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MALE FERTILITY IN BEEF CATTLE

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Introduction

Reproductive performance and fertility are critical to the economic profitability of a beef operation. Fertility is broadly defined as the ability to conceive viable offspring, but males and females must be sufficiently fertile to produce a viable embryo (Utt, 2016). A beef herd's overall fertility rate is generally measured by its pregnancy rate or the percentage of cows that successfully became pregnant during their first, second, or third estrus cycle of the breeding season (Hopper, 2014). Conception is impacted by various factors, including age, nutrition, health, and environmental conditions (Chacón et al., 2002; Nichi et al., 2006; Barth, 2007; Koivisto et al., 2009). Furthermore, genetic factors such as the inbreeding coefficient (Karoui et al., 2011) and breed composition(Barth and Waldner, 2002; Koivisto et al., 2009) can impact reproductive traits.

Most genetic selection tools available to beef producers focus on female fertility. Expected progeny differences (EPD) have been created to estimate the probability of pregnancy in first-calf heifers, the probability of calving as a three-year-old given she calved as a first-calf heifer, and the probability that a female will produce a calf every year to at least six years of age (Doyle et al., 2000; RAAA, 2018; AGA, 2022). Several beef breeds have published a scrotal circumference EPD which predicts the ability of an animal to influence scrotal size in their offspring (Angus Beef Bulletin, 2015). However, it does not account for semen production or semen quality measures, which can be major determinants of conception. Heritability estimates and genetic correlations that have been published for scrotal circumference, semen production measures, and semen quality measures illustrate the potential for increasing beef bull fertility.

Genetic Parameters

Tables 1 and 2 outline the reported heritabilities published within the scientific literature for semen production and quality traits, respectively. All studies from scientific literature utilize a best linear unbiased prediction (BLUP) univariate or multivariate animal model. The two exceptions were Smith et al. (1989) and Kriese et al. (1991), who analyzed their data with a sire model and least square procedures. Each study's model had varying fixed effects, but most included bull age, season, and year. Studies that utilized information from artificial insemination (AI) centers generally included fixed effects such as the day of the week when semen collection occurred, ejaculate number, and semen collector.

Scrotal Circumference

Scrotal circumference is correlated with daily spermatozoa production, semen quality, paired testis weight, and offspring reproductive performance (Lunstra et al., 1978; Coulter and Foote, 1979; Brito et al., 2002; Barth, 2007). The SC is measured by gently forcing the testes to the bottom of the scrotum and placing the measuring tape level with the skin around the widest part of the scrotum (Hopper, 2014). Heritability estimates in the literature for SC range from 0.36 to 0.75. In studies examining British-type yearling bulls, moderate heritability estimates were reported ranging from 0.36 to 0.56 (Neely et al., 1982; Knights et al., 1984; Kriese et al., 1991; Christmas et al., 2001). Scrotal circumference in *Bos indicus* bulls has been reported as moderately to highly heritable. Carvalho et al. (2023) estimated a SC heritability of 0.75 in 18-month-old Nellore bulls. Another study in Nellore bulls estimated a moderate heritability for SC (Silva et al., 2013). The Corbet et al. (2013) study estimated SC heritabilities in 6, 12, 18, and 24-month-old Brahman and Tropical composite bulls and reported similar heritability estimates within each breed. Therefore, age may have less effect on SC heritability than breed origin.

Semen Production Traits

Volume is the total amount of semen in an ejaculate, measured in millimeters (Butler et al., 2021). Most studies reported low heritability estimates for volume. Kealey et al. (2006) and Kapš et al. (2000) reported low heritability estimates for volume in semen collected from Line 1 Hereford and Simmental bulls, respectively, during a BSE. Carvalho et al. (2023) published a similar heritability estimate for volume in Nellore yearling bulls. Estimates from beef bulls at AI centers range from 0.11 to 0.32 (Butler et al., 2021; Rostellato et al., 2021; Cesarani et al., 2023). Heritability estimates from AI dairy bull semen range from 0.18 to 0.65 (Ducrocq and Humblot, 1995; Atagi et al., 2017), with most between 0.22 and 0.26 (Mathevon et al., 1998; Druet et al., 2009; Karoui et al., 2011; Suchocki and Szyda, 2015). The higher heritabilities reported in dairy compared to beef cattle could be due to breed. The studies with data from AI centers could have higher estimates than BSE studies because some centers combine multiple ejaculates into one collection day observation.

Semen concentration is the density of sperm cells in an ejaculate, measured in millions/ milliliter. Most estimates for concentration are lowly heritable in beef and dairy AI bull populations. However, one study reported a moderate to high value for concentration heritability in a population of Holstein bulls (Mathevon et al., 1998). The Mathevon et al. (1998) study only had 137 bulls in their population, which is smaller than other populations in the literature. Interestingly, heritability estimates for concentration from AI dairy bulls tended to be higher than estimates from beef bull semen (Knights et al., 1984; Gredler et al., 2007; Butler et al., 2021).

The total number of spermatozoa in an ejaculate is calculated by multiplying the volume and concentration values. The number of spermatozoa is expressed in millions. Taylor et al. (1985) noted that the accuracy of genetic estimates for number of spermatozoa in a multi-trait model could be affected by it being a function of two other traits. Heritability estimates for number of spermatozoa range from 0.03 to 0.38 in beef and dairy studies (Knights et al., 1984; Taylor et al., 1985; Mathevon et al., 1998; Butler et al., 2021). Similar heritability estimates have been reported in Alpine and Saanen goats (Furstoss et al., 2009). Estimate differences could be attributed to population size or model effects.

Semen Quality Traits

Semen motility is the percentage of sperm cells progressively moving forward in an ejaculate. Multiple studies have determined that motility is an essential indicator of fertility in beef (Chenoweth and Lorton, 2021), sheep (David et al., 2015), and humans (Nel-Themaat et al., 2006). Christensen et al. (1999) reported that motility was statistically correlated to non-return rates. Heritability estimates for beef bull motility obtained from yearling bull BSEs had low heritability estimates (Smith et al., 1989; Christmas et al., 2001; Garmyn et al., 2011). Heritability estimates for motility phenotypes obtained at bull semen collection facilities were higher than those recorded from BSEs and ranged from 0.12 to 0.37 (Ducrocq and Humblot, 1995; Mathevon et al., 1998; Kealey et al., 2006; Suchocki and Szyda, 2015; Berry et al., 2019; Butler et al., 2021). The variation in heritability estimates for motility obtained in the study's model. The heritability of motility is important to bull fertility because if sperm are not motile enough to traverse the female tract, the sperm cannot fertile the ovum (Chenoweth and Lorton, 2021).

Heritability estimates for the percentage of morphologically normal spermatozoa (%Norm) in literature have a wide range of values. Smith et al. (1989) reported a low heritability of 0.07±0.06 from their study of BSEs from Hereford, Angus, and Red Angus bulls. Recent studies reported similar estimates in Angus and Italian Simmental AI bull populations (Butler et al., 2021; Cesarani et al., 2023). Conversely, Kealey et al. (2006) and Corbet et al. (2013) published moderate estimates for %Norm in Line 1 Hereford and Tropical Composite yearling bulls, respectively.

In literature, sperm abnormality traits have been reported in various ways. Primary abnormalities most likely arise during spermatogenesis. Common primary abnormalities are abnormal heads, midpieces, and proximal cytoplasmic droplets (Kealey et al., 2006). Secondary abnormalities are caused by faulty epididymal sperm maturation. Spermatozoa with bent tails, coiled tails, or distal cytoplasmic droplets are considered to have a secondary abnormality. The Kealey et al. (2006) study suggested that genetics could greatly influence secondary abnormalities. Heritability estimates for primary abnormalities in the literature ranged from 0.03 to 0.35 (Smith et al., 1989; Christmas et al., 2001; Garmyn et al., 2011; Butler et al., 2021). Butler et al. (2021) utilized semen collected at an AI center on bulls of various ages. In contrast, the other studies utilized BSE data from yearling bulls. Those same studies reported low heritability estimates for secondary abnormalities (Christmas et al., 2001; Garmyn et al., 2001; Garmyn et al., 2011; Butler et al., 2021).

Major defects decrease fertility when present in an ejaculate. The classification of spermatozoa as a major abnormality includes proximal cytoplasmic droplets, head, and midpiece abnormalities, and any single abnormality with significant presence in the ejaculate (Menon et al., 2011). Minor defects do not significantly impact fertility unless present in a high percentage. Looped tails, distal cytoplasmic droplets, and detached heads would be classified as minor (Menon et al., 2011). Two studies estimated low heritabilities for major and minor abnormalities in Nellore AI bulls. Carvaho et al. (2023) reported an estimate of 0.15 for major abnormalities and 0.04 for minor defects. Silva et al. (2013) reported similar heritability estimates for the percentage of major and minor defects.

In 2016, a differential counting scheme was adopted by the Society of Theriogenology (SFT), which groups defects under the classifications of head, midpiece, and principal piece (tail) abnormalities (Society for Theriogenology, 2018). Duret et al. (2009) reported a moderate heritability estimate for head abnormalities and a low estimate for tail abnormalities.

Heritability estimates for total abnormalities in an ejaculate range from 0.15 to 0.3. Christmas et al. (2001) and Garmyn et al. (2011) reported estimates of 0.29 and 0.25, respectively, for Angus bulls. Estimates of 0.15 and 0.30 were reported in Nellore bulls by Carvalho et al. (2023) and Silva et al. (2013), respectively. Ducrocq and Humblot (1995) published a total abnormality estimate of 0.19 in dairy bulls.

Heritability estimates appear to be highest when abnormalities are classified by anatomical location on the sperm cell or when analyzed as a total amount. However, more research needs to be done on the genetic effects and heritability of sperm abnormalities.

Overall, many of the heritability estimates for semen production and quality traits are low to moderate, but most of the standard errors were small, and the estimates were different from zero, so it is possible to improve male fertility. For example, the Canadian Dairy Industry released a daughter fertility (DF) index for their national breeding program (Fleming et al., 2019) with heritability estimates for the traits within the DF index ranging from 0.02 to 0.07. During the first five years of genomic implementation, the national estimated breeding value (EBV) for the DF index increased by 1.78 EBV points per year (Canadian Dairy Network, 2017). Similar genetic gains could be made in the United States beef population if genetic tools are made available to producers.

Genetic and Phenotypic Correlations

Scrotal Circumference with Semen Production Traits

Table 3 presents the reported correlations between SC and sperm production traits, but the research is limited in the literature. Scrotal circumference is the easiest measurement for veterinarians to take and is less subjective than other measurements taken during a BSE, which is why understanding genetic and phenotypic correlations between SC and ejaculate characteristics is important for improving bull fertility. Barth (2007) published that SC measurements were highly phenotypically correlated with paired testes' weight and daily sperm production. Kealey et al. (2006) reported favorable genetic correlations between SC and volume and concentration. The favorable correlations are promising for improving male fertility because SC is moderate to highly heritable.

Scrotal Circumference with Semen Quality Traits

Many studies published favorable genetic and phenotypic correlations between SC and semen motility which are presented in Table 3. Corbet et al. (2013) published a strong genetic correlation and moderate phenotypic correlation in 12-month-old Brahman bulls. Christmas et al. (2001) and Kealey et al. (2006) reported favorable, moderate genetic correlations of 0.56 and

0.34, respectively, in British-type bulls. However, Smith et al. (1989) reported a negative genetic correlation of -0.04 ± 0.40 between SC and motility, but the estimate was not different than zero.

Corbet et al. (2013) tested the phenotypic and genetic correlations between SC and %Norm in bulls at 12, 18, and 24 months. The authors reported positive, favorable phenotypic and genetic correlation estimates (Corbet et al., 2013). However, Smith et al. (1989) reported an unfavorable, negative genetic correlation. The difference in results could be because the Smith et al. (1989) estimates were from a small population (549) of yearling Hereford bulls, and the Corbet et al. (2013) utilized a large population of 12, 18, and 24-month-old Brahman and Tropical Composite bulls.

Silva et al. (2013) found negative, low genetic correlations between SC and sperm defects in yearling Nellore bulls. Other studies have reported negative genetic associations between SC and sperm traits, with estimates ranging from -0.19 to -0.36, -0.11 to -0.45, and -0.12 to -0.23, for genetic correlations between SC and primary, secondary, and total sperm defects, respectively (Knights et al., 1984; Kealey et al., 2006; Garmyn et al., 2010). These results suggest that direct selection to increase SC could reduce abnormal spermatozoa, which could improve the semen quality of young bulls and subsequently increase the number of males passing a BSE.

Semen Production Traits

Most phenotypic and genetic correlations reported between volume and concentration are negative and unfavorable because as volume increases, concentration decreases. Druet et al. (2009) and Burren et al. (2019) estimated moderate genetic correlations in dairy AI bulls. A lower estimate was published by Rostellato et al. (2021) in a population of Piemontese bulls. Phenotypic correlations ranged from -0.01 to -0.35 (Berry et al., 2019; Rostellato et al., 2021, respectively). Table 3 presents the reported correlations.

Literature estimates for correlations between number of spermatozoa and volume are varied. Gredler et al. (2007) estimated the strong phenotypic and genotypic correlations in a population of dual-purpose Fleckvieh bulls. Similarly, Butler et al. (2021) estimated phenotypic and genetic correlation to be 0.75 ± 0.08 and 0.66 ± 0.01 , respectively. While Rostellato et al. (2021) and Druet et al. (2009) published moderate genetic correlation estimates between number of spermatozoa and volume. The published genetic correlations between concentration and number of spermatozoa are moderate in strength. Druet et al. (2009) reported one of the lower estimates between number of spermatozoa and concentration and it has a large standard error that could be attributed to population size. Higher genetic correlation estimates were published by Gredler et al. (2007), Butler et al. (2021), and Rostellato et al. (2021). Literature estimates for phenotypic correlations range from 0.52 to 0.71 (Gredler et al., 2007; Druet et al., 2009; Butler et al., 2021). The published genetic and phenotypic correlations between number of spermatozoa and volume and concentration should be expected as number of spermatozoa is a function of the two.

Semen Production Traits with Semen Quality

Genetic correlation estimates between volume and initial motility are mostly weak and positive as summarized in Table 3. Relatively few studies have quantified the interrelationships between

volume and morphology. Butler et al. (2021) reported a positive genetic correlation between volume and primary abnormalities. While their estimate between volume and secondary abnormalities was negative and weak. Both estimates were not different than zero (Butler et al., 2021). Druet et al. (2009) reported similar results between volume and numerous individual sperm defects. Berry et al. (2009) reported unfavorable, positive phenotypic and genetic correlation estimates between volume and total abnormalities. Conversely, Ducrocq and Humblot (1995) reported favorable weak correlations between the two traits.

Berry et al. (2019) found a low, favorable genetic correlation between concentration and motility. Similarly, Karoui et al. (2011) reported a moderate, positive correlation between the two traits, but the authors did not report a standard error. Butler et al. (2021) reported negative phenotypic correlations between concentration and primary and secondary abnormalities, so as concentration increases, sperm abnormalities would decrease, which is similar to the results seen in SC correlations. Druet et al. (2009) published many genetic correlations between concentration and various sperm defects, but most estimates were not different than zero. Genetic correlations between concentration and percentage of viable spermatozoa have been estimated to be moderate and positive in several studies (Gredler et al., 2007; Druet et al., 2009; Berry et al., 2019).

Atagi et al. (2017) and Butler et al. (2021) both reported positive and favorable genotypic and phenotypic correlations between number of spermatozoa and motility. Phenotypic correlations for number of spermatozoa and semen morphology are low and negative (Druet et al., 2009; Butler et al., 2021). Butler et al. (2021) genetic correlations between number of spermatozoa and primary and secondary abnormalities both had large standard errors. Knights et al. (1984) reported that correlations in their study indicated that selection to increase the number of spermatozoa would be accompanied by an increase in sperm quality. More research is necessary on the effects between semen production traits and sperm morphology because many current estimates are not different from zero.

Semen Quality Traits

Table 3 also includes genetic and phenotypic correlation between semen quality traits. Butler et al. (2021) estimated a strong and favorable genetic correlation between motility and %Norm. In contrast, Smith et al. (1989; 0.43) and Kealey et al. (2006; 0.51) reported only a moderate, favorable correlation between motility and %Norm. Genetic correlations between motility and primary and secondary abnormalities reported in the literature but some estimates are not statistically significant (Smith et al., 1989; Butler et al., 2021). Druet et al. (2009) reported motility had negative, favorable genetic correlations with head, tail, and total sperm abnormalities. These results indicate that lower motility is associated with a higher percentage of abnormal sperm cells; however, selecting to increase motility could decrease the number of abnormal sperm in an ejaculate.

Current State of Male Fertility Selection Tools

The only available male fertility selection tool for beef producers is the SC EPD. The SC EPD evaluation predicts the difference in an animal's ability to transmit scrotal circumference to its

male offspring compared to other animals (AGA, 2022; AAA, 2023). Moser et al. (1996) reported that Limousin bulls with higher SC EPDs tended to have fewer abnormalities in their semen, and their daughter reached puberty at significantly earlier ages when compared to bulls with lower SC EPDs. Butler et al. (2021) utilized the BLUPF90 family of programs (Misztal et al., 2014) to correlate SC EPDs, provided by the American Angus Association, with beef bull fertility EBVs to determine if SC could be a potential indicator of beef bull fertility. The authors reported that SC was not a good predictor of fertility due to low correlations (Butler et al., 2021).

The literature provides evidence that genetic selection tools could impact beef bull fertility. However, there are few male fertility selection tools currently available within the industry. These tools could allow producers to make selection decisions on younger animals for reproduction traits which require an animal to be at least 12 months old or older to record a phenotype. Additionally, utilizing genomic technology could give producers more predictive power and more confidence when incorporating young, unproven sires into their breeding programs.

Conclusion

Due to its economic importance, additional research into beef bull fertility is warranted. Increased bull fertility could increase beef production, improve an individual herd's efficiency, and provide insight into male fertility traits in other species. Furthermore, improvements to bull fertility could be expedited with genetic selection tools. If beef producers could utilize phenotypic measures from BSEs to make selection decisions for improved male fertility, it would improve efficiency, save on labor and resources, and increase profitability (Rodgers et al., 2012).

Trait	n	Estimate	Standard Error	Breed	Reference
	2617	0.25	0.03	Swiss Cattle	Burren et al. (2019)
	1626	0.09	0.02	Angus	Butler et al. (2021)
	515	0.19	0.05	Holstein	Druet et al. (2009)
Concentration	301	0.14	0.04	Fleckvieh	Gredler et al. (2007)
	717	0.13	0.06	Angus	Knights et al. (1984)
	137	0.52		Holstein	Mathevon et al. (1998)
	1212	0.34	0.068	Holstein-Friesian	Suchocki and Szyda (2015)
	1626	0.08	0.02	Angus	Butler et al. (2021)
Number of Spermatozoa	758	0.15	0.04	Apline Goats	Furstoss et al. (2009)
	535	0.25	0.02	Saanen Goats	Furstoss et al. (2009)
	717	0.24	0.05	Angus	Knights et al. (1984)
	137	0.38		Holstein	Mathevon et al. (1998)
	2351	0.03	Standard Error Breed 0.03 Swiss Cat 0.02 Angus 0.05 Holstein 0.06 Angus 0.07 Holstein 0.06 Angus 0.06 Angus 0.06 Angus Holstein 0.068 Holstein 0.02 Angus 0.04 Apline Ga 0.05 Angus 0.04 Apline Ga 0.05 Angus 0.06 Magus 0.07 Saanen Ga 0.08 Brahma 0.08 Brahma 0.08 Brahma 0.08 Brahma 0.06 Angus Herefor 0.06 Angus Nellore 0.09 Brahma 0.06 Angus Nellore 0.09 Brahma 0.09 Brahma	Holstein	Taylor et al. (1985)
Scrotal Circumference	1608	0.46	0.08	Brahman	Corbet et al. (2013)
Circumference (6 months)	2388	0.41	0.08	Tropical Composite	Corbet et al. (2013)
	1282	0.56		Angus	Christmas et al. (2001)
	1447	0.65	0.08	Brahman	Corbet et al. (2013)
Scrotal	2092	0.46	0.06	Tropical Composite	Corbet et al. (2013)
(12 months)	717	0.36	0.06	Angus	Knights et al. (1984)
(12 monuis)	10511	0.53		Hereford	Kriese et al. (1991)
	578	0.44	0.24	Hereford	Neely et al. (1982)
	18435	0.75		Nellore	Carvalho et al. (2023)*
Scrotal	1409	0.75	0.09	Brahman	Corbet et al. (2013)
(18 months)	2081	0.43	0.09	Tropical Composite	Corbet et al. (2013)
	51161	0.4	0.02	Nellore	Silva et al. (2013)*
Scrotal Circumference	1403	0.75	0.09	Brahman	Corbet et al. (2013)
(24 months)	2067	0.44	0.09	Tropical Composite	Corbet et al. (2013)
	2065	0.159	0.022	Holstein	Atagi et al. (2017)
	1626	0.11	0.02	Angus	Butler et al. (2021)
	15882	0.05		Nellore	Carvalho et al. (2023)*
Volume	622	0.32	0.11	Italian Simmental	Cesarani et al. (2022)
	515	0.22	0.05	Holstein	Druet et al. (2009)
	1644	0.65		Normande	Ducrocq and Humblot (1995)
	955	0.04		Simmental	Kapš et al. (2000)
	502	0.22		Holstein	Karoui et al. (2011)
	840	0.09	0.08	Line 1 Hereford	Kealey et al. (2006)
	137	0.24		Holstein	Mathevon et al. (1998)
	693	0.219		Piemontese	Rostellato et al. (2021)
	1212	0.26	0.062	Holstein-Friesian	Suchocki and Szyda (2015)

Table 1. Reported heritabilities for semen production traits which define bull fertility. *Indicates semen ejaculate records instead of individual animals.

Table 2. Reported heritabilities for semen quality traits which define bull fertility. *Indicates semen ejaculate records instead of individual animals.

Trait	n	Estimate	Standard Error	Breed	Reference
Initial Matility	794	0.37	0.03	Beef and Dairy	Berry et al. (2019)
Initial Motility	1626	0.12	0.03	Angus	Butler et al. (2021)
	1282	0.07		Angus	Christmas et al. (2001)
	1245	0.05	0.03	Angus	Garmyn et al. (2011)
Motility	137	0.31		Holstein	Mathevon et al. (1998)
Motinity	423	0.08	0.07	Hereford, Angus, & Red Angus	Smith et al. (1989)
	1212	0.31	0.06	Holstein-Friesian	Suchocki and Szyda (2015)
Motility Score	1644	0.35		Normande	Ducrocq and Humblot (1995)
	841	0.22	0.09	Line 1 Hereford	Kealey et al. (2006)
	549	0.07	0.06	Hereford, Angus, & Red Angus	Smith et al. (1989)
	1626	0.09	0.04	Angus	Butler et al. (2021)
Percentage of Normal Spermatozoa	622	0.16	0.10	Italian Simmental	Cesarani et al. (2022)
	837	0.35	0.10	Line 1 Hereford	Kealey et al. (2006)
	970	0.41	0.10	Tropical Composite	Corbet et al. (2013)
	1626	0.03	0.03	Angus	Butler et al. (2021)
	1282	0.35		Angus	Christmas et al. (2001)
Drimary Abnormalities	1238	0.27	0.07	Angus	Garmyn et al. (2011)
Timary Abiofinanties	839	0.3	0.10	Line 1 Hereford	Kealey et al. (2006)
	549	0.31	0.09	Hereford, Angus, & Red Angus	Smith et al. (1898)
	1626	0.18	0.04	Angus	Butler et al. (2021)
	1282	0.26		Angus	Christmas et al. (2001)
Secondam. Abnormalities	1238	0.23	0.08	Angus	Garmyn et al. (2011)
Secondary Abnormanues	838	0.33	0.09	Line 1 Hereford	Kealey et al. (2006)
	549	0.02	0.05	Hereford, Angus, & Red Angus	Smith et al. (1898)
	14312	0.15		Nellore	Carvalho et al. (2023)*
Major Sperm Abnormalities	17648	0.16	0.02	Nellore	Silva et al. (2013)*
	13743	0.04		Nellore	Carvalho et al. (2023)*
Minor Sperm Adhormanues	17648	0.04	0.01	Nellore	Silva et al. (2013)*
Percentage of Spermatozoa with Abnormal Head	515	0.35	0.12	Holstein	Druet et al. (2009)
Percentage of Spermatozoa with Abnormal Tail	515	0.19	0.12	Holstein	Druet et al. (2009)
	14621	0.3		Nellore	Carvalho et al. (2023)*
	1282	0.29		Angus	Christmas et al. (2001)
Total Abnormalities	1644	0.19		Normande	Ducrocq and Humblot (1995)
	1238	0.25	0.07	Angus	Garmyn et al. (2011)
	17648	0.15	0.01	Nellore	Silva et al. (2013)*

n	rp	rg	Breed	Reference			
Scrotal Circu	Scrotal Circumference and Volume						
626		0.2	Hereford	Kealey et al. (2006)			
Scrotal Circumference and Concentration							
626		0.77	Hereford	Kealey et al. (2006)			
Scrotal Circu	Scrotal Circumference and Motility						
1282		0.56	Angus	Christmas et al. (2001)			
1447	0.47	0.70 ± 0.08	Brahman	Corbet et al. (2013)			
626		0.34	Line 1 Hereford	Kealey et al. (2006)			
423	0.13	-0.04 ± 0.40	Hereford, Angus, & Red Angus	Smith et al. (1898)			
Scrotal Circu	mference (12 mont	th) and Percenta	age of Normal Spermatozoa				
2092	0.31	0.55 ± 0.13	Tropical Composite	Corbet et al. (2013)			
549	0.17	$\textbf{-0.36} \pm 0.34$	Hereford, Angus, & Red Angus	Smith et al. (1989)			
Scrotal Circu	imference (18 mont	th) and Percenta	age of Normal Spermatozoa				
1409	0.31	0.50 ± 0.13	Brahman	Corbet et al. (2013)			
2081	0.22	0.21 ± 0.16	Tropical Composite	Corbet et al. (2013)			
Scrotal Circu	mference (24 mont	th) and Percenta	age of Normal Spermatozoa				
1403	0.12	0.22 ± 0.19	Brahman	Corbet et al. (2013)			
2067	0.13	0.20 ± 0.14	Tropical Composite	Corbet et al. (2013)			
Scrotal Circumference and Primary Abnormalities							
1238	-0.10	-0.19 ± 0.17	Angus	Garmyn et al. (2011)			
626		-0.36	Line 1 Hereford	Kealey et al. (2006)			
549	-0.09	0.14 ± 0.22	Hereford, Angus, & Red Angus	Smith et al. (1989)			
Scrotal Circumference and Secondary Abnormalities							
1282		-0.32	Angus	Christmas et al. (2001)			
1238	-0.11	$\textbf{-0.23} \pm 0.18$	Angus	Garmyn et al. (2011)			
Volume and Concentration							
794	-0.01	-0.40 ± 0.20	Beef and Dairy	Berry et al. (2019)			
2617	$\textbf{-0.28} \pm 0.01$	-0.56 ± 0.05	Swiss Dairy	Burren et al. (2019)			
515	$\textbf{-0.02} \pm 0.02$	$\textbf{-0.55} \pm 0.18$	Holstein	Druet et al. (2009)			
693	-0.35	-0.44	Piemontese	Rostellato et al. (2005)			
Volume and Initial Motility							
2065	0.047 ± 0.024	$\begin{array}{c} 0.165 \pm \\ 0.146 \end{array}$	Holstein	Atagi et al. (2017)			
2617	0.01 ± 0.02	0.19 ± 0.11	Swiss Dairy	Burren et al. (2019)			
1819	0.13 ± 0.01	0.23 ± 0.16	Angus	Butler et al. (2021)			
Volume and	Gross Motility Sco	re					
515	0.01 ± 0.03	-0.17 ± 0.19	Holstein	Druet et al. (2009)			
840		-0.04	Line 1 Hereford	Kealey et al. (2006)			
Volume and Primary Abnormalities							
1626	-0.09 ± 0.01	0.52 ± 0.61	Angus	Butler et al. (2021)			

Table 3. Phenotypic and genetic correlations between semen production and semen quality traits.*Indicates semen ejaculate records instead of individual animals.

Volume and Secondary Abnormalities						
1626	$\textbf{-0.01} \pm 0.01$	$\textbf{-0.13} \pm 0.17$	Angus	Butler et al. (2021)		
Volume and T	otal Abnormaliti	es				
794	0.63	0.66 ± 0.16	Beef and Dairy	Berry et al. (2019)		
1644	-0.13	-0.26	Normande	Ducrocq and Humblot (1995)		
Volume and N	lumber of Sperma	atozoa				
1626	0.66 ± 0.01	0.75 ± 0.08	Angus	Butler et al. (2021)		
515	0.61 ± 0.03	0.47 ± 0.18	Holstein	Druet et al. (2009)		
301	0.70	0.83 ± 0.13	Fleckvieh	Gredler et al. (2007)		
693	0.53	0.51	Piemontese	Rostellato et al. (2005)		
Concentration	and Number of S	Spermatozoa				
1626	0.61 ± 0.01	0.55 ± 0.13	Angus	Butler et al. (2021)		
515	0.71 ± 0.04	0.46 ± 0.18	Holstein	Druet et al. (2009)		
301	0.52	0.60 ± 0.07	Fleckvieh	Gredler et al. (2007)		
693	0.56	0.56	Piemontese	Rostellato et al. (2005)		
Concentration	and Motility					
794	0.20	0.29 ± 0.04	Beef and Dairy	Berry et al. (2019)		
502	0.33	0.54	Holstein	Karoui et al. (2011)		
Concentration and Primary Abnormalities						
1626	-0.03 ± 0.01		Angus	Butler et al. (2021)		
Concentration	and Secondary A	bnormalities				
1626	-0.13 ± 0.01	0.04 ± 0.19	Angus	Butler et al. (2021)		
Concentration	and Percentage	of Spermatozoa w	vith Abnormal Cytoplasmic			
Droplet	0.08 ± 0.03	0.00 ± 0.28	Holstein	Drugt at al. (2000)		
Concentration	-0.08 ± 0.03	-0.09 ± 0.28	with Abnormal Head	Diuet et al. (2007)		
515	0.02 ± 0.03	0.23 ± 0.24	Holstein	Drugt at al. (2000)		
Concentration	-0.02 ± 0.03	-0.23 ± 0.24	with Abnormal Tail	Diuet et al. (2007)		
515	-0.06 ± 0.03	0.33 ± 0.30	Holstein	Druet et al. (2009)		
Concentration	and Percentage	of Vishle Snerma	tozoa	Didet et al. (2007)		
23614		0.37 ± 0.23	Reef and Dairy	Borry et al. (2010)		
515	0.13	0.37 ± 0.23	Holstein	Drugt et al. (2017)		
301	0.04 ± 0.05	0.29 ± 0.20	Fleckvieh	Gredler et al. (2007)		
$\frac{1}{10000000000000000000000000000000000$						
1626	0.16 ± 0.01	0.23 ± 0.18	Angus	Butler at al. (2021)		
1020	0.10 ± 0.01	0.23 ± 0.13	Aligus	Duilei et al. (2021)		
2065	0.23 ± 0.022	0.146	Holstein	Atagi et al. (2017)		
Number of Spermatozoa and Primary Abnormalities						
1626	-0.10 ± 0.01	0.08 ± 0.73	Angus	Butler et al. (2021)		
Number of Sp	ermatozoa and Se	econdary Abnorm	nalities			
1626	-0.09 ± 0.01	$\textbf{-0.10} \pm 0.20$	Angus	Butler et al. (2021)		
Number of Spermatozoa and Percentage of Spermatozoa with Abnormal Cytoplasmic Droplet						
515	-0.05 ± 0.02	0.33 ± 0.43	Holstein	Druet et al. (2009)		
Number of Spermatozoa and Percentage of Spermatozoa with Abnormal Head						
515	-0.02 ± 0.03	-0.38 ± 0.36	Holstein	Druet et al. (2009)		

Number of Spermatozoa and Percentage of Spermatozoa with Abnormal Tail						
515	-0.03 ± 0.03	0.14 ± 0.54	Holstein	Druet et al. (2009)		
Number of Spermatozoa and Percentage of Viable Spermatozoa						
717	0.79		Angus	Knights et al. (1984)		
Initial Motility and Percentage of Normal Spermatozoa						
1626	0.20 ± 0.01	0.77 ± 0.09	Angus	Butler et al. (2021)		
Motility and Percentage of Normal Spermatozoa						
423	0.38	0.43 ± 0.64	Hereford, Angus, & Red Angus	Smith et al. (1898)		
Gross Motility Score and Percentage of Normal Spermatozoa						
837		0.51	Line 1 Hereford	Kealey et al. (2006)		
Initial Motility and Primary Abnormalities						
1626	$\textbf{-0.21} \pm 0.01$	0.33 ± 0.20	Angus	Butler et al. (2021)		
Initial Motility and Secondary Abnormalities						
1626	-0.15 ± 0.01	0.63 ± 0.82	Angus	Butler et al. (2021)		
Motility and Primary Abnormalities						
423	-0.31	-0.36 ± 0.55	Hereford, Angus, & Red Angus	Smith et al. (1898)		
Motility and Secondary Abnormalities						
423	-0.22	0.71 ± 0.89	Hereford, Angus, & Red Angus	Smith et al. (1898)		
Motility and Percentage of Spermatozoa with Abnormal Cytoplasmic Droplet						
515	-0.07 ± 0.03	0.13 ± 0.23	Holstein	Druet et al. (2009)		
Motility and Percentage of Spermatozoa with Abnormal Head						
515	0.17 ± 0.04	-0.56 ± 0.18	Holstein	Druet et al. (2009)		
Motility and Percentage of Spermatozoa with Abnormal Tail						
515	$\textbf{-0.11} \pm 0.03$	$\textbf{-0.24} \pm 0.24$	Holstein	Druet et al. (2009)		

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