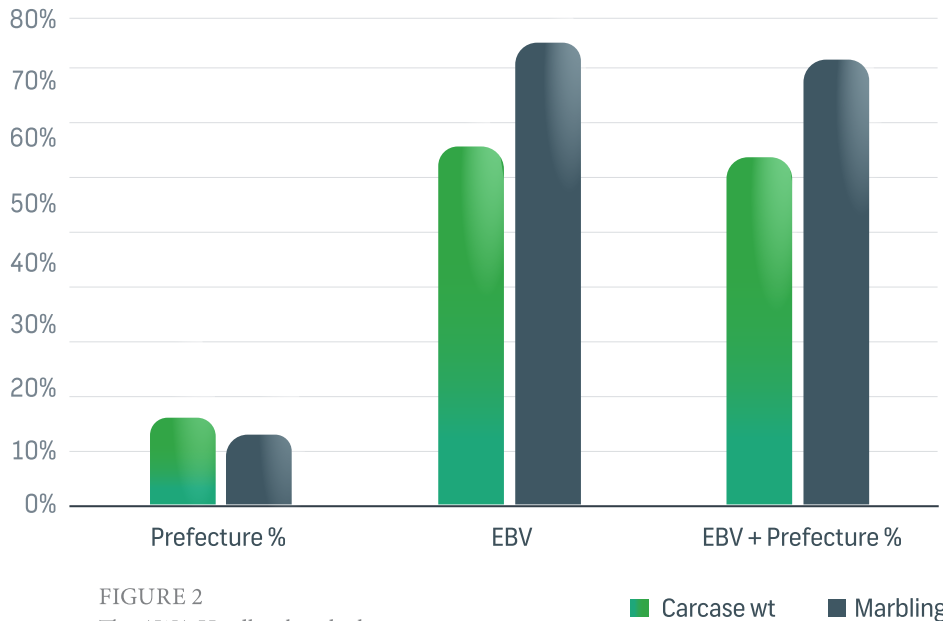
FIGURE 2
The AWA Herdbook – the largest Herdbook registry outside of Japan.

PREFECTURAL ANALYSIS REDUCES THE AVAILABLE DIVERSITY FROM INDIVIDUALS IN EACH PREFECTURE

100% of prefectural or bloodline information is inherited from the parents. Reducing the available diversity from the 364 individuals down to 7 prefectures or bloodlines results in a significant loss of useful pedigree information that is beneficial for managing genetic gain and maintaining genetic diversity. Prefectural analysis ignores the genetic diversity between individuals of given prefectural composition.

> " The result is quite dramatic – prefectural composition is nowhere near as good at predicting performance as is an EBV ...

Taking this one step further, we determined the relationships between prefectural composition, EBV, or EBV plus prefectural composition, and carcase weight and carcase marbling – in all cases, taking account of contemporary group structure and age of the animal.

The result here is quite dramatic. As shown in Figure 2, prefectural composition is nowhere near as good at predicting performance as is an EBV, and in fact, adding prefecture information to

EBV in the analysis reduces the ability to predict genetic merit.

The height of the bars in Figure 2 tells how well that analysis is predicting performance. For example, Prefecture % predicts carcase marbling performance with approximately 12% accuracy, whereas EBV predicts it with approximately 75% accuracy – it's a much better guide.

An important question is "why is the EBV so much better at predicting performance?" The answer is simple – using prefectural composition is based on assuming that all animals of a particular prefecture are genetically the same, and that is simply not the case.

EBVs take account of how good or bad every animal in the population is, and by looking at the performance of related animals, obtains a picture of the value

of the genes themselves. (Incidentally, genomics takes this even further).

This also means that knowledge of the actual pedigree (whether as recorded, or as calculated using DNA) is a much better basis for managing inbreeding and diversity – because we track the actual genes of individuals across pedigrees, and pick up differences at that level amongst animals that seem to have the same prefectural makeup.

IN SUMMARY

Prefectural analysis is possible and has been completed but doesn't add any information you don't already have either in terms of genetic diversity, inbreeding, or Genetic merit.

Balancing diversity and genetic progress is best done using mate selection (MateSel), based on the information in recorded pedigrees, or genomics, coupled with EBVs.

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MORE INFORMATION
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