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USE OF GENOMIC SELECTION IN A TROPICALLY ADAPTED COMPOSITE BEEF PROGRAM

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SUMMARY

Popplewell composites objectively breed tropically adapted multi-breed composite bulls for beef production. They recently genotyped the whole herd and this paper reports analysis of this data. The data was analysed using G-BLUP using a genomic relationship matrix based on 23,094 polygenic markers for 1,104 animals. Preliminary estimates of heritabilities and variances were close to published estimates for similar cattle from northern Australia. Heterozygosity effects were substantial for reproduction and growth.

INTRODUCTION

The Popplewell Composite program was established in 2008 using objectively selected genetics from Angus, Belmont Red / Bonsmara, Senepol and Brahman population. The objectives of the program are to deliver continuous additive genetic improvement in meat production and 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 to introgression of favourable qualitative alleles such as Poll and slick coat.

Genetic evaluation of livestock has traditionally been based on information on genetic relationships between animals (pedigree) and performance of animals or their relatives. Initially this was using sire models, then all known relationships could be modelled using the relationship matrix and analysing the data using best linear unbiased prediction based on the so called animal model (Quaas and Pollak 1980). There have been numerous developments to this method over the years (Graser *et al.* 2005). However, the system has limitations when animals with limited pedigree information are included, especially in tropical beef populations with large use of multiple sire mating systems before the availability of parentage testing technology. Genomic selection as proposed by Muewissen *et al.* (2001) with further developments (e.g. Hayes and Goddard 2011) enables breeding value estimation based on DNA rather than pedigree information. Furthermore, for composite herds a "genetic groups" effect (Gilmour *et al.* 2009) is often included but a genomic relationship matrix can simultaneously account for both between and within-breed genetic variation.

Female reproductive performance is an important profit driver for northern Australian beef production systems. The aim of this paper is to report preliminary genetic parameters for reproduction, growth and carcass quality traits using a genomic relationship matrix in a tropically adapted composite herd. Heterozygosity effects which reflect heterosis or dominance effects which are commonly large for female reproduction traits in taurine x indicine hybrids (Pitchford *et al.* 1993) are also reported.

MATERIALS AND METHODS

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

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

Prior to G-BLUP, hair and or semen samples for DNA extraction had always been collected and stored on all nucleus animals and DNA technology use had been limited mainly to parentage determination and introgression of favourable Poll genes. The commitment to storing tissue and collecting economic relevant phenotypes provided a bank of DNA and data ideal for whole herd G-BLUP without the need for blending of pedigree and genomic relationships. Pedigree data allowed for comparison of pedigree BLUP and G-BLUP models.

Processing marker data. Animals were genotyped on either the Illumina GeneSeek GGP Bovine LD chip (versions 3 and 4) or Illumina BovineHD chip. A matrix of AB genotype calls for 1,119 animals and 29,464 SNPs were extracted from text output files and the minor alleles counted for each genotype (i.e. 0, 1, 2), where the minor allele was calculated across the 1,119 animals. Duplicate animals were removed, monomorphic SNPs and those with minor allele frequency less than 0.01 were also removed, leaving 23,094 SNPs on 1,104 animals. Heterozygosity for each animal was calculated by summing the number of heterozygous genotypes as a proportion of all called genotypes. Heterozygosity is a measure of dominance and reflects heterosis. The values ranged from 25-47%.

A standardised matrix of counts for each SNP was generated by subtracting its mean and dividing by its standard deviation. Missing values were replaced by the standardised mean (0). This starting matrix was multiplied by its transpose and divided by the number of SNPs to generate a relationship matrix which was then inverted ready for analysis.

Statistical analysis. Phenotypes were available for up to 3,934 animals depending on the trait but only 1,104 were genotyped. This paper reports analysis of a subset of phenotypes for animals present in the relationship matrix. The data was analysed using a linear mixed model in ASREML-R (Butler *et al.* 2009). Fixed effects were birth year (2008-2015), sex (male, female), dam age (2-10 years but coded as heifer or mature), age (by fitting birth date as a covariate within year), and heterozygosity (Het%). Contemporary group was defined as management group within birth year and sex. Management groups for later ages were comprised of current management group and previous management groups as described by Graser *et al.* (2005). Ultrasound traits included day of measurement in the contemporary group definition and included weight as a covariate within contemporary group. Scrotal size included a covariate of age within contemporary group. Lastly, the random animal effects were fitted as the inverse of the genomic relationship matrix.

The traits analysed were birth weight, weights at 200, 400 and 600 days (kg), ultrasound loin eye muscle area (cm^2), P8 fat depth, rib fat depth (mm) and intramuscular fat content (%). Maternal genetic effects were not included in initial analyses but will be for birth and 200 day weights in future.

Fertility was measured only on naturally mated females as days from joining to calving with yearling heifers (HDC) separate from those joined from 2 years old (mature, MDC). Those that failed to calve had a 32 day penalty added to the maximum DC value in their management group. Sex, dam age and heifer age effects were not included in the analysis of HDC or MDC. Mature weight was analysed using fixed effects of age in years, lactation number and heterozygosity.

RESULTS AND DISCUSSION

The population is a composite of Africander (Bonsmara and Belmont Red), Senepol, Red Angus and Brahman. A summary of the genetic variation is presented based on principal component analysis of the SNP genotypes (Figure 1). The G-BLUP performed well at describing both between and within breed variation in a single step. Fitting calculated heterozygosity avoided bias in BLUP estimates resulting from heterosis, especially for fertility.

The combination of breeds during the development was expected to lead to large variation in traits that differ between breeds. However, for most traits the variances and heritabilities (Table 1) were very similar to those reported by Wolcott *et al.* (2014) and Johnston *et al.* (2014) for tropical composite cattle measured as part of the CRC for Beef Genetic Technologies. A small exception would be that herein the cattle were younger when ultrasound scanning so the mean and variance in the fat traits was lower than the CRC cattle.

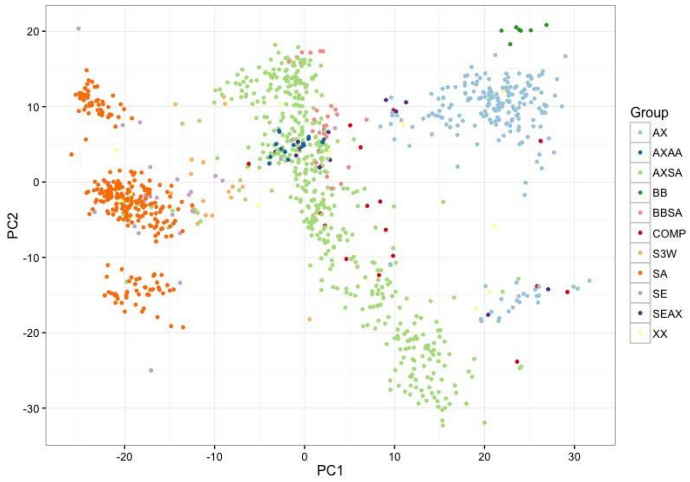

Figure 1. Genetic variation coded by breed of origin. AX is Africander (right), AXSA is Africander x Senepol/Angus (middle), BB is Brahman (top right) and SA is Senepol x Red Angus (left). Other combinations are minor.

Numbers of cattle were a limitation for accurate heritability estimation (Table 1). The numbers for growth and carcass traits was around 800 but for male (scrotal size) and female fertility traits, numbers were very small. Despite this and the fact that a genomic rather than an animal relationship matrix was used, heritability estimates were very close to published values for equivalent breeds and traits (Barwick *et al.* 2009). It is especially encouraging that the preliminary heritability estimates herein for days to calving for first parity and mature cows were almost identical to those presented by Johnston *et al.* (2014). However, a difference herein is that heifers were joined at 15 rather than 27 months. To conceive to calve at 2 years, heifers need to be cycling by around 400 days. Johnston *et al.* (2009) reported that composite heifers averaged 650 days at puberty. Thus, the program herein is putting substantial phenotypic and genetic selection pressure on heifer puberty because it is such a large profit driver and given the number that conceived, it must be working.

Those with greater heterozygosity were bigger and had better female reproduction (conceived faster, Table 1). All of these are as expected based on heterosis in taurine x indicine crosses (e.g. Pitchford *et al.* 1993). This would likely have a significant effect on profitability of commercial herds.

The practical outcome of this work is that this breeding program should achieve significant gains for commercial clients. A selection index was developed based on a combination of approximate economic values and desired gains. The 2016 mating decisions will lead to cattle with higher growth, more fat and improved fertility through both increased scrotal size and decreased days to calving. In addition, there will be small decreases in birth weight and mature cow weight as well as a small increase in eye muscle area. There was no direct selection for fat but this was a correlated response resulting from positive correlations with growth and fertility. There is expected to be

ongoing improvement due to the extensive measurement program, all animals genotyped and mating allocations based on optimising breeding value and genetic diversity outcomes. In addition, the program will further accelerate in scale through strategic partnerships with bull customers using genotypes and phenotypes from their bull multiplier and commercial tier herds.

Table 1. Summary of data, phenotypic variance, heritability and heterozygosity estimates.

Trait	No.	Mean	SD	Min	Max	σ_P^2	h^2	Het%
Birth weight (kg)	892	36.8	5.3	21	55	16.9	0.41	0.32**
200 d weight (kg)	883	204	51	75	415	460	0.11	1.65**
400 d weight (kg)	801	320	64	152	528	905	0.35	3.17**
600 d weight (kg)	351	374	66	232	694	1078	0.56	2.70**
Eye muscle area (cm^2)	790	55.3	12.8	23	96	27.9	0.39	0.31**
Rump P8 fat (mm)	790	3.8	1.6	1	10	1.18	0.23	0.060
Rib fat depth (mm)	790	2.9	1.1	1	7	0.57	0.15	0.021
Intramuscular fat (%)	790	3.5	1.0	1	6	0.45	0.20	0.017**
Scrotal size (cm)	409	29.8	4.0	20	41	8.03	0.62	0.13
Heifer DC	255	348	33	271	393	1021	0.21	-2.77*
Mature DC	503	333	21	271	368	1099	0.14	-2.43**
Mature weight (kg)	433	486	68	324	666	2510	0.60	2.26*

DC is days to calving from date of joining to calving with a 32 day penalty for non-calvers.
Het% is regression of trait on percentage of polymorphic SNPs that were heterozygous.
Approximate standard errors of preliminary heritability estimates were large for all traits and >1 for some. * P<0.05, **P<0.01

In conclusion, this tropical composite breeding program has been innovative in storing DNA and then genotyping all animals. This has enabled genomic analysis of both traditional BREEDPLAN and new traits important for reproduction. Preliminary estimates of heritabilities are similar to other studies and important heterozygosity effects have also been reported.

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