POPPLEWELL COMPOSITES: ADDING VALUE TO OUR CUSTOMERS' TROPICAL BEEF SUPPLY CHAINS THROUGH GENOMIC EVALUATION AND SELECTION

G.I. Popplewell[1], R.G. Tearle[2], R.A. McEwin[2], M.L. Facy[1] and W.S. Pitchford[2]

[1]Popplewell Composites, 33 Tom Schmidt Court, Mount Samson, QLD, 4520 Australia
[2]Davies Research Centre, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, 5371 Australia

SUMMARY

Popplewell Composites has been supplying objectively evaluated Tropical Composite bulls to commercial breeders since 2008. All active and historic animals in its nucleus breeding program were genotyped and Genomic Evaluation (G-BLUP) first conducted in 2016. Since first presenting at AAABG in early 2017, the GenoRater™ genomic evaluation program, built in collaboration with the University of Adelaide, has been used to evaluate more phenotypes, genotypes and traits. Now emerging customer multiplier tier herds are being added to the evaluation. This paper provides an update on the program and data, demonstrating the collaborative growth and connection the breeding program has achieved through application of scientific principles.

INTRODUCTION

Popplewell Composites' nucleus herd was established using animals from Angus, Belmont Red and Bonsmara, Senepol and Brahman breeds, objectively selected on their genetic makeup. The objectives of the program are to deliver meat quality and female fertility improvement through replacement of traditional *Bos indicus* dominated herds with Taurus/Sanga/Indicus Tropically Adapted Composites (Burrow *et al.* 2003). In addition, the aim is to provide continuous additive improvement through quantitative trait selection and introgression of favourable qualitative alleles (e.g. Poll genes for no horns).

The company's value proposition, direct approach to customer and research collaboration and how it conducts its genetic evaluation are all not typical of an Australian beef cattle seed-stock operation. In these aspects, it has more similarities to the operations of some modern Poultry, Pork and Aquaculture breeding companies. Popplewell Composites bulls do not fit into a purebred description or 'breed standard', but instead they are hybrid and multi-breed composite line bulls. The company uses an in-house genomic evaluation tool (GenoRater™) which focuses on being nimble, innovative and combining nucleus and customer herd data.

Customers with very large commercial herds (>10,000 breeding females) are being serviced via development of 'turn-key' bull multiplier herds that are run on the customers' own properties with Popplewell Composites supplying the sires, technology, sample collectors, ear tags, performance recording planning and support. Popplewell Composites also have a loyal client base of progressive family businesses that purchase bulls direct from the nucleus herd.

MATERIALS AND METHODS

Herd management. The Popplewell Composites nucleus cow herd is run in coastal South East Queensland, rotationally grazed on tropical species-based pastures and exposed to tropical parasites. The herd is phenotyped for fertility, birth weight, growth, mature weight, flight speed, tick resistance, coat score, and live-ultrasound carcass traits. Semen tested yearling bulls are sold to commercial and bull multiplier herds in Tropical, Subtropical and Arid regions of Australia. All heifers born into the

program are first mated as yearlings which is not typical of tropical breed seed-stock herds.

Multiplier tier herds are located on customers' own properties in North West Queensland and the Pilbara, Western Australia. These herds are phenotyped for fertility, growth, mature weight, flight speed, and live-ultrasound carcass traits. Birth weight and birth date are not recorded in these herds due to the extensive nature of their operations, however an estimated conception date, captured using pregnancy foetal aging techniques, is used to measure female fertility and adjust other traits for age. Birth Weight genomic estimated breeding values are calculated for multiplier animals using data from Nucleus genomic relatives in combined herd analysis.

Genotyping and processing of marker data. At the last AAABG Pitchford *et al.* (2017) presented the results of analysing all of our current and historic animals records and DNA samples (1,104 head combined). These included all animals with phenotypes genotyped on the Illumina GGP Bovine LD chip (versions 3 and 4) and sires genotyped on the Illumina BovineHD chip.

Since our last paper, 579 more animals have have been added from the Popplewell nucleus. All have been genotyped and many have been phenotyped. Also 1,125 animals with genotypes some associated phenotypes have been added from customers' bull multiplier tier herds. Processing of genotypes of calves born in late 2018 in now underway and will further expand the analysis, along with more genotypes and phenotypes from the multiplier herds this year.

The GGP Bovine LD chip is no longer available, so the program has started using a 50K SNP chip from Weatherbys Scientific Australia. This initially presented some difficulties, overcome by imputing up to the original GGP Bovine LD chip.

To create a Genomic Relationship Matrix (GRM) for the statistical analysis, monomorphic SNPs, those with a call rate less than 0.05 and a minor allele frequency (MAF) less than 0.01 are removed, leaving 29,433 SNPS to be used in the analysis. Heterozygosity for each animal is calculated by summing the number of heterozygous genotypes as a proportion of all called genotypes. A standardised matrix of counts for each SNP is generated by subtracting its mean and dividing by its standard deviation. Missing values are replaced by the standardised mean (0). This starting matrix is multiplied by its transpose and divided by the number of SNPs to generate a relationship matrix which is then inverted, ready for trait analysis.

Statistical analysis. As per Pitchford *et al.* (2017); data is analysed using a linear mixed model in ASREML-R (Gilmour *et al*. 2009). Fixed effects are birth year (2008-2017), sex (male or female), dam age (heifer or mature), age (by fitting birth date as a covariate within year), and heterozygosity (% , labelled Het%).

Contemporary groups are defined as management groups within birth year and sex. Management groups for later ages are comprised of current management group and previous management groups as described by Graser *et al.* (2005). Ultrasound traits include day of measurement in the contemporary group and weight as a covariate within contemporary group. Scrotal size included a covariate of age within contemporary group. Lastly, the random animal effects are fitted as the inverse of the GRM.

The carcass, growth, temperament, adaption and carcass traits analysed are; birth weight, weights at 200, 400 and 600 days (kg), tick resistance, log flight time, ultrasound loin eye muscle area (cm^2), P8 fat depth, rib fat depth (mm) and intramuscular fat content (%).

Female fertility is analysed only on naturally mated females as days from joining to calving (Days to Calving or DC) with yearling heifers (HDC) separate from those joined at 2 years or older (mature, MDC). Those that failed to calve have a 32-day penalty added to the maximum DC value in their management group. Dam age and heifer age effects are included in the analysis of for HDC but not MDC, but both include heterozygosity. Mature weight is analysed on lactating cows only, using fixed effects of age in years and heterozygosity.

RESULTS AND DISCUSSION

Significant programming has gone into GenoRater™ to streamline data handling, accommodate for new traits and also new SNP Chip formats since our last report. The analysis continues to perform well at estimating both within and between breed group differences using G-BLUP methods. Using Het% in the analysis continues to be particularly important for female fertility traits, highlighting the importance of the non-additive benefits (hybrid vigour) of composite breeding the program is providing customers, whose breeding objectives' place large economic values on female fertility.

Table 1. Nucleus Traits and Data Volumes as at 15/9/2018

Trait	# Records	Heritability	Standard Error
Birth Weight (kg)	1352	0.51	0.06
200 Day Weight (kg)	1420	0.30	0.06
400 Day Weight (kg)	1380	0.38	0.06
600 WT (kg)	518	0.37	0.12
U Eye Muscle Area (cm)	1361	0.40	0.06
U_P8 Fat (mm)	1359	0.48	0.06
U_Rib Fat (mm)	1361	0.38	0.06
U_Intramuscular Fat (%)	1361	0.26	0.06
Scrotal Circumference (cm)	696	0.47	0.09
Flight Time (Log Sec)	1268	0.15	0.06
Tick Resistance (Score)	589	0.37	0.10
Coat Type (Score)	991	0.72	0.05
Heifer (Yearling Mated)_DC	374	0.32	0.18
Mature DC	1083	0.16	0.04
Mature Cow WT	688	0.58	0.06
Total Animals/Genotypes	1,683		

Although standard errors for most traits are now low, it is expected those higher standard errors for traits Heifer Days to Calving and 600 Day weight will reduce with extra data expected soon.

Genotype and Phenotype volumes have increased significantly from within the nucleus, which is growing in numbers. Pregnancy records, calves and associated data is now starting to flow from the multiplier herds. Multiplier herds will contribute significantly more phenotypes for more traits over the next 12 months.

CONCLUSIONS

The increase in annual numbers of herds, phenotypes and genotypes entering the analysis can be largely attributed to an increase in customer satisfaction and industry demand for the nucleus bred bulls being described and bred objectively, fuelling and funding nucleus herd growth.

Implementing these genomic approaches is allowing the rapid start-up of the integrated multiplier tier herds, as animal pedigrees (in this case for starting base multiplier cows) are not required for (Meuwissen *et al.* 2001; Hayes and Goddard 2011). This was foreshadowed for this program by Pitchford *et al.* (2017) and is now being exploited.

Planned future research includes exploration of using a dominance matrix in the analysis instead of Het% and further incorporation of back-solving to estimate the effect of individual SNPs on traits. There are also plans for new traits and the inclusion of carcass grading data and corresponding genotypes from bull customers' commercial tier herds.

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