437. Polled Accelerator – a unique application of genomic technologies to address a beef breeding challenge

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Abstract

Genetic improvement requires selection for all traits in the breeding objective and increasingly this includes consideration of traits associated with animal welfare and social licence. A unique program called the 'Polled Accelerator' was developed for a large beef cattle population to rapidly increase the frequency of polledness. The program was constructed using a unique combination of existing and emerging genomic technologies and methods including DNA tests for polled/horn and Pompe's disease, DNA sire assignment, genomic breed composition, imputation and single-step genomic evaluation. Phenotypically polled young males were harvested from the commercial tier and through the program, high genetic merit polled animals were eligible for promotion to the multiplier and nucleus tiers of the breeding program. The application of multiple genomic technologies will allow the rapid introgression of polledness into this population without compromising the composite breed composition, breeding program structure, future genetic progress or genetic diversity.

Introduction

Surgical removal of horns from beef cattle (called dehorning) is becoming an animal welfare and management issue, and is associated with increased calf losses. Dehorning of calves improves safety of both cattle and people during handing and reduces the risk of bruising to cattle. Pain mitigation strategies are available, however there is a permanent alternative to dehorning through genetic selection, though the speed at which it can be achieved may be slow for breeds with low gene frequency for the polled allele. This is the challenge facing the breeding program of The North Australian Pastoral Company (NAPCO) that developed its own composite breed in an extensive northern Australian production environment. The breeding program is closed and relies on retained heterosis, especially for adaptation and reproduction traits. NAPCO is a vertically integrated operation, retaining ownership and management from breeding to slaughter, including a short phase in the company's feedlot prior to slaughter. The foundation breeds were horned and therefore the opportunity to change from within the nucleus tier would be very slow and there is a risk of increased inbreeding, loss of genetic diversity, change of breed composition and slower genetic progress. Selection occurs based on a defined breeding objective, however there is increasing demand to make the composite genetically polled. The Polled Accelerator (PA) program is addressing this breeding challenge through the use of new and emerging genomic tools to enable the rapid increase in polled allele frequency, without compromising the original composite breed makeup, existing genetic merit, future progress or diversity while maintaining manageable levels of inbreeding.

Materials & methods

The cattle used were a composite beef population developed at Alexandria Station, a 1.6M ha property on the Barkly Tableland region of the Northern Territory in northern Australia. The Alexandria Composite (AC) development commenced in 1982 with the crossing of the foundation breeds of Shorthorn to Brahman, and was followed by crossing those progeny with Charbray and Belmont Red (Kowald 2019). The composite was closed in 1990 and has been *inter se* mated since for 5-6 generations in the nucleus tier, resulting in a theoretical stabilised composition of 3/8 Brahman, ¼ Shorthorn, ¼ Belmont Red, 1/8 Charolais.

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Breeding structure. A classical pyramid breeding design was implemented, with a nucleus (approx. 1,200 cows), a bull multiplier (BM) tier (approx. 2,500 cows) and a commercial tier comprising of approximately 50,000 cows. The initial composite development program and subsequently all 3 tiers of the breeding program have been run in the same location.

Performance recording and genetic evaluation. Intensive recording and genotyping occurs in the nucleus tier with approximately 1000 calves born per year. Recording includes: date of birth, birth weight, weaning weight, 400d and 600d weights, flight time, cow weight, carcase scanning, feedlot performance test, scrotal circumference and days to calving, and recently feed intake and abattoir carcase traits. Data is analysed through AC BREEDPLAN evaluation with genetic parameters and adjustment factors estimated from their own data. The evaluation is full multiple-trait, and recently transitioned to a single-step evaluation (Johnston et al. 2018) using a genomic relationship matrix (GRM) with 10,131 genotyped individuals from the nucleus tier.

Sourcing polled commercial bulls and heifers. During annual branding muster of the commercial herd, structurally sound and phenotypically polled males and females were retrieved, (males remained entire) and DNA samples taken. A total of 1,036 males (termed AC_PA animals) and 1,604 females (termed polled AC_BM breeders) were initially retained in the first two years of the program.

DNA testing. Genotyping AC nucleus animals has been occurring for more than a decade using a range of commercially available SNP chips. AC_PA and recent nucleus cohorts were genotyped and tested for polled/horn (PP, PH, HH) and Pompe's disease. All SNP genotypes were processed through the BREEDPLAN genomic pipeline (Connors et al. 2017) and all genotypes are imputed to a common density using an AC reference with 800K genotypes.

Genomic breed composition. SNP frequencies for AC were used to genomically define breed composition using the procedure described by Borner (2017). Principal component analyses were undertaken to compare the AC to the foundation breeds (viz: Brahman, Shorthorn, Belmont Red and Charolais) and the AC_PA individuals.

Single-step evaluation and selection of AC PA males. AC_PA genotypes were processed through the genomic pipeline and those that could be matched, passed SNP QC, and were >80% related to the AC genomic reference, and which were PP or PH, were included in AC BREEDPLAN single-step evaluation through their inclusion in the GRM (n=421). This generated the full suite of EBVs and AC specific BreedObject selection index ($EBV) for the AC_PA subsets of PP and PH animals, which could be selected based on direct comparisons with all 2018 born nucleus animals (NU18).

Transition of the BM tier from horned to polled. The retained young females (polled AC_BM breeders) were selected as the foundation of a new BM herd. While the contribution of these females to increasing the rate of genetic progress will be limited, their role in introducing polled alleles to the breeding program is valuable. Over a period of 6 years, the existing BM females (which are predominantly horned) will be superseded by polled AC_BM breeders. Only polled sires are selected for mating to the polled AC_BM females and these are sourced from the nucleus tier and AC_PA cohort.

Results

Genomic breed composition of AC is presented in Figure 1a and show AC is a distinct population with the first principal component differentiating on the basis of Brahman versus Charolais and Shorthorn. AC_PA

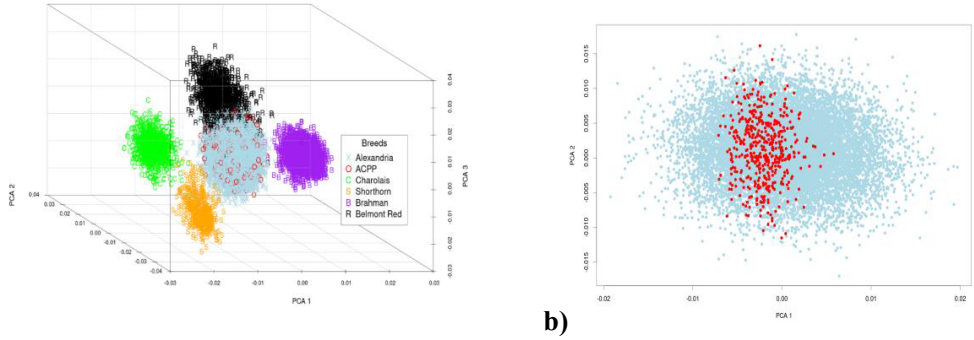

Figure 1. Principal Component analyses (a) AC and foundation breeds and (b) AC (blue) and AC_PA (red)

individuals ranged in genomic breed composition from 40-93% with 69% greater than 80% threshold and are shown in Figure 1b.

Of the 421 AC_PA eligible for inclusion in the GRM, a total of 117 were PP and 304 were PH. The frequency of polled in the NU18 was 11% with only 5 PP bulls in total. Summary statistics for $EBV (Table 1) and key EBVs and accuracies (Table 2) show the EBVs for the two groups of AC_PA (i.e. PP and PH) were similar but lower than NU18, clearly showing the commercial tier animals were genetically inferior. Long term genetic trend of 0.9 kg 600d/yr suggesting the AC_PA animals were genetically about 16 years (or 3 generations) behind the nucleus tier. However, there is considerable spread in AC_PA with a total of 16 and 28 bulls with average or above $EBV and 600d EBV, respectively.

Discussion

The PA program has identified commercial males that could be promoted to the nucleus tier to increase frequency of polled in the AC. The lower average genetic merit and differences in foundation breed percentage highlighted the risk to the program of simply promoting a polled commercial animal to the nucleus. The use of elite AC_PA will still give up some selection differential compared to using top nucleus (horned) bulls but that would likely change if polled was included in $EBV with a high economic value. Also, the AC_PA have lower individual accuracies but this risk could be minimised by using a syndicate of AC_PA selected bulls. AC_PA could be used directly in the nucleus tier (especially PP) but could also be used in the polled BM to increase the number of PP bulls introduced to the commercial tier, resulting in an immediate reduction in horn phenotype (polled being dominant) even though the commercial cow herd would remain predominantly horned in immediate future generations.

Table 1. Summary statistics for self-replacing Index ($EBV) for the 3 groups.

Group[1]	N	Mean	Std	Min.	Max.
PP	117	16.6	8.2	-6.6	40.6
PH	304	17.5	8.7	-4.2	45.6
NU_18	908	34.3	12.7	-2.4	73.5

[1] PP =AC_PA homozygous polled; PH=AC_PA heterozygous polled; NU_18=Nucleus 2018 born animals.

Table 2. Summary statistics for key EBVs from single-step BREEDPLAN evaluation.

		EBV				Accuracy			
trait[1]	Group[2]	Mean	Std	Min.	Max.	Mean	Std	Min.	Max.
BW, kg	PP	0.7	1.0	-1.8	3.3	40.6	6.9	34	57
	PH	0.8	1.1	-2.3	3.9	42.1	7.6	33	69
	NU18	1.6	1.8	-3.9	6.3	70.5	3.4	43	75
600d, kg	PP	17.1	9.2	-6.3	42.9	44.0	7.2	37	59
	PH	17.6	9.7	-4.8	51.5	45.6	7.9	36	71
	NU18	32.3	12.7	-11.9	64.0	73.2	6.1	34	82
DC, d	PP	-0.6	1.3	-4.2	3.5	15.8	5.7	11	29
	PH	-0.7	1.4	-4.7	2.8	17.1	6.4	10	37
	NU18	-2.2	2.6	-10.3	4.5	33.4	4.4	5	42
SC, cm	PP	0.4	0.7	-1.0	2.6	36.1	9.1	28	54
	PH	0.4	0.7	-1.4	3.0	38.2	9.9	27	64
	NU18	1.1	1.1	-2.0	4.7	59.5	6.0	13	68

[1] BW=birth weight; 600d=600 day weight; DC=days to calving; SC=scrotal circumference.

[2] PP=AC_PA homozygous polled; PH=AC_PA heterozygous polled; NU18=Nucleus 2018 born animals.

The PA program highlights the potential risk of simply introducing outside genetics; it could result in a change to the breed composition with no guarantee of improving genetic merit. Depending on the breed of outside genetics chosen, there could also be consequences for progeny adaptation as well as the logistical challenge of sourcing sufficient numbers for such a large herd. There is an opportunity to use mate allocation algorithms to optimise the use of AC_PA animals and to manage potential inbreeding. Gene flow analyses could be used to model the increased polled allele frequencies and to explore where the use of AC_PA animals would have the greatest benefits. EBV accuracies of future AC_PA animals could be increased by expanding the reference population for key traits. Multiple genomic technologies have been exploited in NAPCO's Polled Accelerator program to address a challenge in the breeding program where a non-genomic solution would be slow and introduce additional compromises. Opportunities exist to use more genomic technologies to further increase progress towards a polled population whilst maintaining the benefits and genetic progress for this composite breed.

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