

NOVEL STRATEGIES TO IDENTIFY BEEF BULLS WITH SUPERIOR FERTILITY

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Introduction

Bull fertility is affected by several factors; in a Breeding Soundness Evaluation (BSE), physical soundness, scrotal circumference and sperm quality are evaluated to predict bull fertility (Barth and Oko, 1989; Barth and Waldner, 2002; Barth, 2007; Barth, 2018; Koziol and Armstrong, 2018). Further, sperm quality may be affected by spermatogenesis, sperm maturation, and sperm interaction with testis, epididymis and seminal plasma milieu, especially their proteins (Barth and Oko, 1989; Amann and Hammerstedt, 1993; Johnson et al., 2000; Barth and Waldner, 2002; Saez et al., 2003; Sullivan et al., 2005; Barth, 2007; Saacke, 2008; Caballero et al., 2011; Sullivan and Saez, 2013; Sullivan, 2016; Dalton et al., 2017; Sullivan and Belleannée, 2017; Amann et al., 2018; Barth, 2018; Staub and Johnson, 2018). Also, when sperm is processed for artificial insemination (AI), semen handling plays a very important role in maintaining sperm quality, especially in cryopreserved semen, because sperm have to endure the process of freezing and thawing (Januskauskas et al., 2001; Januskauskas et al., 2003; Rodriguez-Martinez, 2003; DeJarnette, 2005; Dalton et al., 2017; Harstine et al., 2018; Dalton, 2019; DeJarnette et al., 2021). In the female, vaginal, cervical, uterine, and oviductal environment affect sperm transport, hyperactivation, capacitation and sperm-egg interaction (Austin, 1951; Chang, 1951; Austin, 1952; Austin, 1975; Yanagimachi, 1994; Suarez, 2006; Suarez and Pacey, 2006; Suarez, 2008; Sutovsky, 2009; Florman and Fissore, 2015; Suarez, 2015, 2016; Sutovsky, 2018). Thus, bull fertility and sperm quality are very complex and depend on a multitude of events that must occur in an orderly fashion in order for a viable pregnancy to be established.

Bull fertility has been measured by evaluation of sperm morphology and motility for many decades, several tests have been developed during this time to evaluate and predict bull fertility; however, bull fertility prediction has not changed considerably and most of the livestock industry still relies on motility and morphology to predict sperm fertility (Barth and Oko, 1989; Utt, 2016; Dalton et al., 2017; Barth, 2018; Harstine et al., 2018; DeJarnette et al., 2021). Nevertheless, several advances in understanding sperm biology and its impact on field fertility (i.e. pregnancy success) has been accomplished. In this proceeding paper, we will discuss some of the work that has been done in semen preparation, handling, and sperm biology, and how that may influence our ability to identify bulls with superior fertility.

Abbreviations

AI = Artificial insemination; **AKAP4** = A-kinase anchor protein-4; **ALH** = Amplitude of lateral head displacement; **BSE** = Breeding Soundness Exam; **BSP1** = Binder of sperm protein 1; **CALM1** = Calmodulin; **CASA** = Computer Assisted Sperm Analysis; **DAG1** = Dystroglycan; **FAA** = Fertility-associated antigen; **FTAI** = Fixed-time Artificial Insemination; **NAAB-CSS** = National Association of Animal Breeders-Certified Semen Services; **PEBP4** = Phosphatidylethanolamine-binding protein 4; **SERPINA5** = Plasma serine protease inhibitor; **sncRNA** = Small non-coding RNAs; **SNP** = Single nucleotides polymorphism; **SPADH2** = Spermadhesin Z13.

Sperm Preservation and Evaluation

In 1940, bovine semen was successfully cooled after being diluted with an egg-yolk extender and sperm survived for several days (Phillips and Lardy, 1940). Later, the use of antibiotics was reported to improve pregnancy rates (~10% improvement), and the discovery of glycerol as cryoprotectant allowed for cryopreservation of sperm and successful long-term storage of sperm (Almquist et al., 1946; Almquist et al., 1949; Polge et al., 1949; Almquist, 1951; Polge and Rowson, 1952). These advances in sperm storage were key components for the success and dissemination of AI in cattle. Presently, 90% of dairy cattle and approximately 15% of beef heifers and 5% of beef cows are AI'd (USDA, 2018, 2020). The protocols for bovine sperm cryopreservation have not changed considerably in ~50 years, despite the fact that sperm viability is greatly affected in the process resulting in approximately 50% of sperm death during freezing and thawing (Robbins et al., 1976; Parrish et al., 1986; Gunasena and Critser, 1997). Nevertheless, fertility of frozen sperm reaches acceptable successful rates for both AI and *in vitro* fertilization in cattle (Holt, 2000).

Evaluation of fresh ejaculated semen at AI centers that is destined for cryopreservation has a greater motility threshold ($\geq 60\%$ progressive motility) compared to semen evaluation during a BSE ($\geq 30\%$ progressive motility) (DeJarnette, 2005; DeJarnette, 2012; Lone et al., 2017; Harstine et al., 2018; Koziol and Armstrong, 2018; DeJarnette et al., 2021). Conversely, the percentage of morphologically normal sperm is similar ($\geq 70\%$) between a BSE and quality control analysis at AI centers, as samples above this threshold have small to no correlation to fertility (DeJarnette, 2005; DeJarnette, 2012; Harstine et al., 2018; DeJarnette et al., 2021). The cryopreservation process is the reason for pre-freeze higher standards in AI centers. Sperm are damaged during the freezing and thawing process (~50% loss); additionally, lower insemination doses (10 to 40 million sperm per insemination dose) are used for AI, in the uterine body, compared to greater insemination dose (several billions) being deposited in the female vagina during natural service by the bull (Zoca et al., 2020; DeJarnette et al., 2021).

Insemination dose

Sperm dose used for AI has been reported to affect pregnancy rates. Pregnancy rates increase with increased sperm per dose until a plateau is reached which is dependent on the maximum fertility of the female population and/or the sire (Fig 1.) (Salisbury and VanDemark, 1961; Sullivan and Elliott, 1968; Saacke et al., 1994; Den Daas et al., 1998; Saacke, 2008). Den Daas et al. (1998) demonstrated that the insemination dose at which each bull reaches its maximum fertility varied from ~1 million to ~10 million viable sperm per dose, which is consistent with sperm doses commercially available between 10 and 40 million sperm per dose (DeJarnette, 2005; Amann and DeJarnette, 2012; Harstine et al., 2018). A more recent study has reported no effect of sperm insemination dose when varying from 10 to 40 million sperm per dose, agreeing with previous reports (Fig. 2) (Zoca et al., 2020). The reason different bulls reach their maximum fertility at different doses is explained by “compensable” and “uncompensable” sperm traits (originally described by (Saacke et al., 1994). Compensable sperm traits refer to the inability of sperm to fertilize an oocyte which is associated with failure of sperm transport and initiation of fertilization. Examples of compensable sperm traits include lower percentage of progressive motile sperm and high percentage of sperm with disrupted plasma membrane (Saacke et al., 1994; Saacke, 2008; Amann et al., 2018). In fig. 1, bulls A and B are a good example of compensable sperm traits, where it is overcome by increasing insemination dose until they reached the optimum fertility of

the female population. Uncompensable sperm traits pertain to sperm that successfully initiate fertilization, however, are unable to support development of viable embryos, an example of an “uncompensable” trait is sperm with damaged DNA (Eid et al., 1994; Saacke et al., 1994; Saacke, 2008; Amann et al., 2018). Although an increase in sperm dosage increased the fertility level of bulls C and D (Fig. 1), they never reached the optimum female fertility, thus these bulls are a good example of uncompensable sperm traits.

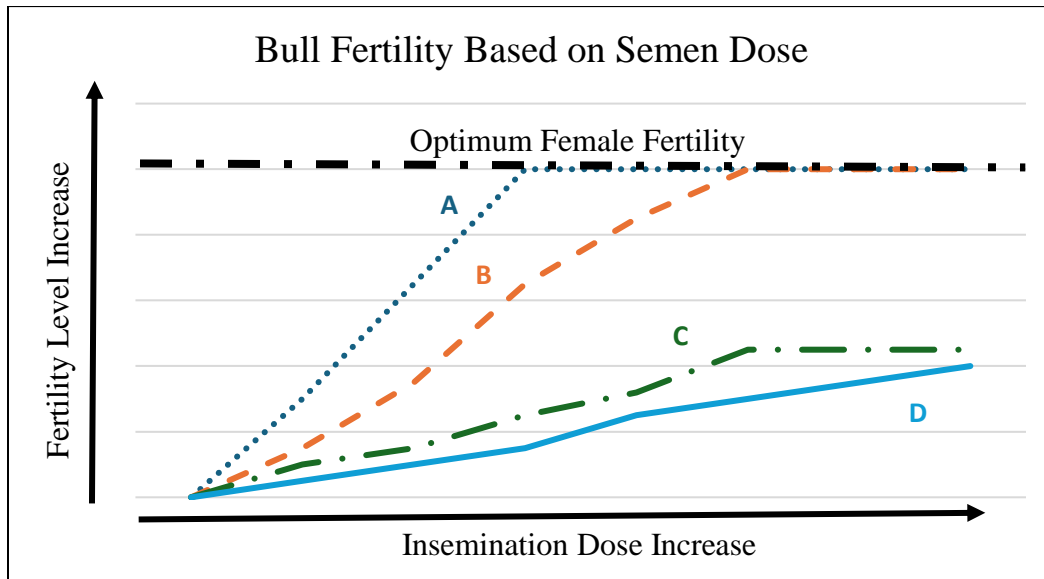


Figure 1. Illustration of change in bull fertility relative to insemination dose and optimum female fertility. Bull fertility increases as the number of viable sperm inseminated increases until it reaches the optimum female fertility or male maximum fertility (Adapted from Salisbury and VanDemark, 1961; Sullivan and Elliott, 1968; Den Daas et al., 1998).

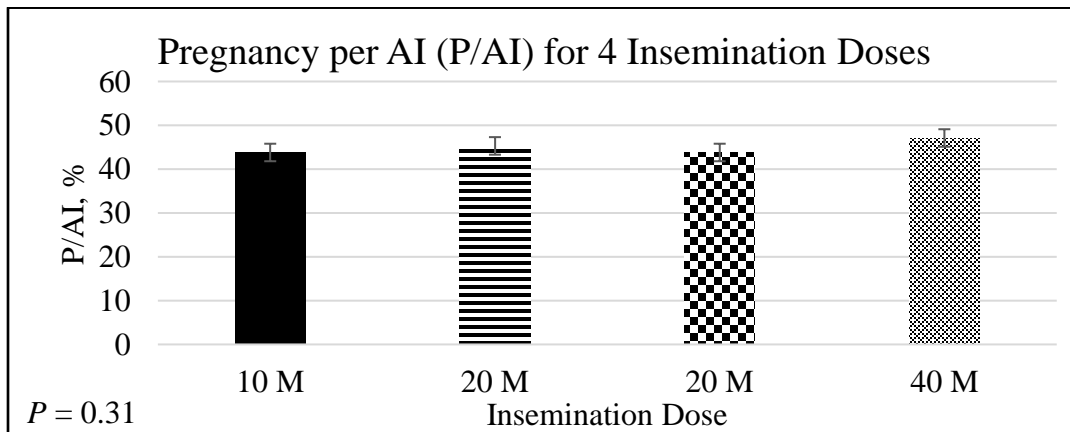


Figure 2. Pregnancy rates for insemination doses ranging from 10 to 40 million sperm per ml. Difference between the two 20 M was only the color of the semen straw. No difference was detected between all four doses ($P = 0.31$) (adapted from (Zoca et al., 2020)).

Only one sperm is required for successful fertilization of an oocyte. The fertilizing sperm that reaches the site of fertilization and successfully completes fertilization, must have normal morphology, progressive motility, intact membranes (plasma and acrosomal membrane), stable and intact DNA, be able to be capacitated and hyperactivated, be able to fertilize, activate the

oocyte and block polyspermy, and support early embryonic development (Rodriguez-Martinez, 2003; Saacke, 2008; Vincent et al., 2012; Garner, 2014; Lockhart et al., 2023; Costes et al., 2024). One single sperm containing all these characteristics is sufficient for fertilization; however, for a bull to be highly fertile (great proportion of females pregnant by single insemination), a great proportion of inseminated sperm need to display these desired characteristics. Increases in pregnancy rates by increasing insemination dose, previously mentioned, is due to sufficing the “compensable” characteristics of the sperm (Saacke, 2008). Further, the maximum fertility of a bull or the level at which a bull’s fertility plateaus (considering that the female population fertility is optimum) is determined by its “uncompensable” characteristics (Saacke, 2008). Finally, the ejaculate is composed of three sperm populations, 1) sperm that cannot initiate fertilization (compensable), 2) sperm that initiate fertilization but do not generate a viable embryo (uncompensable), and 3) fully competent sperm that can generate a viable embryo; therefore, each bull’s fertility is dependent on the proportion of each of these populations in an ejaculate or insemination dose (Amann et al., 2018). Nevertheless, pregnancy rates following AI are dependent on multiple factors beside the quality of an ejaculate or insemination dose, including female’s health and management, semen storage and handling, and proper AI technique (Saacke, 2008; Vincent et al., 2012; Dalton et al., 2017; Amann et al., 2018). It is also necessary that the fertilizing spermatozoon be at the correct place (ampullae or ampullary isthmus junction) and at the correct time (when the oocyte reaches the right place; Amann et al., 2018). This becomes a concern especially when implementing AI and females are AI’ed at different intervals after the onset of estrus. It was reported that females AI’ed shortly after the beginning of behavioral estrus had decreased fertilization rates compared to females AI’ed toward the end of estrus; however, embryo quality was greater in those females AI’ed at the beginning of estrus compared to those AI’ed towards the end of estrus (Saacke et al., 2000; Dalton et al., 2001). This is an even greater challenge when FTAI is used, because females are AI’ed regardless of expression of behavioral estrus. Females that expressed behavioral estrus, i.e., they were exposed to high levels of estradiol prior to FTAI, had conception rates, on average, 27% greater than those that did not expressed behavioral estrus (Perry and Perry, 2008; Larimore et al., 2015; Richardson et al., 2016). Thus, the use of an insemination dose of high sperm quality that can maximize pregnancy rates with one single insemination is necessary for optimization of beef cattle production.

Prediction of Fertility

The delivery of a high-quality sperm dose, one that meets or exceeds industry standards is the responsibility of AI centers and is accomplished by meeting or exceeding the guidelines established by the NAAB-CSS (DeJarnette, 2012; Mitchell, 2012). Sperm analysis is improved greatly when more objective methods are used, such as CASA and flow cytometry, compared to previous subjective methods (visual microscopy), mainly because of the increase in number of individual sperm evaluated by these machines (thousands) compared to microscopy (few hundreds); however, microscopy is still the main method of sperm analyses for a BSE and morphology (Barth and Oko, 1989; Rodriguez-Martinez, 2003; Barth, 2007; Vincent et al., 2012; Barth, 2018). A semen quality control was added to the NAAB-CSS audit program in 2011; however, quality control minimum standards and procedures are held privately (Mitchell, 2012). Although each company may have different standards, quality control minimum standard procedures for pre-freeze and post-thaw (usually motility and morphology) must be approved by an NAAB-CSS auditor (Mitchell, 2012). Commonly used methods of quality control in AI centers involve: morphology ($\geq 70\%$ normal sperm is usually used), motility ($\geq 60\%$ for pre-freeze in a

subjective assessment and $\geq 30\%$ for post-thaw in an objective assessment are usually used), viability (usually only post-thaw and a threshold for this characteristic was not clearly identified; (Rodriguez-Martinez, 2003; DeJarnette, 2012; Garner, 2014; Thundathil et al., 2016; Harstine et al., 2018; DeJarnette et al., 2021). Also, it has been reported that most bulls from AI centers will have fertility within 3% of the average fertility, either above or below (Clay and McDaniel, 2001)

The search for a method to predict male fertility has been the aim of several investigators, probably since the first reports of a sperm by Hamm and Leeuwenhoek in 1677 (Amann and Hammerstedt, 1993; Rodriguez-Martinez, 2003; Utt, 2016; Smith et al., 2018; Costes et al., 2024). Male fertility depends on multiple factors as discussed previously. Each ejaculate/insemination dose must contain sperm with “enough” of the required characteristics that allow sperm to reach the site of fertilization, fertilize an oocyte and produce a viable embryo; however, it is not known what is “enough” for all sperm traits (Amann and Hammerstedt, 1993; Rodriguez-Martinez, 2003). Several sperm characteristics have been evaluated and reported to be correlated with bull fertility, some positive and others negative; however, results across studies are not consistent, as demonstrated by great variation in correlations, from strong to weak or no correlation (Rodriguez-Martinez, 2003; Utt, 2016). Even though motility is one of the key components utilized in a BSE and at AI centers to predict bull fertility. In an unselected population, bulls that have above minimum standards for motility, correlation with fertility is variable; from non-significant to significant; $r^2 = 0.01$ to $r^2 = 0.63$ (Kjoestad et al., 1993; Stålhammar et al., 1994; Farrell et al., 1998; Gillan et al., 2008; Kathiravan et al., 2008; DeJarnette et al., 2021).

As previously stated, bull fertility is multifactorial and dependent on a series of sperm characteristics and biological functions that sperm is required to go through in order to develop a viable embryo. Current sperm analysis can explain 50 to 60% of fertility variation of bulls (Saacke, 2008). It is unlikely that a single sperm characteristic will explain most of the variation between bulls, thus, a multivariate approach is more likely to accurately estimate the fertility level of a bull or ejaculate. When multiple CASA parameters were included in a regression analysis, the correlation with fertility was increased from $r^2 = 0.34$ with only total motility in the model to $r^2 = 0.68$ with amplitude of lateral head displacement (ALH) and progressive motility, and was reported to be as high as $r^2 = 0.98$ when five CASA characteristics were included in the model (Farrell et al., 1998). In another study, single sperm characteristic correlation with fertility varied from $r^2 = 0.28$ to $r^2 = 0.45$, while multiple (4 or 5) characteristics ranged from $r^2 = 0.50$ to $r^2 = 0.58$ (Januskauskas et al., 2001). Researchers, AI industry personnel and veterinarians aim to predict bull fertility by identifying a threshold for sperm characteristics that will correctly predict a bull’s fertility, such as $\geq 70\%$ normal sperm and $\geq 30\%$ motile sperm; however, with such variability in correlation with fertility it makes it exceedingly difficult to develop an accurate predictive model. Also, several of these characteristics were strongly correlated with motility, morphology, or both (Rodriguez-Martinez, 2003; Utt, 2016). Consideration should be taken in the selection of sperm parameters that will be included in a multiple regression analysis. It is important that sperm parameters are not correlated or the correlation between sperm parameters is weak (Utt, 2016). As described by Utt (2016), when parameters in a multiple regression analysis are correlated, it can lead to an incorrect estimation of fertility by the regression model which decreases the predictive ability of the model when applied in a greater population. Thus, when developing a fertility predictor/estimator multiple regression model, researchers or industry must first evaluate whether parameters included are measuring correlated characteristics or not.

In combination, predicting bull fertility based on sperm analyses is extremely complex. The correct prediction of a bull's fertility (more likely on the ejaculate level than the whole animal's life), if possible, will require the development of new markers of fertility that are not correlated with motility and morphology, and most likely will involve a combination of several sperm characteristics in a multifactorial equation. In the near future, it is more likely that scientists will improve the ability to detect lowly fertile animals through new tests compared to predicting highly fertile ones (DeJarnette, 2005; Dalton, 2019).

Fertility Markers

Flow cytometry:

Initially, only fluorescent microscopy would be used to make inference on a few hundred sperm and that would be extrapolated to the whole population; however, flow cytometry can increase the number of cells evaluated for a specific sperm trait of interest from a few hundred to several thousands which gives us more confidence that the true value of the population is being evaluated. Flow cytometry has been used to measure several characteristics in sperm, such as plasma membrane integrity (viability), acrosomal membrane integrity, the energy potential present in the mitochondria of the sperm, the changes in the fluidity of the plasma membrane associated with sperm capacitation, intracellular ions (e.g.: calcium and zinc), reactive oxygen species concentration, ability to respond to an oxidative stress, and many others. As previously mentioned, the sperm must have 'enough' of all desired characteristics in order to fertilize the oocyte. Further, the ejaculate is composed of a heterogeneous population of sperm, thus, a large proportion of this population must display enough of all desired characteristics for a bull to be of high fertility. Nevertheless, we don't know how much is enough for several characteristics.

The relationship of intact plasma membrane (viable), intact acrosome, concentration of reactive oxygen species, ability to react to oxidative stressors, mitochondrial energy potential and DNA integrity and bull fertility have been demonstrated in several studies (Oliveira et al., 2014; Kumaresan et al., 2017; Bernecic et al., 2021). Bulls with greater proportion of viable sperm with intact acrosome, greater mitochondrial energy potential, lower reactive oxygen species, lower DNA fragmentation would be the desired population; however, how much is necessary to be of high fertility is unknown. Therefore, other studies have failed to identify a relationship between some of these characteristics and field fertility (Zoca et al., 2020; Zoca et al., 2023a), likely, bulls in these studies had enough of these characteristics, even the lower fertility bulls. Fertility difference between high and low fertility bulls in Zoca's study ranged from 4.6 to 7.4 percentage points (pregnancy rates difference) whereas the fertility variation for the other studies mentioned was 11 to 28 percentages points (pregnancy rates). Thus, the greater the fertility difference, the more likely more sperm characteristics will be associated with fertility as a bigger disruption to sperm biology would be expected.

In our recent study, however, we were able to identify a relationship between viability, and zinc signature (a measure of sperm capacitation) and field fertility (Zoca et al., 2023a). The zinc signature assay used in that study classified sperm in four populations: 1) sperm with high intracellular zinc that is considered non-capacitated and with high fertilization ability; 2) sperm with moderate intracellular concentration of zinc that have started the process of capacitation but has high fertilization ability; 3) intracellular zinc is limited to the acrosomal region and/or midpiece, sperm have undergone capacitation and is in the process of cell death, and have low or no fertilization capacity; 4) no intracellular zinc, sperm is dead and may or may not have gone

through capacitation before dying. Thus, in the referred study, high fertility bulls had greater viability and greater proportion of sperm in the signatures 1 and 2 combined. Flow cytometry can be used to measure several sperm characteristics as mentioned above. Another use of flow cytometry would be to identify proteins in the sperm, either presence and absence or even concentration of those proteins. Some of the studies in the protein section below have used flow cytometry to study sperm proteins and their association with bull fertility (Odhiambo et al., 2014; Zoca et al., 2023a).

Proteins:

Sperm biological processes are regulated through proteins, such as sperm hyperactivation and capacitation, formation of the sperm reservoir, induction of the acrosome reaction, and fertilization (Sutovsky, 2009; Florman and Fissore, 2015; Suarez, 2015, 2016; Sutovsky, 2018; Saint-Dizier et al., 2020; Mahé et al., 2021). Sperm has a very limited metabolic function, and it is dependent on the media/environment surrounding them, such as the testicular and epididymal fluids, and seminal plasma in the male, semen extenders when used in assisted reproductive technologies, and the fluid in the female's vagina, cervix, uterus, and oviduct. In the female tract, viable sperm reaches the oviduct 6 to 12 hours after insemination and populates the isthmus where they form the sperm reservoir (Hunter and Wilmot, 1984; Wilmot and Hunter, 1984; Lefebvre et al., 1995), these interactions are dependent on proteins (glycoproteins). Thus, cell-to-cell interactions (i.e. sperm to oviduct and sperm to oocyte) are essential processes during fertilization and may be drivers for fertility variation between bulls. Variation in protein expression between bulls may serve as fertility markers and aid in the selection of highly fertile bulls, as several studies have reported their correlation or association with field or *in vitro* fertility.

Several sperm proteins have been tested as fertility markers and demonstrated promising results. A study focused on a sperm protein of 25 kDa (called P25b) reported that this 25 kDa sperm protein was lowly expressed in some subfertile bulls compared to high fertility and some low fertility bulls; also, this protein was present on the acrosomal region and the principal piece of sperm tail (Parent et al., 1999). Others have described that osteopontin (Ca²⁺-binding protein) was more abundant in semen samples from high fertility bulls compared to low fertility bulls (Killian et al., 1993; Cancel et al., 1997; Moura et al., 2006) and when osteopontin was added to fertilization media (10 µg/mL) cleavage and blastocyst rate of *in vitro* fertilized oocytes were improved compared to control media without osteopontin (Monaco et al., 2009). Further, phospholipase A2 was more abundant and spermadhesin Z13 (SPADH2) was less abundant in high fertility compared to low fertility bulls (Moura et al., 2006); however, in a different study, it was reported that calmodulin (CALM1), SPADH2 and phosphatidylethanolamine-binding protein 4 (PEBP4) were in greater concentration in semen samples from bulls of high fertility compared to low fertility and binder of sperm protein 1 (BSP1) was more abundant in low fertility bulls (Somashakar et al., 2015; Somashakar et al., 2017). Ibrahim et al. (2000) investigated the relationship of sperm protein clusterin with bull fertility and other sperm parameters, although clusterin was negatively correlated with nonreturn rates (raw and adjusted; $r^2 = 0.09$ and $r^2 = 0.33$, respectively) and estimated relative conception rate ($r^2 = 0.36$), it was also negatively correlated with motility and positively correlated with morphology abnormalities ($r^2 = 0.10$ to $r^2 = 0.60$).

A protein called fertility-associated antigen (FAA; previously called heparin-binding proteins) was characterized on ejaculated sperm and demonstrated association with bull fertility (natural service). Bulls with sperm positive for FAA had greater pregnancy rates (9 to 40

percentage points) compared to bulls that sperm lacked FAA (Bellin et al., 1994; Bellin et al., 1996; Bellin et al., 1998). Bulls used for AI with sperm positive for FAA had greater pregnancy rates (7 to 9 percentage points) compared to bull with sperm negative for FAA (Spratt et al., 2000); however, in a different study, pregnancy rates of bulls with sperm positive for FAA were not different (41.5% vs. 39.3%, respectively) or were lower (33.7% vs. 40.7%, respectively) than bulls with sperm negative for FAA (Dalton et al., 2012). Additionally, it was described that A-kinase anchor protein-4 (AKAP4) was present on the sperm principal piece and this protein was related to sperm motility (Moss et al., 1999). Later it was reported that the expression level of this protein differed between high and low fertility bulls with high fertility bulls having greater expression (Peddinti et al., 2008) and a commercial kit is available for testing AKAP4 on sperm samples (Sergeant et al., 2019).

Ubiquitin has been intensively studied and was reported as a negative marker of fertility, as bulls with greater sperm ubiquitination was associated with greater numbers of sperm defects (Sutovsky et al., 2001; Sutovsky et al., 2002; Sutovsky et al., 2007; Odhiambo et al., 2011; Kennedy et al., 2014). In an *in vitro* trial, nanopurification of sperm with anti-ubiquitin improved fertilization rates in comparison to control; however, when sperm was nanopurified with anti-ubiquitin and used for AI, there was a decrease in pregnancy rates when nanopurified sperm at 10 million sperm per dose was compared with control sperm at 20 million sperm per dose, but no difference in fertility was detected with the same insemination dose between nanopurified and control (10 million sperm per dose; (Odhiambo et al., 2014).

Recently, we worked with three sperm proteins, plasma serine protease inhibitor (SERPINA5), dystroglycan (DAG1), and CD9, and their potential as bull sperm fertility markers. We reported those proteins to be attached to the sperm (Zoca et al., 2022) and confirmed their presence in bull sperm (Fig. 3 and 4). However, there was no relationship between SERPINA5 or DAG1 and sire conception rate (dairy bulls), total and progressive motility, plasma membrane integrity (viability), or *in vitro* embryo production outcomes (cleavage and blastocyst rate, and their ratio; (Zoca et al., 2023b). Nevertheless, when we investigated CD9, fertility differences between 5 angus bulls were explained by dead CD9+ populations (Fig 4A), where bulls with superior fertility had lower proportion of sperm categorized as dead CD9+ compared to lower fertility bulls. However, these results need to be validated in a larger population of bulls with known fertility.

These are some examples of proteins that have been used as fertility markers in bovine. Several other examples can be found in bovine, laboratory animals, men and other livestock species and poultry. If the words “sperm” and “protein” and “fertility” are entered into a literature (<https://pubmed.ncbi.nlm.nih.gov/> search, since 1946, 9,491 results are found and 7,151 of those publications happened in the past 20 yr, 4,655 in past 10 yr and 2,824 in the past 5 years (searched on August 21, 2024). In combination, these studies demonstrated the challenge in identifying a new biomarker of bull sperm fertility. Some biomarkers are associated or predictive of bull fertility in a small group but not in the population, as illustrated by Spratt et al. (2000) and Dalton et al. (2012) results. Others are correlated with motility and morphology and the additive predictive value of those biomarkers is debatable (Ibrahim et al., 2000). Further, some demonstrate promising results in laboratory studies but not in the field (Odhiambo et al., 2014). Some lack field validation or are not used by the industry as a fertility marker.

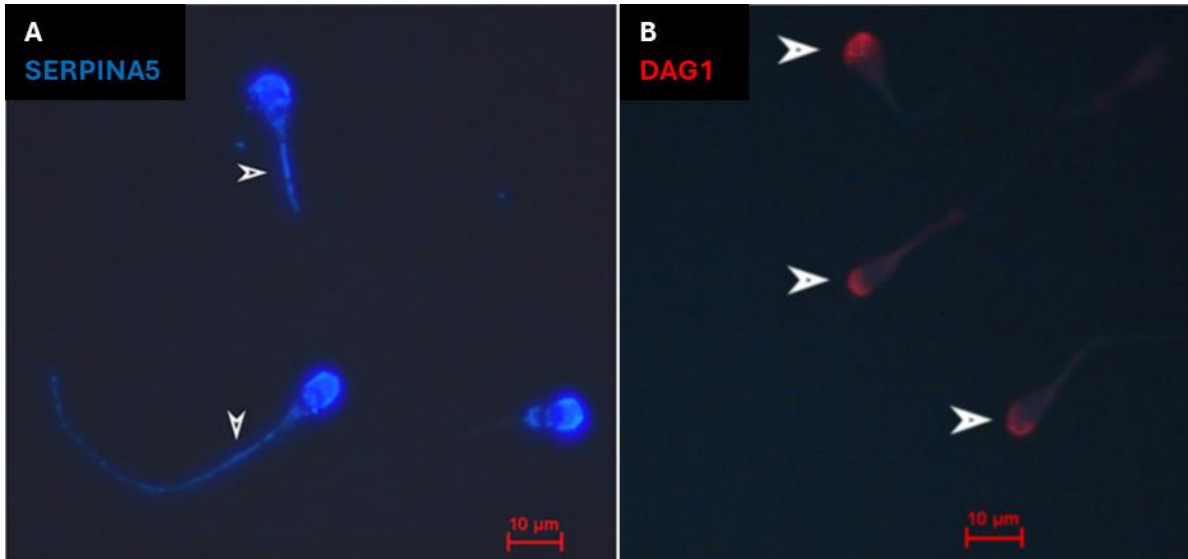


Figure 3. Immunofluorescence picture of sperm labeled with anti-SERPINA5 antibody (A) and anti-DAG1 (B; adapted from (Zoca et al., 2023b).

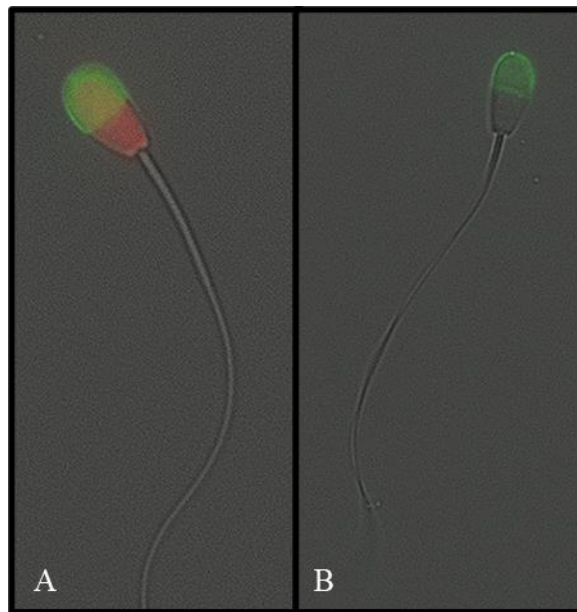


Figure 4. Immunofluorescence picture of two sperm labeled with anti-CD9 antibody (green) where one has the plasma membrane disrupted (dead; A) and the other is a viable sperm (B; adapted from (Zoca et al., 2023a).

Omic's

More recently we have started to investigate the relationship of “Omic’s” in sperm biology and bull fertility. The omic’s world involves analyses of DNA (genomics), RNA and miRNA (transcriptomics), proteins (proteomics), metabolites (metabolomics), DNA-methylation and histone acetylation (epigenomics), lipids (lipidomic) and others. Previously, it was believed that sperm only delivered the paternal genome to the oocyte; however, research has provided evidence that in addition to the sperm’s centrosome for reactivation of meiosis II (Albertson, 1984) and sperm specific phospholipase C- ζ which plays a role in activation of embryonic development

(Saunders et al., 2007), approximately 5 to 10 fg of paternal RNA can be delivered to the oocyte (Boerke et al., 2007). Recently, some studies have used multiple of these omics together in a multiomics approach to investigate bull fertility (Talluri et al., 2022; Costes et al., 2024). Very briefly, Talluri et al. (2022) used transcriptomic, proteomic, and metabolomic analyses of sperm from high and low fertility dairy bulls. They reported that in several levels (transcript, protein, and metabolite), sperm metabolism of high fertility bulls was different than low fertility bulls where energy utilization/production was one of the major differences. More specifically, low fertility bulls had genes involved in oxidative phosphorylation, and proteins involved in metabolic pathways downregulated compared to high fertility bulls. Further, in the multiomic's approach, major metabolic pathways that were dysregulated in individual approaches were revealed to be interactive between transcriptomic, proteomic, and metabolomic that included Butanoate metabolism, Glycolysis and gluconeogenesis, and Methionine and cysteine metabolism dysregulated in low fertility bulls which are molecules associated with energy productions in the sperm. Other dysregulated pathways were Phosphatidyl inositol phosphate, pyrimidine metabolism and saturated fatty acid beta oxidation. The authors concluded that sperm metabolism is likely involved in bull fertility regulation.

In the other multiomic's approach to understand bull fertility, Costes et al. (2024) used genotypes, sperm DNA methylation at CpGs and sperm small non-coding RNAs (sncRNA) and semen parameters from 98 dairy bulls with contrasting fertility. All semen used for their study was from commercially available bulls in France, no surprising semen parameter included in the analyses (sperm motility, velocities, and viability) had little to no correlation to fertility as a rigorous quality control was implicated before semen was approved for breeding. As previously mentioned, semen quality as commonly measure (motility, morphology, and viability) are associated to fertility to a certain level; however, above a certain threshold, little to no correlation is observed. Nevertheless, the authors observed a great relationship between genotypes (measured by single nucleotides polymorphism; SNP), DNA methylation, and sncRNA and fertility. More specifically, 170 regions were more methylated and 83 sncRNA were greatly expressed in low-fertility bulls while only 3 regions were more methylated and 120 sncRNA were greatly expressed in high fertility. Most of these sncRNA were miRNA and ribosomal RNAs derived fragments.

Roughly 20% of miRNA present in sperm are contributed to the oocyte during fertilization (Amanai et al., 2006), and miRNA families that have had predictive ability of bull fertility were associated with developmental process (cell differentiation, and embryonic and fetal development) (Yuan et al., 2016; Wang et al., 2017; Alves et al., 2019). Many research groups have identified miRNA that are differentially expressed between different fertility classifications (Fagerlind et al., 2015; Alves et al., 2019; Alves et al., 2020; Menezes et al., 2020; Keles et al., 2021; Werry et al., 2022; Salas-Huetos et al., 2023), but the lists of differentially expressed miRNA varies among the studies conducted. These differences are likely due to how fertility classifications were made and the fact that they play a larger role post fertilization compared to other factors that would play a role in sperm transport, formation of the sperm reservoir or fertilization.

In summary, multi-omic's studies, have demonstrated a potential in improving our predictive models of bull fertility. The use of omic's is likely the next step in identifying superior sires and potentially predicting the fertility of bulls. Further, not only using omic's but a multiomic approach to combine two or more of these high-throughput methods of analyzing sperm will increase our predictive ability.

Summary

Methods of bull fertility evaluation have not changed significantly in the past several years. In order to improve identification of higher fertility animals, and, consequently, removal of subfertile animals from the breeding population, it is necessary to validate biomarkers of fertility already identified or newly developed. Thus, evaluation of bull fertility will begin with a thorough BSE which evaluates the physical soundness, scrotal circumference, and sperm quality of a bull. For a bull to have potential high fertility, it must be healthy, produce an ejaculate with a great proportion of sperm with high levels of desirable traits, and a scrotal circumference sufficient for daily sperm production during the breeding season. Other areas that are involved in fertility but not measured in a breeding soundness exam are sperm membrane integrity, stability of the DNA, ability to undergo hyperactivation, capacitation, and the acrosome reaction, traverse the female barriers, fertilize the oocyte and generate a viable pregnancy.

As new tests of fertility are developed, they need to be easy to perform by AI industry personnel and veterinarians in the field. Identification of new fertility markers may improve the ability to detect lower fertility bulls that need to be culled before they enter the breeding season or predict which bulls will have high fertility. Genotypes (SNP), sperm DNA methylation at CpGs, sncRNA, proteins, metabolites, and lipids are all potential targets for new fertility markers that may influence fertilization and early embryonic development. Since sperm population is heterogeneous, studies should focus on methods to identify sperm population within an ejaculate that could generate a viable embryo and bulls that would possess a greater proportion of their ejaculate with these characteristics. Thus, the understanding of what is 'enough' of each characteristic is a crucial step in prediction of bull fertility.

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