Bull Fertility

Introduction

Predicted transmitting ability (pta) figures associated with a bull are for his female offspring (including fertility index) and do not relate to the ability of a bull to get a cow in calf. Observations within the CAFRE Greenmount Dairy Herd indicate that there are considerable differences in different bull's abilities to result in a pregnancy. Unfortunately, data on bull fertility is not available to farmers (at least in the UK) to aid bull selection based on this trait.

Setting the scene

Fertility traits are arguably good examples of complex phenotypes—traits that are influenced simultaneously by a large number of small effect genes and environmental factors. They are undoubtedly complex traits of great economic importance to the dairy industry. Although genomic prediction for improved cow fertility has received much attention, bull fertility has largely been ignored. Abdollahi-Arpanahi, (R. *et al.,* 2017).

Bull fertility, defined as the ability of the spermatozoon to fertilise and activate the ovum and then support embryonic and foetal development, is a crucial factor influencing animal reproduction and production efficiency. Despite significant influences of fertility on herd genetic improvement and efficient cattle production, the mechanisms regulating this phenotype and reliable biomarkers associated with bull fertility are poorly defined, (Parisi, M. *et. al.,* 2014).

Establishment of pregnancy in cattle is complex and encompasses ovulation, fertilization, blastocyst formation and growth into an elongated conceptus, pregnancy recognition signalling and development of the embryo and placenta. There is strong evidence that service sire fertility plays an important role in these development processes, (Ortega, M. 2018). Much less emphasis has being placed on male fertility and as a consequence, the influence of the bull on herd fertility in both dairy and beef herds has been somewhat overlooked.

Male and female fertility are positively correlated, but the correlation is low and genetic predictions for fertility are currently only produced for females, (Taylor, J. *et. al.,* 2018). The UK 'predicted transmitting ability' figures generated for bulls are in relation to the female offspring and have no connection with the ability of the bull to fertilise an egg in utero and produce offspring.

The ability to predict a bull's fertility before semen is released into the field has been a long-term objective of the animal breeding industry. Despite animal breeding centres employing stringent pre- and post-thawed quality control checks, significant variation still exists in bull field fertility. Furthermore, while routine laboratory tests assess sperm function in terms of motility and morphology, they do not differentiate between sperm transport through the female reproductive tract, sperm fertilizing ability or the ability to sustain early embryo development, (O'Callaghan, E. *et al.,* 2020).

Relevant links between bull fertility and reproductive success have been observed, not only in the fertilization process through differences in semen quality, but also in embryo preimplantation and development, as well as in offspring performance in later life. Moreover, there is recent evidence that embryos from bulls with lower fertility have a reduced ability to establish pregnancy and this depends on several factors, such as sperm fertilizing ability, pre-implantation embryonic development and development of the embryo and placenta after conceptus elongation and pregnancy recognition. Studies have highlighted the importance of understanding genetic contributions of the sire to

pregnancy establishment that is crucial to increase reproductive efficiency in dairy cattle, (Ortega, M. *et. al.,* 2018).

Although fertilization success is typically high, (>85%), following artificial insemination (AI) in cattle, many of the resulting embryos fail to develop to term. A significant proportion of this loss occurs between fertilization and maternal recognition of pregnancy, (Fair, S. *et al.,* 2018).

Evaluations for male fertility are usually undertaken within breeding companies. Because the methodology used by different breeding companies may not always be similar and results are not often made publicly available, the end user, the farmer, is unable to consider male fertility when making breeding decisions and the methodology used to rank bulls on male fertility may be sub-optimal, not accounting for confounding factors effects, such as herd and cow-specific factors, including the genetic merit of the animal and the level of inbreeding, (Berry, D. *et. al.,* 2011).

The intensive use and high rate of AI sire turnover leaves insufficient time to adequately assess the fertility status of a bull before wide-scale use of his semen in the field, (Fair, S. *et al.,* 2018).

General aspects of fertility

Bull fertility is an economically important trait and is defined as the ability of the sperm to fertilize and activate the egg, and to sustain embryo development which is crucial for efficient reproduction of cattle. Fertility is a complex trait with numerous determinants including molecular genetics, epigenetics, cellular and physiological aspects of sperm. Traditional semen evaluation techniques include analyses of sperm motility, membrane integrity and morphology to estimate bull fertility. However, they are both tedious and unreliable. As such, fertility differences among males cannot be accurately determined by these conventional methods. Identification of molecular, cellular and physiological biomarkers associated with fertilizing ability is vital for evaluation of semen quality and prediction of bull fertility.

In the full cycle of reproduction, endpoints that can be clearly identified are: gamete formation, fertilization, pre-implantation embryo and post-implantation foetal development, birth of normal young, and growth to sexual maturity. Often one is measuring one trait to estimate another, such as sperm motility, that has some value as a correlate of fertility, (Foote, R. 2002).

Measurements of testis size and consistency are highly repeatable, ($R^2 > 0.90$). Total sperm output is highly correlated with testicular circumference, ($r = 0.81$) and firmness of the testes with fertility in bulls, ($R^2 = 0.67$). Testis size also is highly inherited in bulls. Several seminal plasma proteins have been reported to be associated with fertility differences in bulls. This could lead to a genetic marker for bull fertility being developed, (Foote, R. 2002).

Fertility differences between bulls may be obscured if there are enough normal sperm, unless defective sperm somehow inhibit normal ones. The many complicating factors influencing fertility indicate that multiple characteristics need to be estimated with precision, so that multiple regression equations can be developed to estimate the relative fertility of a semen sample more accurately. The absolute degree of fertility achieved in practice will depend upon the fertility of females involved and a host of contemporary environmental factors, (Foote, R. 2002).

Prediction of fertilizing ability of bulls is still largely a mystery, owing to the fact that abnormal sperm coexist along with normal sperm cells, (Parisi, M. *et. el.,* 2014). Bull fertility is often assessed as the return or non-return to service after artificial insemination and/or pregnancy diagnosis. The end point is often day 56, but this outcome can be influenced by animals culled in the interim, use of natural service and/or an insemination by a different organisation/person and not recorded by the semen

supply company. Adjusted sire conception rate models account for environmental factors; (herd, technician, month of insemination, age of cow, cow genotype, days in milk, milk production, level of inbreeding in sire and dam, etc,) and express a bull's fertility relative to a population mean of 0% for all bulls under investigation, (Fair, S. *et al.,* 2018).

Bull fertility can only be accurately determined under conditions where sperm numbers are limiting. It is not surprising that there is difficulty in identifying the causes of bull subfertility when a dubious fertility phenotype is used at the start. Ideally, the number of sperm at which a bull's fertility reaches a plateau should be determined, but tracking semen straws with varying sperm concentrations in the field poses major logistical issues for most AI companies, (Fair, S. *et al.,* 2018).

Semen Quality

Traditional in vitro evaluation of semen quality usually involves the subjective assessment of motility, an estimate of the proportion of spermatozoa with normal morphology and an estimate of the concentration of spermatozoa in a unit dose. While these tests set minimum standards for semen used for AI, they have limited value for predicting the subsequent fertility of the sample when an animal is inseminated. While routine laboratory tests assess sperm function in terms of motility and morphology, they do not differentiate between sperm transport through the female reproductive tract, sperm fertilizing ability, or ability to sustain early embryo development. The multifactorial aspect of semen fertility can result in misevaluation of semen quality when assessing only a few parameters, (Vincent, P. *et al.*, 2012).

Semen production centres are now moving away from subjective semen assessment, which is largely uncorrelated to field fertility, (see paragraph above), to objective semen analyses that incorporate **computer assisted sperm analysis** (CASA) and flow cytometry. CASA can provide information about sperm concentration, morphology, viability and index of DNA fragmentation of frozen-thawed sperm. The parameters typically collected using CASA systems are motility, velocity, linearity and lateral displacement of spermatozoa as they progress along their trajectories in a sample. However, these more specialized techniques are not routinely used for regular analysis of frozen-thawed semen in AI centres, (Vincent, P. *et al.*, 2012).

Flow cytometry analyses cells suspended in a stream of fluid passing at high velocity in front of one or several lasers. The light emitted by fluorochrome bound cells is captured by photomultiplier tubes and converted into an electronic signal and subsequently digitalized by cytometry software. Flow cytometry allows a better characterization of the spermatozoa because it has the potential for a multi-parametric analysis of spermatozoa. Key features of flow cytometry are the acquisition and analysis of thousands of cells within seconds. Evaluation of sperm plasma membrane integrity (PMI) has increased in precision thanks to flow cytometry. PMI was shown to be highly correlated with microscopic evaluation of that trait, (Utt, M. 2016).

Multi-parametric analyses of semen with CASA and flow cytometry demonstrates a very high predictive potential for semen quality and fertility. Research and development of new markers to identify high fertility semen needs to be undertaken, (Vincent, P. *et al.*, 2012).

Consequently, attention has been directed towards the assessment of other aspects of semen quality using these techniques as predictors of fertility, such as sperm viability, acrosomal integrity, membrane status, DNA integrity, membrane proteins and the ability of spermatozoa to swim-up. A stepwise regression analysis identified tests which, when combined, produced models with a strong correlation with field fertility. A stepwise regression analysis identified tests which, when combined,

produced models with a strong correlation ($R^2 > 0.9$) to field fertility, (10 bulls with a range of fertility results). (Gillan, L. *et al.,* 2008)

In a review of Holstein bull fertility in the USA, using over 2000 bulls with a median of 1867 serves per sire, it was found that 93% of the sires were within 3% of the breed average for sire conception rates, (based on confirmed pregnancy), (Harstine, B. *et. al.,* 2018).

A retrospective study demonstrated that the performance of bull spermatozoa in a number of in vitro diagnostic tests can be correlated with adjusted field fertility. Spermatozoa from bulls with superior fertility displayed high motility, (subjectively-assessed), viability and straight-line velocity had few abnormal morphological forms and an ability to swim-up and penetrate artificial cervical mucus in large numbers. Moreover, when a number of in vitro tests were combined into a mixed model, the correlation with established field fertility was extremely high. Therefore, it is to be expected that semen assessments incorporating several in vitro diagnostic tests would be more representative of the many functions spermatozoa perform and of their varied characteristics, (Gillan, L. *et al.,* 2008).

Fertility differences may be obscured if there are enough normal sperm in each straw, unless defective sperm somehow inhibit normal ones. Competitive fertilisation or heterospermic insemination is a unique procedure where sperm from more than one male are combined to compete for fertilization of oocytes to which they are exposed in vitro or in vivo. Because sperm compete within the same female at the same time, many extraneous variables associated with homospermic insemination are eliminated. This experimental design increases efficiency at least 10-fold, greatly reducing the number of observations and cost required to achieve a desired level of statistical significance. It is a procedure that has been underutilized in accurately ranking animals based on fertility, (Foote, R. 2002).

The ability to predict the fertility of bulls before semen is released into the field has been a long-term objective of the animal breeding industry. However, the recent shift in the dairy industry towards the intensive use of young genomically selected bulls has increased its urgency. Such bulls, which are often in the highest demand, are frequently only used intensively for one season and consequently there is limited time to track their field fertility. A more pressing issue is that they produce fewer sperm per ejaculate than mature bulls and therefore there is a need to reduce the sperm number per straw to the minimum required without a concomitant reduction in fertility. However, as individual bulls vary in the minimum number of sperm required to achieve their maximum fertility, this cannot be currently achieved without extensive field-testing. **Although an *in vitro* semen quality test, or combination of tests, which can accurately and consistently determine a bull's fertility and the optimum sperm number required represent the 'holy grail' in terms of semen assessment, this has not been achieved to date**. Understanding the underlying causes of variation in bull fertility is a key prerequisite to achieving this goal. In this review, we consider the reliability of sire conception rate estimates and then consider where along the pregnancy establishment axis the variation in reproductive loss between bulls occurs. We discuss the aetiology of these deficiencies in sperm function and propose avenues for future investigation, (Fair, S. *et al.,* 2018).

Genetics of bull fertility

The genetic improvement of bull fertility has been largely ignored. This appears to be contradictory considering that semen from one service sire bull may be used to inseminate hundreds of cows and thus, one sub-fertile bull would have a larger impact on overall herd fertility than a single cow with fertility problems, (Abdollahi-Arpanahi, R. *et al.,* 2017).

Prior to genomics, bulls at approximately one year of age typically entered a progeny-test program as a method to determine their breeding value. Bulls were at least five years old when their semen could

be marketed based on progeny-test results. However, this has changed dramatically in recent years with the advent of genomics and now the vast majority of semen is being marketed based exclusively on the genetics of the young bull.

The heritability of sire conception rate, (based on parous females) is very low, which confirms that sire conception rate does not accurately reflect true male fertility, (Taylor, J. *et. al.,* 2018). Given the low heritability of non-compensatory fertility, it is not surprising that the correlation between predicted and true breeding value for this trait is expected to be low, (Blaschek, M. *et. al.,* 2011).

Practically no genetic variation in non-return rate measured in artificially inseminated bulls exists. This is most likely due to selection since generally only bulls with sufficiently high semen quality are considered for use in AI. No genetic correlations between semen quality measures and field non-return rate have been documented. Documented genetic correlations among many of the semen quality characteristics suggest that larger scrotal circumference is associated with a greater volume and concentration of sperm, a larger proportion of live sperm with greater motility, and a larger proportion of normal sperm. Although no study estimated the genetic correlation between scrotal circumference and sperm number, the positive genetic correlations between scrotal circumference and both sperm concentration and volume suggest the correlation between scrotal circumference and total sperm number may also be positive, (Berry, D, *et. al.,* 2014).

Relevant links between bull fertility and reproductive success have been observed not only in the fertilisation process through differences in semen quality but also in embryo preimplantation and development as well as in offspring performance in later life. Moreover, there is recent evidence that embryos from bulls with low fertility have a reduced ability to establish pregnancy and this depends on several factors such as: sperm fertilizing ability, preimplantation embryonic development and development of the embryo and placenta after conceptus elongation and pregnancy recognition

The accurate prediction of yet-to-be observed fertility phenotypes is very challenging and the in-corporation of different sources of information can help to improve model predictive performance. However, there is growing evidence that bull fertility is influenced by genetic factors. The genomic prediction of service sire fertility is possible, and this could have a great impact on the dairy industry worldwide, (Nani, J. *et. al.,* 2019).

In a recent study, a comprehensive genomic analysis was performed with the purpose of unravelling the genetic architecture underlying sire conception rate in Holstein dairy cattle. Genomic regions in BTA5, BTA9, BTA13, BTA15, BTA21 and BTA25 were found to be associated with sire fertility. Most of these regions harbour genes with known roles in sperm biology, including sperm maturation, motility and fertilization. Another study found that Holstein bulls with greater CRISP2 and lower CCT8 mRNA expression in sperm had higher probabilities of siring calves, (Han, Y. *et. al.,* 2016).

In multivariate regression models, CRISP2 and CCT8 mRNA expression in sperm accounted for 95% of the variance in Holstein bull's sire conception rate scores. In conclusion, Holstein bulls with greater CRISP2 and lower CCT8 mRNA expression in sperm had higher probabilities of siring calves. Hence these markers could be incorporated into gene analysis of young sires' ability to sire offspring, (Arangasamy, A. *et. al.,* 2011).

A US study with 795 bulls with known conception rates were genomically assessed for regions associated with non-compensatory bull fertility. Heritability of non-compensatory fertility in the current data set was very low, making the identification of genomic regions associated with the trait difficult, (Blaschek, M. *et. al.,* 2011).

A study was carried out to investigate the feasibility of genomic prediction of sire conception rate (SCR) in US Holstein dairy cattle. Interestingly, a set of candidate regions and individual genes strongly associated with SCR was identified; most of the genes were closely related to sperm physiology and male biology. Overall, our findings suggest that genomic prediction of bull fertility is feasible.

A recent study based on a large data set of 100,058 ejaculates from 2,858 Nordic Holstein bulls, reported low to moderate heritability and moderate to high repeatability estimates for semen quality traits, including pre- and post-cryopreservation semen concentration, sperm motility, sperm viability, ejaculate volume, and number of doses per ejaculate. These results indicate the possibility of implementing selective breeding to improve semen quality traits in the Nordic Holstein. Additionally, our study found moderate to high genetic and phenotypic correlations between non-return rate and some of the semen quality traits. The results indicate that some of the semen quality traits, specifically pre- and post-cryopreservation sperm viability, post-cryopreservation sperm motility, and pre-cryopreservation sperm concentration, can be useful predictors for service sire non return rate. Positive and strong genetic correlations between these semen quality traits and service sire non return rates also indicate that selection for the semen quality traits might be favourable for improving service sire non return rate, (Gebreyesus, G. *et. al.,* 2021).

In dairy cattle, there is an opportunity to rapidly develop genomic predictions for male fertility (in both sexes), considering the large number of genotyped animals and the availability of sire conception rate phenotypes. However, these phenotypes should be based on inseminations made by yearling bulls in which sperm dosages have been standardized and this will require collaboration between AI organizations, (Taylor, J. *et. al.,* 2018).

New technologies will undoubtedly produce lists of biomarkers that are different between bulls of varying fertility. The major challenge then is to define which ones are physiologically important. For this, we need novel functional approaches comprising of both in vitro and in vivo methods. However, before we go down this path we must be cognisant of the limitations of sire fertility estimates, especially when inseminations are performed with high numbers of sperm. Then, we should ensure experiments are sufficiently powered with bulls across a wide range of the fertility spectrum in the quest to identify the reasons for the variation in sire conception rates, (Fair, S. *et al.,* 2018).

Bull subfertility/infertility

To precisely and accurately estimate sire fertility, one must have sufficient 'complete records' with: a) a common basis for decision to inseminate (standing heat, rubbed tail paint, timed-AI); b) a common unit of measure for how females are judged pregnant at a stipulated and consistent interval after AI; c) no error in outcome measurement, be it detection of females returning to oestrus, trans-rectal palpation, or ultrasonographic evaluation; and d) no error in recorded data, such as wrong date for AI, or identity of the bull or female. These four criteria are not achieved perfectly in any data set, and these failures contribute to unexplained variation in the population estimate of relative sire fertility. It is not surprising that there is difficulty in identifying the causes of bull subfertility, if a dubious fertility phenotype is used at the start. Ideally, the number of sperm at which a bull's fertility reaches a plateau should be determined, but tracking semen straws with varying sperm concentrations in the field poses major logistical issues for most AI companies.

Bulls in AI studs are generally fertile, (at least in comparison to other bulls in the same stud). Where sire conception rates are available, most bulls are within three percentage units of the mean for all the bulls assessed, (Amann, R. *et. al.,* 2012). This is largely due to the removed of bulls with poor

quality semen and doses of semen of below standard quality, as assessed by various techniques highlighted in this investigation.

Bull subfertility/infertility can be divided into compensatory and non-compensatory components, where compensatory refers to infertility that can be overcome by increasing sperm numbers and non-compensatory infertility represents the remainder, presumably due to molecular and genomic defects that cannot be compensated for by increasing sperm numbers per straw, (Amann, R. *et. al.,* 2012). However, few un-compensable sperm defects are 'clean', and at least some also seem to have a compensable component and/or have an expression modified by other compensable factors or environmental-management factors. No one knows with certainty if a given sperm defect is entirely compensable, entirely un-compensable, or contributes to both types of outcomes, (Amann, R. *et. al.,* 2012).

To mitigate against low bull conception rates, AI centres often inflate the number of spermatozoa within insemination doses, (Fair, S. *et al.,* 2018). However, this has been shown to be effective only against compensable sperm defects, whereby fertility is typically improved with increasing sperm number until a threshold level is reached. This strategy limits the supply of straws that can be processed from an individual ejaculate and disseminated into the field and is especially problematic for young, genomically selected dairy bulls, which are in high demand, but produce low quantities of semen.

In order to minimise differences in pregnancy rates among individual sires, over-compensation of sperm numbers typically occurs in the preparation of frozen-thawed semen, resulting in a sperm concentration that considerably exceeds the number of sperm necessary for maximum fertility. Thus, the 'true fertility' potential of a bull in the field is masked by the greater sperm number per insemination dose and this needs to be considered when attempting to understand the variation in sire conception rates using in vitro assays. Therefore, fertility can only be determined under conditions where sperm numbers are limiting, (Fair, S. *et al.,* 2018).

In vitro methods of assessing bull semen quality in artificial insemination (AI) centres are unable to consistently detect individuals of lower fertility. A research study in Ireland assessed cryopreserved spermatozoa from a number of high and low fertility bulls as measured by pregnancy status. Spermatozoa were assessed for motility and kinematic parameters, morphology, acrosome integrity, plasma membrane lipid packing, viability, (or membrane integrity), superoxide production, and DNA integrity. In addition, spermatozoa were used for in vitro fertilization to evaluate their capacity for fertilization and successful embryo development. Acrosome integrity and viability were the only sperm attributes that were significantly different between high and low fertility bulls. However, the variable nature of low-fertility bulls suggests that additional, in-depth characterization of spermatozoa at a molecular level is required to further understand the etiology of these low fertility bulls, (Bernecic, N*. et. al.,* 2021).

A study provided evidence that the most precise estimation of a bull's non-return rate can be achieved through flow cytometric detection of sperm concentration and viability in neat semen, combined with flow cytometric detection of post-thaw sperm viability, although the effects of those seminal measures are of moderate magnitude, (Christensen, P. *et. al.,* 2011).

Another study found that while differences in field fertility among AI sires used in the study were not reflected in fertilization rate, differences in embryo quality were apparent as early as day 7. These differences likely contributed to the higher proportion of conceptuses surviving to day 15 in high fertility bulls. The present studies highlight influences of the sire genome on a continuum of early

pregnancy events from fertilization and pre-implantation development to post-elongation implantation and embryogenesis. Thus, the inability to develop genetic predictors of sire conception rate is due to the various phenotypes involved in the trait. To date, genomic regions associated with sire conception rate have been identified in genes influencing semen quality and fertilization. Future investigations should focus on identifying genetic variants in bulls that govern early embryonic mortality that are not based solely on the sire conception rate value and incorporate other traits including return to oestrus to identify fertilization and preimplantation defects, (Ortega, M. *et. al.,* 2018).

Optimum fertility can be achieved with a much lower sperm number when fresh (liquid) rather than frozen-thawed semen is used, (2 to 5 million v. 15 to 20 million sperm, respectively). The higher sperm numbers in cryopreserved semen compensate for the damage during the freeze-thaw process compared with fresh semen and on average, the same level of fertility is achieved with both types of semen by increasing sperm numbers in cryopreserved straws, (Fair, S. *et al.,* 2018).

In a US study researchers obtained a global view of different classes of proteins expressed in the accessory sex gland fluid of proven, high use Holstein bulls with documented fertility history. The recognized characteristics of the accessory sex gland proteins suggest they modulate important sperm functions after ejaculation and in the female reproductive tract. Some of these proteins are described for the first time as part of the accessory sex gland fluid. **These analyses and observations provide justification for studies to explore and better understand the mechanisms by which accessory sex gland proteins influence male fertility,** (Moura, A. *et al.,* 2007)**.**

The main findings of a study of a field fertility study among AI sires were not reflected in fertilization rate; however, a greater proportion of embryos were at a more advanced stage of development at day 7 following AI with semen from high fertility bulls versus low fertility bulls; mean embryo cell number on day 7 was greater in embryos derived from high fertility bulls versus low fertility bulls, the number of sperm in the vicinity of the oocyte at fertilization, as assessed by accessory sperm number, was greater in high fertility bulls and despite no difference in the mean length of recovered conceptuses, the proportion of conceptuses surviving to days 15 was greater in high fertility bulls, (O'Callaghan, E. *et al.,* 2020).

A North American study concluded that several sperm and seminal plasma proteins were expressed in greater abundance in high-fertility compared with low-fertility bulls. These proteins involved in several key biological functions including sperm-egg interaction and embryonic development. Since protein concentrations differed in high and low fertility bulls, efficiency of associated sperm functions that are necessary for fertility may also differ between high and low fertility semen. Therefore, varying concentrations of sperm and seminal plasma proteins in high and low fertility bulls were likely related to differences in fertility, (Kasimanickam, R. *et. al.,* 2019).

Bull age

Total sperm production increases with age up to about 4 years old. With the advent of the genomic era, most bulls in stud are young, (1-2 years old, based on their high genetic merit). Bulls younger than one year old produce less sperm than bulls greater than 1 year old. These young animals produce limited volumes and concentration of semen and consequently, there is a limited number of straws available for the market, (Murphy, E. *et. al.,* 2018). The volume and concentration of sperm increases with age, but by that stage the next generation of young bulls have arrived, often before there is much information available on conception rates, etc. The low semen ejaculate volume typically associated

with young bulls not only reduces sperm numbers but also pre-freeze and post-thaw sperm motility, (Murphy, E. *et. al.,* 2018).

The collection of a second consecutive ejaculate does not affect post-thaw sperm motility and therefore, should be considered, particularly for bulls in high demand, Murphy, e. et al., (2018). A recent paper from Ireland concluded that collecting ejaculates more frequently from post pubertal dairy bulls, reduced the number of days required to obtain a target number of straws, increased sperm motility pre-freeze and post-thaw at 2 hours and increased semen quality in terms of lower superoxide production. Critically, collecting ejaculates more frequently resulted in increased field fertility, and may be a strategy to improve outcomes from AI, leading to increased productivity of cattle. The first ejaculate yielded more total sperm and higher pre-freeze motility than the second ejaculate, but there was no difference in post thaw motility, (Taffe, P. *et al.,* 2022)

Total sperm production can be predicted with >90% accuracy up to 4 months into the future, (based on current production). Sperm production is highly repeatable. Management factors, such as age at collection, frequency of collection, breed, barn, year, season, and scrotal circumference contribute to prediction accuracy, (Quick, A. *et al.,* 2020).

The challenge for the AI industry in todays' genomic era is that the highest demand, most valuable sires are among the youngest in the population and produce smaller quantities of semen that possess more age-associated quality issues as compared with the mature, proven sires of yesteryear. Timely access to fertility data of these young sires is becoming increasingly important to maximize their utilization while maintaining their fertility potential, (Harstine, B. *et. al.,* 2018).

Comments

Bull fertility as measured by non-return rate, or positive/negative diagnosis of pregnancy are seldom, if ever made available to farmers, even if such measures are collected by the AI centre. While this type of information is collected in the USA, Israel and some European countries, it is not available in the UK. Non-return rates by a pre-set time, often between day 56 and 70 give a reasonable measure of bull fertility, but do not account for cows culled in the interim, natural service, or service by a different technician. In the UK a considerable amount of AI is undertaken by the farmer and as such, no feedback on conception rates are available to the AI Company. Even when AI technicians do the inseminations, there may be no ongoing recording of non-return rates to determine proficiency of the operator. Sire inbreeding level, number of sperm/straw, quality of semen, cow inbreeding level, cow age, milk yield, lactation number, evidence of oestrous, signs of uterine infection, environmental factors such as nutrition, lameness, ill-health, level of circulating progesterone, semen handling pre and post thaw etc., all impact the end result, a pregnancy that is carried to term, with live healthy offspring produced.

Going forward, it would be beneficial to the industry as a whole to have all services and pregnancy results recorded on a central database. This would allow bull fertility to be accessed quickly and on an ongoing basis and aid farmers in their selection of bulls, not just based on bull genetics, but sire conception rate as well. The standardisation of sperm numbers per straw would also help greatly in the comparison of relative bull fertility, while taking into account many of the factors that impact on possible outcomes, such as level of inbreeding, season of collection, number of straws marketed, etc.

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