THE *REPRONOMICS* PROJECT - ENABLING GENETIC IMPROVEMENT IN REPRODUCTION IN NORTHERN AUSTRALIA

D.J. Johnston[1], T.P Grant[2] T.J. Schatz[3], B.M. Burns[4], G. Fordyce[5] and R.E. Lyons[6]

[1] Animal Genetics and Breeding Unit*, University of New England, Armidale, NSW 2351
[2] Queensland Department of Agriculture and Fisheries, Toowoomba, QLD
[3] NT Department of Primary Industries and Fisheries, GPO Box 3000, Darwin, NT
[4] QLD, Department of Agriculture and Fisheries 25 Yeppoon Road, Parkhurst, QLD
[5] Queensland Alliance for Agriculture and Food Innovation, UQ, Charters Towers, QLD
[6] Animal Genetics Laboratory, University of Queensland, Gatton, QLD

SUMMARY

This paper provides a brief description of a large breeding and genotyping project currently being conducted in northern Australia using three tropically-adapted beef breeds. Intensive recording of early-in-life female reproduction phenotypes using real-time ultrasound on large numbers of females will significantly increase the size of the genomic reference populations for these key traits and breeds. This phenotypic data, along with high density SNP genotypes, will provide crucial data to enable the effective implementation of new BREEDPLAN genomic evaluations currently being developed for the Australian beef industry, and will assist in increasing the accuracy of selection, especially in young bulls. The project design will also allow investigations of *GxE* interactions for female reproduction traits; the potential development of new traits; and methodologies required for the implementation of across-breed genomic evaluations.

INTRODUCTION

Reproduction is a key profit driver in northern Australia and the recent Beef CRC northern reproduction project, and earlier research (e.g. Hetzel *et al.* 1989), showed there is a clear role for genetics in improving commercial weaning rates. Heritability and genetic variance estimates for reproduction traits from the Beef CRC suggest considerable genetic progress is possible in both Brahmans and Tropical Composites. This is particularly the case for component traits of reproduction measured earlier in a cow's reproductive life. Two of these traits identified as important for genetic improvement are heifer age at puberty (Johnston *et al.* 2009) and first-lactation anoestrous interval (Johnston *et al.* 2014a). Male reproductive measures are also heritable (Corbet *et al.* 2013) and can be used with other novel traits as indirect measures of reproduction (Johnston *et al.* 2014b; Barwick *et al.* 2014). Genomics research has also shown that this emerging technology has the potential to add significantly (Hawken *et al.* 2012 and Zhang *et al.* 2014) to our ability to make genetic progress in reproduction (Barwick *et al.* 2014). However to move the research outcomes more rapidly into industry breeding programs requires the collection of considerably more reproductive phenotypes and genotypes to build the size of the genomic reference populations across an increased number of northern beef breeds. This is the aim of a new 5 year project (MLA *B.NBP.0759*) known as the Repronomics*TM* project that has been running for 3.5 years and has generated significant numbers of calves and has recorded large numbers of females for age at puberty, lactation anoestrous interval, calving and weaning rates, along with many other traits in 3 major northern beef breeds. These records are being combined with DNA SNP genotypes on all project animals, as well as key industry animals, to drive new genomics enhanced BREEDPLAN evaluations. This paper provides a brief description of the experimental design and an update on the recording that is occurring in the project.

---

*AGBU is a joint venture of NSW Department of Primary Industries and the University of New England

LOCATION AND BREEDS

The project is utilising the 3 numerically largest tropically adapted beef breeds (*viz*. Brahman, Droughtmaster and Santa Gertrudis) in northern Australia. The research is being conducted on Queensland Department of Agriculture and Fisheries (DAF) research facilities (Brian Pastures, Gayndah; Spyglass, Charters Towers) and the Northern Territory Department of Primary Industry and Fisheries' Douglas Daly Research Farm, Daly River. The project is also utilizing industry seedstock herds located throughout Queensland. The Douglas Daly Brahman herd is part of a large long-term fertility selection experiment (Schatz *et al.* 2010). The Brian Pastures and Spyglass herds consist of pedigree and performance recorded females, and include a proportion of ex-Beef CRC cows used as base females. All herds are fully BREEDPLAN recorded and genetic linkages exist with the Beef CRC project, the Brahman Beef Information Nucleus herds, the Smart Futures Fund Next-Gen project industry herds and other key industry seedstock herds. At Brian Pastures, all 3 breeds are present, whereas at Spyglass there are Brahman and Droughtmasters. At each location, the breeds are managed and recorded together, and this is providing unique data for the future development of across-breed EBVs.

SIRES USED

The sires used in the project include naturally mated bulls purchased by DAF, and in recent years AI sires have been chosen that are currently influential in each of the breeds in terms of the number of offspring generated in the last 5 years. In addition, some emerging young sires have been used in each breed. The sires are chosen particularly if they have limited or no daughters recorded for reproduction in BREEDPLAN. Poll status is considered, but is not the primary selection criterion. The aim is to generate 15-20 daughters from each sire and intensively record them for early reproduction. For Droughtmasters, a selection of older sires has also been used to allow estimation of breed genetic parameters, particularly for female reproduction traits. To-date, the project has generated progeny on 236 sires, with 86 currently having 10 or more daughters, not including calves generated in the latest 2017 born calf crop.

FEMALES GENERATED AND KEY TRAIT RECORDING

Currently the project has generated approximately 4,200 calves from 4 year drops. Breeding is by natural mating for maidens and first-lactation cows. At the Douglas Daly herd, heifers are mated as yearlings, but in the DAF herds the heifers are mated first as 2-year olds. The majority of older cows have been used for AI (2 rounds fixed-time program) to generate progeny on the key industry sires, and although the project has experienced below average seasonal conditions in the first 2 years, the resultant calving rates to AI have been very good, averaging 50%.

The project is using real-time ultrasound and highly skilled ultrasonographers to perform regular ovarian assessments on all females to accurately determine the follicle development, and importantly, the presence of a corpus luteum (CL). Every year the cohort of maiden heifers are regularly scanned to determine age at observed CL (see Figure 1) which is used as a measure of age at puberty for each heifer. All first-lactation cows are also regularly scanned during the mating season to determine their time to return to cycling post-calving. Post-weaning all acyclic females continue to be scanned until a CL is observed. To-date the project has recorded more than 1,500 heifers on the research station herds for age at puberty and about 1,000 first-lactation cows for their anoestrous interval.

All females are regularly recorded for body weight, hip height, body condition score, subcutaneous fat depth, and eye muscle area. At calving, each cow is scored for calving ease, teat and udder score, maternal behaviour and body condition. The data is checked to ensure highest quality and continuously loaded onto a custom-built project database. All BREEDPLAN traits are

regularly extracted and sent to ABRI's northern multi-breed research database and made available for use in routine BREEDPLAN evaluations of the 3 breeds.
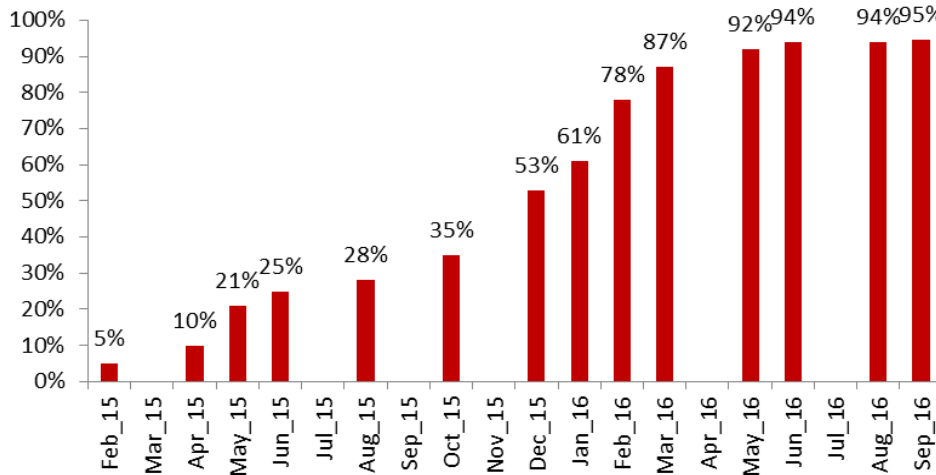

Figure 1. Cumulative frequencies of first observed CL from regular ovarian scanning of the 2014 drop Spyglass heifers weaned mid-2014

DNA GENOTYPING

To enable the development of genomic selection, all females have been DNA parent verified and genotyped with a 25K SNP chip, and all project sires are genotyped with an 80K *Bos indicus* SNP chip. Large numbers of seedstock animals have also been genotyped, including sires in co-operator industry herds (2-3 herds/breed) and other sires in Brahman and Santa Gertrudis with high accuracy BREEDPLAN days to calving EBVs. As the project progresses, cohorts of young bulls in co-operator seedstock herds will be genotyped, and will provide a demonstration of the benefits in increased accuracy from the project recording. All DNA data is checked and stored on the project database and is available for inclusion in subsequent genomic evaluations.

STEER PROGENY

All calves generated in the project are intensively recorded from birth to weaning - including accurate birth date, birth weight, gestation length (AI calves only), calving ease and survival, weaning weight, flight time, plus several other research measures. The Douglas Daly male calves remain entire, whereas at branding the DAF bull calves are castrated. After weaning, several steer cohorts have entered a northern MLA Donor Company-funded BIN project. The steers are grown-out and recorded for post-weaning performance and subsequent full abattoir carcase and meat quality assessments. The steer recording complements the female recording at the research stations, and completes the suite of key profit driver traits for northern beef production systems.

ENABLING GENOMIC SELECTION

The new single-step procedure represents a seminal change in the evolution of the BREEDPLAN genetic evaluation system. Single-step evaluations (Misztal *et al.* 2009) allow simultaneous use of existing pedigree relationships (for the majority of animals) in conjunction with a genomic relationship matrix (GRM) of genotyped animals from high density SNP profiles (e.g. 20K or 50K). The procedure simplifies, and is equivalent to, the use of genomic information currently using estimated genomic values derived from genomic prediction equations, and allows

the evaluation to be continually updated as additional phenotypes and genotypes are added. Currently, the existing pedigree relationship matrix allows differences in phenotypic performance to be transmitted to known relatives, whereas the single-step evaluation will allow genetic differences between individuals to be influenced through their degree of genomic relationship. Therefore animals with large amounts of phenotypic information when genotyped will influence the EBVs and accuracies of any animal that is genomically related.

As the genetic evaluations of the tropical breeds move towards single-step methodologies, the data and research outcomes from this project will be pivotal in driving this new era of genetic evaluation. While the Beef CRC genotyped and phenotyped large numbers of tropically adapted cattle for female and male reproduction traits, it did not include Santa Gertrudis or Droughtmaster breeds, a gap that this project is addressing. The project is also generating phenotypes and genotypes on current industry-relevant genetics and this provides the northern breeding industry with the unique opportunity to implement genomic selection, increasing the accuracy of selection of young bulls, particularly for important female reproduction traits.

CONCLUSIONS

The project is well underway and achieving its targets in generating females and intensive recording of female reproduction. Levels of recording of the project-generated females are increasing and the data is feeding into new BREEDPLAN evaluations that will enable tropical breeds to make genetic change in improving female reproduction rates. The project is building uniquely recorded herds that will allow genetics to be compared across environments, and will be a powerful resource enabling industry herds to be benchmarked for reproduction traits, as well as many other traits including overall genetic merit. Finally, the head-to-head management of breeds will provide the necessary data to generate across-breed genomic EBVs for large numbers of traits.

ACKNOWLEDGEMENTS

REFERENCES

Barwick SA, Johnston DJ, Holroyd RG, Walkley JRW, Burrow HM (2013) *Anim. Prod. Sci.* **54**: 97.

Corbet NJ, Burns BM, Johnston DJ, Wolcott ML, Corbet DH, Venus BK, Li Y, McGowan MR, Holroyd RG (2013) *Anim. Prod. Sci.* **53**: 101.

Hawken RJ, Zhang YD , Fortes MRS, Collis E, Barris WC, Corbet NJ, Williams PJ, Fordyce G, Holroyd RG, Walkley JRW, Barendse W, Johnston DJ, Prayaga KC, Tier B, Reverter A, Lehnert SA (2012) *J. Anim. Sci.* **90**: 1398.

Hetzel DJS, Mackinnon MJ, Dixon R, Entwistle KW (1989) *Anim. Prod.* **49**: 73.

Johnston DJ, Barwick SA, Corbet NJ, Fordyce G, Holroyd RG, Williams PJ, Burrow HM (2009) *Anim. Prod. Sci.* **49**: 399.

Johnston DJ, Barwick SA, Fordyce G, Holroyd RG, Williams PJ, Corbet NJ (2014a) *Anim. Prod. Sci.* **54**: 1.

Johnston DJ, Corbet NJ, Barwick SA, Wolcott ML, Holroyd RG (2014b) *Anim. Prod. Sci.* **54**: 74.

Misztal I, Legarra A, Aguilar I (2009) *J. Dairy Sci.* **92**: 4648.

Schatz TJ, Jayawardhana GA, Golding R, Hearnden MN (2010) *Anim. Prod. Sci.* **50**: 345.

Zhang YD, Johnston DJ, Bolormaa S, Hawken RJ, Tier B (2014) *Anim. Prod. Sci.* **54**: 16.