

Evaluating long term benefits of genomic selection programs in beef cattle breeding programs in Western Canada

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By Tess Mills

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OR

Dean
College of Graduate and Postdoctoral Studies
University of Saskatchewan
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Saskatoon, Saskatchewan, S7N 5C9
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ABSTRACT

A study was conducted to evaluate long-term benefits of genomic selection programs in natural service multi-sire breeding programs in Western Canada. A total of 24 breeding groups and 117 sires (some repeated) were followed over 6 breeding and calving years to determine the association between sire performance over multiple years, number of calves sired, calf performance, and replacement heifer performance over multiple years. To evaluate sire performance and account for the different numbers of cows and sires in each breeding group, bull prolificacy indexes (BPI) were calculated. BPI ranged from 0-4 and sires were categorized based on BPI for analysis with groups representing bottom 25% of sires BPI, middle 50%, and top 25%. Age of sires influenced sire prolificacy between yearlings, 2-year-olds, and mature sires. Twenty sires were used for 3 or more years of breeding and performance was not found to be repeatable across years.

Genomic testing (EnVigour HX™, Delta Genomics, Edmonton, Alberta, Canada) was performed in two years of the six year study. EnVigour HX™ testing provided vigour scores and breed composition of the animals tested. The 2018 heifers from the cooperating producer had an average vigour score (VS) of 69% with a standard deviation of 10.5% and range of 66% with most calves having 5 breeds detected. The 2019 heifers from the cooperating producer had an average VS of 75% with a standard deviation of 11.5% and range of 58 percent.

Replacement heifers produced from targeted sires in 2015 were evaluated for 1 to 3 breeding and calving seasons to evaluate grand-calf performance. A total of 16 sires produced the 74 heifers selected for replacement in 2015. A total of 171 calves were produced from the 2015-born replacement heifers between the 2018-2020 calving seasons. The top 25% of sires, based on BPI, had a higher proportion of replacement heifers retained in 2015, and therefore

more grand-calves attributed to them. The bottom 25% of sires had a greater number of heifers retained over multiple calving seasons compared to the middle and top groups. Heifers born in the first 21d of the calving season tended to have more calves also born in the first cycle ($R^2 = 0.5239$). Calving interval tended to decrease as a heifer matured across three calving cycles. There is a benefit of informed sire selection using DNA parentage. The data can help improve overall calf numbers and improve replacement heifer performance in the herd.

A two-year net return analysis of using EnvigourHXTM testing in the herd was performed based on differences between low vigour score and high vigour score heifers. Total kg weaned over two parturitions was valued based on CanFax reported average market prices for 182kg steers in October 2020 and 205kg steers in October 2021. Based on cost of testing and total return there was a loss of \$3,409 for the operation. Longer term analysis will need to be performed to see if costs can be recouped for genomic testing on a commercial operation.

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LIST OF ABBREVIATIONS

ADG	Average Daily Gain
AFC	Age at First Calving
BCS	Body Condition Score
BMP	Best Management Practices
BPI	Bull Prolificacy Index
BW	Body Weight
BSE	Breeding Soundness Evaluation
CI	Calving Interval
DF	Degrees of Freedom
DFI	Days to First Insemination
DMI	Dry Matter Intake
DNA	Deoxyribonucleic acid
DO	Days Open
EPD	Expected Progeny Difference
FIC	Days From First Insemination to Conception
FSH	Follicle Stimulating Hormone
gEPD	Genomic Expected Progeny Difference
GHG	Greenhouse Gas
GL	Gestation Length
gRH	Genomic Retained Heterosis
GnRH	Gonadotropin-releasing Hormone
IN	Number of Inseminations per Conception

kg	Kilograms
lbs	Pounds
LH	Luteinizing Hormone
NC	North Carolina
PCR	Polymerase Chain Reaction
RFI	Residual Feed Intake
SC	Scrotal Circumference
SD	Standard Deviation
SK	Saskatchewan
SNP	Single Nucleotide Polymorphism
SW	Southwest
UK	United Kingdom
USD	United States Dollar
VS	Vigour Score
WCCCS	Western Canadian Cow Calf Survey
WW	Weaning Weight

1.0 INTRODUCTION

For beef cow-calf producers, reproductive capabilities of the herd are more important than the sale of calves for both seed stock and commercial producer profitability. Without proper reproductive abilities, there is no production and therefore no calves to sell for breeding stock or to produce meat (Chenoweth 2011). Therefore, having management and selection focused only on production traits can negatively impact reproduction and fertility within the herd (Cushman et al. 2019). Poor reproductive performance is one of the main reasons for culling beef cows (Thundathil 2016) and a bulls reproductive ability is commonly tested with a breeding soundness evaluation (BSE) to determine if a bull is suitable for breeding (Chenoweth and McPherson 2016). Because of the importance of reproductive management within a herd, use of genomic testing has become popular to assist with these decisions and help make them more accurate (Van Eenennaam et al. 2007; Pollak et al. 2012).

Bull selection is an important decision for a cow-calf operation that will impact future genetic and economic potential for the herd. Bulls that produce more progeny will increase profitability and bulls passing on superior genetics to improve calf productivity are the most beneficial to an operation (McGowan et al. 2002). Proper bull management and nutrition during development and maturity is key to achieve their potential (Walker et al. 2009). Bull selection is based on many factors including multiple expected progeny differences (EPDs), breed, and reproductive ability which is determined through a BSE exam evaluating physical and semen characteristics (Makarechien et al. 1987; Walker et al. 2009; Chenoweth and Mcpherson 2016). Ensuring proper bull selection to align with and achieve herd breeding objectives is critical.

Bull performance can be impacted by multiple factors including physical health, nutrition, bull to cow ratio, environment, and libido (Blockey 1981; López et al. 1999; Van

Eenennaam and Drake 2012). In single sire breeding management, it is simple to determine a bull's performance. However, this is not the case with multi-sire breeding groups as it is more difficult to tell how a specific bull is performing amongst the rest. This can make bull culling decisions difficult, because calf output is one of the major economic inputs of a bull (Drake et al. 2011). Previous studies have shown that all bulls may not be siring their expected number of progenies, if they are producing any at all (Holroyd et al. 2002; Van Eenennaam et al. 2007; Domolewski 2017). Without the use of DNA testing there is no way to be sure how a bull is performing, or which progeny belong to him (Drake et al. 2011), and that could mean potential income may be lost due to poor producing bulls. Therefore, it is important to evaluate the economic potential of using DNA testing to identify prolific sires, in multi-sire commercial breeding herds.

Parentage testing using DNA is only one of several currently available genetic tests, while genomic testing is increasing in popularity and accessibility for producers even outside the dairy and seedstock industries. However, all tests may not be of equal value to producers, and it is important that the data obtained from these tests is used to make informed management decisions that will benefit the herd economically in the long run.

The objectives of this review are to 1) discuss factors considered for bull selection, 2) discuss multiple factors that can impact fertility, and 3) introduce genomic testing currently available and if these tools can help determine sire performance repeatability across multiple years.

2.0 LITERATURE REVIEW

2.1 Bull Selection

Reproduction in livestock operations is essential for proper production and economic viability (Chenoweth 2011). For beef cattle producers, bull selection can be seen as one of the most important decisions for several reasons (Stokes 2010). Primarily, bulls are an essential part of the breeding stock with the potential to transmit desired genetic traits to a large percentage of the herd (Chenoweth 2011). A bull can influence overall herd fertility and genetics more than any other single animal, while poor fertility by a bull can cause a substantial loss to the potential calf crop and herd as a whole (Walker et al. 2009). The majority of commercial beef producers use natural mating systems, and the success of these programs depends on the reproductive capacity and fertility of the sires used (Lunstra 1985). Therefore, selection of herd sires is an important consideration for commercial producers, and traits to consider include breed, price, and EPD rank of specific desired traits.

2.1.1 Expected Progeny Difference's (EPD)

Expected progeny differences (EPDs) provide estimates of the genetic potential of an animal as a parent in several different categories (Greiner et al. 2002). Purebred producers submit production data to their respective breed association for the calculation of EPDs. Expected progeny differences have been around for over 50 years, and accuracy has been improved through ge-EPDs introduced in 2009 (Gonda 2020)

Typically, when a bull is sold, the buyer is provided with EPDs for traits of interest to a commercial buyer which may include – calving ease, birth weight, wean weight, yearling weight and milk. For example, EPDs between two individuals predicts differences in performance of their future offspring when mated to animals of the same genetic merit, however, the two

individual bulls must be of the same breed for comparison (Greiner et al. 2002). It is also possible to look at how a bull will rank within their breed for specific traits of interest, such as birth weight, calving ease direct, weaning, and yearling weight, maternal milk, carcass traits, and many others.

As there is no progeny performance information available, when a producer purchases a yearling bull, EPDs are useful to determine what traits the bull potentially excels in and use this information to support the overall operations genetic/breeding program objectives. However, a bull with superior EPDs will not be useful to a producer or provide any genetic merit if he does not sire any calves (Drake et al. 2011). If a producer has no breeding goals or objectives, the usefulness and importance of an EPD is greatly reduced because no traits are predetermined to meet a future goal.

2.1.2 Breeding program objectives

Depending on the overall reproductive objectives for the cattle operation, many producers will be looking for different bull genetic characteristics to pass on to future progeny. For a commercial producer, crossbreeding programs are typically used because they can optimize productivity in the herd (Van Eenennaam 2017). A simple two-breed terminal cross involves straight bred cows bred to a bull of another breed, therefore depending on the breed currently used, a producer may want to select bulls of different breeds that have specific characteristics that may be less prominent in the main breed their herd is composed of (Herring 2016). The specific characteristics can be based on general breed characteristics or the specific EPD for that bull. However, both physical and genetic characteristics should be considered because the sire will inevitably contribute a major percentage of the genetic change in a herd (Chenoweth 2011). It has been reported that there are large differences between bulls for reproductive ability due to

individual characteristics of bulls more so than their age, the bull to cow ratio, or mating system (Makarechian et al. 1987).

2.1.3 Bull fertility

Ideally, having one test to determine a bull's fertility would be very useful to producers, however, there have been no tests that are both reliable and easy to perform on the farm. Tests such as serving capacity, libido, semen traits, behaviour and dominance, and scrotal circumference have all shown varying results in their ability to determine bull fertility (Makarechian et al. 1987; Coulter and Kozub 1989; Holroyd et al. 2002). Bull fertility can be influenced by a variety of factors including, breeding soundness evaluation (BSE) results, individual bull factors, breeding management on pasture, behaviour and dominance in a group, and a bull's nutrition (Chenoweth 1997; Utt 2016). Which could determine why no single/stand-alone test has been able to accurately predict fertility in bulls to date.

2.1.4 Breeding Soundness Evaluation (BSE)

A breeding soundness evaluation (BSE) is a test performed by veterinarians to determine if a bull meets the minimum standards for breeding in four categories (Alexander 2008). Typically, bulls are subject to a BSE exam prior to sale and many producers will test their bulls each year before the breeding season (Waldner et al. 2010). The four categories a bull must pass are a physical examination, scrotal circumference based on age, semen motility, and sperm morphology (Alexander 2008). Based on the results of the BSE, a bull is then classified as satisfactory, questionable, or an unsatisfactory potential breeder (Farin et al. 1989). Issues in any of the four categories can have negative impacts on breeding potential of the bull and therefore it is important to ensure all breeding bulls are physically capable of breeding before the breeding

season.

Testicular measurements have been found to be linked to semen quantity and quality in bulls (Coulter and Foote 1979). Typically, scrotal circumference (SC) is used as an indirect measure of testicular weight (Kastelic 2014). Scrotal circumference has been shown to be an accurate measure of puberty, predictor of semen quality, and positively associated with growth characteristics (Kastelic 2014). However, a variety of factors can influence SC including breed, age, and environmental influences (Coulter and Foote 1979; Kastelic 2014). In a study by Waldner and colleagues (2010) cows that were exposed to bulls with a smaller SC were less likely to be diagnosed pregnant than those bulls with a larger scrotal circumference.

Semen evaluation in terms of sperm motility and morphology are an important part of the BSE exam, and can relate to a bull's ability to breed a female as well (Chenoweth and McPherson 2016). With this evaluation, certain sperm defects can be identified and considered based on the potential they will have on the sperm reaching the site of fertilization or making a viable embryo (s). Studies suggest bull health and plane of nutrition in early life can impact semen quality and delay sexual maturity (Montanholi et al. 2016). Without testing a bull, its breeding potential remains unknown. In order to ensure optimized reproductive potential in a breeding bull, the bull should be known to produce large numbers of morphologically normal sperm (Kastelic 2014), making it important to test a bull's semen before the breeding season.

Previous studies in a variety of locations have shown that between 65-85% of bulls subjected to a BSE were determined to be satisfactory potential breeders, but this can vary from a multitude of bull factors and external factors as well (Chenoweth and Mcpherson 2016). According to Chenoweth (1994), the reproductive capabilities of bulls are influenced by multiple factors including, semen quality and quantity, libido and mating ability, and social interactions

between bulls or dominance effects on breeding pastures. A BSE is recommended for bulls (Chenoweth 1994), however the exam only assesses the bull physically and his semen characteristics, and does not determine sexual drive or libido (Chenoweth 1997).

2.2 Factors affecting fertility

Bull efficiency, as well as performance, should be considered to maximize profit potential. Under natural breeding systems, there are a number of factors that can impact herd fertility, including male, female, and environmental factors (Chenoweth 2011). A bull's age, lifetime nutrition, and breed can all play a role. Puberty in bulls is regulated by multiple hormones changing concentration and being up regulated or downregulated including luteinising hormone (LH), follicle-stimulating hormone (FSH), testosterone, and gonadotrophin-releasing hormone (GnRH) (Thundathil et al. 2016). Bull reproductive development occurs in three phases - infantile, prepubertal, and pubertal - with rapid testicular development occurring through puberty (Thundathil et al. 2016). Therefore, it is important to ensure a bull has not been negatively influenced during pubertal development to prevent negative impacts on their fertility.

2.2.1 Nutrition

Under natural breeding systems, there are a number of factors that can impact overall herd fertility (Chenoweth 2011). A bull's diet during his lifetime can have a long-term effect (Coulter 1994). Nutrition management of a bull needs to consider all phases of a bull's lifetime including their early life (pre- and post-weaning), prior to breeding, breeding season, and post breeding (Walker et al. 2009).

2.2.1.1 Early-life nutrition

Early-life nutrition of a bull will impact their reproductive potential for breeding for the remainder of their life (Thundathil et al. 2016). That means if a bull has poor nutrition before the onset of puberty, this may delay puberty, result in smaller testes size at maturity, and reduced sperm production potential (Thundathil et al. 2016). To ensure proper development pre-weaning, it is important there are adequate nutrients supplied in the diet for the growing calf, including adequate milk production from the dam (Walker et al. 2009).

If a bull calf is provided with the required nutrients in the diet early in life, they may have an earlier onset of puberty (Coulter 1994). In a study by Byrne et al. (2018), it was reported that age at puberty is regulated by diet before 6 months of age in Holstein-Friesian bulls, with no diet influence after 6 months of age. The onset of puberty relies on the initiation of GnRH, which will signal the anterior pituitary to secrete FSH and luteinizing hormone. The timing of the LH rise is important to determine the age of puberty (Thundathil et al. 2016; Byrne et al. 2018). It is important to ensure proper nutrition for growing bulls to prevent any negative impact on hormones leading to a reduction of reproductive potential later in life. The key to a well-balanced feeding program during a bull's life is to ensure nutrient requirements are met and that nutrients are neither under or over fed (Walker et al. 2009).

2.2.1.2 Effects of high-energy diets

It is recommended bulls be developed at moderate rates of gain rather than high rates of gain to prevent negative impacts from the diet (Walker et al. 2009). Feeding a high energy diet can have detrimental impacts on the testes, feet, and legs, impacting a bull's ability to properly breed (Coulter and Kozub 1989; Walker et al. 2009). In an earlier study, it was shown that bulls

on a high energy diet had an increase in backfat thickness and reduced epididymal sperm reserves (Coulter and Kozub 1989). Another study, Coulter (1994) showed that feeding a high-energy diet did not improve reproductive capacity, and harmed the bull's reproductive potential. The study concluded that bulls on a medium-energy diet over the high energy diet had higher sperm reserves and overall sperm production. During a 3-year field study by Coulter and Kozub (1989), the authors determined that as a bull's backfat thickness increased, fertility under multi-sire range breeding conditions declined.

2.2.1.3 Effects of undersupplying nutrients

During post-weaning both over- and under-nutrition can have negative impacts to the growing bull (Walker et al. 2009). Underfeeding or improper nutrition composition of the diet can cause deformities or make a bull prone to injuries (Massip 1975), which will negatively impact his breeding ability. Underfed bulls may also have a delayed onset of puberty (Walker et al. 2009). In terms of libido in underfed bulls, a study by Wierzbowski (1978) compared twin bulls, the lower weight bull (235 kg less body weight) on reduced feed had an enhanced libido expression compared to their twin. There was also no adverse effects on sexual behaviour in the lighter bull, and they were shown to be more efficient (Wierzbowski 1978). In other studies, semen quality was shown to be unaffected by underfeeding, but testes size was shown to be reduced (Moule 1963).

The impact of improper vitamin and mineral supply should not be ignored when balancing bull nutrition. Previous studies showed that a lack of vitamin A can reduce libido and cause sperm abnormalities (Moule 1963) and deficiencies in numerous minerals such as calcium and sodium can cause bone deformities (Massip 1975).

2.2.1.4 Feed efficiency and fertility

There is an increased tendency to select for beef cattle with improved nutritional efficiency (Thundathil et al. 2016). Feed costs are the largest variable cost in commercial beef production so improving the feed efficiency of the cattle may improve profitability (Awda et al. 2013). Residual feed intake (RFI) is a measure of feed efficiency that has increasing interest in beef cattle research. Residual feed intake is the difference between actual feed intake and the expected feed requirements given the body weight and other measures of production (Awda et al. 2013). However, many studies have shown that improved RFI in a bull correlates with decreased reproductive ability. In a study by Wang et al. (2012), it was found that a majority of the bulls that failed the sperm motility assessment had greater feed efficiency. It was also found that more feed efficient bulls also showed a delay in sexual maturity (Fontoura et al. 2016). This difference in timing of sexual maturity is likely due to the metabolic differences in energy partitioning between higher and lower feed efficient animals (Fontoura et al. 2016). Since a bull's main purpose on a commercial operation is his ability to breed and reproduce, it is important to consider if the benefits of a lower RFI outweigh the negative impacts on fertility.

2.2.2 Breeding management systems

Natural mating is the predominant method used by commercial producers in the United States and Canada (Van Eenennaam et al. 2014; BCRC 2019). For natural mating systems, producers will either use a single-sire or multi-sire breeding system. It has been reported that single-sire breeding systems can have a large range in pregnancy rates compared to multi-sire breeding (Lunstra and Lasterb 1982; Lunstra 1985). There are certain management considerations for producers when deciding between single or multi-sire breeding. Cow

numbers, pasture size, pasture availability, and bull cost are all considerations a producer needs to assess which system works best for their operation.

2.2.2.1 Single-sire breeding system vs multi-sire breeding system

For commercial producers, breeding bulls have a major influence on income for the operation. Bulls are valuable to a producer in two respects, his ability to impregnate as many cows/heifers as possible, and passing on superior genes to his offspring that will influence the herd for years to come (Drake et al. 2011). In single-sire breeding systems, all the potential income and genetic influence is placed on one bull, but his impact and ability to reproduce is easily known. In multi-sire groups, producers have no guaranteed way of knowing which bulls are reproducing efficiently and which are essentially wasting time and resources of the operation (Holroyd et al. 2002). There have been early arguments about the fertility rates among cows with single-sire or multi-sire groups. It has been assumed that using multiple sires in a breeding group can compensate for less fertile bulls, however, there have been conflicting results in the past whether pregnancy rate is higher or not for multi-sire breeding groups compared to single-sire groups (Lunstra 1985). However, there are multiple factors that play a role on bull fertility in multi-sire groups, that do not apply for single-sire groups. This includes, age differences, bull/cow ratio, and the social interaction between bulls (Makarechian et al. 1987).

Multiple factors influence a bull's ability to reproduce including age, health, and libido. These factors play a role in single-sire mating groups, but their effects can usually be detected early on based on observation during the breeding season or results at calving (Lunstra 1985). In multi-sire mating groups these factors also can be influential, however, social dominance in the group will also play a major role. Unfortunately, identifying bulls with high libido or higher

social dominance is not easily determined (Abell et al. 2017b). This results in variability in the number of offspring born per bull in multi-sire mating groups (Makarechian et al. 1987; Holroyd et al. 2002; Abell et al. 2017a). A previous study by Drake et al. (2011) found that a small majority of sires produced over 50% of the calves in a mating group, with multiple sires producing no offspring at all.

2.2.2.3 Behaviour and Dominance

The reproductive capabilities of bulls involve more than just their physical attributes and ability to breed. In multi-sire breeding systems, each bull's behaviour and dominance status will impact how they perform during the breeding season (Blockey 1979). Individual bull's libido, or their willingness to breed, will also influence their breeding season performance (Ologun et al. 1981; Chenoweth 1997; Abell et al. 2017a) regardless of whether they are in a multi-sire breeding group or not. Currently, there is no simple on farm test to determine a bull's libido. Previous studies have looked at the use of serving capacity (SC) tests to determine libido (Chenoweth et al. 1979; Blockey 1981; Godfrey and Lunstra 1989), however these are time consuming, and there are welfare concerns for the animals involved so they are no longer used. Therefore, a bull's willingness to breed cannot necessarily be determined prior to the breeding season like their abilities with a breeding soundness evaluation.

In groups of bulls with different ages, social dominance and age influenced the social rankings of the bulls (Blockey 1979) which impacted their breeding opportunities. However, Godfrey and Lunstra (1989) reported that bulls with a higher SC mounted more females than a bull with a lower SC even if the higher SC bull was less dominant. However, the study used all younger bulls who may not have had a determined social dominance structure. Another study

found that with the physical presence of a mature male, younger bulls' sexual activity was negatively affected (López et al. 1999). Therefore, multi-sire groups with both mature and young bulls may negatively influence the reproductive abilities of the group as a whole, resulting in some bulls performing much worse than others. However in contrast, another study found no relationship between social dominance structure and calf output (Holroyd et al. 2002). A bull's age and lack of experience may also impact their performance. The influence of age may be related to less mating experience of yearling bulls compared to mature bulls (Coulter and Kozub 1989). Overall, there are a multitude of factors that interact and influence the number of calves sired per bull, and therefore it can be difficult to predetermine a reason for poor or excellent performance.

2.3 Genomic Testing

In the Canadian beef industry, the use of genomic testing has grown as testing becomes more cost effective and more widely available. Genomic testing is predominantly used to identify a variety of genetic markers that can be useful for breeding to improve traits in a herd more quickly and accurately, or test for genetic defects to remove them from the herd (Hocquette et al. 2007; Van Eenennaam and Drake 2012). More specifically, genomic testing such as DNA testing, is being used to determine parentage in multi-sire breeding groups (Van Eenennaam et al. 2007). Other genomic tests include genomic prediction of breed composition, determining dry matter intake (DMI), growth, and feed efficiency, to name a few (Saatchi et al. 2014; Akanno et al. 2017a).

2.3.1 Single nucleotide polymorphism (SNP) and DNA parentage

In natural service breeding systems using multi-sire breeding groups, the performance of an individual sire is unknown (Gomez-Raya et al. 2008). For natural service breeding systems, a bull is expected to impregnate a certain number of cows in a breeding season, and it is assumed all bulls in a multi-sire breeding group will sire the same number of calves (Abell et al. 2017b). However, previous research has shown that this is not the case (Holroyd et al. 2002; Van Eenennaam et al. 2007; Drake et al. 2011), and that a small number of bulls in a group may sire a majority of the calves, while other bulls may sire little to no calves. This can be determined by conducting parentage testing on the bulls and calves. Previously, microsatellites had been more commonly used for bovine parentage testing (Heaton et al. 2002). However, with technological advancement, single nucleotide polymorphism (SNP) markers are most commonly used today. Using SNP testing has become a popular technique because they are abundant in cattle, the technique can be automated, has low error rates, and can be standardized across many laboratories (Heaton et al. 2002; Van Eenennaam et al. 2007). As this technique has increased in popularity, cost has decreased and made it more accessible for commercial producers as well.

Single nucleotide polymorphism parentage testing uses DNA markers to eliminate non-potential sires until a sire cannot be further eliminated. The International Society for Animal Genetics (ISAG) recommends at least 100 markers be used (Strucken et al. 2016). According to a study by Strucken et al. (2016), 200 SNPs need to be used to reduce the potential for false-negative results, but to eliminate false-positive results they found 700 SNP markers were needed for cattle. A study by Buchanan et al. (2017) looked at comparing three types of parentage testing: microsatellite, real-time quantitative PCR, and SNP arrays of various sizes (100, 200, 500, and 1000 respectively). Buchanan et al. (2017) found 1000 SNPs had the lowest mismatch rate at 2% and highlighted the influences of population size, genotyping error rates, and the

specificity and sensitivity of certain parentage analysis types on the testing results. Each year testing improves its accuracy and becomes more accessible to producers with reduced cost.¹

2.3.2 Genomic testing available currently

Since cattle were domesticated 8000-10,000 years ago, over 800 breeds have been established, and provide a significant source of nutrition and livelihood to nearly 6.6 billion people worldwide (Elsik et al. 2009). And over the past 50 years, researchers have created specific recommendations for nutrition and management of cattle across the world (Kononoff et al. 2015). With the sequencing of the cattle genome (Elsik et al. 2009), and advancements in genomics, genetic testing of cattle is becoming more available, allowing identification of the impact that gene variation has on animal performance (Kononoff et al. 2015).

The advancement of using SNP arrays for testing cattle have identified genetic markers associated with traits that can be used for improved breeding and selection programs for producers (Seabury et al. 2017). This has reduced the cost for testing over the years and introduced a wide variety of tests available for producers. This includes tests for specific traits that are beneficial to a producer such as, beef tenderness (Miller 2010; Walter et al. 2014), feed efficiency and growth traits (Seabury et al. 2017), leptin testing (Kononoff et al. 2015), and recessive defect and mutations (Charlier et al. 2008; McClure et al. 2014). However, many of these tests are marketed to purebred producers.

Current tests available for commercial producers is limited in Canada. There are only two available, and there is no scientific information evaluating the use of either of these tests by independent studies. Quantum Genetix has a product called Q-select advertised as a powerful

¹ Current pricing for parentage testing is \$15.43 (Neogen) to \$20 CAD per test (Quantum 2024).

selection tool for your herd (Quantum Genetix 2024). This is marketed to commercial producers and claims to focus on beef production traits that are economically important. Using this information is supposed to help select the best bulls and replacement heifers. The second test available is EnVigourHX™ by Delta Genomics (now Neogen Canada). This test was developed based on results from a study by Basarab et al. (2018) and is described in more detail below.

2.3.3 EnVigour HX™

In the commercial beef production sector, using crossbred cattle for the benefit of heterosis, or hybrid vigour, in the herd has a benefit of increasing overall production efficiency and increases longevity and reproductive rate of beef cows (Cundiff et al. 1992; Núñez-Dominguez et al. 1992; Macneil et al. 1994). In the cow-calf sector, the greater number and weight of weaned calves per cow is an important economic output value and can be increased from the effect of heterosis with crossbred cattle over straight and purebred cattle (Cundiff et al. 1992). The value of a new genomic tool could help producers understand their animal's hybrid vigour and make an optimal crossbreeding strategy for their herd (Delta Genomics 2018).

EnVigour HX™ is a tool developed by Delta Genomics®² to help producers develop an optimal cross breeding strategy for their herd when they have defined goals for their herd (Delta Genomics 2018). EnVigour HX™ uses gEPDs (genomic expected progeny differences) to determine a genomic breed composition of each animal and assign a vigour score, the test also gives parentage verification, providing three tests from one sample. A benefit of this information is which bulls to put in which mating group, based on the cow's vigour scores and breed composition, the bull's vigour score and breed composition, as well as a bulls past history of the

² EnVigourHX™ and Delta Genomics have now become iGenity and Neogen

number of offspring he sired. However, each individual producer will need to determine if the benefit and usefulness of the results will outweigh the cost of testing (\$45 per head in 2018).

EnVigour HX™ is promoted as a tool for replacement heifer selection (Delta Genomics 2018). The vigour score (VS) is reported as a percentage, where the lower the number the less hybrid vigour the animal is deemed to have. Scores typically range from 20 for straightbred animals to above 80 for crossbred/composite animals. A 10% increase in VS has been estimated to increase 200 d weaning weights by 1.4 kg, shorten age at first calving by 2 d, increase pregnancy rates 2% and increase wean rates 3% (Basarab 2018; Delta Genomics 2018). The suggested guidance is to EnVigour HX™ test all breeding females and breeding bulls in the first year and match bulls with cows that are least like them in terms of breed composition to increase VS of progeny with strategic crossbreeding.

At the Lacombe Research Station, 412 replacement heifers were followed for 5 calvings and split into High and Low vigour groups based on their vigour scores. The high vigour (VS >48.6%) females had 47% retention to third parity while only 32% of the low vigour (VS ≤ 48.6%) females remained after three calvings. Across five parities, the high vigour heifers had higher retention levels and the improved performance provided a \$161 per head per year benefit (Basarab et al. 2018).

Currently, the only information available about EnvigourHX™ is from the lab that developed it (Delta Genomics), and one study whose results were used to develop the test (Basarab et al. 2018). All claims of the value and performance benefits obtained from using the test are from one of these two sources. Therefore, details and results of this test may be biased with no current third party analysis having been performed or tested on the validity.

2.3.4 Use in commercial herds

The popularity of genomic testing services for the beef industry has been increasing in recent years (Thompson 2018). The benefit of genomic testing is the use of more informed genetic selection, which can help to increase prediction accuracy and selection intensity in crossbred programs (Thundathil et al. 2016). In turn, genetic selection can help improve a herds long term profitability through production efficiency improvements (Ochsner et al. 2017). Genomic testing in cattle can be done with simple traits (controlled by a single pair of genes) or complex traits (controlled by multiple pairs of genes), however, complex traits are more difficult to match with SNPs (Ballenger et al. 2016). And testing for simple or complex traits can have economic benefits, such as testing for horned or polled (simple), coat colour (simple), reproductive performance (complex), or feed efficiency (complex). However, all traits of interest will have varying levels of heritability (Ballenger et al. 2016) and therefore affect selection ability.

The information provided for producers from genomic testing has potential to generate value in the beef industry, however, the beef cattle supply chain is made up of several separate sectors, and as a result, the distribution of value down the supply chain will depend on the application (Van Eenennaam and Drake 2012; Thompson 2018). Therefore, the value of genetic tests relates to the benefit of the results for the producer outweighing the cost. Genomic testing has the potential to generate value for each sector of the supply chain, depending on what testing is done and how the information is used. For example, Van Eenennaam and Drake (2012), determined that the value of genomic testing that improves selection accuracy would be highest for the breeding sector and replacement stud animals. And testing to improve replacement female selection accuracy would be most beneficial for commercial producers. In general, commercial

beef producers tend to be slower adopters to new technology because of the lower business margin compared to other sectors, like dairy producers (Berry et al. 2016). Therefore, a clear economic incentive needs to be available for producers to decide to use the tests.

2.4 Sire repeatability

The use of DNA parentage testing for multi-sire breeding groups is a simple way to determine progeny numbers of each sire, thus allowing more informed selection decisions of herd bulls and their progeny. In this situation, the value of a bull comes from his ability to impregnate as many cows in the group as possible, and pass on superior performance genes to his offspring (Van Eenennaam et al. 2014). However, it is important that a bull's performance is consistent over time, and not just one year. If a bull cannot impregnate cows and produce progeny, he will not be able to pass on the desired traits he may have been purchased for (Van Eenennaam et al. 2014). Also, if a producer keeps and uses replacement heifers from herd bulls, a bull's genetics will stay in the herd for many years (Van Eenennaam et al. 2014). Depending on whether a sire is selected for replacement heifer production or terminal carcass characteristics, it is important to know if the sire is performing adequately.

2.4.1 Progeny number per sire

If a bull's performance could be predicted, multi-sire breeding would be very efficient (Bennett et al. 2017). However, for yearling bull, this is difficult to do accurately. Previous studies have attempted to find out how to accurately and simply predict a bulls' performance, but the wide range of variables make it difficult (Blockey 1979; Chenoweth et al. 1979; Henney et al. 1990; Abell et al. 2017a). With the use of DNA parentage testing, knowing a bull's

performance after a breeding season has become possible even in multi-sire breeding groups. However, with the use of this technology, previous studies have shown that in many multi-sire breeding pastures it is typical that a disproportionately high number of calves are sired from one bull, and another bull may only sire one calf (Van Eenennaam et al. 2014; Abell et al. 2017b; Domolewski 2017)

An important factor of bull performance is their ability to sire a large number of calves and pass on their genetics, but equally as important is the sire's ability to repeatedly perform well in this sense. If a bull outperforms others one year, but performs poorly the next, is he worth keeping and how will he perform in subsequent years? Therefore, it's important to determine if sire repeatability with calf numbers is possible. In an Australian study by Holroyd et al. (2002), using mixed *Bos indicus* bulls, the authors found calf output of their bulls to be moderately repeatable (0.43-0.69) across years at four of their five sites under extensive range conditions. In another study by Van Eenennaam et al. (2014) using *Bos taurus* bulls, repeatability of bull prolificacy over 3 years was also moderately repeatable (0.33-0.37) under more intensive pasture conditions. In a study evaluating sheep by Juengel et al. (2018), using rams under multi-sire mating conditions, they found ram mating success to be moderately repeatable and heritable (0.30) among 15 flocks across 2-3 years (Juengel et al. 2018). If a sire can consistently be a top performer, and this can be determined early on, then beneficial management and economic decisions can be made by a producer to keep well producing bulls, and cull poor producing bulls.

2.4.2 Replacement heifers

According to the Western Canadian Cow-Calf Survey in 2017, 69% of producers who responded retained heifers for replacement (WCCCS 2017). Replacement heifers are a key part of the profit potential and genetic improvement of the herd (Corah 1991). In commercial

crossbreeding systems, it is important for a producer to decide if they will be purchasing or raising their own replacements (Yadav et al. 2018). To ensure multiple years of consistent replacement heifers are produced, it is essential that an appropriate crossbreeding system is used based on management goals of the operation (Theunissen et al. 2011). In any crossbreeding system, it is important to have a long-term plan focused on specific ideal traits, to ensure maximum benefits from crossbreeding (Yadav et al. 2018). Therefore, when selecting a bull it is important to realize that the presence of a bull in a breeding group is not necessarily a guarantee of any offspring, or ones that are sufficient to use as replacement heifers (Drake et al. 2011). It is important to ensure herd sires are producing offspring, as well as passing on the desired traits to produce daughters for use as replacement females in the herd. Ideally, these daughters will remain in the herd for multiple years, meaning a bull's genetics will be a large part of the genetic potential of the cow herd (Corah 1991) and can remain in the herd for a long period of time.

Crossbreeding programs can focus on traits ideal for terminal calves or maternal replacement calves, the latter of which is most important for producing quality replacement heifers. Longevity of a beef female is very important for profitability of an operation (Cushman et al. 2013), and crossbreeding focused on maternal traits can help. For a commercial producer, reproduction is more economically valuable than growth traits, and herd selection programs focused on production traits could have a negative impact on reproductive performance (Cushman et al. 2019). It is important to use separate sires and dams, and base selection decisions on whether they are producing terminal progeny or replacements (Weaber 2015).

One of the benefits of DNA parentage testing is the ability to select replacement females more accurately in the herd (Van Eenennaam and Drake 2012). When keeping replacement females, confirming their sire through DNA parentage testing will make breeding group

selection easier, and help prevent inbreeding. If a producer is consistently keeping their own replacements, identification, and use of genomic markers for sire selection of female fertility traits can ensure maternal trait sires are passing on the desired traits (Thundathil et al. 2016). However, it is also important that producers have a heifer development program in place, to ensure the quality females chosen to be kept are meeting the reproductive and growth production targets determined by the operation (Engelken 2008).

According to Corah (1991), there are five phases in replacement heifer selection and development: sire selection, preweaning, weaning to breeding, breeding to calving, and calving to rebreeding. Throughout development producers invest a substantial amount of time and resources into these females, so it is important producers are able to get a return on their monetary and time investment (Engelken 2008). Ideally, replacement females will be used for multiple generations and incorporate new and improved genetics into the herd (Bridges 2013) half from the female and half from the sire in each progeny. Sire selection is an important component of heifer development and management decisions, as females will produce typically one calf a year, but a sire will produce multiple calves and perhaps multiple replacement females. This means his genetics will remain in the herd for many years and generations if their replacement female offspring perform well and remain in the herd. A future study following replacement females of highly prolific sires through multiple generations and following subsequent calf performance would be useful to determine how much of a continued influence well performing sires have on an operation.

2.4.3 Carcass Characteristics

For all sectors of the beef industry, increased growth rates are associated with higher economic returns (Buchanan et al. 2005). In the cow-calf sector, this is typically represented in

weaning weights of calves in the fall balanced with high conception, good calving distribution and reduced early calf death. Over the years, growth has increased in all industries with new technological adoptions. For backgrounding and finishing sectors, the use of implants to improve feed to gain in calves has improved the system, and selective breeding through EPDs and improved genetics has helped improve weaning weights for cow-calf producers (Buchanan et al. 2005). The use of organized crossbreeding systems allows for improved efficiency of beef production through heterosis benefits, including breeding and carcass traits (Theunissen et al. 2013). The use of breed differences from a crossbreeding system can allow for higher productivity and profitability in a herd, through improved reproductive potential, growth improvement, and an overall better performing calf (Theunissen et al. 2013). It is also important to ensure a sire with the desired terminal traits is being used to produce terminal calves, so positive carcass traits can be passed on.

For carcass traits, selection is an especially beneficial tool because unlike reproductive traits, most carcass traits have moderate to high heritability (Theunissen et al. 2011; Van Eenennaam and Drake 2012). These traits are also realized sooner in the production system compared to reproductive traits. For example, carcass traits can be realized when the calf is sold, however, reproductive traits and breeding capability are not realized until the heifer gets pregnant, has her first calf, and then is bred back again in a timely fashion (Engelken 2008). However, for specific carcass traits like marbling, yield grade, and ribeye area, producers who sell calves at weaning gain little value in the selection process focused on these end-product qualities (Weaber 2015). Also, it is difficult to find sires that are able to meet the goals for both terminal calves and replacement heifers. One study found that exclusive selection for terminal carcass traits has negatively impacted the improvement of maternal traits in the UK beef suckler

herd (Roughsedge et al. 2005). One solution presented by Weaber (2015) suggests having two separate breeding decisions for maternal vs. terminal traits. This will improve selection intensity for both groups and limit the issues that arise when trying to balance qualities for both terminal carcass and maternal traits in a single sire (Weaber 2015).

However, economically it may not be desirable for cow-calf producers to focus on breeding for specific carcass traits. It would only be beneficial if the producer was to receive differential (quality based) prices for their calves, however, this does not typically occur (Melton 1994). An example would be a premium paid back to the producer for specific carcass attributes and carcass quality (Van Eenennaam and Drake 2012). In a study by Van Eenennaam and Drake (2012), the average gross return including a quality premium per sire was \$712 USD, but when you look at gross revenue of all male offspring by sire it ranges from \$4881 to \$55,889 US dollars. This is because of the difference in prolificacy. Even a sire that passes on the most desirable carcass traits to get the best premium is useless if he cannot impregnate cows and produce multiple offspring year after year (Van Eenennaam and Drake 2012). Essentially, producers who market calves at weaning should place the most economic emphasis on reproductive traits (~47%) and focus less on production traits (~24%), and consumption (meat quality) traits (~30%) (Melton 1994; Van Eenennaam and Drake 2012).

In terms of carcass characteristics, it has been shown previously that there is a positive relationship between a sire's carcass EPD and their progeny phenotype ($P < 0.001$) (Crews 2002). Therefore, EPDs would be a useful determinant for selecting a sire to produce terminal calves. But EPDs do not determine sire prolificacy, so DNA parentage testing can be used to verify if a sire is producing the quality of calves expected based on his EPD scores. With EPDs (Crews 2002) and moderate to high heritability of carcass traits (Crews and Kemp 2002), for

terminal progeny for commercial producers, it may be best to focus on ensuring the sires are producing a high number of calves because that is where the greatest economic value will come from.

2.5 Summary

A herd sire has a very important role on a cow-calf operation. In a multi-sire breeding program, it is assumed that all sires will produce the same number of offspring. However, there are multiple variables that impact this expected outcome. A bull's age, dominance status, early life nutrition, health, behaviour, and libido all play a role in a bull's ability to produce offspring. But at the end of the day, a bull's main job is to produce multiple offspring per year and pass on his desired traits. Therefore, selecting the right sire to fit the production goals of the operation is very important. With the use of proper crossbreeding programs, offspring with desired maternal or carcass traits can be produced. And in any crossbreeding program, proper management and informed breeding decisions are important, and they can be assisted with the use of genomic testing.

Genomic testing can help determine which calves belong to which sire, prolificacy of each sire, the hybrid vigour of mature and replacement females, and many other specific traits. While many factors can impact a bull's ability to sire calves, genomic testing like DNA parentage can help determine a bull's performance in multi-sire breeding groups. And if a sire's performance is repeatable across years, testing can help determine early whether keeping the sire is economically beneficial to the operation.

The objectives of the following research are to 1) determine paternity in multi-sire breeding groups, number of progeny per bull, and describe and assess repeatability of the sires'

contribution through progeny number per year, 2) evaluate replacement heifer performance from sires and, 3) evaluate EnVigour HX™ testing in a commercial herd and assess economic benefit of using the program for the producer.

3.0 EVALUATION OF BULL PROLIFICACY ACROSS MULTIPLE YEARS AND THE IMPACT ON HEIFER PERFORMANCE

3.1 Introduction

Cattle breeding programs are one of the most important considerations for a cow-calf beef cattle operation, as economic potential of a ranch is highly related to the herd's reproductive performance (Chenoweth 2011). While proper health and management of breeding animals are important for a producer's economic benefit, it is also important to improve herd efficiency overall to be able to feed a growing population (Thundathil et al. 2016). In Western Canada, the use of multi-sire breeding pastures for beef cattle is a common practice, especially with industry consolidation leading to increasing herd sizes (Makarechian et al. 1987; Tang et al. 2011). However, in this system, producers may not know for certain the number of progeny sired by each bull, and they will not be able to determine if performance traits were passed on (Van Eenennaam et al. 2007).

According to the Canadian Cow-Calf Cost of Production Network the sale of weaned calves is the primary source of income for cow-calf producers which ranged from 70-85% of enterprise revenues in 2022 (Canfax 2023). Weaned calf revenues are based on the number of calves sold and their market value at sale, therefore, a bull's value is related to his ability to sire as many offspring as he can and his ability to pass down desirable genes to his offspring (Van Eenennaam et al. 2014). In many multi-sire breeding groups, it is typical that a disproportionate number of calves are sired from one bull, while another bull will only sire one calf (Abell et al. 2017a; Domolewski 2017). This can be influenced by a variety of behavioural influences on the bull, including the bull's libido (Blockey 1979). However, with DNA parentage testing, a producer can eliminate low producing bulls not economically beneficial to the operation (Holroyd et al. 2002). The use of DNA parentage technologies in commercial herds enables a producer to identify and cull low producing bulls and retain high producing bulls (Gomez-Raya

et al. 2008). Although there is an obvious cost to producers for this testing, it would be profitable when the benefits of an overall increase in calf production overrides the cost of the test (Gomez-Raya et al. 2008).

Selecting which bulls to mate with which females is important to consider for herd improvement. Selections made by producers can impact the herd for multiple generations, especially when replacement females are selected from within the herd (Wiggans et al. 2017; Ortega et al. 2018). According to surveys conducted in the US and Western Canada, selecting replacement females from within the herd is common practice; 80% of US producers raise replacements (NAHMS 2008) and 80% of WCCCS survey respondents indicated they retain heifers for replacement (WCCCS 2014). Because impacts from selection are long-lasting it is important for a producer to set goals and to make informed selection decisions in their herd.

Crossbreeding programs are used by producers to optimize productivity through the exploitation of hybrid vigour, or heterosis, to improve overall production efficiency, and increase longevity and reproductive rate of beef cows (Cundiff et al. 1992; Núñez-Dominguez et al. 1992; Macneil et al. 1994). Heterosis, or hybrid vigour, refers to the performance advantages of the crossbred offspring from their pure/straight bred parents (Akanno et al. 2017a). Breed complementarity results from crossing breeds from different, but complementary, biological types (Van Eenennaam 2017). When considering breed complementarity in crossbreeding programs, record keeping is essential, to make decisions based on a set goal of traits for the calves (Van Eenennaam 2017). Genomic testing can also be used to determine breed composition in crossbred cattle as well. This type of genomic testing is promoted as beneficial for heifer retention selection as well as for breeding group selection.

Few studies have examined the variation of calves sired in multi-sire breeding pastures and evaluated the consistency of an individual bull's performance over time. Also, genetic tools for selecting bulls with superior breeding performance that would be passed along to male or female progeny are in short supply and generally come at a higher cost to the producer.

The objectives of the following study are 1) to determine paternity in multi-sire breeding groups, number of progeny per bull, and describe and assess repeatability of the sire's contribution through progeny number per year, 2) to evaluate the performance of sires' daughters to second parity and 3) to evaluate the EnVigour HX™ test with an economic analysis for a commercial beef producer.

3.2 MATERIALS AND METHODS

Data collection involved collaboration with a commercial cow-calf ranch operation located in Saskatchewan over a 6-year period and a genomic testing company in Edmonton, Alberta.

The ranch operation was located in southwest Saskatchewan, 26 kilometers north of Eastend, Saskatchewan. Ownership of the herd changed hands in 2018. Data for the herd was collected working with private owners for the 2014-2018 breeding seasons and a nearby Hutterite colony for the 2019-2021 breeding seasons. The cow herd consisted of approximately 400 breeding females and approximately 20 bulls per year. This operation started calving in late April each year. The operation retained 75 to 90 replacement females per year.

Four breeding groups were used each year, two mature cow groups, one 2-year-old group, and one replacement heifer group. During breeding season, each of the mature cow groups had access to approximately 360 ha each of native pasture and mixed grass legume

pasture stand. The 2-year-old group and replacement heifer group each had access to approximately 120 ha of a mixed grass legume pasture stand. Access to free choice mineral was available year-round. Details on winter feeding programs for bulls and females was unavailable.

3.2.1 Breeding group descriptives

A total of 43 different bulls were used over the 6 year period, with 20 bulls being used for 3 or more years. The herd animals were crossbred with Red Angus, Black Angus, and Beefbooster influence. Each year there were 4 multi-sire breeding groups: Groups 1 and 2 included mature cows (> 3 year of age), group 3 included 2-year-old females, and group 4 included yearling replacement heifers (Table 3.1). Age of bulls and cows were recorded each year from producer records. Bulls and cows were not assigned to the same breeding group each year but were assigned based on the judgement of the producer. No information was provided by the producer on how they selected which bulls go to which breeding group. Bulls were removed from the breeding pasture if injured and typically replaced with a spare from the replacement group. During the study period no bulls were pulled in the middle of the breeding season.

Table 3.1 Summary of breeding group management

		Breeding group ¹			
		1	2	3	4
2014					
	Number of sires	5	6	3	4
	Number of cows	130	136	67	75
	Bull:cow ratio	1:26	1:23	1:22	1:19
	Bull age, year	1-4	1-5	2-3	1-4
	BPI ² range	0.3-1.7	0.2-2.5	0.6-1.4	0.7-1.4
	Breeding season length (d)	66	66	59	56
2015					
	Number of sires	6	6	3	4
	Number of cows	162	154	70	85
	Bull:cow ratio	1:27	1:26	1:23	1:21
	Bull age, year	1-4	1-5	3-4	1-3
	BPI range	0.35-2.4	0.26-2.5	0.5-1.4	0.2-2
	Breeding season length (d)	74	64	68	68
2016					
	Number of sires	7	6	2	3
	Number of cows	172	159	39	71
	Bull:cow ratio	1:26	1:27	1:20	1:24
	Bull age, year	1-4	1-4	4-5	2-4
	BPI range	0.2-2.5	0-2.6	1.02-1.8	0.2-2
	Breeding season length (d)	66	61	61	67
2017					
	Number of sires	8	6	3	3
	Number of cows	154	159	71	78
	Bull:cow ratio	1:19	1:27	1:24	1:26

	Bull age, year	1-5	1-4	1-6	1-4
	BPI range	0-3.3	0-2.4	0.6-1.5	0.1-1.9
	Breeding season length (d)	67	64	67	50
2018					
	Number of sires	8	7	3	3
	Number of cows	184	148	79	79
	Bull:cow ratio	1:23	1:21	1:26	1:26
	Bull age, year	1-7	1-5	2	1-5
	BPI range	.05-3.3	0.1-1.7	0.3-1.5	0.12-2.2
	Breeding season length (d)	60	60	60	51
2019					
	Number of sires	7	7	3	4
	Number of cows	157	157	79	90
	Bull:cow ratio	1:22	1:22	1:26	1:23
	Bull age, year	1-4	1-4	2-3	2-3
	BPI range	0-4	.25-2.4	0.9-2.8	0.2-2.1
	Breeding season length (d)	60	60	55	45

¹Breeding groups 1 and 2 are mature cows, group 3 is two-year olds and group 4 is replacements.

²BPI is Bull prolificacy index where a value of 1 means that after adjusting for conception, a bull bred the number of females he was expected to. The index is defined in equation 3.1 in Section 3.2.6.

In 2014, 18 bulls and 450 cows were used, managed in four separate breeding groups. In 2015, 19 bulls and 471 cows were used, managed in four separate breeding groups. In 2016, 18 bulls and 441 cows were used, managed in four separate breeding groups. In 2017, 20 bulls and 462 cows were used, managed in four separate breeding groups. In 2018, 21 bulls and 490 cows were used, managed in four separate breeding groups. In 2019, 21 bulls and 483 cows were used,

managed in four separate breeding groups. Individual group breeding dates, cow and sire details varied across years and breeding groups (Table 3.1).

Figure 3.1 represents the bull:cow ratio for the 4 breeding groups across all 6 production years (2014-2019). Each year, groups 1 and 2 had the highest number of bulls (5-8) and groups 3 and 4 had the least number of bulls (2-4). As shown in Figure 3.1, the cow number per group ranged throughout the years. The mature cow breeding groups, group 1 and 2, had an average of 156 cows over 6 years. The two-year-old groups, group 3, had an average of 68 cows over 6 years. The yearling heifer group, group 4, had an average of 80 cows over 6 years. Breeding season was between July and September with the calving season spanning 69-85 days (Table 3.2)

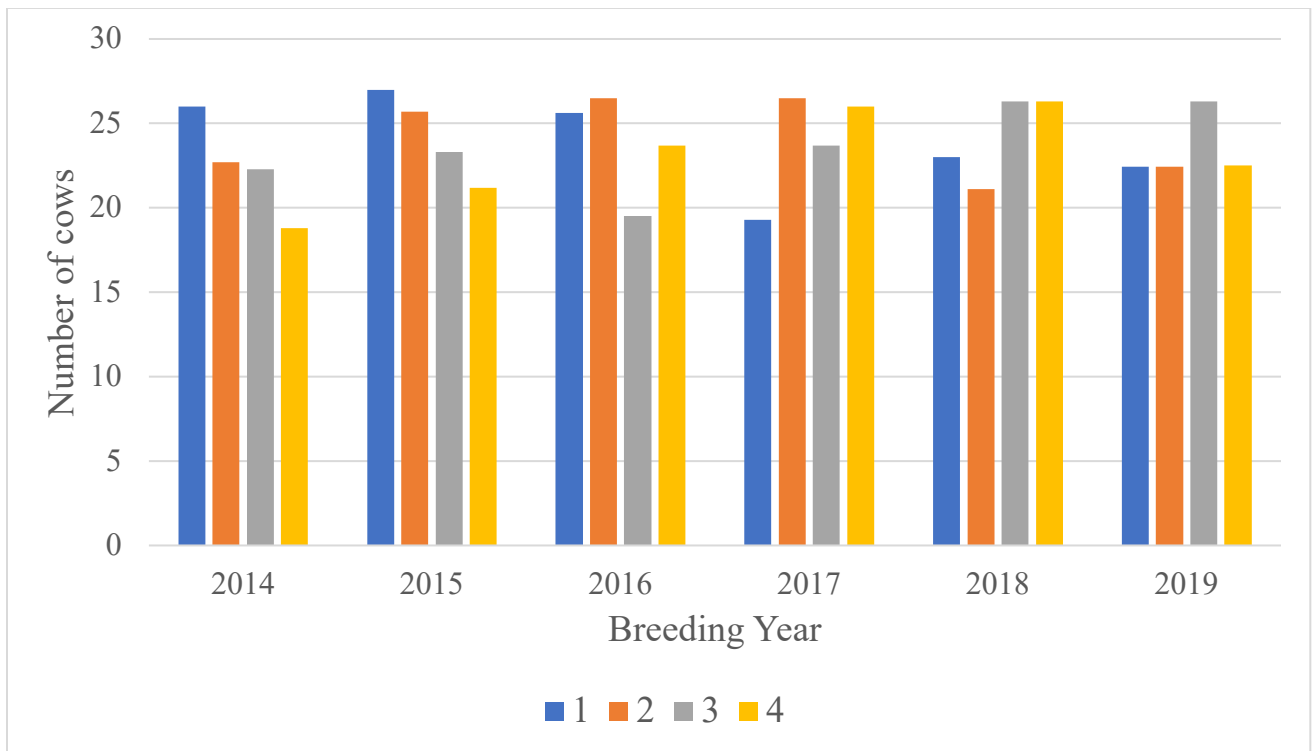


Figure 3.1. Number of cows per bull for each breeding group by year.

Table 3.2 Summary of breeding and calving management over 6 yr

	2015	2016	2017	2018	2019	2020
Breeding season start	13-Jul-14	11-Jul-15	14-Jul-16	11-Jul-17	16-Jul-18	12-Jul-19
Breeding season end ¹	17-Sep-14	15-Sep-15	18-Sep-16	16-Sep-17	14-Sep-18	10-Sep-19
Calving season start	05-Apr-15	11-Apr-16	15-Apr-17	07-Apr-18	30-Mar-19	10-Apr-20
Calving span d	77	85	78	81	85	69

¹Breeding season end date based on 2 mature cow groups, first calvers and replacement heifers ending 5 and 10 d sooner, respectively.

3.2.2 Replacement heifer selection criteria

From 2015 to 2018 the herd was owned and managed by one owner, then sold to new owner/management in 2019. Replacement heifer selection criteria changed slightly from 2018 to 2019 due to ownership and management changes. All management decisions were made by the owner and the research study did not have influence on any management decision making.

Between 2015 and 2018 a heifer was ineligible for selection as a replacement if: a) she was a twin with a bull; b) she had been treated with antibiotics as a suckling calf; c) her dam's weight exceeded 771 kg; d) her temperament was a concern, or; e) she was a daughter of an unwanted bull. After culling, heifers were weighed, and the top 90 females were retained.

When the herd changed ownership in 2019 selection criteria included culling heifers: a) from temperamental dams; b) with poor conformation (including if a heifer's dam had a poor udder, feet or body); c) born in third cycle, or; d) low body weight of the heifer at weaning. Additional notes were made during post-weaning feeding management and used in the selection process.

3.2.3 DNA sampling and animal data collection

In order to calculate calving cycle, the calving season start date was based on when the first mature cow (>3 year) had her calf. The calving season ranged from 69 to 85 d each year (Table 3.2)

Each year, at calving notches of ear tissue were collected from all calves, both live and dead. A specialized Tissue Sampling Unit (TSU) tagger by Allflex® was used to collect ear tissue samples from each calf. Samples were collected using instructions provided by Allflex® (Allflex 2021). This involved removing a TSU vial unit from packaging and inserting it into the tissue applicator. Once the TSU vial was inserted the retention ring was closed to lock the tube in place. The applicator handle was then squeezed together until locked. The handle was then released and the red plastic clip was removed meaning the applicator was loaded and ready to take a sample.

To take the sample once the gun was loaded, the gun opening was slid over the calf ear and positioned approximately 1 inch from the edge of the ear. The handles were squeezed together to take a sample and then released to free the ear. The TSU tube was then removed.

Tissue samples were then either frozen or stored at room temperature depending on the vial used for collection which varied by year. Ear tissue samples were used for DNA parentage testing and couriered to a lab for testing. Each ear tissue sample sent was correlated with a calf ear tag identification number and a list of potential sires was sent as well.

For all bulls used for breeding, tail hairs were collected for lab analysis each year, with approximately 20 tail hairs with follicle attached collected from each bull (McGrath 2014). Bull tail hair only needed to be collected once per animal and were typically collected at a time when the bulls were brought to the chute for processing. Once the lab had the bull's DNA profile on record, they did not require future submission of DNA (tail hairs).

All samples from 2015 to 2017 were sent to Quantum Genetix in Saskatoon, Saskatchewan for DNA parentage testing, while samples from 2018 to 2020 were sent to Delta Genomics (now Neogen Canada) in Edmonton, Alberta for parentage testing.

Calf birth date and dam and calf identification were recorded at calving each year based on dangle tag number and letter (n=2374). Calves were numbered based on the order they were born with #1 being the first born, and the letter provided after was based on the letter year (BIF 2021). As well, calf birth weights were obtained within 24 h of birth and weaning weights were obtained in October each year, at approximately 172 days of age. Some years there were missing weaning weights that were not collected by the operation.

3.2.4 Sample analysis

All DNA samples were analyzed using SNP technology for sire verification. At Quantum Genetix, analysis followed the procedure outlined by Domolewski (2017) for all samples prior to 2018. Similar testing was performed for all samples submitted from 2018 onward at Delta Genomics lab. All calf ear tag samples from 2018 were analyzed for parentage and genomic testing on breed composition and vigour score (EnVigour HX™, Delta Genomics, Edmonton, AB, Canada). All calf ear tissue samples from 2019 were tested for parentage, while replacement heifers were also tested for breed composition and vigour score (EnVigour HX™ analysis). All DNA samples genotyped at Delta Genomics followed the procedure outlined by Basarab et al. (2018). Calves tested with EnVigour HX™ ® were given a vigour score (VS) and a percentage of breed composition. In 2018/2019 the test was able to detect 13 different breeds, including Angus, Brown Swiss, Charolais, Galloway, Gelbvieh, Hereford, Holstein, Jersey, Limousin, Maine Anjou, Salers, Shorthorn, and Simmental. If an animal had evidence of a breed in addition

to these 13 or portions that could not be determined to be of the above breeds it was assigned a percentage “indeterminate.”

3.2.5 Statistical Analysis

Statistical analysis was performed using SAS 9.3 (SAS version 9.3; SAS Institute Inc., Cary, NC). Descriptive statistics were performed using Microsoft Excel spreadsheets. The coefficient of determination or R² values was calculated to determine if there is a relationship between bull performance in their yearling year versus two-year old year based on their Bull Prolificacy Index (BPI).

An index called the Bull Prolificacy Index was calculated using the equation developed by Domolewski (2017):

$$BPI = \frac{\text{No. of sampled calves attributed to sire}}{\frac{\text{Number of calves born}}{\text{Number of bulls in breeding pasture}}} \quad (3.1)$$

Where *BPI* is calculated with number of calves attributed to a sire through genomic parentage testing, the total number of calves born in the breeding pasture, and the total number of sires in the breeding pasture. The BPI index allows for standardized comparison across breeding groups per year by accounting for different bull to cow ratios and pregnancy rates. An index value of 1 means a bull sired the “expected” number of calves (e.g., an equal proportion) based on total bulls in the breeding group and number of calves born and parentage verified. A score above 1 means the bull exceeded expectations and sired a higher number of calves than expected. A score below 1 means the bull sired fewer calves than expected for that breeding season. It is more accurate to use BPI, when analyzing sire performance, over total calves sired because calves attributed to sire alone does not account for cow pregnancy rate or bull to cow ratio. Using a BPI

score to analyze a sire's performance accounts for the bull to cow ratio differences and cow impact. BPI represents the proportion of a sires' contribution based on their expected contribution and the opportunity to contribute.

A BPI score was calculated for every individual bull each year to determine BPI variation across years. Based on a bull's individual BPI score in a year, those bulls were sorted into groups: Bottom 25%, Average, and Top 25% BPI bulls, and evaluated based on their average BPI group.

Sire performance by age and when grouped by average BPI score was analyzed using the ANOVA procedure of SAS (2020). For age influence on BPI analysis, the equation:

$$BPI = year + age + (year \times age) \quad (3.2)$$

was used. Where *BPI* is each sire's calculated bull prolificacy index in a given year, *year* is specific breeding year and *age* is the sire's age in years.

For daughters sired by bulls based on BPI grouping, the equation:

$$BPI = year + daughters\text{sired} + (year \times daughters\text{sired}) \quad (3.3)$$

was used. Where *BPI* is each sire's calculated bull prolificacy index in a given year, *year* is the specific breeding year, and *daughters sired* is the number of daughters sired by each individual bull. Differences in means were determined significant when $P \leq 0.05$.

Performance of sires used for ≥ 3 years was analyzed using the MIXED procedure in SAS to help determine repeatability. The model used was:

$$BPI = year + BPI\text{Group} + (year \times BPI\text{Group})$$

Where *BPI* is bull prolificacy index, *BPIGroup* represents the grouping of sires (low, average, high) based individual BPI and *year* is specific year.

A general Satterthwaite's approximation was performed on degrees of freedom for means. The Tukey method was used for multi-BPI group comparisons. Differences in treatment means were considered significant when $P \leq 0.05$.

3.3 RESULTS AND DISCUSSION

3.3.1 Bull prolificacy

Sire prolificacy varied by group and individual bull across years. Descriptive statistics based on breeding group per year of calf output are shown in Table 3.3. There was variation in calf numbers between both breeding groups and between individual sires within breeding groups. Calf number per sire ranged from 0 to 71 across all six years. These results are consistent with previous research evaluating sire prolificacy (Holroyd et al. 2002; Van Eenennaam et al. 2007; Domolewski 2017). In the study by Holroyd et al. (2002), 235 sires were tested and 58% sired 10% or less calves in their respective breeding groups, while 14% sired over 30% of the calves in each of their breeding groups.

In the current study, most breeding groups had sires differing in age. The maximum number of calves sired was influenced by bull performance, cow to bull ratio, and breeding season length, which also varied across breeding groups (Table 3.3). It is not clear how large of an impact each measurement has on bull performance in terms of number of calves sired. Unlike previous studies (Holroyd et al. 2002; Abell et al. 2017a), all breeding groups had a mix of bull ages, including yearling bulls in the same group as mature bulls. Replacement heifers were in their own breeding group (group 4) and the bulls used each year in that group had less days of potential breeding. These differences impacted results in the current study compared to previous studies comparing sire performance and DNA parentage testing.

Table 3.3 Descriptive statistics for each breeding group by year

Breeding group	Breeding group type	Breeding year	Number of sires	Number of cows	Bull:Cow ratio	Mean sire age, year	Calves Verified Per Sire			
							Total number of calves ¹	Min number of calves	Max number of calves	Mean number of calves
1	Mature	2014	5	130	1:26	2	130	10	44	26
2	Mature		6	136	1:22.7	3.9	127	5	53	21
3	Heifer		3	67	1:22.3	2.5	63	14	29	21
4	Yearlings		4	75	1:18.8	2.5	70	12	24	18
1	Mature	2015	6	162	1:27	2	138	8	54	23
2	Mature		6	154	1:25.7	2.7	139	2	38	23
3	Heifer		3	70	1:23.3	3.7	59	4	35	20
4	Yearlings		4	85	1:21.2	2.1	38	2	19	10
1	Mature	2016	7	172	1:25.6	2.4	156	4	55	22
2	Mature		6	159	1:26.5	2.2	129	0	56	22
3	Heifer		2	39	1:19.5	4.8	34	6	28	17
4	Yearling		3	71	1:23.7	2.5	60	0	31	20
1	Mature	2017	8	154	1:19.3	2.3	111	0	46	14
2	Mature		6	159	1:26.5	2	91	0	36	15
3	Heifer		3	71	1:23.7	3.4	62	12	30	21
4	Yearling		3	78	1:26	2.9	59	2	37	20
1	Mature	2018	8	184	1:23	2.9	152	1	63	19
2	Mature		7	148	1:21.1	3	122	2	30	17
3	Heifer		3	79	1:26.3	2	69	6	34	23
4	Yearling		3	79	1:26.3	4.3	73	3	54	24
1	Mature	2019	7	157	1:22.5	2.8	124	0	71	18
2	Mature		7	157	1:22.4	3	142	5	48	20
3	Heifer		3	79	1:26.3	2.3	70	18	28	23
4	Yearling		4	90	1:22.5	3	82	4	42	21

¹Only includes calves with a matched sire. Any calves with a no sire match were not included in the total for this column.

Each year a BPI value was calculated for each sire and was used to categorize sires based on performance. Three categories were used each year, top 25% of sires based on BPI, middle 50% BPI, and bottom 25% BPI values. Each year there was a large range in the BPI values of sires in each breeding group (Table 3.4). Recall, a BPI of 1.0 represents a sire that produced the expected number of calves after accounting for cow to bull ratio, conception and calving rate in the breeding group. Every year there was at least one sire per group that was able to achieve above the expected BPI value of 1.0 (Table 3.4).

Table 3.4 Number of sires, bull to cow ratio per breeding group per year, and corresponding BPI range

Breeding year	Breeding group	Number of sires	Bull:Cow ratio	Minimum BPI	Maximum BPI
2014	1	5	1:26	0.3	1.7
	2	6	1:23	0.2	2.5
	3	3	1:22	0.6	1.4
	4	4	1:19	0.7	1.4
2015	1	6	1:27	0.35	2.4
	2	6	1:26	0.26	2.5
	3	3	1:23	0.5	1.4
	4	4	1:21	0.2	2
2016	1	7	1:26	0.2	2.5
	2	6	1:27	0	2.6
	3	2	1:20	0.35	1.65
	4	3	1:24	0	2
2017	1	8	1:19	0	3.3
	2	6	1:27	0	2.4
	3	3	1:24	0.6	1.6
	4	3	1:26	0.1	1.9
2018	1	8	1:23	0.05	3.3
	2	7	1:21	0.1	1.7
	3	3	1:26	0.3	1.5
	4	3	1:26	0.12	2.2
2019	1	7	1:23	0	4
	2	7	1:22	0.25	2.4
	3	3	1:26	0.9	2.8
	4	4	1:23	0.2	2.1

Over 6 years, 113 BPI values were calculated for sires, with a median of 0.92 and an average value of 1.02. The highest BPI value was 4 and the lowest was 0, and sires with a BPI in the bottom 25% over all years had a BPI of less than 0.35, while bulls in the top 25% across all years had a BPI greater than 1.45. Based on the BPI values from the current study herd, 0.35, or the bottom 25% of sires' BPI, was arbitrarily determined to be the minimum value needed for

sires that would be recommended to remain in the breeding group. Over 6 years, there were 17 breeding groups with at least 1 bull BPI in the bottom 25 percent. One breeding group had no sires below an average BPI of 1.02, breeding group 3 in 2016. However, the group only had 2 sires (Table 3.4). In total, seven sires were recorded with a BPI of 0 over 6 years (Figure 3.2).

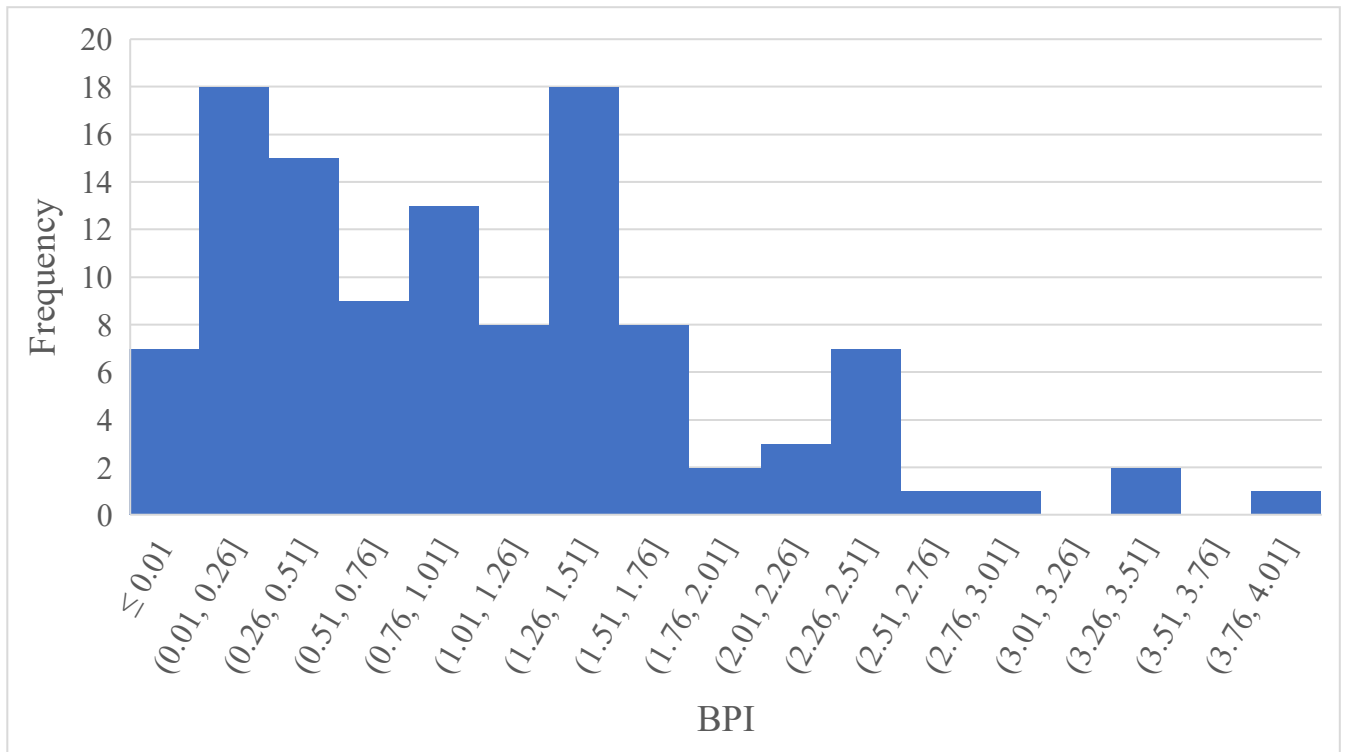


Figure 3.2 Histogram representing the BPI values of sires used from 2014 to 2019

3.3.2 Sire age

The age of sire had an influence on their BPI value (Figure 3.3). Sire age ranged from 1 to 5 year of age. Yearlings had a significantly lower BPI ($P < 0.05$) value compared to 2-year-old bulls and mature bulls (≥ 3 years). This result is in line with the expected lower performance of yearling bulls compared to 2-year-olds and mature bulls (Domolewski 2017). The 2-year-old bulls tended to have the highest BPI range overall, however, only 31 were used over 6 years, compared to 33 yearling bulls, and 52 mature bulls. The highest BPI value was for a mature bull in 2019 (Table 3.4), and greatest variation was in 2-year-old and mature groups, with a standard deviation of 0.86 and 0.88, respectively. The yearling group had a standard deviation of 0.54. In a study by Van Eenennaam et al. (2014) they found no significant relationship between calf number and bull age, though bulls of increasing age tended to have higher maximum number of calves. However, analysis of young bulls included bulls ranging from 1.4 to 2.9 years of age, while our study segregated yearling bull performance from two-year-old and mature bull performance. Their analysis of bull performance was also using calf number sired only, and this does not account for bull:cow ratio and cow fertility like our results do. Another study looking at both *Bos indicus* and *Bos taurus* cattle found that age had a significant effect ($P < 0.01$) on calf output in Brahman but not in other breeds (Holroyd et al. 2002). However, in this study no yearling bulls were used so a lower performance for yearling bulls could not be determined. Also, the analysis of sire performance in the current study is based on a BPI and not solely on number of calves sired, which can account for differences seen in the current study compared to previous studies.

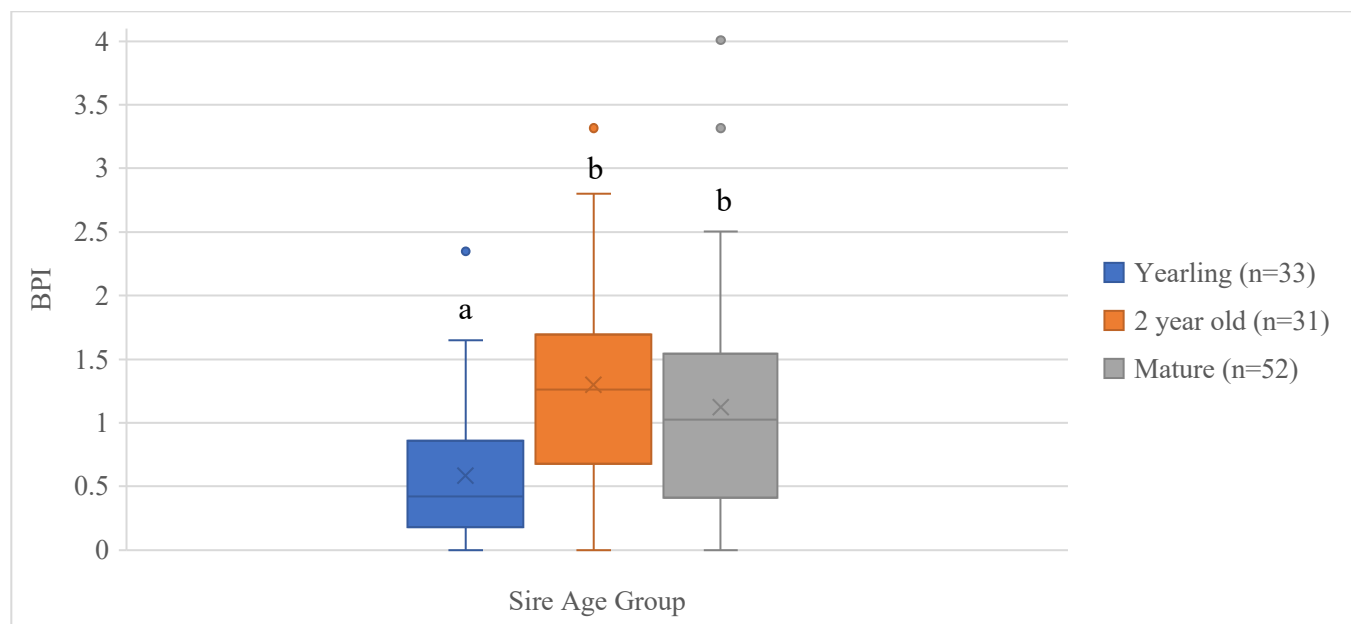


Figure 3.3 Range of BPI values based on sire age over 6 year

Sires tended to have increased BPI values as a 2-year-old compared to yearling sires (Figure 3.4). Most sires that exceeded the expected BPI ($BPI > 1$) as a yearling remained above the expected BPI as a 2-year-old. There was a slight positive relationship ($R^2 = 0.32$), for an individual bulls BPI value to increase from first to second year of breeding (Figure 3.4). Each dot represents an individual bull and their BPI score in their first year of use and second year of use (Figure 3.4). This suggests bulls may tend to improve their BPI from a yearling to a 2-year-old.

Poorer yearling performance compared to 2-year-old and mature bull performance cannot clearly be determined in the current study. Hypotheses can be made based on the lower maturity of yearling bulls compared to older bulls. Reproductive development potential of sires can be influenced by early nutrition, factors include age at puberty, sperm production potential, and testis size at maturity (Thundathil et al. 2016). Another study looking at the influence of age groups on bull performance determined that in the young and mature sire groups, the presence of a dominant or mature sire influenced the performance of other bulls in the group by reducing their attempts at females nearby (López et al. 1999). Therefore, if there is a strong mature sire

influence in multi-sire groups, that could negatively impact the yearling sires' performance in the mixed age group.

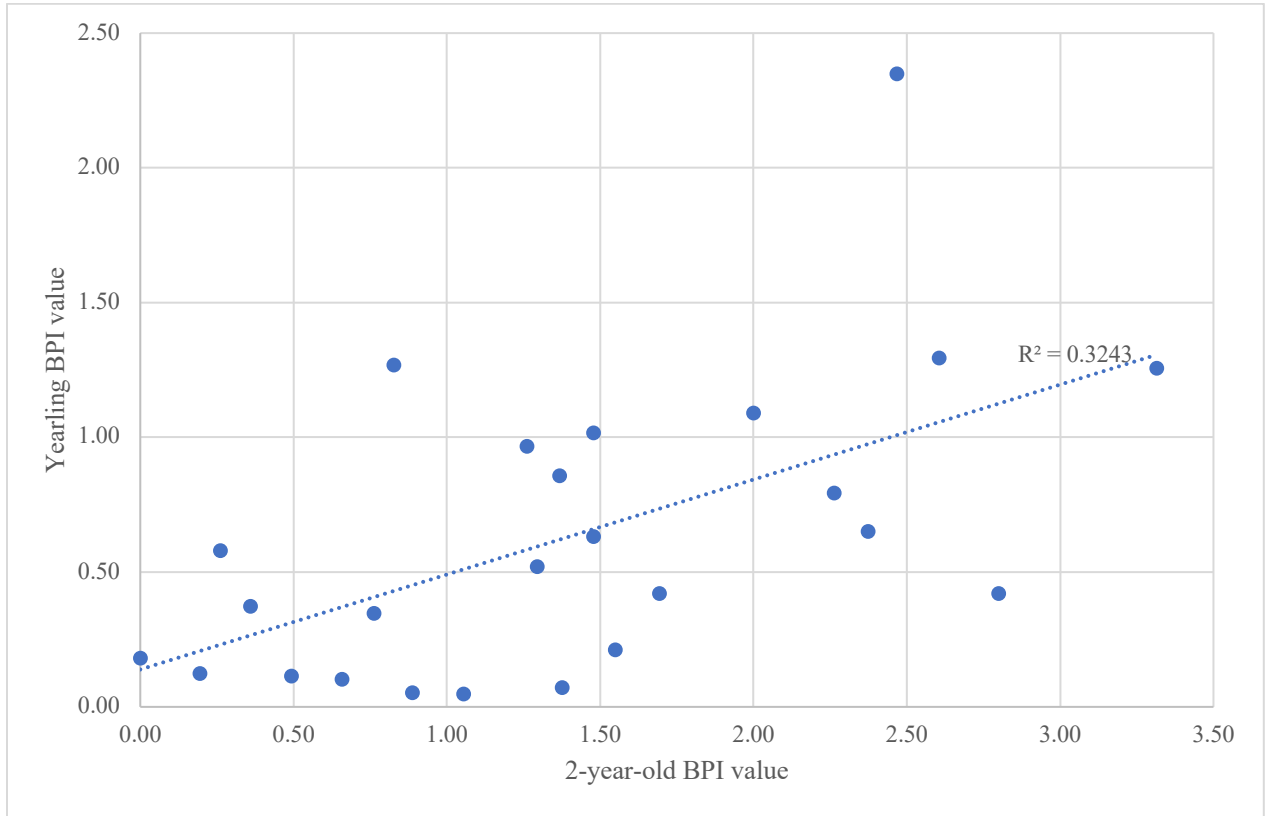


Figure 3.4 The BPI value of yearling bulls compared to their BPI value as 2-year-olds.

For bulls used for more than one year of breeding, 9 bulls had a BPI value in the first year of breeding below the minimum BPI value of 0.35, with an average BPI value of 0.14. However, several bulls with a BPI value below the minimum value of 0.35 in their first year of use, had an increased BPI above 0.35 in the next year of use (Table 3.5). The group of bulls above 0.35 BPI as yearlings also increased their BPI as a 2-year-old and remained above 0.35 for all years used.

Table 3.5 Bull BPI value as a yearling, 2-year-old, and overall

	Bottom 25% BPI	
	Bulls ¹	All Other Bulls
Number of bulls	9	16
Yearling BPI average value	0.14	0.91
2-year-old BPI average value	0.78	1.74
Overall BPI value	0.48	1.38
Average years used	2.3	3.4

¹Used a pre-determined BPI value of 0.35 as a cut off for the low group and grouping was determined in the sires first year of use

The results from the study indicate a lower BPI performance for yearling bulls when used in mixed age breeding groups. Therefore, culling based on yearling performance may not be indicative of a bulls long term performance. It would be beneficial to evaluate a bulls performance as they age to see if they have the potential to improve their performance.

3.3.3 Bull repeatability across years

A total of 20 sires were used for multiple years, between 3 to 5 years in the current study (Table 3.6). Sires were grouped based on their overall average BPI value for all years used, and not just their BPI in their first year of use (Table 3.6). The high BPI group of sires ranked as the top 25%, had sires used for the greatest number of years, were the youngest in their first year of use and had an overall average BPI value of 2.08 (Table 3.6). The bottom 25% of sires based on all years of use had an average BPI value of 0.42 (Table 3.6). There was variation in BPI values across years for most sires. However, sires who had higher BPI values tended to remain higher each year.

Table 3.6 Average BPI of sires used for breeding for > 3 year, by year, over 6 yr

	BPI Group ¹			SEM	BPI Group	P-value	
	Bottom 25% of sires	Middle 50%	Top 25% of sires			Year	BPIGroup x Year
# of sires	5	10	5	-	-	-	-
Avg age in Year 1 ²	1.6	1.4	1	-	-	-	-
Avg number of years used ³	3.2	3.8	4	-	-	-	-
Group AVG BPI over 6 years	0.42	1.03	2.08	0.171	<0.01	0.37	0.56

¹Grouping of bulls was based on their average BPI for all years the bull was used (up to 6)

²Year 1 represents first year of data for that bull since the study began

³Average number of years the individual sires were used within the 6 years

In this study, year effect was not found to be significant for sire BPI in any year ($P>0.05$). This could be interpreted as BPI being consistent or repeatable across multiple years. However, that hypothesis cannot be accepted as the sample size was small and the data was highly variable. There are no statistically significant results that were able to determine sire repeatability in the current study. Therefore, we cannot definitively say sire performance based on BPI was repeatable in the current 6 year study. A larger group of bulls for repeatability analysis would be required for future studies.

If sire repeatability were able to be determined, those results would agree with results found in previous studies. In a study by Van Eenennaam et al (2014), sire repeatability for sires over 3 years of age was found to be 0.37 and for all sires was slightly lower at 0.33 (Van Eenennaam et al. 2014). A Holroyd et al. (2002) study found sire repeatability to be slightly higher under their extensive Australian conditions at 0.43 to 0.69 (Holroyd et al. 2002). The conditions of the current study were similar to Van Eenennaam et al. (2014), meaning sire

performance in the current study may reflect similarly to those found by Van Eenennaam et al. (2014).

If a sires' performance is repeatable, it would be beneficial information for a producer. This would allow them to select the top producing sires and cull the bottom producing sires, in theory producing more calves. However, a non-repeatable performance can indicate an increase in BPI over the years which is important to recognize as sires may become more efficient as they age over years.

For the 20 bulls used for more than 3 years, their BPI value for each year of use is shown in Figure 3.5. The highest BPI value was for a 4 year old bull in his third year of breeding (No. 5; Figure 3.5). The majority of bulls (55%) saw increased BPI values from their first to their second year of breeding. In total, 6 bulls increased their BPI, 3 decreased, 8 had BPI remain fairly consistent (whether high or low), and 3 had BPI values go up and down each year. However, these are just descriptive based on the data and not statistically significant results.

Most bulls had variable BPI scores across years (12), with only a few bulls remaining at relatively same BPI value across years (8) (Figure 3.5). The top 3 bulls (5, 11, and 15) based on their BPI value were above an ideal BPI of 1.0, and the determined minimum expected BPI value of 0.35 in all their years of use (Figure 3.5). Nearly two-thirds (13 of 20) of the sires analyzed had at least one year where they sired fewer calves than expected (i.e. BPI below 1). Four bulls had a BPI value of zero in one of their multiple years of breeding. A value of zero results from no calves being assigned to a specific sire during DNA parentage testing. This could be due to poor calf or sire samples, or from lack of calf production by the individual sire. Without all poor samples being re-tested it is not possible to determine the actual cause. No sires were indicated in records as being injured or pulled early.

Repeatability of sires used for multiple calf crops was evaluated in a California study by Drake et al. (2011). Sire prolificacy and combined weaning weight per sire was found to be moderately repeatable (0.5) over consecutive calf crops. Similar to the current study, sires used in the study by Drake et al. (2011) had different sire groupings with each calf crop, yet sires producing a larger number of calves in a calf crop tended to remain prolific regardless of sire groupings. However, the influence of sire grouping on BPI cannot be definitely determined in the current study.

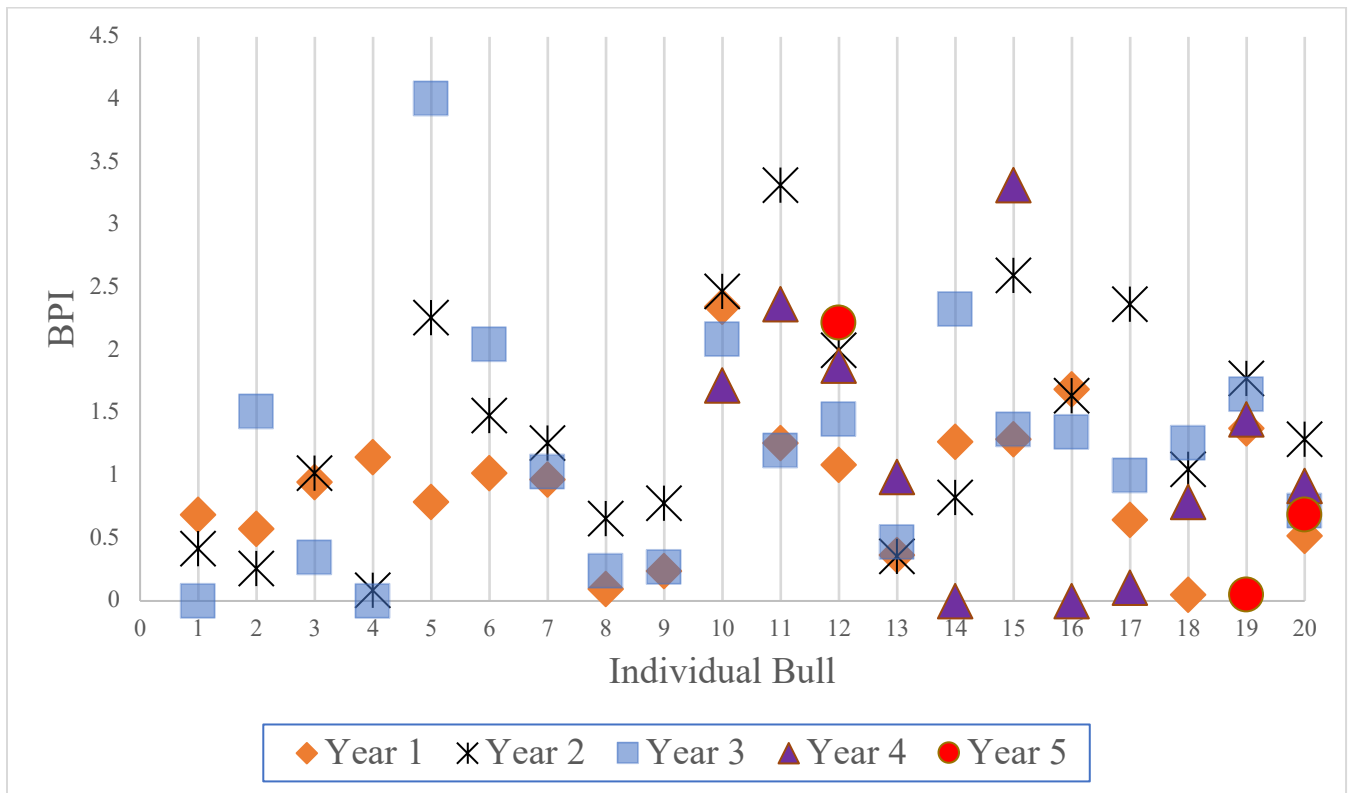


Figure 3.5 Dot plot of bulls (n=20) used over multiple breeding year and BPI value each year of use

3.3.4 Sire performance based on calves born in the first 21 d of the calving season

Of the 24 breeding groups evaluated over 6 years, 16 groups had 50% or more of the calves born in the first 21 d of the calving season, with at least one breeding group per year (Figure 3.6). Reproductive traits such as fertility, calving ease, libido, adaptability and structural soundness are important to consider, as they can drastically improve or reduce cattle productivity, this includes having more calves produced in the first 21 d (Gutiérrez et al. 2002).

It is recommended that 60% of the calf crop is born in the first 21 d based on improvements in fertility and longevity for the cows and positive influences on increased weight gain for calves by weaning (Cushman et al. 2013; Damiran et al. 2018). In this herd, the 60% of calves born in the first 21 d benchmark was only achieved 5 times in 6 years, with all four breeding groups meeting the target in year 5 (2019) (Figure 3.6). However, the heifer breeding group (group 4) consistently had over 50% of calves born in the first cycle across all 6 years.

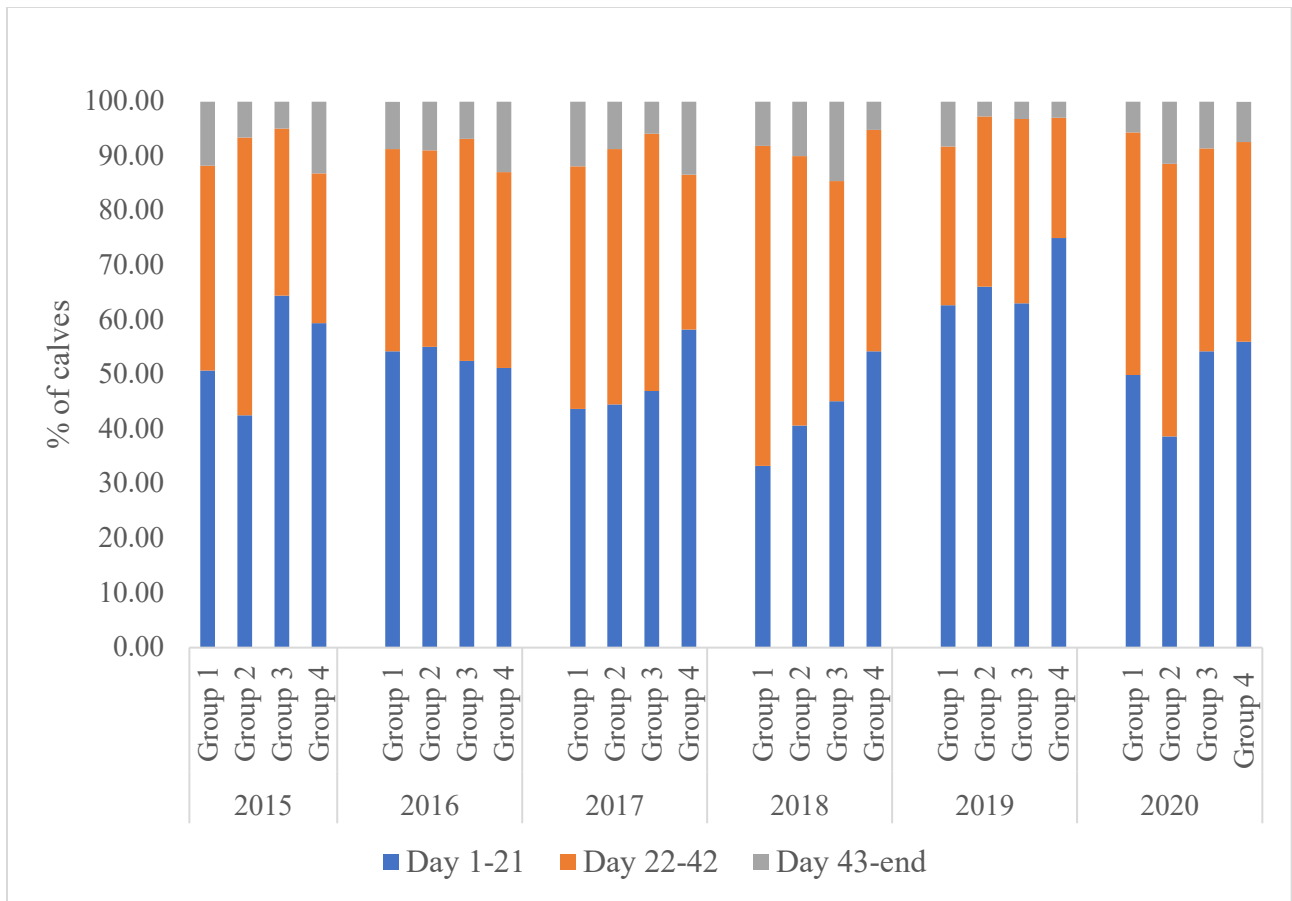


Figure 3.6 Percentage of calves born in each breeding cycle by breeding group per year

Most years, the low BPI value group was < 0.5 , average group was above 1.0, and high BPI value group was above 1.5 (Figure 3.7). When correcting for calves born in the first 21 cycle, the BPI value of the low group increased, the BPI value for the high group increased in year 1 and 4, and the value for the average group only increased in year 2, and was either lower or unchanged in all the other years. When looking at high performing bulls, it is important to consider how many calves they sired that are born in the first 21 d, as it is beneficial for both the calves and dams. Commercial cow-calf producers tend to calve in spring and wean all calves on the same date regardless of age or weight at weaning and most cow-calf producers sell their calves at or shortly after weaning (BCRC 2019). Calves born earlier have more days to grow

before weaning, and heifers born in the first cycle are more likely to produce a calf in the first 21 d as well (Funston et al. 2012; Cushman et al. 2013). Producing a calf in the first 21 d is especially important for heifers to ensure they have enough time to recover and cycle again to maintain a 365 day calving cycle and increase longevity in the herd (Damiran et al. 2018).

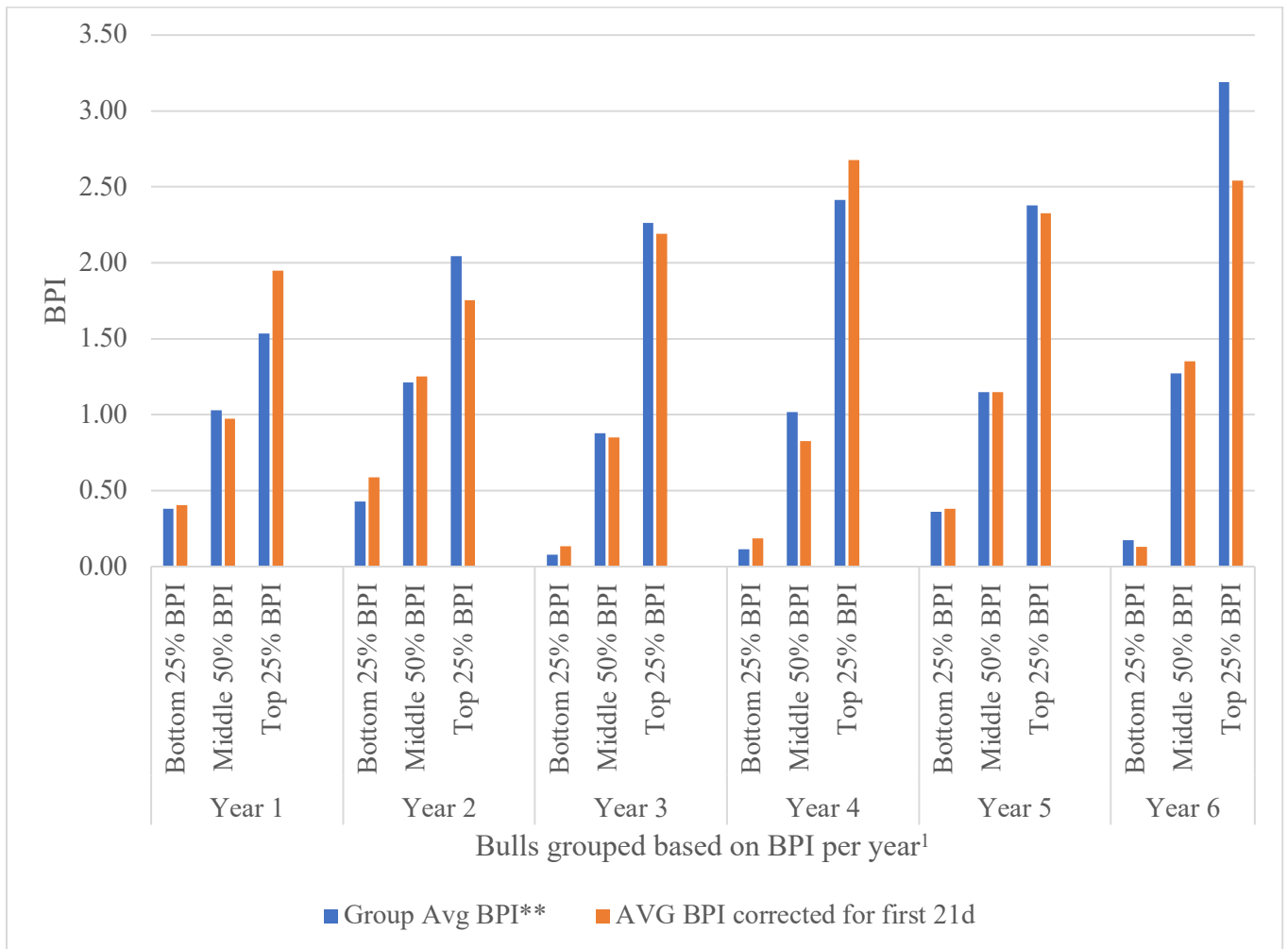


Figure 3.7 Bulls used for >3 years and grouped by BPI per year and the corrected² BPI based on calves born in the first 21d

¹Year 1 included 9 bulls (2 bulls in top and bottom group; 5 bulls in middle group)

Year 2 included 11 bulls (3 bulls in top and bottom group; 5 bulls in middle group)

Year 3 included 15 bulls (4 bulls in top and bottom group; 7 bulls in middle group)

Year 4 included 16 bulls (4 bulls in top and bottom group; 8 bulls in middle group)

Year 5 included 14 bulls (4 bulls in top and bottom group; 6 bulls in middle group)

Year 6 included 9 bulls (2 bulls in top and bottom group; 5 bulls in middle group)

²BPI correction changed total calves born to only number of calves born in the first 21d

** Bulls were sorted into the BPI groups individually each year based on their individual BPI in that year

A study by Funston et al. (2012) found that the calving cycle of when both heifer and steer calves are born, significantly impacts performance. The authors found that steer calves born in the first 21 d had increased weaning weight, increased hot carcass weight, improved marbling score ($P < 0.01$), and a greater ($P = 0.01$) percentage of calves achieved USDA choice quality grading or greater. For heifer calves born in the first 21 d, weaning weight ($P = 0.03$) and prebreeding weight ($P < 0.01$) was highest, and percentage of heifers cycling at the beginning of the breeding season was 70% ($P < 0.01$) versus 58% and 39% for second and third cycle born heifer calves (Funston et al. 2012). These are all economically important traits, and therefore bulls that produce more calves in the first cycle will have increased economic benefit to the herd (Damiran et al. 2018). For example, as determined in a study by Damiran et al. (2018), a heifer in western Canada has a cost of production of \$962 per cow wintered, and to recoup her development costs, will need to produce a minimum of five consecutive calves (Damiran et al. 2018). The major finding of this paper was that based on the analysis of calving records from the western Canadian herd, heifers born in the first cycle (21d) stayed in the herd longer and weaned more total kg per calf.

3.3.5 EnVigour HX™ genomic tool

During the 2018 calving season, 398 calves were then tested with EnVigour HX™, and as the study herd was largely crossbred, between 2 and 8 breeds were detected per calf tested

(Table 3.7). As breed count increased per calf, vigour score (VS) also increased. The calf crop had an average VS of 69% with the highest calf at 86% and the lowest VS at 19 percent.

According to Delta Genomics (Delta 2017), with every 10% increase in VS there should be a 1.36 kg increase in wean weight, females are 2 d earlier age at first calving, females have 2% higher conception rates, and 3% higher wean rates. If these results were accurate, this would suggest for the 2018 heifers we should expect to observe 8.2 kg higher WW ($1.36 \text{ kg} \times 6$), females 12 d earlier age at first calving, females with 12% higher conception rates, and 18% higher wean rates between the lowest and highest VS ranked animals.

Table 3.7 EnVigour HX™ vigour score for calves born in 2018

Breeds Detected	Number of calves tested	Average Vigour Score	Max Vigour Score	Min Vigour Score
2	23	31%	41%	19%
3	55	48%	72%	30%
4	69	72%	82%	40%
5	156	76%	84%	60%
6	78	78%	86%	66%
7	17	80%	85%	75%
Total	398	69%	86%	19%

The majority of calves had 5 breeds detected, with all calves having some percentage being indeterminate and Angus (Table 3.8). Breed detection ability using this testing is not entirely accurate, resulting in all calves having a portion of their breed composition unable to be determined, and was indicated as “indeterminate”. Almost all calves had some Hereford breed detected (92%), while 59% of calves had Gelbvieh breed detected. However, both of those breeds on average only represented about 20% and 10% inclusion, respectively. Knowing which calves are majority Angus, or British breeds, versus continental breeds can assist with herd management decisions based on breed traits. For example, replacement heifer performance as a

terminal or maternal line can be pre-determined by knowing the breed composition makeup in a crossbred herd.

Vigour score is related to the potential for increased heterozygosity from crossbreeding and can be of economic value to the herd (Akanno et al. 2018). Akanno and colleagues found that genome-based estimates of breed fractions are similar when compared to pedigree-based predictions (Akanno et al. 2017). Basarab et al. (2018) also found when compared to pedigree breed fractions, genomic based breed fractions were similar and can be accurately predicted (Basarab et al. 2018). Therefore, if the genomic-based breed predictions are accurate, vigour score may be a useful tool for multiple aspects of beef production, including exploiting specific crossbreeding strategies to improve terminal or maternal traits in the herd. Another benefit of this type of testing includes ensuring there is no loss of diversity in a crossbred herd, and the ability to reduce inbreeding when combined with parentage testing (Gorbach et al. 2010).

Table 3.8. EnVigour HX™ breed composition of 2018 born calves

Breeds	Number of calves tested with breed inclusion	Percent calf crop with specific breed inclusion*	Average percent breed composition of calves
Angus	398	100	47%
Brown Swiss	12	3.0	7%
Charolais	69	17.3	8%
Galloway	1	0.3	7%
Gelbvieh	234	58.8	10%
Hereford	367	92.2	19%
Holstein	11	2.8	7%
Jersey	49	12.3	8%
Limousin	117	29.4	9%
Maine Anjou	40	10.1	7%
Salers	15	3.8	7%
Shorthorn	29	7.3	8%

Simmental	114	28.6	9%
Indeterminate	398	100	20%

* Percent of calf crop with at least 6% of the breed included

In the current study, there were 20 sires used in the 2017 breeding season. Sixteen sires were Beefbooster breed (composite breed), 2 were Red Angus, and 2 were Black Angus (Table 3.9). Vigour score (VS) was higher for Beefbooster sires, compared to the purebred breeds of Red and Black Angus. Beefbooster is a composite breed, designed to capitalize on heterosis (Stothard et al. 2015). Akanno and colleagues found that the Beefbooster composite breed had more genomic retained heterosis (gRH) compared to all other breeds and composites tested (Akanno et al. 2018). This is beneficial, as the amount of heterosis retained for each generation is proportional to breed heterozygosity retained (Akanno et al. 2017). However, even with composite sires being used, all of the calf crop born in 2018 was almost 50% Angus breed (Table 3.8).

Table 3.9. EnVigour HX™ vigour score and breed composition of 2018 bulls

	Red/Black Angus	Beefbooster
Vigour score		
Average	34%	86%
Minimum	21%	83%
Maximum	41%	88%
Average number of breeds detected*	2.5	6.6
Number of breeds	4	16

*All breed counts include indeterminate

The use of genomic testing can improve management decisions in the herd, and help support decisions on improving specific traits based on certain genetics available in the herd

(Windig and Engelsma 2010). Specifically, matching sires and cows to optimize heterosis can result in progeny with improved performance and improved lifetime productivity (Basarab et al. 2018).

3.3.6 Performance of replacement heifers from targeted sires

In the current study, 177 heifer calves were born in 2015 from 19 different sires, with 16 of those sires producing heifers that were then retained as replacements. Those 16 sires were ranked based on their BPI in 2015 (Table 3.10). Among the 16 sires, 159 heifers were born and from these, 74 heifers were selected as replacement females. These 74 heifers weaned 161 calves between 2017 and 2020. In the first year of calving for the replacements, only 54 heifers weaned a calf, or 78 percent of total heifers. By the fourth parturition (2020), only 29 (39%) of the original 74 replacement heifers remained in the herd.

Between the 2017 and 2020 calving years, each sire is attributed to between 4 and 23 grand-calves. The variation in grand-calf numbers is influenced by the number of replacement heifers they produced in 2015 and the longevity of those heifers through the 4 calving seasons measured. There was no significant interaction between BPI Group and year ($P > 0.05$) of the number of grand-calves born across the 4 calving seasons measured (Table 3.10).

Retention of replacement females is of major importance for sustainability and profitability on beef operations (Cushman et al. 2013). This means sires that can produce high quality replacement heifers with increased longevity in the herd are economically beneficial to an operation. Each year, a sire contributes 50% of the genetic make-up of the calf crop, and if a producer retains their own replacement heifers, a sire's influence is even higher (Dhuyvetter et al. 1996). Although replacement heifer selection in this study was not based on a sire's calculated BPI, the top 25% BPI group had a higher proportion of daughters retained (34.6%) based on the total number of daughters born (Table 3.10). This means that the sires in the top 25% BPI have the highest genetic input in the calf crop long term and highest value in production economically.

Retaining heifers that will remain in the herd for many years as a cow is more economically efficient (Werth et al. 1991). Results from a model study by Werth et al. (1991) found that management practices which maintain a higher percentage of mature cows in the breeding herd will optimize economic and reproductive efficiencies because more calves and heavier calves are produced relative to the feed necessary for maintenance and lactation, compared to a herd with a high number of younger replacement heifers.

Table 3.10 Replacement heifer¹ progeny performance

Sire BPI rank ²	Bull number	Female s sired	Females retained	Calves Born to Heifers ¹				Total calves ³	Remaining females after 4 calving years (%)	No. grand-calves per sire
				2017	2018	2019	2020			
Bottom 25%	4	21	10	9	6	6	7	28	70	7
Middle 50%	8	81	38	26	22	20	13	81	34.2	10.1
Top 25%	4	57	26	19	14	10	9	52	34.6	13
<i>Total</i>	16	159	74	54	42	36	29	161	-	-

¹2015 born heifers from 2014 breeding sires.

² Overall BPI from 2015 calving year

³Total calves from 2017-2020 calf crops born to the 2015 heifers

The BPI values of sires used for breeding in 2015 and that produced replacement heifers, ranged from 0.38 to 2.5. The bottom ranked 25% had an average BPI value of 0.40, and the top ranked 25% of bulls had an average BPI of 1.74 (Table 3.11). Of the 74 total replacement heifers retained, 46 heifers (62%) were born in the first breeding cycle (Table 3.11). Four sires had all heifers born in the first breeding cycle, while 4 sires had no heifers born after the first breeding cycle. High BPI value sires had the most daughters retained compared to average or low BPI

ranked bulls at 6.5 heifers per sire (Table 3.11). When looking at daughters retained as a percentage of females sired there is minimal difference with 46-48% across all three groups.

When correcting BPI value for number of calves born in the first 21 d cycle, the top ranked 25% BPI group was still higher (1.73) than the other two ranked groups, with the bottom ranked 25% BPI group still having the lowest BPI value (0.61). However, the bottom 25% BPI group improved their average BPI slightly when corrected for 21d, while the other two groups' BPI slightly declined after the correction.

In a study by Gutierrez et al. (2002) looking at genetic relationships between major reproductive traits in beef cattle, they determined age at first calving has the largest heritability over calving interval and calving day. Therefore, knowing which bulls produce more calves in total, as well as more calves in the first 21 d may have a positive genetic improvement on the herds reproductive capabilities in the long run (Dhuyvetter et al. 1996; Drake et al. 2012; Diskin and Kenny 2014). Another study by Drake et al. (2012) determined that calves born in the first 21 d of the calving season accounted for 40% of the total feeder calf or retained ownership value to the ranch. The data from this study suggested that selecting sires to increase the proportion of calves born early in the calving season (and two other traits, scrotal circumference, and cow energy value EPDs) could increase total ranch income per sire and the overall ranch efficiency (Drake et al. 2012). However, sire selection is not the only driving force behind calves being born in the first cycle (21 d), female influence needs to be accounted for as well.

Table 3.11 Bulls sorted based on their respective 2015 BPI score, showing their 2015 born heifer calves' reproductive performance

	Bottom 25% BPI	Middle 50% BPI	Top 25% BPI	SEM	P-Value
# of bulls	4	8	4	-	-
2015 AVG ¹ BPI	0.40	0.96	1.74	0.11	0.0003
2015 AVG BPI corrected for 21d ²	0.61	0.82	1.73	0.178	0.0045
# Daughters retained in 2015	10	38	26	10.6	0.254
# Daughters born in first 21 d	6	14	8	0.25	0.906
% of retained born in first 21d	60	36.8	30.8	-	-
AVG # of daughters kept per bull	2.5	4.75	6.5	-	-
Total calves born from replacement heifers ³	30	87	52	41.25	0.462
AVG # of calves born in first 21d	14	40	26	10.79	0.377
% of calves born in first 21d	47	46	50	-	-
# of grand calves per bull	7.5	10.9	13	-	-
% heifers remaining after four calvings	70	34	35	-	-

¹AVG = average

²Average BPI of sires in 2015 corrected for only daughters born in the first 21 d of the calving cycle

³between 2017-2020

The bottom 25% BPI had the highest percentage of heifers born in the first 21 d (60%) compared to the other two groups (36.8 and 30.8 respectively) (Table 3.11). When looking at the calves born to the 2015-born replacement heifers, sires in the top 25% BPI group had numerically more daughters produce calves in the first cycle, with half (50%) of the calves produced from daughters of top 25% BPI sires born in the first cycle. However, these results were not statistically significant ($P > 0.05$). In a Saskatchewan study by Damiran et al. (2018), one major outcome showed that females who calve earlier as heifers were able to produce more overall kg of weaned calf, resulting in an additional \$773 to \$1160 in revenue for the operation, over their lifetime compared to heifers who calved in the second or third cycle (Damiran et al. 2018). The value of a sire to an operation will vary significantly based on their overall production goals. For an operation that desires more calves born in the first cycle (21 d), calves sired will not be the best indicator of value. If that was the case on this operation, sires in the bottom 25% may have been of more value. Using BPI as an indicator of sire success is just one of many ways a sires performance can be valued, and these results cannot assume to be applicable to other operations.

The top 25% BPI group also had the most grand-calves on a per sire basis at 13, compared to 7.5 and 11 for the other two BPI groups (Table 3.11). However, the top 25% group had the least amount of replacement heifers remaining in the herd and producing a calf after 4 calving years, with only 35% (9 of 26) heifers remaining. In contrast, 70% of the heifers selected (7 of 10) from the Bottom 25% BPI sire group still remained in the herd after four parturitions. This may be due to the bottom 25% BPI group having less than 3 females retained from each bull while the top 25% BPI group had over 6 retained from each bull (Table 3.11).

This might suggest that the low BPI sires are producing higher quality calves from their smaller calf crop compared to those sires producing a larger number of calves. It is important to consider the overall goal of an operation when determining sire quality for selection. If the goal is to produce a large number of calves for sale at weaning, than calf numbers in the first cycle may not be relevant or of importance. However, if the operation plans to retain a large number of females, female reproductive efficiency and calf quality are important considerations for sires in the herd.

3.3.6.1 Calving interval of heifers

An important management consideration for an operation is calving date of the replacement heifers. Both maternal and fetal effects can contribute to gestation length, which influences a cow or heifer's calving date, but paternal contributions to gestation length are less clear (Fang et al. 2019). Previous studies have shown that heifers who initially calve earlier, tend to calve earlier for the remainder of their reproductive years, and have improved lifetime production (Lesmeister et al. 1973; Funston et al. 2012). Therefore, heifers born in the first cycle, or first 21 d of calving, tend to be more influential to the reproductive output of the herd. The largest improvements to a herd can come from selection and reproductive management of herd bulls, therefore, understanding paternal contributions to pregnancy establishment could be beneficial to advance overall herd fertility (Ortega et al. 2018). In the current study, individual sires with a greater percentage of heifers born in the first cycle (21 d), tended to have a greater percentage of grand-calves from those heifers also born in the first cycle ($R^2 = 0.3896$) (Figure 3.8). For 2015 and 2016, 20 bulls sired selected replacement heifers. Three bulls did not sire any replacement heifers that were born in the first 21 d of the calving period (Figure 3.8).

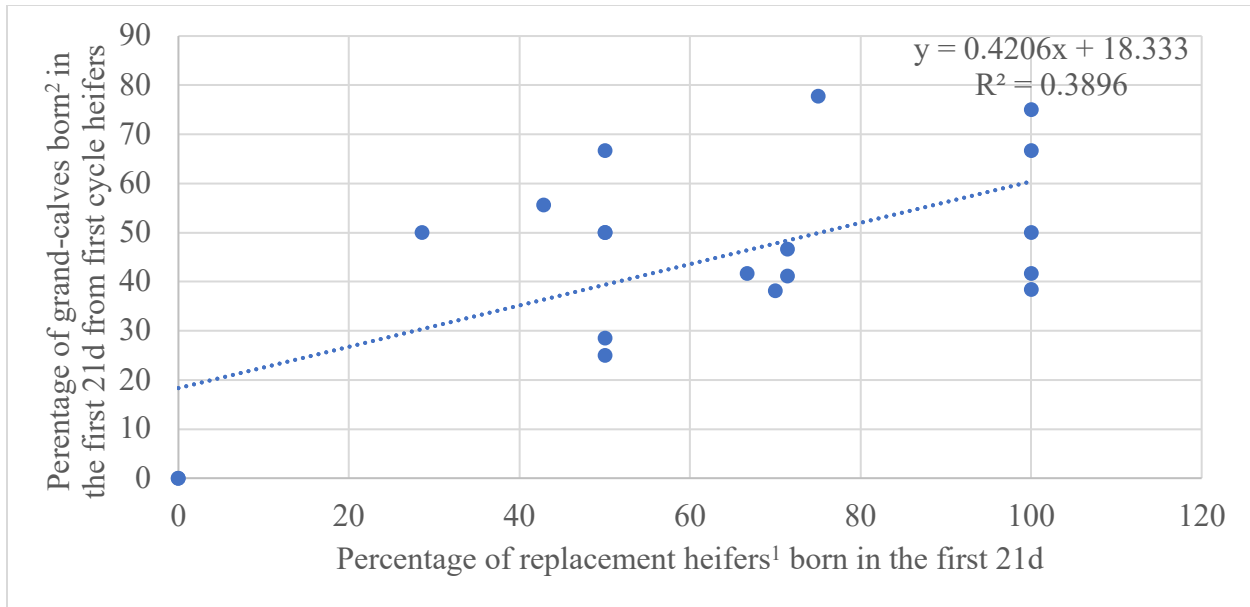


Figure 3.8 Relationship of heifers born in the first breeding cycle and their subsequent progeny birth cycle on a per sire basis.

¹Replacement heifers (n=49) were born in 2015 and 2016. Only heifers with ≥ 3 years of calving data were included.

² Grand-calves (n=72) were born between 2017-2020.

Ideally, a cow is expected to produce a calf every 365 days (Vinet and Zhedanov 2011). The gestational length for a beef cow is 283 days, and in order to produce a calf every year, she needs to be cycling again and bred within 82 days of calving to maintain a 365 d calving interval (Walker and Perry 2007; Damiran et al. 2018). The average calving interval for replacement females retained in 2015 and 2016 in the producer collaborator’s herd, was 371 d between their first and second calf (Figure 3.9). The calving interval between their second and third calf was 365 d, and between their third and fourth calf, the interval was 367 d on average. These results agree with previous studies evaluating calving interval, where it was reported that as a cow matures their calving date becomes progressively earlier (Dunn and Kaltenbach 1980; Werth et al. 1996). The longest calving interval in the current study was 424 d, with the heifers first calf born at start of the calving season (April 15 2018), and the second calf was born at the end of the

third cycle (June 13 2019). However, this cow had a reduced calving interval for the third calf at 326 d in 2020 (Figure 3.9). The shortest calving interval was 308 d, with the second calf being born in the fourth cycle, June 19 2018, and the third calf born close to the start of calving season, April 23 2019. The female's calving interval was greatest between the first and second calf at 419 d and went up again between her third and fourth at 383 d. These results agree with findings from Werth et al. (1996) who found a negative association between calving intervals within individual cows between 2 and 3 year of age, and 3 and 4 year of age.

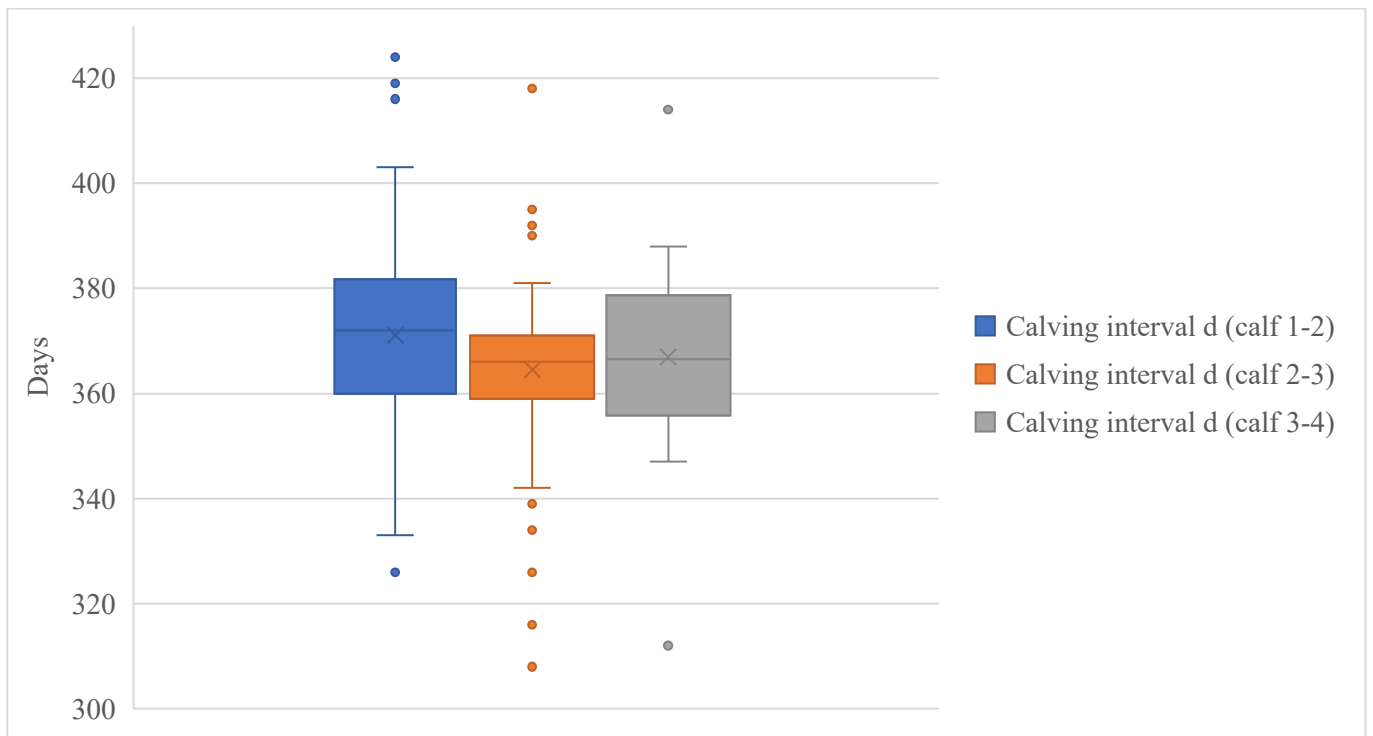


Figure 3.9 Calving interval (d) of 2015 and 2016 born replacement females for their 2nd, 3rd, and 4th calf.

Age at first calving (AFC) and calving interval are typically used as indicators of fertility by breed organizations (Gutiérrez et al. 2002). Fertility traits are important to consider for the herd and are influenced from both maternal and paternal genetics as well as environmental and

management influences (Gutiérrez et al. 2002; Utt 2016). In the study herd, average calving interval decreased for all heifers between the second and third calf born (Figure 3.10). For females sired by the top 25% ranked sires based on BPI value, their calving interval continued to decrease each year. Calving interval is influenced both by gestation length, and conception date during the breeding season (Yagüe et al. 2009). A study by Yagüe et al. (2009), looked at the genetic influence of multiple fertility traits from beef cows managed using artificial insemination (AI) including, days to first insemination (DFI), days from first insemination to conception (FIC), number of inseminations per conception (IN), days open (DO), gestation length (GL) and calving interval (CI) (Yagüe et al. 2009). This study found highly significant genetic correlations for FIC, IN, DO, and CI. Genetic correlations between DO and CI were similar and higher than 0.85. Calving interval is also an important consideration for natural mating, so selecting females with shorter CI is beneficial for overall herd fertility.

While maternal and fetal influences are clear contributors to gestation length, a study by Fang et al. (2019) looked at potential genetic and epigenetic effects of paternal influence on gestation length (Fang et al. 2019). The study looked at both genomics and sperm epigenomics data in dairy cattle and found 25 candidate genes related to gestation length, and determined the paternal influence is likely related to regulation of embryo development (Fang et al. 2019). With this information, a high performing bull that can reduce gestation length may be more economically beneficial to the herd, relating to calf weaning performance as well as heifer performance and longevity.

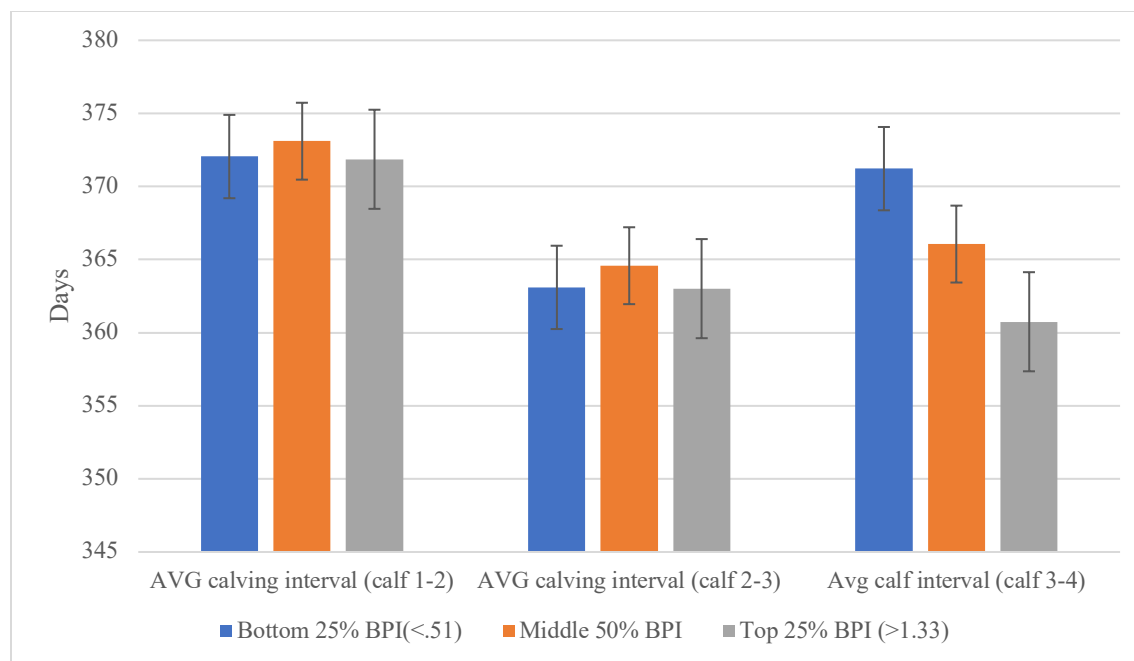


Figure 3.10 Average calving interval (d) of the heifers born from targeted sires in 2015 and 2016 (sorted based on BPI) from their first calf to their fourth between 2017 and 2020

3.3.6.2 Performance of grand-calves born to 2015 and 2016 heifers based on sire BPI values

In 2015, the top 25% BPI-ranked sires produced 35% of the selected replacement heifers, with the bottom 25% ranked sires producing only 13.5% of the replacement heifers (Table 3.12). Heifers from sires ranked in the top 25% produced almost double the kg of weaned calves, compared to heifers born from the bottom ranked 25% of sires, though not significantly different ($P > 0.05$). Even though both groups had the same number of sires, the differences in total kilograms weaned is related to the ability of replacement heifers to raise a calf to weaning for multiple years, as well as the bottom 25% of sires siring a smaller amount of replacement heifers. Based on the number of calves weaned by replacement heifers from 2017-2020, on a per bull basis, the top 25% of bulls had more grand-calves weaned than the other two groups. However, the average kg per calf weaned off the heifers was lowest for bulls of the high BPI group on average numerically, but not significantly different ($P > 0.05$).

In 2016, sires in the top 25% based on BPI group produced over 50% of the selected replacement heifers of that year (Table 3.12). While the bottom 25% of sires based on BPI group only produced 13% of the replacement heifers, even though both groups had the same number of sires. The replacement heifers born from sires of the top 25% BPI group produced and weaned significantly more calves ($P = 0.0052$) and ($P = 0.0079$), respectively, during the trial collection period than replacement heifers born from sires of the other two groups. The replacement heifers born from sires in the top 25% BPI group also weaned 4-fold greater total kg of calves than heifers born to sires from the bottom 25% BPI group ($P = 0.012$). Total kilograms weaned per calf on an individual sire basis was higher for the top 25% group, which was almost double compared to the middle group and four times higher than the bottom 25% group. However, on an individual calf basis, the calves born from heifers sired by the top 25% BPI group had slightly lighter weight calves on average than the middle BPI group, but still heavier than the bottom 25% BPI group though not significantly different ($P > 0.05$).

Prolificacy of a sire essentially determines their long-term contribution to the genetic composition of the herd (Drake et al. 2011) and this is accentuated when their heifer calves are also retained as replacements within the herd. The difference in heifer performance based on sire BPI ranking was more profound in 2016 than 2015, meaning a smaller number of sires produced a larger number of calves and replacement heifers. This variability in sire performance agrees with findings in previous studies as well (Holroyd et al. 2002; Van Eenennaam et al 2007; Domolewski 2017), and this performance can directly impact herd genetics and potential profitability in the long term, as those replacement heifers remain in the herd and continue to produce calves.

Table 3.12 Performance of replacement heifers born in 2015-2016 from targeted sires (based on BPI)

	2015 born replacement heifers			SEM	P-Value
	Bottom 25% BPI	Middle 50% BPI	Top 25% BPI		
Number of sires	4	8	4	-	-
Number of replacement heifers born	10	38	26	10.6	0.254
% of total replacement heifers	13.5%	51.4%	35.1%	-	-
Number of calves ¹ born to replacement heifers	30	87	52	41.25	0.462
Number of calves ¹ weaned from replacement heifers	27	83	52	40.65	0.377
Total kg weaned	5309	16167	10009		0.3402
Average kg weaned ² per sire	1327	2021	2502	-	-
Average kg/calf	195.1	197.6	194.8	1742.4	0.967
	2016 born replacement heifers			SEM	P-Value
	Bottom 25% BPI	Middle 50% BPI	Top 25% BPI		
Number of sires	4	7	4	-	-
Number of replacement heifers born	7	34	46	10.05	0.0027
% of total replacement heifers	8.0%	39.1%	52.9%	-	-
Number of calves ¹ born to replacement heifers	16	77	86	37.08	0.0052
Number of calves ¹ weaned from replacement heifers	16	74	81	36.04	0.0079
Total kg weaned	3295	15386	15950		0.0120
Average kg weaned ² per sire	824	2198	3988	-	-
Average kg/calf	146.9	207.2	197.3	670.36	0.285

¹Calves born to replacement heifers are considered grand-calves of the sires in the BPI groups

²Average kg weaned of all grand-calves born from heifers (2018-2020) sired by each sire

3.3.6.3 EnVigour HX™ results of replacement heifers born in 2018-2019

A majority of heifers in both years had a vigour score (VS) of 75% or greater (Figure 3.11). According to a study by Basarab et al. (2018), a 10% increase in VS improved cow longevity in the herd, and increased total calf wean weight per cow by 35.7 kg ($P = 0.019$) (Basarab et al. 2018). That resulted in an extra \$161 per heifer per year (Basarab et al. 2018). Therefore, with a herd producing high VS heifers, there can be an economic benefit per heifer each year they remain in the herd. Also, heifers with higher VS are supposed to be younger at first calving, with every 10% increase resulting in calving 2 d earlier (Basarab et al. 2018).

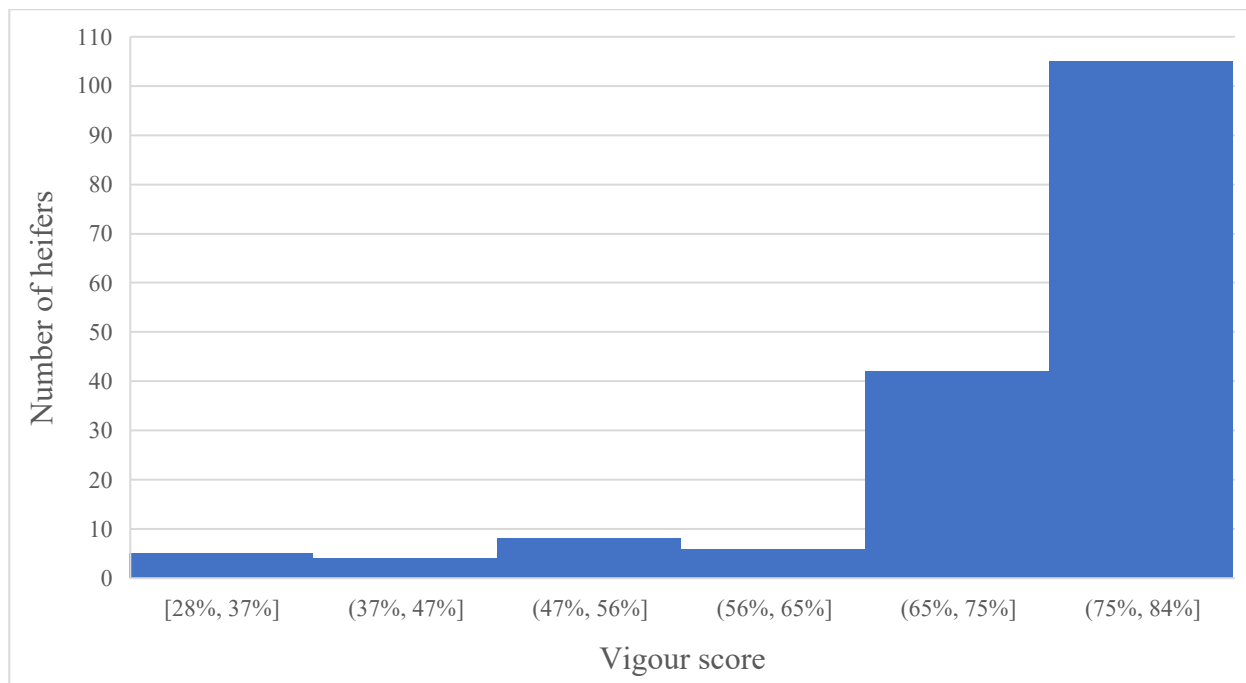


Figure 3.11 Histogram of vigour scores from all replacement heifers in 2018 and 2019 (n=170)

In this herd, vigour score increased numerically on average of all heifers born from 2018 to 2019 (Table 3.13). Average VS was 69% in 2018 born heifers and increased 8.7% in heifers born in 2019. Average number of breeds found per heifer also slightly increased from 2018 to 2019 from 4.7 to 4.9. This represents more heifer calves on average having a greater number of breed influences genetically.

Table 3.13 Vigour score and breed composition of all heifers born in 2018 and 2019 calving seasons

	2018		2019	
	Vigour score	Number of breeds ¹	Vigour score	Number of breeds ¹
AVG	69%	4.7	75%	4.9
MIN	19%	2	28%	2
MAX	85%	7	86%	8

¹Number of breeds determined by testing to be part of the heifers breed composition. Indeterminate (portion unable to be linked to a specific breed) is included as a breed number.

According to Basarab et al. (2018) when selecting heifers, it would be economically beneficial to select those with higher VS scores, however VS was not a basis for replacement selection in the current study herd. Although VS was not a basis for replacement heifer selection, those selected in 2018 had slightly higher average VS than the average of all heifers (Table 3.14). However, replacement heifers selected in 2019 had a slightly lower average VS than all heifers born, but both groups were higher than in 2018. However, on average, the heifers born in 2018 and 2019 have a high VS, above 70%, and are mixed with at least 4 different breeds (Table 3.13). Therefore, in a herd like this they may not benefit from this type of genomic testing to make additional changes. However, it did confirm that the incorporation of composite bulls in the study herd to increase hybrid vigour was successful.

Table 3.14 Selected replacement heifer vigour score compared to all heifers born in 2018 and 2019 calving

	2018		2019	
	Replacement heifers	All heifers born	Replacement heifers	All heifers born
AVG	72%	69%	73%	75%
MIN	31%	19%	28%	28%
MAX	84%	85%	83%	86%

In 2018, a majority of replacement heifers (62%) had a VS between 71 and 81 percent (Figure 3.11). In 2019, a majority of replacement heifers were between 70 and 80% as well, with 63% of heifers falling between these VS values (Figure 3.11). In a study by Akanno et al. (2017), they found positive association of nonadditive genetic effects for growth traits in particular, thus reflecting the importance of heterosis to improve these traits in a herd (2017). Another study by Akanno et al. (2018) confirmed those results using the same methods that the EnVigour HX™ testing uses, and they also found positive heterosis effects for growth traits but not for carcass traits (2018).

There were two related studies using this testing approach (Akanno et al. 2018; Basarab et al. 2018), and one that could be used to compare (Basarab et al. 2018). This study is also the basis for claims made by the testing company on what results can be expected applying EnVigour HX™ results to replacement selection. The study is by Basarab et al. (2018) and found genomic retained heterozygosity and retained heterosis were positively and linearly related to cow fertility, longevity, and overall lifetime productivity of the heifers tested. Specifically, they found that a 10% increase in their RHETg (retained heterozygosity) resulted in 51 d longer survival in the herd ($P = 0.011$) and 35.7 greater calf wean weight per cow ($P = 0.019$) over five parities. Those increases resulted in \$161 per heifer per year, which if related back to the current

herd would result in \$14,490 more per year if all 90 heifers weaned an improved calf and maintained in the herd.

However, this genomic test is based on population data from one study (Basarab et al. 2018), and no economic analysis has been done yet evaluating the cost benefit analysis for commercial producers using the test. Based on the high percentage of replacement heifers in the current study herd with a vigour score above 70%, there may not be an economic benefit to using the test.

3.3.6.4 2018 Replacement heifer performance based on EnVigour HX™ vigour score

Heifers tested in 2018 were followed through first and second parity, and their performance was analyzed based on vigour score. The VS range for heifers was 31 to 84% (Figure 3.11) with majority of heifers having a score between 70-79 percent (Table 3.15). Age at first calving (AFC) was expected to decrease by 2 days for every 10% increase in vigour score. According to Delta genomics, every 10% increase in VS should improve specific performance parameters (1.36 kg higher WW, 2 d earlier AFC, 2% higher conception rates, and 3% higher wean rate) (2017). However, AFC was lowest for heifers with a VS between 60-69 percent. This group also had the highest conception rate compared to all other groups, and the highest WW and adjusted wean weights (Table 3.15). However, the 60-69% group also had the smallest number of heifers in it with only 6 animals.

The use of crossbreeding programs has been well documented and so have the benefits obtained from such a program (Theunissen et al. 2013; Van Eenennaam 2017; Basarab et al. 2018). Heterosis is the superiority of the crossbred animal when compared to its straightbred parents, and tends to have the largest improvements in lowly heritable traits (Van Eenennaam

2017). However, it can be beneficial for a variety of traits, and in a study looking at heterosis effects on milk yield based on different management levels, the authors found an economic advantage of crossbreeding for all management levels (Kargo et al. 2012). In another study, Penasa et al. (2010) looked at the effect of the environment on expression of heterosis and found that heterosis effects were generally larger in harsher environments compared to supportive ones. Therefore, if an operation is looking to adopt or improve their crossbreeding program, the use of a genomic test, such as EnVigour HX™, could improve crossbreeding management. The adoption of crossbreeding may be easier with the testing, for any management level, and have slight benefits in areas of more stressful environments.

Table 3.15. 2018 replacement heifer performance based on EnVigour HX™ score with expected differences and actual differences between each 10% change in vigour score

	0-59% VS	60-69% VS	70-79% VS	80% and over VS	Expected difference ¹	Actual difference ²
# of heifers	10	6	56	14	-	-
AVG EnvigourHX score	0.43	0.66	0.76	0.81	-	-
Age @ 1st calving (d)	733	730	733	734	-2d	-3d, +3d, +1d
Calving interval (d)	370	369	366	361	None expected	1d dec, 3d dec, 5d dec
Conception rate 1st calf (%)	90.0	100.0	86	100	+2%	+10%, -14%, +14%
Conception rate 2nd calf (%)	70	100	73	93	+2%	+30%, -27%, +20%
Wean rate - first calf(%)	90	100	86	100	+3%	+10%, -14%, +14%
Wean rate - 2nd calf (%)	70	100	73	93	+3%	+30%, -27%, +20%
Avg WW (kgs)	199.5	207.7	197.7	197.7	None expected	+8.2 kgs, -10 kgs, no difference
205d adjusted WW (kgs)	195.8	210.6	202.3	199.7	+1.36 kgs	+14.8 kgs, -8.3 kgs, -2.6 kgs

¹Based on values provided by Delta genomics (2017) for every 10% increase in VS

²Between each 10% group difference

Further testing with more herds, to obtain a larger sample size, may show improved performance expected by improving VS, however that was not the case in this study. In the study by Basarab

et al. (2018) an economic benefit was only found after 5 years of use, and in the current study the test was only evaluated over two calving years. There also may be an influence on calf weaning rate performance based on sire breed. While all heifers were in the same breeding group in their first breeding season, once they aged to mature cows they were in different breeding groups. Within each breeding group there were some purebred Angus bulls and some composite Beefbooster bulls. The study herd's use of beefbooster bulls demonstrates their interest in hybrid vigour. The use of EnVigour HX™ testing confirmed hybrid vigour exists in their herd. In general, based on the results from this herd, and with the large number of females already above 70% VS, there may be no benefit for adoption of this testing for this herd. It would be beneficial to do a long term comparison across straight and crossbred herds between using EnVigour HX™ and VS as a selection tool versus traditional selection with no genomic testing. This can better determine if there is an economic benefit of utilizing this tool for a commercial producer.

3.4 CONCLUSION

Bulls in multi-sire breeding groups were found to sire a different number of calves across all years. When evaluating bulls based on BPI value, sire age played an influence with yearling bulls having lower BPI than mature bulls ($P < 0.05$). On average, most bulls tended to have a smaller range of BPI variation across years compared to a larger range of BPI variation between bulls. A larger sample of bulls is needed to determine repeatability of performance based on BPI value. When looking at bull BPI based on calves born in the first cycle, low BPI bulls improved while high and average BPI bulls decreased or stayed the same most years, only increasing two or one years, respectively. This may indicate low BPI sires are producing well at the beginning

fo the breeding season but reproductive capacity diminishes as the season progresses, while high Bpi sires are able to maintain reproductive ability throughout the breeding season.

High BPI bulls produced a greater number of heifers and had more of their heifers subsequently retained as replacements, however, the low BPI bulls had a greater number of heifers born in the first cycle (21 d) and a greater number of replacement females remaining in the herd after four parturitions. Other reproductive measures such as calving interval was lowest, for those heifers born from high BPI bulls. Although they produced less heifer calves, those heifers had good performance to remain in the herd for multiple calving seasons. Therefore, BPI alone should not be a determination for bull value on an operation. It is a useful measure to aid in informed decision making that is based on an operations long-term goal. However, the use of DNA parentage testing is required to determine bull BPI and is a useful tool for informed decision making and breeding selection decisions.

In general, BPI is not useful to determine a sire's ability to produce high quality heifer calves, but only calf number overall. It can however be used to evaluate sires that produced more calves in the first cycle. Heifer performance based on VS was not clearly able to be differentiated in this study as most heifers tested (86%) had a high VS. EnVigour HX™ testing was likely not beneficial for the study herd because any more increase in VS for heifers would likely not see enough monetary gain to cover the additional cost of testing.

4.0 ECONOMICS OF GENOMIC TESTING FOR COMMERCIAL BEEF HERDS

4.1 INTRODUCTION

Major advances in technology, specifically with genomic testing in livestock, has improved the tests and technology available to all producers, not only seedstock, and has reduced the cost of some simpler and more common testing such as DNA parentage testing.

Genomic testing is promoted as a way to make informed management decisions related to replacement selection and sire matching (Delta Genomics, 2017). As with any new technology or practice, producers will consider the costs and benefits prior to adoption. With profit margins averaging \$75 per cow in cow-calf production (AB Agriculture and Forestry 2020), commercial cow-calf producers may be reluctant to spend dollars on a genomic test costing \$45 per test.

EnVigour HX™ provides parentage, breed composition and a vigour score (VS). The vigour score is reported as a percentage, where the lower the number the less hybrid vigour the animal is deemed to have. Scores typically range from 20 for straightbred animals to above 80 for crossbred/composite animals (Furber 2017). A 10% increase in VS has been estimated to increase 200 d weaning weights by 1.36 kg, shorten age at first calving by 2 d, increase pregnancy rates 2% and increase wean rates 3% greater. The recommendation is to EnVigour HX™ test breeding females and breeding bulls and then match bulls with cows that are least like them in terms of breed composition to increase VS of progeny with strategic crossbreeding.

At the Lacombe Research Station, 412 replacement heifers were followed for 5 calvings and split into High and Low vigour groups based on their vigour scores. The high vigour (VS >48.6%) females had 47% retention to third parity while only 32% of the low vigour (VS ≤ 48.6%) females remained after three calvings. Across five parities, the high vigour heifers had

higher retention levels and the improved performance provided a \$161 per head per year benefit (Basarab et al. 2018).

The collaborating operation in the current study had all calves tested using EnVigour HX™ in 2018 and all heifers born tested in 2019. The producer did not use VS results in management decisions. The testing was provided at no cost to the producer and ownership of the herd changed during the study. Therefore, both these factors may be reasons explaining the non-use of VS scores in heifer replacement selection.

Adoption of technologies can be negatively impacted if there is risk of obsolescence or complexity in learning to use the technology (Weersink and Fulton 2020). Commercially available genomic testing is continuing to evolve and may need more improvements to see an economic benefit for commercial producers. For this reason, in this chapter an economic evaluation will be used to evaluate the cost and benefit of using the genomic test EnvigourHX™, to determine if these tools are useful for the commercial cow-calf producer.

4.2 MATERIALS AND METHODS

Economic analysis of DNA testing and utilizing a genomic selection tool involved using assumptions and values provided by the testing company, from their own research trial, as well as utilizing data collected from the operation used in Chapter 3.0. For the EnVigour HX™ analysis, real values were used from the collaborating operation, with assumed costs and gains values used from the testing lab and a previous research study (Basarab et al. 2018). These analyses were done to determine if there is an economic benefit to the cost of the testing for a commercial beef operation.

Specific values claimed to be improved by previous research and the testing company included age at first calving, conception rate, wean rate, and 205 day adjusted weaning weight

(WW) and the assumed gains were used along with the data collected from the operation. Expected differences were based on claims made by the company, and actual differences were what was seen between heifers tested on the operation based on their vigour scores. Heifers (n=86) born and retained in 2018 were sorted into groups based on their VS assigned by EnvigourHX™ testing. Low VS heifers (VS <0.74), Average VS heifers (0.74-0.77), and high VS heifers (>0.77). Heifers were followed over two parturitions to evaluate age at 1st calving (d), calving interval (d), conception rate for 1st and 2nd calf (%), wean rate (5), average WW (kg), total kg weaned, and 205d adjusted WW (kg). Replacement heifer performance was analyzed to compare the if the heifer data met, exceeded, or did not meet the expected differences based on vigour score.

A two-year value of production comparison was done to compare the actual differences observed between low VS and high VS heifers. Heifers (n=54) born and retained in 2018 were sorted into groups based on their VS assigned by EnvigourHX™ testing as mentioned above. Heifers in the average VS group were excluded for this analysis to ensure an average VS spread difference of at least 10%. Heifers were followed over two parturitions to evaluate number calves weaned and calf WW.

Due to an uneven number of heifers between groups, group size used was 100 heifers and values were based on the actual heifer data collected from the herd over two years (2018 and 2019). The cost of EnvigourHX™ was \$45 in 2018 and this value was used. Wean weight values were obtained using Canfax's reported average market price for 182kg steers in October 2020 (\$5.42/kg) and average market price for 205kg steers in October 2021 (\$5.28/kg). A two-year net return analysis was performed using the equation:

$$\text{Net return} = \text{testing cost} - \text{total kg weaned}$$

Where *net return* was the two-year net return value, *testing cost* was the total cost for testing 200 heifers with EnvigourHX™ in 2018 at \$45 per head, and *total kg weaned* was the difference of total kg weaned per 100 retained heifers between the low VS and high VS heifers.

4.3 RESULTS AND DISCUSSION

According to Delta Genomics (2017) every 10% increase in EnVigour HX™ score will have multiple benefits for various traits. These benefits include 1.36 kg increase in the 200 d wean weight, 2 d reduction in age at first calving, 2% increase in pregnancy rates, and 3% increase in wean rates. For the 2018 heifers, as seen in Table 4.1, there was a 20% increase in VS between the low and high group and therefore improvements expected are doubled. The results for the 2018 heifers show no improvement in age at first calving, however, the benefit may be for their heifer calves. For conception rates each year, there was only a 1.2 or 1.3% difference between the low and high group with 4% expected, however the conception rates in the heifers were already high. The 205 d adjusted WW did not meet the 2.72 kg expected difference, but was close at 2.5 kilograms. Definitive cost-effectiveness in genomic testing is difficult to determine, whether that be if the value of genomic information results are great enough or if the cost of the test is low enough (Thompson 2018). DNA parentage testing can be more simple to understand and implement to improve the accuracy of replacement female selection or bull performance (Van Eenennaam 2012). Our results do not provide a clear determination if genomic testing with EnvigourHX™ is beneficial, and there is a gap in the literature of other studies evaluating this test at all.

Table 4.1. Replacement heifer performance based on EnVigour HX™ score with expected differences and actual differences between groups

	Low Envigour heifers (<0.74)	AVG	High Envigour heifers(>0.77)	Expected difference ^b	Actual difference ^c
No. of heifers	28	32	26	-	-
AVG Envigour score	0.61	0.76	0.80	-	+0.19
Age at 1st calving (d)	733	733	733	-4d	0
Calving interval (d)	337	367	363	None expected	+26d
Conception rate 1st calf (%)	96.5	95.3	97.7	+4%	+1.2%
Conception rate 2nd calf (%)	92.2	88.3	93.5	+4%	+1.3%
Wean rate (%)	100	96.875	100	+6%	0
Avg WW (kgs)	194.2	197.0	198.4	-	+4.2 kgs
Total kg weaned ^a	9304	10263	8923	-	-381 kgs
205d adjusted WW (kg)	197.8	203.4	200.3	+2.72 kgs	+2.5 kgs

^a number of heifers was not equal across groups.

^b based on 20% spread between the average VS for the low and high group and Delta Genomics expected production differences

^c between low and high group

The cost of EnVigour HX™ testing was \$45 per head in 2018 and was performed on all heifers as calves. Therefore, the cost of testing all heifers was \$4,140. Because this testing is done on heifers as calves, each heifer now has cost the producer \$45, regardless if the female ever produces a calf. Currently, genomic tests range from \$10 to \$79 per head depending on the

company and level of information the testing provides (Ballenger et al. 2016), which can be costly when done on all or half of the calf crop each year.

After two parities, the low VS heifers and high VS heifers had differences in conception and weaned calf numbers, but they were minimal despite the 20% difference in average VS score between low VS and high VS heifers (Table 4.2). Between the two groups, the high VS heifers weaned 711 more kgs than the low VS heifers providing a \$3,854 return for the high VS group in 2020. The high VS heifers weaned more kgs in 2021 as well, at 329 more kgs for a \$1,737 return over the low VS heifer group (Table 4.2). Overall, the two-year net return was a loss of \$3,409. After two calf crops, the improved performance observed among high VS heifers generated enough revenue to recover 62% of the investment. There may be potential to eventually break even or have a positive return over more years, however this was unable to be determined in the current studies timeframe. These results cannot be compared to other studies evaluating this testing as there is a gap in the literature for this genomic test.

Table 4.2 Two-year value of production comparison 2018-born females categorized as low or high EnvigourHX, per 100 heifers

	Low VS heifers ¹	High VS heifers ²	Actual difference	Returns, \$
Cost of test ³ (\$)	-	-		-9000
2020				
% that weaned a calf	89	92	+3	-
Avg WW (kg)	184.6	186.3	+1.7	-
Total kg weaned per 100 retained	16,429	17,140	+711	+3,854 ⁴
2021				
% that weaned a calf	79	81	+2	
Avg WW (kg)	213.2	212	-1.2	-
Total kg weaned per 100 retained	16,843	17,172	+329	+1,737
2 Year Net Return over Testing Cost				(\$3,409)

¹Low VS heifers had n=28 and <74 VS.

²High VS heifers had n=26 and >77 VS.

³Testing cost \$45 per test and assuming 100 heifers tested per category

⁴Additional wean weight values using Canfax's reported average market price for 182kg steers in October 2020 (\$5.42/kg) and average market price for 205kg steers in October 2021 (\$5.28/kg)

Another consideration when adopting new technology is the importance of understanding how to use the results to assist in management decisions. In this study, the testing results were

supplied to the producer, but they did not use the parentage or EnVigour HX™ results when making culling or breeding decisions. This was for a variety of reasons, the main one was the delay of results after sample submission. From 2018-2020, complete test results took an average of two months turn around time, which was too long to incorporate results for breeding decisions as the breeding season had already begun. Although they did keep the parentage data in their records, it was not used in decision making during the same year.

EnVigour HX™ testing results done in 2018 and 2019 were not used at all by the operation. This may be due to unfamiliarity with the information provided by the test. Support was not provided by researchers or lab personnel to the owners of collaborating operation on what the test results represented or how they can be used for breeding management decisions. Although the benefit from crossbreeding is clear in many ways, the financial benefit from utilizing this testing to aid in crossbreeding decision making may not be as obvious.

The adoption of genomic technology is important to ensure the beef industry continues improving and adapting to the challenges and variable markets in the future. However, any new decision or adaptation comes down to the economic benefit back to the operation. And not all technology is relevant or feasible for every operation. Therefore, it is important that the financial investment translates to a clear benefit whether monetary, improvement in sustainability, ease of management, or all three factors.

Typically, beef cattle operations are slower to adopt new technology when compared to the dairy industry (Berry et al. 2016). However, this does not mean the adoption rates can not or will not increase. A major reason for lack of adoption of new technology could be due to limited support after adoption, or unclear return on investment for the producer. As was the situation with the genomic testing used in the current study. Therefore, providing support, such as

interpretation of the results and examples of implementation on farm, could be invaluable to producer adoption. The seedstock industry utilizes genomic testing much more frequently than the commercial sector, but they have the support of the breed association to assist and clarify questions and concerns about new technology. Options for support to commercial producers when adopting new technologies could help bridge the gap.

4.4 CONCLUSION

There is a clear economic and social importance to improve beef production globally and improving and optimizing breeding strategies and reproductive performance in the herd is essential for improvement. The benefit from crossbreeding is clear and has been well established for many years. However, based on our economic analysis, the benefit utilizing genomic test for improving heterosis was not clear in this herd. There may be an economic improvement over a longer period of time, but another study would need to be conducted. It may be beneficial to find a larger population of heifers with lower vigour scores and follow them over multiple years to determine if and when an economic improvement occurs. It would also be important to consider how long the testing needs to be used before the use will not provide any more significant improvement, perhaps when the herd average vigour score is around 75% as was the case with this herd.

In conclusion, improvement of breeding programs in the commercial beef cattle sector is important for longevity and sustainability. However, the current genomic tests available, such as EnVigour HX™, may not be easily integrated without financial support or compensation to allow these programs to be economically feasible for a commercial producer. Based on the results obtained from the current study herd, over the timeframe used, EnvigourHX™ testing could not be recommended for use with this herd. Applicability to other herds cannot be determined at this time.

5.0 GENERAL DISCUSSION AND CONCLUSIONS

In each year of the current study, there was a wide range in number of calves sired per bull. Regardless of purchase price, the cost to maintain a sire is the same for all sires, meaning low producing sires can economically hinder the operation. Furthermore, higher purchase prices of the bull will not guarantee prolificacy. Therefore, identification of high and low producing sires is a valuable asset when making selection decisions.

A BPI score was calculated for each bull to account for different bull to cow ratios between each breeding group each year. The BPI value allows for standardized comparison across breeding groups per year with different bull:cow ratios and variation in cow fertility. A score of 1 represents the expected number of calves to be sired based on total bulls in the breeding group and number of cows available. A score above 1 represents the bull exceeding expectations and producing a higher number of calves than expected. A score below 1 represents the bull not producing their expected number of calves for that breeding season.

Sire age was determined to influence performance for yearling bulls compared to two-year-olds and mature bulls based on BPI value. Overall, yearlings had the lowest BPI value compared to 2-year-old and mature sires. However, mature bulls showed the largest variation in BPI compared to yearlings and 2 yr old bulls. The use of DNA parentage testing could identify these mature sires earlier as low progeny producers which could decrease the variation and help to improve the mature sire performance overall.

Sires used for multiple years had varied performance during the study period. Some sires who produced a higher number of calves early numerically tended to continue to produce a higher number of calves, compared to sires who produced a low number of calves in the first breeding season. However, this was not always the case, and it was unclear if bull repeatability

can be determined early on, and it was not able to be determined in this study statistically as there was too small a sample size to work with. If sire long term performance could be determined early on, that would be beneficial when making management decisions to ensure poor producing sires are not being kept.

When the calf crop was tested using EnVigour HX™, the average vigour score was 69% with all calves' breed composition being majority Angus cross calves. The benefit of crossbreeding has been well documented over the years, and the use of both purebred Angus bulls and composite breed Beefbooster bulls, this herd has been able to have a higher vigour score on average. However, the information obtained from testing was not used to make any management decisions, and with the high cost of the test at \$45 each, it would not have been beneficial for this herd to do the testing as no positive net financial return was calculated.

Sires with high prolificacy will produce more calves and have their genetic influence be retained in the herd for more generations. Although sires in the low prolificacy group had a higher percentage of daughters remain in the herd, they had a lower percentage of grand-calves overall compared to the average and high prolificacy sire groups. This is beneficial because sires with ideal genetics will only be beneficial if they produce enough calves to pass on those genetics for many generations. A sire with the best potential of genetics cannot perform and produce calves with higher genetic potential if they cannot produce calves first.

Replacement heifer performance, like sire performance, is related to calf production. Therefore, it is important that a heifer or cow is provided with proper management that will improve their ability to get pregnant and produce a calf. Previous research has shown that heifers born in the first 21 d are more likely to remain in the herd and produce a calf. In this study heifers born in the first cycle tended to also produce calves in the first cycle of the calving

season. Producing a calf early in the calving season allows the female more time to recover and be able to cycle early in the breeding season. Producing a calf early also benefits calves as they have more time to gain weight before weaning.

Replacement heifers in this study had the shortest calving interval between their second and third calves. This means most heifers were able to produce calves early on or recover sooner after a late calving date. Replacement heifers from high BPI sires also tended to have the shortest calving intervals compared to heifers from low or average BPI sires.

The investment in genetic potential of highly prolific sires is realized for multiple generations. Valuable sire performance can also vary across different operations based on their goals. But identifying calves to sires based on number of calves or calves born in the first cycle (21 d) is useful information for selection decisions. But in multiple sire breeding groups, an individual sire's performance is not known. So, in combination with genomic testing for parentage, and an investment in ideal genetics, more informed decisions can be made yearly to help promote greater economic return on investment.

Adoption of new technology is an important financial decision on any operation. There needs to be a clear realized economic value that the adoption would bring to the operation. In this study, the current operation did not see an economic benefit with two years of use of the new genomic EnVigour HX™ test. The previous study that utilized the test only realized an economic return with five years of testing (Basarab et al. 2018). However, the test was developed based on the study results from Basarab et al. (2018), and with no other independent study or reference population evaluating the economic benefit from using the genomic test, it is unclear if there would be a benefit for most commercial operations.

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