Breeding Focus 2021 - Improving Reproduction

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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

The influence of bull fertility on beef herd productivity

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Abstract

Reproductive performance of beef breeding herds is the most critical aspect of livestock systems as it constrains the productivity of the entire supply chain worldwide. If reproductive performance is low, productivity is impaired, and the system is less sustainable. Reproductive performance is complex and requires contributions from both male and female fertility. Compounding this dichotomy, underlying fertility traits are polygenic in nature and multifactorial. Female fertility has received focussed attention for several years resulting in improved management strategies, biotechnologies for its physiological control, and genomic selection approaches that target fertility indicator traits. Although improvements are still possible, great advances have been achieved in recent years. On the other hand, bull fertility has received relatively little attention. This could be partly because most bulls have some degree of fertility, management strategies are often put in place to overcome the detrimental effects of subfertility, or subfertility (or infertility) is often simply unknown. We would argue that male fertility is largely unexplored in the context of sustainable intensification of animal production and plays a major role.

The relevance of bull fertility in beef production systems

The majority of beef-producing enterprises worldwide use natural mating in their breeding herds. The key objective of such herds is to generate calves that will supply livestock to the whole system. Natural mating is especially important in countries where the adoption of reproductive biotechnologies (e.g. artificial insemination) is restricted either by geographic dispersion compounded with frequent droughts, limiting breeder nutrition, limited access to technology (low-tech countries), or other issues (e.g. perceived high cost for implementation). Herd fertility as a whole plays a preeminent role in low input production systems, which is the case for a large proportion of the Australian beef industry.

The reproductive performance is a crucial productivity metric for the whole herd and is impacted by maternal and paternal attributes. Female fertility has received focused attention in recent years, leading to a greater understanding of female reproductive physiology, the development of biotechnologies for manipulating the estral cycle, and the early stages of genomic selection approaches for genetic improvement (Baruselli *et al.* 2018; D'Occhio *et al.* 2019; Engle *et al.* 2019; Hayes *et al.* 2019). Combined, these strategies have boosted female productivity. On the other hand, the use of male fertility indicators is still lagging behind. The vast majority of working herd bulls in Australia do not go through a formal assessment that considers structural soundness, libido, semen quality, and its genetic potential. Genetic selection for bull fertility is typically limited to one trait only: scrotal circumference. It is well-known that a sire's influence in a breeding herd is much bigger than that of any cow in natural mating systems. On average, one bull each year will serve 25 females, ranging from 20-50 depending on the property (Holroyd *et al.* 2005). Considering five years of working life for a bull and a pregnancy rate of 70%, a single bull will generate around 87 calves in his lifetime, while a good cow will deliver 6-8 calves in total. A bull's influence in a breeding herd is more than ten times bigger than that of a breeding female. Moreover, if male reproductive biotechnologies (e.g. artificial insemination) are used, the bull influence can be even greater.

In a sustainable intensification context for animal production, all actions that can be implemented should be considered (Eisler *et al.* 2014). From selecting breeds adapted to a local environment, better nutrition, health, and management, collectively have an incremental contribution. In this framework, the knowledge that bull fertility plays an essential role in beef production due to its direct and indirect effects opens a "new" opportunity for positive intervention and should not be neglected.

The complexity of male fertility traits

Sexual development and spermatogenesis

Puberty and spermatogenesis are closely linked and finely regulated physiological processes. Although the very first trigger for the onset of puberty is still unknown, its hormonal control is well studied: the hypothalamus – hypophysis – gonad hormonal axis orchestrates these processes.

Puberty is the age at which an animal becomes capable of generating offspring. This broad definition goes beyond the production of sperm cells to also include the development of body condition and sexual behavior needed for mating. For simplicity, puberty in bulls is often defined as the age a bull ejaculates 50 x 10^6 spermatozoa with at least 10% progressive motility (Lunstra *et al.* 1978). Other indicators can also be useful when estimating age at puberty, e.g. in *Bos indicus* cattle, the age in which a bull reaches a scrotal circumference (SC) of 26 cm

(Fortes *et al.* 2012), and some hormonal levels are also correlated with age at puberty such as Inhibin 4 and IGF-1 (Kaneko *et al.* 2001; Burns *et al.* 2013). The age at which animals attain reproductive capacity varies within and across breeds (or populations). This is evident when Tropical Composites are compared to Brahman bulls, using SC and IGF-1 measurements (Figure 1). Brahman are mostly *Bos indicus* cattle, while Tropical Composites have mixed ancestry (Porto-Neto *et al.* 2014).

It is worth noting that age at puberty in males has a genetic component. Several studies have highlighted major differences between *Bos taurus* and *Bos indicus* cattle, with the latter being, in general, late-maturing when compared to European cattle (Lunstra *et al.* 1978; Lunstra and Cundiff 2003b; Corbet *et al.* 2013). In addition to the genetic background, nutrition and health status also have major influences on cattle's sexual development. The rearing environment of young animals directly affects the age at puberty and may have long-lasting effects on lifetime fertility, as seen in bovine females (Wathes *et al.* 2014). After puberty, spermatogenesis, or the process in which stem germ cells differentiate to generate male gametes (sperm) starts.

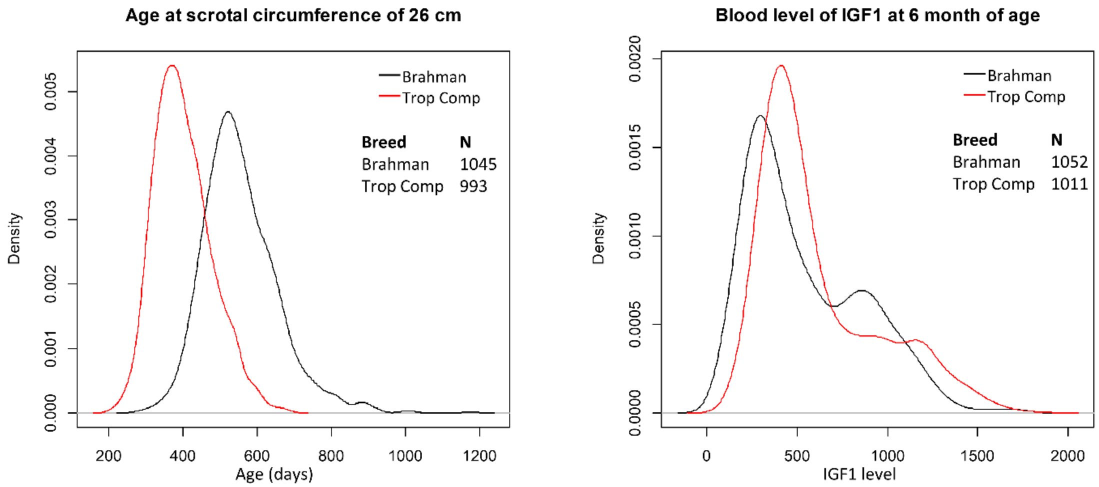

Figure 1. Frequency distribution of two bull fertility indicator traits in Brahman and Tropical Composite cattle exemplifying the variability within and across breeds (data from the CRC for Beef Genetic Technologies)

At the onset of puberty, pulsatile GnRH released by the hypothalamus stimulates the secretion of luteinizing hormone (LH) and follicle-stimulating hormone (FSH) by the anterior hypophysis. In males, these two hormones act at the testicular level on specific cell types to support spermatogenesis, FSH acts on Sertoli cells, which are in close contact with stem germ cells, and LH promotes the production of testosterone by the interstitial Leydig cells (Gadea *et al.* 2013). There are other cell types and hormones involved in spermatogenesis, but these are the key ones.

Spermatogenesis is a process that takes around 61 days in bulls and occurs within seminiferous tubes of the testis (recently reviewed by Staub and Johnson 2018). Briefly, there are three steps from a stem germ cell to a mature sperm: 1) spermatocytogenesis, mitotic division that increases the yield of spermatogenesis by producing stem cells and primary spermatocytes, 2) meiosis, 3) spermiogenesis. Spermiogenesis is one of the best examples in nature of cellular differentiation without division, which creates a sophisticated self-propelling cell: the sperm. Sperm cells coming from seminiferous tubes mature during their migration through the epididymis, then they are combined with the secretions of the auxiliary glands to form the ejaculate. Not surprisingly, external disturbances (e.g. high temperature and humidity) can negatively affect this complex and finely regulated process (for recent reviews, see Boe-Hansen *et al.* 2020; Morrell 2020). External disturbances are more often than not temporary, as is their effects on sperm quality. However, it is worth noting that other issues, such as some infectious diaseases and injury can lead to more permanent detrimental effects. Any disturbance during the whole spermatogenesis process can compromise male fertility.

Bull fertility indicators

The most reliable fertility assessment of a bull is the pregnancy rate, in a defined period, of the mated cow herd. This assessment is not available in most situations due to many factors, mostly associated with logistical problems and parent verification costs. The pregnancy rate of specific bulls is valuable management information; if available, it can distinguish bulls that are sub-fertile relative to those most prolific. The downside is that the bull needs to be used in at least one breeding season. Therefore, this assessment is never available when purchasing young animals.

The bull breeding soundness evaluation (BBSE) was developed to provide an assessment of fertility that could be used prior to the first mating season. To reduce variation in the methodology utilized for bull assessment, the Australian Association of Cattle Veterinarians supported the definition of standards (Entwistle and Fordyce 2003). This assessment is based on structural soundness and fertility indicators associated with the whole of life fertility (Fordyce *et al.* 2006). There are three main components to the BBSE: 1) the physical assessment of an animal considering attributes that support locomotion and the physical integrity of the reproductive tract; 2) microscopic evaluation of a semen sample by the crush-side (e.g. motility and vigor of sperm cells), and 3) microscopic evaluation of a semen sample in the laboratory for assessment and estimation of the number of normal and abnormal sperm cells in the ejaculate. Mating behavior is another essential component of the BBSE but is currently infrequently used in northern Australia. To assist the industry in interpreting BBSE, upper and lower threshold limits for each trait were defined to qualify animals that pass and fail the BBSE (Fordyce *et al.* 2006).

The BBSE provides information that can be used in different ways, depending on the age at the assessment and the objective of the evaluation. When performed at around 600 days of age, prior to sale of the young bulls getting ready for their first mating season, the BBSE can be seen as a "fertility certificate" for the young sire. It is a good evaluation of his ability to produce good quality semen, and certify that he has a sound body conformation. Since most animals have already reached sexual maturity at this age, the phenotypic variation is still observed but reduced. Suppose the breeder's objective is to shift the herd's puberty to a younger age. In that case, the BBSE should be performed at a much younger age, challenging the animals and creating a bigger phenotypic spread, which will be more beneficial for the genetic improvement than a later assessment. The flexibility of interpretation and practicality of the evaluation makes the BBSE a good assessment for bulls.

Genetic parameters of bull fertility indicators in different breeds

Most fertility indicators observed during the BBSE have moderate to high heritabilities (recently reviewed by Butler *et al.* 2020). Although variation exists in the estimated heritability across breeds and populations, the variation seems to be smaller for traits that are measured objectively, e.g. scrotal circumference (0.36 – 0.56), the volume of the ejaculate (0.04 – 0.65), and sperm motility (0.05 – 0.43) (Butler *et al.* 2020). In tropical cattle, there is considerable variation in the age of attainment of puberty, which is partly reflected in the estimates of heritability for SC and the percentage of normal sperm that vary by the age of measurement (Corbet *et al.* 2013). In general, the observation of these traits made in younger animals resulted in higher heritability estimates, possibly hinting at a more effective selection response based on early observations.

Another relevant attribute regarding bull fertility is their genetic correlation to other production-related traits. Corbet et al. (2013) found high correlations between several semen traits (e.g. SC vs. mass and motility measured at 18 months of age, with correlations of 0.82 and 0.79). Interestingly, body weight and hip height at 15 months of age were not significantly correlated to the percentage of normal sperm, in contrast to the body condition score and the depth of fat cover on the ribs at the same age. This demonstrates that energy balance and its reserves play a role in the development of an animals' maturity. Due to its practicality for measurement, one of the most recorded bull fertility indicators is SC, which is favorably correlated to the age at puberty and body weight. Nonetheless, its correlation to the percentage of normal sperm, body condition score, and depth of fat cover is lower than 1, demonstrating the value in measuring complementary characteristics to build a fertility-related profile for each animal.

Quantitative trait loci (QTL) and genetic variants associated with bull fertility traits

Given their complexity, it is no surprise that bull fertility traits are polygenic. Casas's early studies (Casas *et al.* 2004) and McClure (2010) described many QTLs in multiple chromosomes for SC, testicular weight, and volume. Since then, many QTLs and genome-wide association studies have reported genomic regions relevant to a growing number of bull fertility traits (Fortes *et al.* 2013; Taylor *et al.* 2018). Still, many QTLs and genetic variants seem to be breed or population-specific (Fortes *et al.* 2020) and not confirmed in subsequent studies. Nonetheless, recent studies were able to pinpoint some functional mutations affecting male fertility (Iso-Touru *et al.* 2019; Hiltpold *et al.* 2020), which are still to be confirmed if these are segregating and relevant in other populations. There is still much we do not know about the molecular genetics of bull fertility traits. The speculated role of several positional candidate genes deserves further investigation to better understand the biological processes involved and possibly lead to more precise animal selection.

One thing is certain: The X chromosome plays an important role in male fertility. More than 95% of the 3,776 QTLs listed in the *Cattle QTLdb* for semen quality traits, such as the percentage of normal sperm or sperm motility, are located on the X chromosome (https://www.animalgenome.org). Many X-linked genes are germ cell-specific and known for their conserved role in spermatogenesis in mice and humans (Zheng *et al.* 2010). A recent genome-wide association study suggested some of the same X-linked genes are associated with sperm morphological abnormalities in *Bos indicus* and Composite cattle (Fortes *et al.* 2020).

Recent and ongoing improvement of the bovine reference genome, including its functional annotation, can lead to new fertility indicators and biomarkers. The functional annotation of animal genomes, or FAANG project (Tuggle *et al.* 2016), gathers data on RNA expression, DNA methylation, and many other aspects of chromatin structure (Giuffra *et al.* 2019). Datasets on bovine testicular gene expression are also available and can be mined to understand spermatogenesis better (see GEO records: GSE106496, GSE106497, GSE106498). Fully annotated genomes will lead to a better understanding of associated genetic variants that are not related to protein-coding genes.

The economic impact of bull fertility

The impact of using a low fertility bull in a breeding herd extends further than the direct consequence of low pregnancy rates. On top of this direct effect, which is already relevant, we should remember that any new bull increases purchase and maintenance costs. Additionally, the use of a low fertility bull represents a loss of opportunity to improve herd fertility via the increased age of puberty of daughters, extended daughter’s postpartum anoestrus interval, and the reduced selection of improved replacement heifers. There is also an associated cost with running unproductive females. In this section, we will discuss some key drivers of the economic impact related to the fertility of bulls.

The age at puberty

Puberty marks the beginning of a bull’s working life. When it starts early, the generation interval is reduced, and overall herd productivity improves (Fortes et al., 2012). Early puberty in bulls is positively correlated to early puberty in their female offspring, which also impacts pregnancy rates at a fixed age (Moser *et al.* 1996; Fortes *et al.* 2012). Selection for decreased age at puberty must not automatically imply that heifers will be mated younger. It is beneficial if heifers can ‘cycle’ younger and be ready to conceive as soon as mating is planned. They are thereby assisting in a shorter mating period leading to shorter inter calving intervals with reduced calving spreads and tighter weaning groups, thus improving the herds' overall management and efficiency.

There is a sizeable phenotypic variation in age at puberty among cattle breeds. In particular, taurine (*Bos taurus*) breeds are early pubertal compared to zebu (*Bos indicus*) breeds, which present slower testicular development and later sexual maturity (Chase *et al.* 2001; Lunstra and Cundiff 2003a). Pubertal development and sexual maturity have been defined in bulls by measuring certain traits, such as reaching an SC threshold or producing semen of sufficient quality (Brito *et al.* 2004). For example, in a Brahman population, age at puberty was defined as the age when bulls achieved a SC of 26 cm (Fortes et al., 2012). Variation in terms of age at puberty has a genetic component and varies across and within breeds. The heritability for the age at puberty, reported between 0.20 and 0.67 across breeds, indicates that this trait can be improved through genetic selection (Fortes *et al.* 2020).

A few studies have recently investigated the molecular basis of genetic variance in fertility-related traits. Some identified functional mutations affecting specific conditions or production traits (Iso-Touru *et al.* 2019; Fortes *et al.* 2020; Hiltpold *et al.* 2020; Stafuzza *et al.* 2020). In the future, these variations could be incorporated into a blended genomic selection – marker-assisted selection strategy for improving herd fertility.

The ability to impregnate cows

It is easy to argue that a bull's ability to impregnate cows is the single most important trait for a bull in a beef production system, which all other genetic improvements depend upon. However, the conception rate for a given bull is rarely observed, especially in multi-sire mating systems in extensive commercial production systems (e.g. Northern Australia). Consequently, it is not part of the herd management strategy and cannot be part of a genetic improvement plan.

There are many possible reasons for a cow not getting pregnant, and bull fertility is one. The use of fertility indicators, for example, the BBSE, is a fair attempt to alleviate this problem The BullPower studies (Holroyd *et al.* 2005) investigated premating bull fertility measures in multiple sire matings across northern Australia. They identified the relative impact of structural traits relative to mating behavior and testicular and semen traits. Despite the progress in calf output from earlier studies, examining a wide range of fertility measures only accounted for 35 to 57% of calf output variation. These clearly defined traits are moderate to highly heritable (Corbet *et al.* 2013), and, for example, the percentage of normal sperm (<50% vs >70%) had been associated with calf output in a multi-breed, multi-sire evaluation in Northern Australia (Fitzpatrick *et al.* 2002). Nonetheless, the *in vitro* assessment of semen has its limitations: a semen sample with a "pass" in its assessment may not always directly correlate to pregnancy rate in the field, demonstrating the complexity of fertility traits (Fair and Lonergan 2018).

The use of fixed-time artificial insemination has skyrocketed in some of the world's major beef producing regions, with an estimated application on around 16 million cattle in Brazil only (Prof Pietro Baruselli, personal communication). The uptake of this biotechnology allowed international semen companies to start collecting observational conception rates in a large number of dairy and, more recently, beef cows (e.g. Concept Plus, Alta Genetics, https://english.altagenetics.com/dairy/concept-plus-2/ , accessed on 29/10/2020). The application of controlled protocols has generated some of the most reliable fertility indicators to date. For instance, comparing two bulls of the same breed with at least 500 fixed-time inseminations in at least five different properties, their conception rates can vary by more than 20%. This statistically supported difference in conception rate became an important tool for selecting sires for large-scale artificial insemination programs. Nonetheless, despite the value of the observation, little knowledge about its underlying biology opens an opportunity for future studies.

The use of DNA-based predictions of the bulls' conception rates can also be considered to rank bulls for selection and inform management decisions. A cost-effective approach has been developed that allows the use of molecular technology without the need for individual DNA profiling of all animals (Reverter *et al.* 2016; Alexandre *et al.* 2019; Alexandre *et al.* 2020). The method uses an industry-oriented trait, the pregnancy outcome after the mating season, and DNA samples of bulls and cows. The bulls are genotyped individually, while cows have their DNA pooled within the pregnancy outcome result before proceeding for genotyping, resulting in considerable savings on genotyping costs. Using this dataset comprised of individual and pooled genotypes and the trait observations, we can estimate the breeding values for each individual sire. Additionally, this customized dataset can be used to rank candidate sires by their estimated genetic merit for pregnancy outcome before purchase.

"Value-adding" to selection for male fertility: the correlated effect on female fertility

In biology, different physiological processes often share genetic features. These commonalities are translated into phenotypic and genetic correlations between traits. For instance, the age at puberty in Brahman cows is correlated to pregnancy outcome at the first mating (-0.71) and lifetime calving rate (-0.40) (Johnston *et al.* 2014). Genetic correlations between production traits of sufficient strength (very high or very low) have a significant correlated effect on each other. They can be found among female or male traits and across both sexes.

Several male fertility-related traits are correlated to female fertility-related traits. In pedigree-based analyses, the blood concentration of IGF-I measured at 6 months of age in bulls was correlated to the age at puberty in Brahman (-0.56) and Tropical Composite (-0.43) cows (Johnston *et al.* 2014). With the advent of genomic technologies, the analyses were no longer limited to pedigree links. Using a genomic approach, Raidan et al. (2019) estimated the correlations between the percentage of normal sperm at 24 months of age with age at puberty (-0.54) and the length of the postpartum anoestrus at first calving (-0.66) in Brahmans. Both studies confirmed the usefulness of favorable correlations between male and female fertility indicators.

Biological processes supporting these genetic correlations are dynamic. The age at which fertility indicators are observed impacts the correlation's magnitude, such as in an Angus herd, this female trait was more strongly correlated to the scrotal circumference measured at 300 days of age than to 400 or 630 days of age (-0.48, -0.24 and -0.15, respectively) (Bonamy *et al.* 2018). A similar trend was also observed in Brahman cattle for age at puberty and scrotal circumference at 12 (-0.41) and 6 months (-0.30) of age (Johnston *et al.* 2014). These differences could be partly explained by the shared biological process between male and female attainment of puberty, which in the Angus breed is closer to 300 days of age, while in Brahman cattle, it starts at 365 days. It is worth noting that within tropically adapted breeds, the correlations are stronger between age at puberty and the percent of normal spermatozoa at different ages. This observation is not surprising given the lower selection pressure, later age of mating, and generally extended mating periods associated with Brahman cattle in Northern Australia.

Several correlated across-sex fertility indicators have the potential to be explored in breeding selection to improve whole-herd reproductive performance. Not to consider these correlated responses represents an opportunity lost.

The additional benefit of reproductive biotechnologies

Reproductive biotechnologies such as artificial insemination (AI) and fixed-time artificial insemination (FTAI) aim at herd improvement via the uniformity of the herd, ease of management, and the optimization of bull selection. The concept is based on the specific selection of males and their multiplication across herds.

Potentially, with greater adoption, the importance of live breeding bulls is diminished, albeit the geographic dispersion of cattle and the extensive nature of the industry coupled with the frequency of droughts continue to pose a limitation to the broader utilization of these biotechnologies. In the more intensive areas, the number of bulls on a property can be reduced to lower purchase and maintenance costs. This will result in the additional benefit derived from better bulls and easier management due to the reduced calving period. However, several points need to be considered for the implementation of AI or FTAI programs, as not all breeders will benefit from it. Suppose just considering applying the technology on a property is overwhelming (due to the perceived high cost and management barriers), for instance, on large properties across Northern Australia. In that case, an alternative is its application on a smaller herd to allow the introduction or improvement of specific traits in a sub-herd that could later provide bulls to a larger herd. The application of such biotechnologies will not be feasible in all beef production systems, but these should be considered and discussed due to their potentially higher impact.

Final remarks

Bull fertility indicators, as per the Bull Breeding Soundness Evaluation (BBSE), are related to calf output (Holroyd *et al.* 2005).

Traits observed during the BBSE are, in general, moderate to highly heritable. However, variation exists between cattle breeds, populations, and recording age.

The assessment of young bulls between 12-24 months of age is strongly recommended as it enables the informed selection of replacement breeding males.

Early maturing bulls can drive financial benefit. A bull that reaches puberty earlier in life might have one more year of service in its lifetime compared to a late-maturing bull. Even if the management (mating season) does not favor the joining of early maturing bulls, and all bulls are mated at the same time, it is expected that the early maturing bull will be more advanced in his testis development, being more "ready" for service.

The selection for early maturing bulls positively affects the whole herd due to its correlated gain on female fertility. Some bull fertility indicators are favorably genetically correlated to female fertility indicators, including age at puberty.

After the first selection, following the early assessment of bulls, later in life fertility traits are paramount. For instance, calf output and sire prolificacy in multiple sire mating systems using bulls of similar age, are two of the best traits that can be recorded. These traits "capture" the full performance of a bull, being influenced by the structure of the animal, semen quality, libido, etc. However, these traits are often not recorded, mainly due to recording costs.

The mating behavior test that is part of the BBSE has, to date, had limited adoption. This can be partly explained by time constraints for its application and concerns by some community sectors on its interpretation due to variations on its protocol. The development of a genomic test either in isolation or association with a limited mating behavior test would be extremely beneficial, given the association between mating behavior and calf output (Bertram *et al.* 2002). Advanced genomics might play a role in this area in the future.

There seems to be no gene of major effect affecting fertility traits in males and females. Therefore, to improve these traits, the best approach may be via genomic selection strategies.

There is a large discrepancy between the number of herd bulls needed every year to replace old sires or to mate with first-joining heifers and the number of bulls that are formally part of any selection program for genetic improvement. The relatively small uptake of genetic evaluation by beef producers, particularly in Northern Australia, including fertility and other production-related traits, hinders the national herd's genetic improvement.

In addition to genomic technologies, there is an ongoing need to improve the observation of traits (fertility and others) and the uptake of genetic evaluation. Increased use of computerized recording hardware for use in cattle yards has aided producers in capturing some herd performance data and a greater awareness of the difference in herd performance across regions of the country and breed type. The development of strategies for the utilization of commercial data in genetic evaluations and, possibly, the establishment of regional-focused programs might assist a change in the right direction within this area.

Given the large divergence in fertility rates across various land systems across Northern Australia (McGowan *et al.* 2014, Cash Cow report) there is an urgent need to dramatically raise fertility rates on many properties to achieve long-term financial viability. Male and female fertility are key drivers of profitability, playing a major role in beef-producing enterprises' economic and environmental sustainability. An integrated approach that combines improvements in nutrition, disease control (including reproductive illness), management, and herd fertility is needed to lift on-farm productivity.

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