Breeding Focus 2021 - Improving Reproduction

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Published by

Animal Genetics and Breeding Unit

University of New England

Armidale, NSW, Australia

Animal Genetics and Breeding Unit

University of New England

Armidale NSW 2351

Australia

http://agbu.une.edu.au

ISBN: 978-1-921597-86-2

e**ISBN**: 978-1-921597-87-9

Cover design by Susan Joyal

Book design by Kathy Dobos

First published, 2021

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Preface

“Breeding Focus 2021 – Improving reproduction” is the fourth workshop in the series. The Breeding Focus series was developed to provide an opportunity for exchange between industry and research across a number of agricultural industry sectors. With this goal in mind, workshops have included presentations across multiple agriculturally relevant animal species to take participants outside their area of expertise and encourage them to think outside the box. Reproduction is a main driver for profitability and genetic gain. We will discuss existing knowledge, identify gaps and explore genetic and management strategies to improve reproduction further in multiple species.

Successful reproduction is a complex characteristic comprising the formation of reproductive cells, successful mating and fertilisation, embryonic and fetal growth and eventually a successful birthing event. In livestock species, reproduction traits have mostly low heritabilities, which makes it challenging to improve reproduction as part of a multiple trait breeding objective. The complexity arises not just from the cascade of processes required to result in successful reproduction, but the relevant traits are different in males and females and they are influenced through health and fitness, nutrition, climate and other environmental and management factors.

Challenges to the improvement of reproduction can vary widely for different species. For less domesticated species such as abalone, the ability to produce and reproduce the animals in captivity presents a major challenge. In bees, reproduction has not been given great attention and little research has been undertaken to understand the underlying genetics of drone and queen reproduction. However, in all industries reproduction is recognised as the basis for genetic and economic gain. It directly influences the selection intensity that can be applied. It also determines how many animals are not required for replacement and can be sold. In all industries, irrespective of the challenge, cost-effective and easy to measure phenotypes of reasonable heritability are central. New technologies and approaches enable the development of novel phenotypes for genetic improvement which will be combined with a growing amount of genomic data in livestock species and together these developments provide new and exciting opportunities to improve reproduction further.

We would like to thank everyone who has contributed to this event for their time and effort: the authors for their contributions to the book and presentations, the reviewers who all readily agreed to critique the manuscripts. We would like to express a special thanks to Kathy Dobos for her contributions into the organisation of this workshop and the publication. Thank you!

Susanne Hermesch and Sonja Dominik

Armidale, May 2021

Genetic improvement of cow reproduction in northern Australia beef cattle breeds

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Abstract

Northern Australia is characterised by high temperatures, seasonally fluctuating feed quality and unique parasitic challenges. *Bos indicus* and *bos indicus* derived breeds are favoured for their ability to withstand these challenges and produce in the harsh northern Australian environment. Cow reproduction is an important driver for breeding profitable beef enterprises but has typically been difficult to select for with traits generally being lowly heritable, sex-limited and expressed late in life. The key cow reproduction trait in the Australian BREEDPLAN genetic evaluation is days to calving which has been demonstrated to be highly correlated with calving success (i.e. did the cow calve or not). The development of two highly heritable ovarian ultrasound scan traits when implemented as part of genomic selection may be a game changer in creating opportunities for genetic improvement of cow reproduction in northern beef herds. Age at puberty and lactation anoestrus interval are both highly heritable (h^2 estimates of approximately 0.50 and 0.40, respectively) and correlated to days to calving -the key cow reproduction trait currently analysed in BREEDPLAN. The purpose of this chapter was first to outline the current genetic improvement program for female reproduction in northern Australia beef cattle breeds, and secondly to show how the incorporation of ovarian scan traits and genomic selection are providing a new and exciting opportunity to make significant genetic improvement for female reproduction.

Northern Australian beef production

The size of the national beef herd in 2019/20 was estimated to be 21.1 million head with export markets valued at $12.84 billion (ABARES, 2020). Australian beef production is divided into northern (arid, semi-arid and tropical climates) and southern (more temperate) regions, with Queensland, Northern Territory and northern Western Australia constituting the northern region. Martin (2015) reported that in 2013, 79% of all Australian beef cattle were located in the northern region, with 97% of northern Australia beef enterprises located in Queensland, 2% in Northern Territory and 1% in northern Western Australia. In contrast to southern Australia, northern Australia experiences distinct ‘wet’ and ‘dry’ seasons with large variations in the availability and quality of feed (Davis, 1993). Initially, the beef breeds imported to Australia were *bos taurus* British breeds (Tonts *et al.* 2010). In the mid 1900s, importation of *bos indicus* breeds better suited to the tropical climate of northern Australia began. The first of these imports in 1933 were the first Brahmans (Tonts *et al.* 2010). Shortly after, Droughtmaster (a mix of Zebu, Shorthorn and Brahman breeds) was the first Australian breed developed for northern Australia. *Bos indicus* breeds are favoured in northern Australia for their increased ability to withstand and produce in the harsh environment characterised by high temperatures, poor feed quality and increased parasite burden. Since the 1960s, beef breeders in northern Australia increased *bos indicus* influence, with 65% of cattle in Queensland having *bos indicus* content in the 1980s (Bindon and Jones, 2001), while almost all of the current beef population of northern Australia has some *bos indicus* content (Department of Agriculture and Fisheries (DAF), 2018).

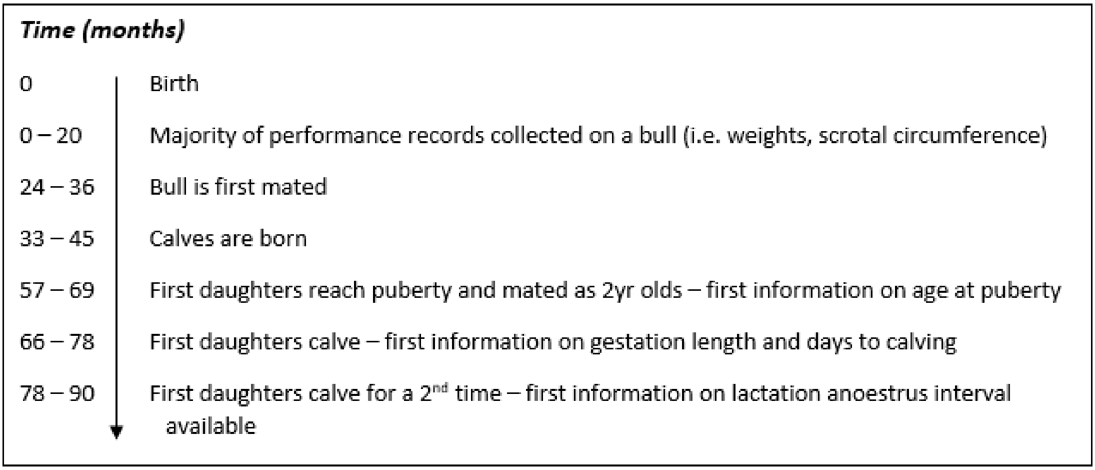
Management practices often vary across northern and southern production systems. In the north, properties tend to be very large with low stocking rates compared with those in southern Australia (Martin, 2015). Cattle are physically located over large areas making relatively simple tasks like mustering more complex and challenging. Not only are the cattle located over large areas, but properties are also themselves in remote locations, often quite a distance from the nearest town. This remoteness can also impact management strategies in northern Australia. For example, short-term supplementary feeding to compensate for poor seasonal conditions may not be a cost-effective strategy in northern Australia once logistics, such as increased transport costs, are considered. For genetic improvement, the collection of basic animal information (i.e. dates of birth) can be challenging, if not impossible.

Cow reproduction is essential for profitable beef production

Cow reproduction is a significant driver for profitability of beef enterprises. Within a season, if a cow fails to wean a live calf, she provides no income to the enterprise (apart from cull cow value) but has been a substantial cost to maintain. The harsh northern Australian conditions make weaning a live calf annually more difficult. Martin (2015) reported that the branding rate in northern Australia was only 70% compared with 86% for beef herds in southern Australia. Johnston *et al.* (2014a) reported lifetime weaning rates of 0.60 and 0.73 for Brahman and Tropical Composite cows from the Beef CRC. Making even small genetic gains for cow reproduction traits can generate large increases in profitability by increasing the number of animals available for sale and selection. In addition, improving cow reproduction increases the efficiency of land and water use and reduces greenhouse gas emissions per kg beef produced without needing to increase the size of the national herd.

Genetic improvement of cow reproduction traits in northern Australia

Achieving genetic improvement for cow reproduction traits can be challenging. The traits are often lowly heritable, sex-limited and/or expressed later in life (Cammack *et al.* 2009). Compared with other economically important traits, the genetic improvement achieved to date for cow reproduction has been limited (Barwick and Henzell, 2005; Barwick *et al*. 2014). This is illustrated in Figure 1 that shows that information about a bull's growth and carcase (via ultrasound) traits is generally available by the time selection decisions are made on that bull. At bull selection, the only information about cow reproduction is limited to information collected from female relatives (i.e. grand dam, dam, half-sisters, half-aunts) and it is not until the bull is at least 6 or 7 years old that the first direct information is obtained on his daughters.



Time (months)	
0	Birth
0 – 20	Majority of performance records collected on a bull (i.e. weights, scrotal circumference)
24 – 36	Bull is first mated
33 – 45	Calves are born
57 – 69	First daughters reach puberty and mated as 2yr olds – first information on age at puberty
66 – 78	First daughters calve – first information on gestation length and days to calving
78 – 90	First daughters calve for a 2nd time – first information on lactation anoestrus interval available

Figure 1. Approximate time line for bulls from birth through to the first direct (via daughters) cow reproduction phenotypes being available

These factors make cow reproduction traits ideal candidates for genomic selection (Meuwissen and Goddard, 1996). Genomic selection has the potential to provide more accurate breeding values shortly after birth, though this is dependent on establishing a reference population which generates the necessary quality and volume of cow reproduction phenotypes, though this is an skilled-, labour- and cost-intensive undertaking.

Generation of breeding values and selection indexes for Australian beef cattle is undertaken via the national genetic evaluation: BREEDPLAN (Graser *et al.* 2005). While there are some differences across breeds, all collect phenotypes to describe genetic differences in a range of growth, carcass and reproduction traits within the breed. In northern Australia, seven breeds are included in the BREEDPLAN evaluation (Belmont Red, Braford, Brahman, Brangus, Droughtmaster, Santa Gertrudis and Tropical Composite). The most numerous breeds are Brahman, Santa Gertrudis and Droughtmaster with 449,620, 280,596 and 232,551 animals, respectively in the national genetic evaluation (Moore *et al.* 2019a).

Cow reproduction traits for genetic evaluation

A number of female reproduction traits have been developed (Cammack *et al*. 2009) and they can be characterised by being lowly heritable and measured late in life as shown in the previous section. Most reproduction traits are defined based on key dates in the production system, such as date of birth or bull in. Female reproduction traits also tend to be biased due to culling of females that fail to calve and/or the management decisions of the herd, such as when the bull is exposed to cows for mating. The following sections outline the traits included in the Australian BREEDPLAN genetic evaluation and alternative traits definitions considered in genetic evaluations around the world.

Female reproduction traits included in BREEDPLAN

Days to Calving

A simple trait by definition, days to calving is difficult to measure in practice, especially in northern Australia. Capturing date of birth data is challenging as it requires a high level of monitoring to ensure accurate records and in northern Australia this is especially difficult when cattle are managed under extensive conditions.

Days to calving is the key descriptor of female reproduction in the BREEDPLAN evaluation for northern beef breeds. It is also included in genetic evaluations for New Zealand, South Africia and Namibia (Johnston, 2014). The trait is defined as the time from bull-in date (i.e. first exposure to the bull) to the birth of the resulting calf (Johnston and Bunter, 1996; Meyer *et al.* 1990). The trait encompasses several facets of reproduction. During this time period, a cow needs to cycle, be mated, conceive, gestate the pregnancy and give birth. The trait is recorded only for naturally mated cows and cows that fail to calve receive a penalty phenotype of the maximum days to calving within the contemporary group plus 21 days for temperate breeds or 42 days for tropical breeds (Johnston and Bunter, 1996).

In BREEDPLAN, days to calving is analysed as a repeated measure of the cow, with up to six days to calving records included in the national genetic evaluation (Graser *et al.* 2005), and has been estimated to be lowly heritable in both temperate and tropical breeds. For Angus cattle, Johnston and Bunter (1996) estimated a heritability of 0.11 and Johnston and Moore (2019) estimated a heritability of 0.09 from a Brahman dataset. Both studies demonstrated that days to calving was a genetically similar trait to calving success (calved / not calved), with cows that successfully produced a calf shown to have shorter days to calving. Johnston and Bunter (1996) estimated a correlation of -0.97 with calving success, and Johnston and Moore (2019) showed that for every one day increase in the days to calving EBV there was a 1.10 decrease in the calving percentage among Brahman sires evaluated.

There is emerging evidence that days to calving as a maiden heifer may be a different trait to days to calving from subsequent matings. Johnston and Moore (2019) estimated a genetic correlation of 0.46 between days to calving records from the first and second matings, suggesting that for

Brahman cows they are different traits. For Angus cattle however, a higher genetic correlation of 0.85 was estimated between the first and second days to calving records (Johnston and Bunter, 1996). Further investigation is required to fully understand the relationship between days to calving at first and second matings, including if they are different traits for other northern beef breeds and understanding why the relationship may vary between temperate and tropical breeds. Jeyaruban and Johnston (2017) considered days to calving in Brahman and Santa Gertrudis cattle, and found days to calving as a repeated trait to be heritable (h^2=0.08). In addition, when considered as separate traits they observed higher (but not significantly), heritability estimates of 0.13 and 0.14, respectively for days to calving at first and second mating in Santa Gertrudis.

In the same study, Jeyaruban and Johnston (2017) also showed a genetic relationship between male reproduction traits and days to calving. Cattle with genetics for shorter days to calving were also those with genetics for higher percent of normal sperm, and to a lesser degree genetics for larger scrotal circumferences. Genetic correlations in Braham ranged between -0.47 to -0.79 depending on how days to calving was modelled and between -0.18 and -0.28 for Santa Gertrudis. Johnston and Moore (2019) also found similar relationships in Brahman estimating genetic correlations of -0.66 and -0.71 between percent normal sperm and days to calving 1 and 2, respectively.

Gestation length

Gestation length is the number of days between conception and birth. However, the date of conception is only available from artificial insemination (AI) matings and there is typically low use of AI in northern beef herds. Like days to calving, knowledge of the date of calving to form the gestation length record can also be difficult. Decreasing gestation length has been shown to reduce calving difficulties and enable more cows to maintain an annual calving pattern (Chud *et al.* 2014, Jeyaruban *et al.* 2016, Paschal *et al.* 1991, Wolcott *et al.* 2015).

Breed differences for gestation length have been reported, with tropical breeds consistently having longer gestation lengths compared with temperate breeds (Corbet *et al.* 1997, Sartori and Barros, 2011). The longer gestation length of tropical breeds may be a contributing reason why tropical breeds are able to withstand, and still perform, in the harsh northern Australian environment. Gestation length for Australian temperate breeds have recently been estimated (Jeyaruban *et al.* 2016) to be highly heritable with direct heritabilities between 0.42 (0.03) and 0.52 (0.02) and maternal heritabilities between 0.03 (0.02) and 0.09 (0.01). A preliminary study considering tropical breeds in northern Australia also found gestation length to be highly heritability, with an estimate of 0.82 (0.08), inclusive of both the direct and maternal components (Moore *et al.* 2019b). There have been very few estimates of genetic parameters in tropical breeds elsewhere. Moderate positive genetic correlations have been shown with birth weight (Chud *et al.* 2014, Jeyaruban *et al.* 2016). Chud *et al.* 2014 estimated no relationship with weaning weight, suggesting that the genes contributing to the relationship between birth weight and gestation length are not the same genes that drive later growth.

Other female reproduction traits considered around the world

Calving success / heifer pregnancy

Calving success is often analysed as a binary trait based on the success or failure of a cow to calve. Other variations in this trait can be heifer pregnancy based on heifers conceiving at their maiden mating. Johnston (2014) reported United States of America, Venezuela, Brazil and France genetic evaluations to include heifer pregnancy or calving success traits. The binary nature of the trait provides a challenge for the analysis of the trait, but this can be accommodated fitting threshold models. Although increasing the percentage of cows producing a calf is the ultimate goal, the trait has a very low heritability. The heritability of heifer calving success of French Charolais has been reported to be just 0.015 (Venot *et al*. 2013). As reported in the previous section, days to calving is the preferred trait in Australia as it is more heritable compared to calving success and is also very highly correlated with calving success.

Calving interval

Calving interval is the number of days between two consecutive calving dates. It is often used when bull in dates are not available to generate the days to calving record. Calving interval encompasses many aspects; the cows ability to recover from birthing, rear the calf, continue to grow depending on her age, cycle again, have the opportunity to be re-mated, conceive, gestate the pregnancy and again give birth. A drawback of this trait is that it is only useful if mating is continuous, otherwise it is a biased trait. A cow that cycles and not provided an opportunity to mate, receives a longer calving interval. Conversely, a cow that is late to cycle and there was not the opportunity to mate ultimately receives a shorter (more favourable) calving interval due to management decisions. While managing contemporary groups may help account for non-genetic management decisions, it will not overcome the inherent bias in the trait definition. Calving interval is included as a trait in the genetic evaluations of Ireland, Denmark and United Kingdom (Johnston, 2014). The heritability for calving interval was estimated to range between 0.04 and 0.13 in a number of *bos taurus* breeds in the UK (Roughsedge *et al.* 2013), which is consistent with estimates for days to calving.

Age at first calf

A proxy for age at puberty is age at first calf, defined as the age of the cow when her first calf is born. This trait requires the date of birth of both cow and calf to be known and like most traits of this nature – derived from date of birth records – age at first calf is subject to being influenced by management decisions i.e. when the bull was introduced. It is common practise to manage the mating period to avoid heifers falling pregnant too young and thus avoid potential calving issues. However, this introduces bias to the age at first calf trait definition. A heifer that cycles before the mating period, artificially receives an older age at first calf record. Age at first calf is included as a trait in the genetic evaluations of Ireland, Brazil and United Kingdom (Johnston, 2014). Compared to the other reproduction traits mined from registration data, age at first calf tends to have higher heritability. Cammack's *et al*. (2009) review paper reported heritability estimates ranging from 0.01 to 0.27. Younger age at first calf has been shown to be associated with increased lifetime productivity (Cammack *et al*. 2009).

Stayability / Lifetime productivity

Increasing the number of calves produced by a cow in her lifetime is a key aspect of reproduction. The trait is included in the genetic evaluations of United States of America, Canada, Venezuela, France, Brazil and United Kingdom (Johnston, 2014). The trait has challenges in that there are issues with data censoring, incomplete or missing data and the phenotype is only known at the end of a cow's lifetime. Not surprisingly, this trait has a very low heritability with Roughsedge *et al.* (2013) reporting estimates ranging from 0.03 to 0.13, and Johnston *et al.* (2014a) reporting heritabilities of 0.04 to 0.16 for tropical beef breeds.

Scrotal circumference / percent normal sperm

Male reproduction traits has been shown to have genetic relationships with some female fertility traits, and are often the first information available to indicate a sires genetic merit for female reproduction. Scrotal circumference is included in a large number of country genetic evaluations; Australia, New Zealand, South Africa, Namibia, Argentina, United Kingdom, Ireland, Brazil, France, United States of America, Canada and Mexico (Johnston, 2014). Compared to many female reproduction traits, scrotal circumference is heritable with estimates ranging 0.29 to 0.78. Cammack *et al*. (2009) reported moderate negative genetic correlations with age at first calf indicating that bulls with larger scrotal circumferences were more likely to produce daughters that reach puberty earlier. Johnston and Moore (2017) estimated genetic correlations indicating that bulls with larger scrotal circumferences were more likely to produce daughters with shorter days to calving, earlier age at puberty and shorter anoestrus interval. Scrotal circumference as a measure of cow reproduction also has the benefit that it can be measured when the bull is approximately 400 days of age, and before significant selection decisions are made.

Percent normal sperm has been linked with female reproduction. Both Jeyaruban and Johnston (2017) and Johnston and Moore (2017) reported negative genetic correlations indicating that sires with higher percentage of normal sperm were more likely to produce daughters with shorter days to calving, earlier age at puberty and shorter anoestrus interval. In the same dataset, Johnston and Moore (2017) found that the strength of the correlations were approximately double for percent normal sperm and female reproduction traits, compared with those estimated between scrotal circumference and female reproduction traits.

Emerging cow reproduction measures

There have been several large research projects focusing on collecting quality phenotypes to enable genetic improvement for reproduction and other hard-to-measure traits. Reproduction data on northern beef breeds has been collected as part of the Cooperative Research Centre for Cattle and Beef Quality (CRC) (Barwick *et al*. 2009, Johnston *et al*. (2014a, 2014b)), the Repronomics^{TM} project (Johnston *et al.* 2017), the Kaiuroo Brahman herd as part of a MLA donor company project (Wolcott, 2019) and the Smart Futures funded project (Hayes *et al*. 2019). In addition to the traits (days to calving and gestation length) already recorded in BREEDPLAN, these projects explored potential novel reproduction traits including ovarian scan traits, which have been included into the suite of BREEDPLAN traits for Brahman, Santa Gertrudis and Droughtmaster.

Ovarian ultrasound scan traits

Two new traits have been defined based on ovarian ultrasound scan information and incorporated into the BREEDPLAN genetic evaluations. Using ultrasound to scan ovaries can identify the presence of a *corpus luteum*, and regular scanning can determine age at puberty and lactation anoestrus interval.

Age at puberty has been shown to be an important aspect of reproduction (Cammack *et al*. 2009) but has been difficult to measure accurately. With ovarian scans taken every four to six weeks, an accurate age that heifers become pubertal can be obtained based on the first observed *corpus luteum*. The first Australian study considering ovarian scanned cattle was the beef CRC, where Johnston *et al.* (2009) considered age at puberty for Brahman and Tropical Composite heifers. They found age at puberty to be highly heritable in both breeds with estimates of 0.57 (0.12) and 0.52 (0.12), respectively. Johnston *et al.* (2014b) extended the research further and highlighted that cows with genetics for early puberty were also the cows with genetics for higher conception, pregnancy, calving and weaning rates and lower days to calving. In Brahman the genetic correlation between age at puberty and days to calving from the first mating was 0.79 (0.14) but only 0.08 (0.27) for days to calving from the second mating. This was different for Tropical Composite cows where genetic correlations of 0.10 (0.27) and 0.43 (0.26) were estimated between age at puberty and days to calving from the first and second matings, respectively. An extensive five-year Repronomics^{TM} project recorded age at puberty for Brahman, Santa Gertrudis and Droughtmaster (Johnston *et al*. 2017) and from an across breeds dataset estimated a heritability of 0.53 (0.07) for age at puberty (Johnston *et al.* 2019). Johnston and Moore (2019) showed a strong positive correlation between age at puberty and days to calving at both the first and second mating with genetic correlations of 0.62 (0.14) and 0.56 (0.14), respectively. Wolcott (2019) in a separate Brahman population also estimated similar heritability for age at puberty (0.56 (0.13)). Age at puberty from ovarian scans is a phenotype that accurately measures a key aspect of female reproduction. However, it does also require repeat scanning of cattle that may not always be possible. Corbet *et al*. (2018) proposed *corpus luteum* score as an alternative measurement for puberty based on a single ovarian scan when animals were on average 600 days of age. *Corpus luteum* score was recorded as a binary trait depending on if a *corpus luteum* was present or not in the scan. Hayes *et al*. (2019) estimated the heritability for *corpus luteum* score in a population of Brahman, Droughtmaster and Santa Gertrudis heifers. The estimated heritability of *corpus luteum* score was 0.24, which was much lower than the age at puberty ovarian scan trait and similar to the age at first calf trait traditionally used as a proxy for age at puberty. The high heritability of ovarian scanned age at puberty provides the beef industry with an excellent trait that has the potential for significant genetic improvement to reduce the age at puberty and days to calving.

Anoestrus interval captures the period post calving until the cow recommences cycling. This is the post partum anoestrus interval, however, animals are not ovarian scanned while they have young calves. Instead Lactation anoestrus interval is the number of days from the commencement of mating until the first *corpus luteum* is identified by ovarian ultrasound scanning in lactating 1st calf cows. Lactation anoestrus interval has been estimated to be heritable, but the size of estimates varied across different datasets. From the beef CRC data, Johnston *et al.* (2014a) estimated heritabilities of 0.51 (0.18) and 0.26 (0.11), respectively for Brahman and Tropical Composite. They estimated that lactation anoestrus interval and days to calving were effectively the same trait, but with lactation anoestrus interval having a much higher heritability compared to days to calving. In an industry Brahman herd, Kaiuroo, estimated lactation anoestrus interval had a heritability estimate of 0.39 (0.27) (Wolcott 2019). The multi-breed Repronomics™ project estimated from an across breed dataset a lower heritability, 0.22 (0.07), compared to the other studies (Johnston *et al.* 2019). Johnston and Moore (2019) considered Brahman animals from the Repronomics™ project and estimated a heritability of 0.40 (0.07). These estimates suggest that perhaps lactation anoestrus interval was more heritable in Brahman compared with other tropical breeds that contained at least some *bos taurus* ancestry. They also showed that lactation anoestrus interval and days to calving at second mating were genetically the same. This was not the case for days to calving from the first mating where a strong correlation of 0.52 (0.19) was estimated with lactation anoestrus interval. Johnston *et al.* (2014a) found strong negative genetic correlations with lactation anoestrus interval and lifetime weaning rate with cows weaning more calves in her life also having genetics for shorter lactation anoestrus interval.

Inclusion into genetic evaluation - Both age at puberty and lactation anoestrus interval capture different aspects of reproductive performance, but are themselves moderately positively correlated. Johnston and Moore (2019) estimating a genetic correlation of 0.29 (0.12) and Johnston *et al.* (2014b) estimated a genetic correlation of 0.31 (0.18) between the two ovarian scan traits. Wolcott (2019) found a higher correlation of 0.62 (0.36) from the Kaiuroo Brahman population.

Both age at puberty and lactation anoestrus interval have been shown to be highly heritable (for female reproduction traits) and provide Australia's northern beef industry with excellent new traits for genetic improvement. The ovarian scan traits show that where key components of reproduction can be accurately measured, the heritability of reproduction traits can be at least as high as those observed for growth and carcase traits and this can help improve genetic response for cow reproduction if selection decisions are made on the basis of those measurements. However, these accurate ovarian scan measurements are hard to measure and not feasible (lack of skilled technicians and the need for multiple scans) for large-scale regular collection in the beef industry. Even if there were skilled technicians available, it would still be an expensive and time-consuming trait to record. However, genomic selection would be an ideal technology to enable wide spread selection for these key fertility traits.

Genomic reference population - An excellent reference population has been developed using records from Repronomics™, Beef CRC and Kaiuroo datasets and this means that the wider industry can use genomic selection to select for age at puberty and lactation anoestrus interval. The use of the new traits via genomic selection provides for the first time tools that can make genetic improvement for cow reproduction at rates of gain akin to what we see for growth and carcase traits. The proviso is that the reference population needs to be maintained with projects like Repronomics™. Although incorporated into BREEDPLAN, separate EBVs for ovarian scan traits are not published. Instead, ovarian scan traits contribute information as correlated traits to days to calving, which is the key breeding objective for reproduction in northern beef. Moore *et al.* (2019a) showed that the three breeds in Repronomics™ had very different performance recording structures and record availability, but all benefited from the additional information provided by ovarian scans and single-step genomic selection. Brahman was the largest population and was already both well recorded and genotyped, the addition of Repronomics™ data and single-step genomic selection increased the average days to calving EBV accuracy of young animals by 14.7%. Santa Gertrudis and Droughtmaster were similar in size and both had limited data already recorded. Santa Gertrudis already has a small number of strategic genotypes while Droughtmaster were not previously genotyped. The addition of Repronomics™ data and single-step genomic selection have increased the average days to calving EBV accuracy of young animals by 6.0 and 6.2%, respectively for Droughtmaster and Santa Gertrudis genetic evaluations.

Emerging technology

Ovarian scans are an emerging technology that has already been successfully utilised to improve female reproduction in northern Australia. Other technologies may provide further opportunities to improve female reproduction. Individual behaviour, mating and calving outcomes and calf survival may all be possible with emerging technology. These technologies may include remote sensing, satellite tracking, pedometers, location loggers, electronic mount detectors for oestrus activity, body temperature or hormone assays.

Conclusion

Genetic improvement for female reproduction has traditionally been limited due to traits being hard to define and lowly heritable. The key reproduction trait for Australian northern beef cattle is days to calving that is highly correlated to calving success. Two new ovarian scan traits, coupled with genomic selection provide an exciting opportunity to the northern beef industry to make significant genetic improvement for female reproduction.

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