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LINKING COMMERCIAL CARCASE DATA TO STUD HERDS: THE POWER OF GENOMICS

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SUMMARY

The prediction of breeding values for beef carcase traits using traditional genetic methods requires that the slaughtered cattle have a full pedigree, linking them back to the stud sector of their respective breed, additionally to accurate contemporary group structure and no selective harvesting. Due to these requirements, progress towards EBV for meat quality and other carcase traits in the beef industry has been slow, especially in Northern Australia. Here, an example of how genomic information can be used to cost-effectively feed information from the meat processing sector back to the breeding sector, using pooled DNA genotyping and placing the genotypes of pooled commercial animals and selection candidates at the stud in a hybrid genomic relationship matrix for estimating breeding values. This approach could be used to quickly and cost-effectively build reference populations for commercial performance traits in many livestock breeding applications.

INTRODUCTION

The use of data from commercial cattle to inform genetic improvement is very limited, mainly because the genetic links between the commercial herds and their stud ancestral herds are poorly known. Additionally, the cost of building large genotyped reference populations for the implementation of modern genomic technologies is still prohibitive in most cases.

An alternative approach has been proposed to draw on performance measures that are routinely acquired in commercial populations, and to cost-effectively use DNA information to link these measures to the animals available for selection in the breeding sector (Bell *et al*. 2017; Reverter *et al*. 2016).

Large volumes of carcase data are routinely recorded in the Australian beef industry, but do not usually contribute to the evaluation of genetic merit in the corresponding stud herds. This study exemplifies a cost-effective method for linking carcase data from un-pedigreed commercial animals to the stud sector.

MATERIALS AND METHODS

Animals and measurements. Tail hair samples were collected from 620 commercial Tropical Composite heifers, across two cohorts of similar size. They were feedlot finished (days on feed ~ 249 or 114) and slaughtered under the Meat Standard Australia recording system, which returned more than ten carcase attributes, including weight, MSA marbling score, pH, and hump height. Here we focused on Hump height (Hump) and MSA Index (MSA), which is an index that combines several factors recorded at the processing plant, weighted by its estimated effect, mainly, on meat eating quality (https://www.mla.com.au/marketing-beef-and-lamb/meat-standards-australia/). Additionally, DNA samples from 100 stud sires were included in the analysis. These sires were part of the herd selection program that could directly benefit from the information of the commercial cattle. Under this selection program, these sires will be grandfathers of future commercial cattle.

Pooling DNA and genotyping. Within each cohort, hair samples from each heifer were pooled in groups of five or four individuals according to their carcase phenotype, either MSA or Hump observations. We assembled 101 pools according to MSA, and 40 pools according to Hump (only

pools from the extreme values). Each hair pool then had DNA-extracted and genotyped as a single sample using the single nucleotide polymorphism (SNP) genotyping platform GGPHD 150K for beef (Neogen Genomics, Lincoln, USA; http://genomics.neogen.com/pdf/AG151_GGP_TS.pdf). The individual stud sires were genotyped for ~ 50,000 SNP (Zoetis, Kalamazoo, USA). The pooled genotypic data was translated into allele calls using the B-Allele Frequency metric output from GenomeStudio software (Illumina Inc, San Diego, USA). After standard quality control on genotypes, SNP that were in common to both platforms (n = 43,807) were kept for further analyses.

Statistical analyses. Descriptive statistics, phenotypic correlations, and linear models were run in SAS (SAS Inst., Cary, NC). The combined pooled and individual genotypes were used to build a hybrid genomic relationship matrix (hybrid-GRM, Reverter *et al.* (2016)). The hybrid-GRM was then used in an additive genomic model to derive genomic Best Linear Unbiased Prediction (gBLUP) values using Qxpak v5 (Perez-Enciso and Misztal 2011). The statistical model included only heifer cohort as a fixed effect, since season of birth, on-farm management group, time on feed, killing day and killing facility were all confounded within cohort.

RESULTS

Using data from 620 carcases we were able to recover the expected MSA Index effect sizes (http://www.redpoll.org.au/documents/June15_BreedingforMSACompliianceandIndex-1.pdf) for the main attributes known to significantly impact MSA Index, which were carcase weight (0.015 ± 0.002, $p < 0.0001$), Hump (-0.048 ± 0.002, $p < 0.0001$), ossification (-0.069 ± 0.002, $p < 0.0001$), and MSA marbling score (0.016 ± 0.000, $p < 0.0001$). The recovery of known effects gives confidence that this is a representative sample for this Tropical Composite breed and its MSA Index does not deviate from the expectation.

To make the DNA pooling approach more effective, smaller management groups were removed from the sample, so data from 501 carcases remained for further analyses. We focused on two traits, MSA and Hump, both traits have distinct, overlapping distributions for each cohort (Figure 1). The strong effect of cohort in this sample was mainly attributed to different age at slaughter and feed length.

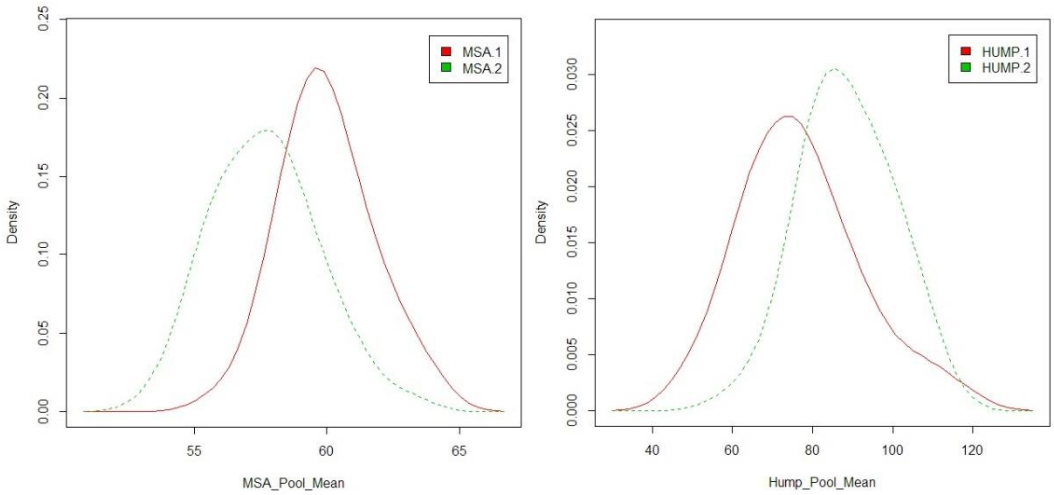

Figure 1. Density plot for observed pooled phenotypes of two cohorts.

For MSA we used data from all carcases (n = 501) as a reference population, split into 101 pooled genotypes, but for Hump we collected only genotypes for pools with extremes values (40 pools, 10

pools of high and low value, within each of the two cohorts of animals). The hybrid-GRM depicted a low relationship between stud sires and all pools. This is not surprising due to the distant relationship between the stud and this generation if the commercial herds. Nevertheless, a variable degree of relationship was detected and can be explored to derive phenotype estimates.

The distribution of gEBV of MSA and Hump for the 100 stud sires is shown in Figure 2A. The MSA gEBV approximates a normal distribution, while the Hump distribution is broader and heavy-tailed. This quite possibly reflects the fact that only the extremes of the phenotypic distribution formed the reference population for Hump, and for MSA the whole distribution of the phenotype was sampled. The negative correlation between Hump and MSA observed in the carcase data, remained present at the level of sire gEBV (Figure 2B). This approach was effective in identifying the potential top and bottom performing sires from the stud herd based on commercial herd performance data.

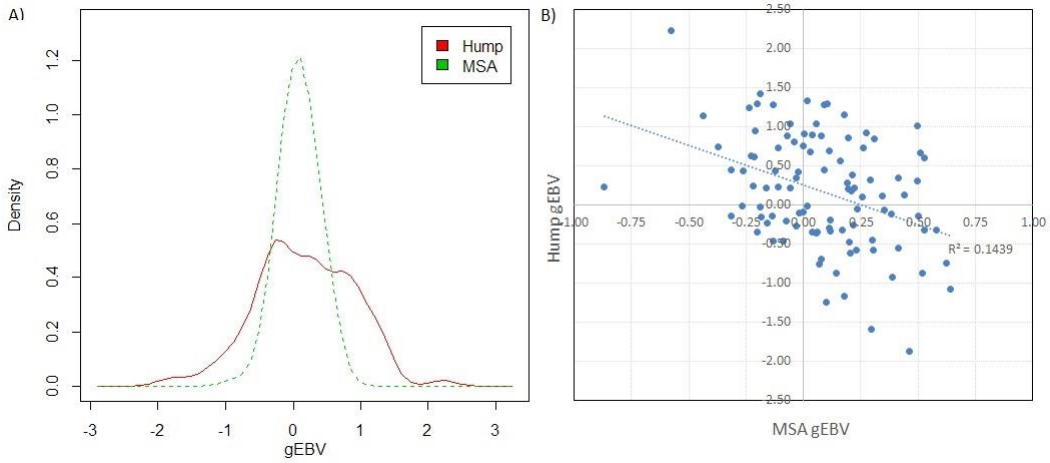

Figure 2. Stud sires (n = 100) evaluation. A) Density plot of gEBV for Hump and MSA and B) scatter plot showing the relationship between gEBV for Hump and MSA.

DISCUSSION

In this study we explored the potential utility of approaches based on DNA pooling to feed performance information from commercial cattle back to stud herds. This approach builds reference populations of commercial cattle, via the generation of genotypic data from animals that *per se* do not have enough value (records and/or pedigree) to justify the investment in individual genotyping, but as a group have valuable performance indicators. Then, the genomic predictions based on this reference population can be used to generate gEBV for animals being selected to enter these herds.

In demonstrating the feasibility of this approach, we have provided further evidence for the flexibility of DNA pooling methodology in dealing with different types of commercial phenotypes. The approach has now been exemplified for evaluation of reproductive performance in cattle (Reverter *et al*. 2016), as well as dag scores in sheep (Bell *et al*. 2017), and carcase data. One limitation of the DNA pooling approach is that genotyped pools are specifically assembled for a given phenotype, so if there are two phenotypes of interest, the pooling process will have to be done twice. If multiple traits of interest have been measured in the reference population and/or genotyping becomes more affordable due to technology developments, the cost savings offered by DNA pooling will be less significant, and individual genotypes may be the better option. In the case of commercial cattle, often no more than one or two key phenotypes are acquired during routine management or monitoring, which means that these approaches are still relevant.

Similar to other methods that estimate breeding values, DNA pooling approaches would also benefit from large reference populations. The larger the reference population is, and the genetically closer to the animals to be tested they are, in general, the more accurate the estimates will be (VanRaden *et al*. 2009). If an equivalent procedure is used to continue collection of commercial phenotypes across different years, the reference population could grow over time, potentially improving the estimates based on it.

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