TWO YEARS IN: LESSONS FROM THE INTRODUCTION OF HEREFORD SINGLE-STEP BREEDPLAN

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SUMMARY

The first multi-country multi-trait single-step GBLUP (ssGBLUP) BREEDPLAN analysis was released for the Hereford breed in October 2017, combining the pedigree, performance and genomic data from Australia, New Zealand and Namibia. Nearly 18 months later, Hereford breeders have embraced genotyping with a 3.8-fold increase in number of animals genotyped. The inclusion of genomic information has influenced the Estimated Breeding Values (EBVs), although this varies by trait and animal. Similarly, exclusion of hard-to-measure phenotypes from the analysis confirms the importance of recording phenotypes for the estimation of accurate EBVs, even when utilising ssGBLUP. The collection of both genotypes and phenotypes, particularly for hard-to-measure traits, remains vital in allowing beef producers to best utilise ssGBLUP.

INTRODUCTION

Since the release of the first genetic evaluation for beef cattle in Australia in the 1980s, the BREEDPLAN model has been continually updated to incorporate new methodology and traits (Graser *et al.* 2005). More recently, several breeds have moved to include genomic information in their BREEDPLAN analyses using ssGBLUP methodology (Johnston *et al.* 2018). This includes the Hereford Single-Step BREEDPLAN (Hereford ssBP) analysis, released in October 2017 and the first multi-country multi-trait ssGBLUP BREEDPLAN analysis. Data from three Hereford associations, being Herefords Australia (HAL), the New Zealand Hereford Association (NZHA) and the Hereford Cattle Breeders Society of Namibia (HCBSN), is combined in a single BREEPDLAN analysis.

Seventeen months on since the release of Hereford ssBP, this paper reviews the size and composition of the Hereford G-Matrix and how this has changed over time. The effect of including both genomic information and phenotypes for hard-to-measure traits on BREEDPLAN EBVs and accuracy is also explored.

MATERIALS AND METHODS

The Hereford ssBP analysis combines pedigree, performance and genomic information from three Hereford breed societies (HAL, NZHA and HCBSN) in a complete multi-trait BREEDPLAN analysis of birth, growth, fertility, carcase and feed intake traits. Calving ease and docility traits are analysed separately using a threshold model analysis (Graser *et al.* 2005) and do not directly incorporate genomic information at present. Twelve standard production analyses are run each year, with 19 trait EBVs reported. For the purposes of the current study, G-Matrix data was extracted from the October 2017, October 2018 and March 2019 Hereford ssBP analyses.

The impact of genomics on EBVs was examined by comparing results from the March 2019 Hereford ssBP analysis with results from the same analysis run without the G-Matrix. Data was analysed for three sets of animals, being (a) sires with an EBV accuracy of $\geq75\%$, (b) young bulls with an EBV accuracy of $\geq50\%$ and (c) non-parent genotyped animals with an EBV accuracy of $\geq5\%$.

Likewise, the impact of hard-to-measure trait phenotypes on EBVs and accuracy was examined by comparing the March 2019 results (which included hard-to-measure trait phenotypes) with results from the same analysis where hard-to-measure trait phenotypes were excluded (HtM- trial run).

RESULTS AND DISCUSSION

Hereford G-Matrix composition. In comparing G-Matrices, the number of animals genotyped has increased by 3.8-fold in 17 months, from 3651 animals in the October 2017 analysis to 13764 animals in the March 2019 analysis. The majority of genotypes were supplied by HAL, although there has been a steady increase in the percentage of the NZHA genotypes (0.8% versus 12.6%) since Hereford ssBP was released. While some HCBSN animals have been genotyped, these are not yet available in the format required for inclusion in the Hereford ssBP analysis. Although HAL genotypes currently dominate the G-Matrix, the benefits arising from Hereford ssBP would extend to members in all three Hereford societies subject to linkage between individual herds and the reference population, regardless of which society provides the genotypes.

In October 2017 the G-Matrix was comprised of animals born 1961 to 2016, with 29% born prior to 2010 and 39% in 2015 or later. Just 16% of the animals in the October 2017 G-Matrix were female. Given that the approach employed to build the Hereford reference population included strategic genotyping of influential sires and genotyping of well-recorded animals in the HAL beef information nucleus (BIN; Banks 2011), it is not surprising that the October 2017 Hereford G-Matrix was comprised of many older animals, mostly male. These strategies have been employed by other beef breeds and the Australian sheep industry (Brown *et al.* 2018) as they moved toward the implementation of Single-Step genomics in their genetic evaluations.

However, composition of the G-Matrix shows marked change in March 2019. Of animals in this G-Matrix, 12% were born prior to 2010 and 67% in 2015 or later. While most animals in the reference population were male, female animals now comprise 29% of those genotyped. The rapid growth in the size of the reference population suggests that Hereford breeders are embracing genotyping technology. In particular, the growth in both the percentage of younger animals genotyped and the percentage of female animals genotyped indicates that in the past 17 months Hereford producers have genotyped not only older sires but are also genotyping the younger animals (e.g. young bulls and replacement heifers) in their herds. This is to be expected as the greatest benefit of genomics will be seen in these animals, with increased EBV accuracy at earlier ages. In addition, changing requirements for animal registration (e.g. parent verification; compulsory SNP genotyping for certain classes of animals) combined with extension messages on the benefits of genotyping are likely to have contributed to this rapid uptake.

Rapid uptake of genotyping following the release of genomic analyses is not unprecedented. The Australian dairy industry first released genomic EBVs in 2010 (Nieuwhof *et al.* 2011) and since then, the number of animals being genotyped commercially has grown considerably, from just over 500 animals genotyped in the 2012/2013 financial year to over 19000 in the 2017/2018 financial year (Williams *pers. comm.* 2019). Much of this growth has been in the genotyping of females. While beef producers are unlikely to embrace genotyping of females to the same extent as their dairy counterparts, the release of a low-density panel for Hereford females in mid-2019 may help drive an increase in the genotyping of Hereford females.

Effect of genomics on Hereford BREEDPLAN. Although the inclusion of genomic information did not change the Hereford breed average EBVs (based on 2017 drop), the EBVs of individual animals have changed considerably, some increasing and others decreasing. EBV movements were more pronounced in genotyped non-parent animals than observed for sires, although EBV movements were evident for both groups. This trend was observed across traits, and likely reflects EBV accuracy

prior to the inclusion of genomic information.

Hereford ssBP has also led to increased EBV variance for most traits. For genotyped non-parent animals, EBV standard deviation is higher for most BREEDPLAN traits. Increased EBV variance is particularly useful for beef producers, as identification of genetically superior and inferior animals informs selection decisions to drive genetic gain.

Lastly, Hereford ssBP has led to an increase in EBV accuracy. This increase has been greatest for animals with a low EBV accuracy prior to the inclusion of genomic data; a trend that holds across traits (Figure 1). However, the magnitude of this increase varies across traits (Figure 1). For 200 Day Weight (200d), the average increase in EBV accuracy for animals with a prior EBV accuracy of ≤20% was 30%; for Days to Calving (DtC) it was 5.5%. Similar results were observed by Johnston *et al.* (2018) following the implementation of ssGBLUP for Australian Angus and Brahman. They concluded that the difference in magnitude of EBV accuracy increase across traits likely varied due to both heritability and the size of the reference population for each trait. Both are likely to be the case here; 200d is moderately heritable while DtC is lowly heritable. Furthermore, over 85% of animals in the March 2019 G-Matrix have a phenotype for 200d, but less than 5% have DtC phenotypes. This is not surprising given the low level of performance recording observed for DtC in the Australian beef industry (Gudex and Millen 2019, these proceedings). Collection of additional phenotypes is likely to drive larger increases in EBV accuracy than currently observed (in turn leading to increased genetic gain), and thus remains a key extension message for industry.
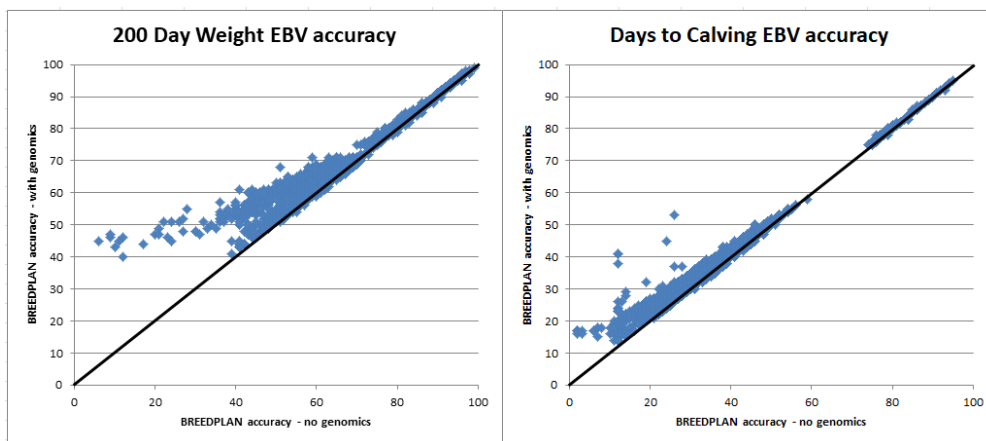
Figure 1. Changes in EBV accuracy for 200 Day Weight and Days to Calving when genomic information is included in the Hereford BREEDPLAN analysis

Effect of hard-to-measure phenotypes on Hereford BREEDPLAN. The removal of DtC and abattoir carcase data had greatest impact on DtC and carcase trait EBVs and accuracy, but little to no effect on EBVs and accuracy for other BREEDPLAN traits. The impact varied by trait, with the biggest impact being evident for DtC. The correlation between the DtC EBV in the ssBP run and the HtM- trial run was 0.35, with the latter results regressed back toward the base (from -2.1 days on average back to -1.7 days) and with reduced standard deviation (from 3.3 days back to 1.6 days). While the average change in DtC EBV was small, substantial changes in DtC EBV were observed for individual animals, the most extreme being changes of ±9.0 days. The exclusion of DtC data also led to a decrease in DtC EBV accuracy, from an average of 80% in the standard production run to an average of 61% in the HtM- trial run.

Less extreme changes were observed for the carcase traits. Correlations between the standard production run and the HtM- trial run varied from 0.95 (for each of Eye Muscle Area (EMA) and Rump Fat (P8)) to 0.99 (Carcase Weight (CWt)). While the exclusion of abattoir carcase data led to small changes in average EBV for the carcase traits, the carcase EBVs did not regress towards the base for all traits and only three of the six carcase traits showed reduced standard deviation in the HtM- trial run (CWt, EMA and P8). Despite this, the exclusion of abattoir carcase data did lead to large changes in carcase EBVs for individual animals. For CWt, changes in EBV ranged from -16.3 to +17.3 kg, and for EMA EBVs, from -5.4 cm^2 to +4.7 cm^2. Small reductions in average EBV accuracy (-1%) were observed for carcase traits in the HtM- trial run.

The exclusion of DtC data had a more extreme impact on DtC EBVs than the exclusion of abattoir carcase data had on carcase trait EBVs. This is most likely due to the multi-trait nature of the Hereford ssBP analysis, where information used in the calculation of carcase EBVs included both abattoir carcase data and correlated ultrasound scan data. Given that ultrasound scan data was not removed, it is likely to have buffered some of the effect of removing abattoir carcase data on the carcase EBVs. The same cannot be said for DtC, where the removal of DtC data led to DtC EBVs regressing towards zero, and with less variation and less EBV accuracy.

This research confirms the importance of a well-recorded reference population for the accurate estimation of breeding values, especially in relation to hard-to-measure traits. In the absence of direct records for these hard-to-measure traits and the absence of significantly correlated trait data, the availability of genotypes and ssBP alone is unlikely to provide sufficient EBV accuracy, limiting the potential for genetic improvements in these traits.

CONCLUSIONS

Since the release of Hereford ssBP, breeders have embraced genomic technology with a 3.8-fold increase in the number of animals genotyped. The inclusion of genomic information does result in EBV movements for individual animals, plus increased EBV variance for most traits and increased EBV accuracy, although this will vary by trait and by animal. This study has also confirmed the value of recording hard-to-measure phenotypes for the accurate estimation of breeding values. To maximise long-term genetic gains, the on-going collection by breeders of both genotypes and phenotypes, particularly for hard-to-measure traits, remains vital.

ACKNOWLEDGEMENTS

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