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Investigating conception rate for beef service sires bred to dairy cows and heifers

T. M. McWhorter,[1*] J. L. Hutchison,[2] H. D. Norman,[3] J. B. Cole,[2] G. C. Fok,[2] D. A. L. Lourenco,[1] and P. M. VanRaden[2]
[1]Department of Animal and Dairy Science, University of Georgia, Athens 30602
[2]USDA Animal Genomics and Improvement Laboratory, Beltsville, MD 20705
[3]Council on Dairy Cattle Breeding, Bowie, MD 20716

ABSTRACT

The widespread use of sexed semen on US dairy cows and heifers has led to an excess of replacement heifers' calves, and the sale prices for those calves are much lower than in the past. Females not selected to produce the next generation of replacement heifers are increasingly being bred to beef bulls to produce crossbred calves for beef production. The purpose of this study was to investigate the use of beef service sires bred to dairy cows and heifers and to provide a tool for dairy producers to evaluate beef service sires' conception. Sire conception rate (SCR) is a phenotypic evaluation of service sire fertility that is routinely calculated for US dairy bulls. A total of 268,174 breedings were available, which included 36 recognized beef breeds and 7 dairy breeds. Most of the beef-on-dairy inseminations (95.4%) were to Angus (AN) bulls. Because of the limited number of records among other breeds, we restricted our final evaluations to AN service sires bred to Holstein (HO) cows. Service-sire inbreeding and expected inbreeding of resulting embryo were set to zero because pedigree data for AN bulls were unavailable. There were 233,379 breedings from 1,344 AN service sire to 163,919 HO cows. A mean (SD) conception rate of 33.8% (47.3%) was observed compared with 34.3% (47.5%) for breedings with HO sires mated to HO cows. Publishable AN bulls were required to have ≥100 total matings, ≥10 matings in the most recent 12 mo, and breedings in at least 5 herds. Mean SCR reliability was 64.5% for 116 publishable bulls, with a maximum reliability of 99% based on 25,217 breedings. Average SCR was near zero (on AN base) with a range of −5.1 to 4.4. Breedings to HO heifers were also examined, which included 19,437 breedings (443 AN service sire and 15,971 HO heifers). A mean (SD) conception rate of 53.0% (49.9%) was observed, compared with 55.3% (49.7%) for breedings with a HO sire mated to a HO heifer. Beef sires were used more frequently in cows known to be problem breeders, which explains some of the difference in conception rate. Mean service number was 1.92 and 2.87 for HO heifers and 2.13 and 3.04 for HO cows mated to HO and AN sires, respectively. Mating dairy cows and heifers to beef bulls may be profitable if calf prices are higher, fertility is improved, or if practices such as sexed semen, genomic testing, and improved cow productive life allow herd owners to produce both higher quality dairy replacement and increased income from market calves.
Key words: sire conception rate, beef on dairy, beef bull fertility

INTRODUCTION

The adoption of beef bull semen in dairy herds presents advantageous opportunities for farmers. Dairy farmers rely on replacement females to be of equal or greater value than those of the previous generation. Until recently, the sex of the calf could not be chosen and a surplus of unnecessary male dairy calves was produced. A breeding strategy that is growing in popularity is to use sexed dairy semen on the best females to generate replacement heifers and to use beef semen on the remainder (Ettema et al., 2017). Although sexed semen is not a reality in all dairy herds, when used, it yields the predetermined calf sex with ~90% probability, minimizing the chance of an unwanted male calf (Holden and Butler, 2018). Beef and dairy crossbred calves produced by the remainder of the dams are to be used as beef output. This breeding strategy would lead to an increase in genetic gain in the dairy herd and an enhanced value of surplus calves as beef production for dairy farmers. Bérodier et al. (2019) found that the highest gains in net margin occurred when combining the use of sexed semen with terminal crossbreeding. It is known that a beef and dairy crossbred calf can produce satisfactory carcass and meat characteristics for consumers (Domingo et al., 2015). Berry et al.

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*Corresponding author: taylor.mcwhorter@uga.edu

(2019) introduced the dairy-beef index to rank beef bulls when mated to dairy cows and maximize the offspring's value. This index evaluates traits pertaining to calf growth and dam performance, however, it does not include traits related to bull fertility.

Breeding strategies heavily depend on the fertility of the mated pair. Conception rate (**CR**) is a measure of the female's fertility, whereas sire conception rate (**SCR**) is a measure of the bull's fertility. The USDA's Animal Improvement Programs Laboratory assumed responsibility for the US dairy bull fertility evaluations from the Dairy Records Management Systems (Raleigh, NC) in 2006 (Kuhn et al., 2006a). Kuhn et al. (2008) developed the SCR evaluation for dairy bulls, which focuses on incorporating multiple services and addressing the expanded service-sire effect, attributes of the bulls, and fertility changes over time. Kuhn and Hutchison (2008) found the heritability of SCR to be almost zero (i.e., 0.02 and 0.013% from linear and threshold models, respectively), meaning the genetic effect for service sire contributes little information to predictions. Therefore, SCR is a phenotypic assessment of bull fertility and is currently used to predict sire fertility for dairy bull breeds, including Ayrshire, Brown Swiss, Guernsey, Holstein, Jersey, and Milking Shorthorn (Norman et al., 2008).

Although very beneficial in dairy cattle, bull fertility has not been given much attention in beef breeds; however, male fertility becomes extremely important if beef bulls are mated to dairy cows or heifers. The objective of this study was to apply the same approach developed by Kuhn et al. (2008) to evaluate SCR when beef breeds are used as service sires on dairy cows in the United States, and to provide a tool for dairy producers to evaluate beef service sires.

MATERIALS AND METHODS

Description of Data

The National Association of Animal Breeders (**NAAB**; Madison, WI) supplied 5,063 beef bull IDs of more than 50 recognized breeds to be cross-matched with dairy cow mating records in the Council on Dairy Cattle Breeding's (**CDCB**; Bowie, MD) National Cooperators Database. Although the bull ID, birth date, breed, and controller stud code were known, there was no access to the beef bull's pedigree or genomic data; consequently, the service-sire inbreeding and expected inbreeding of resulting embryos used in Kuhn et al. (2008) were set to zero, and beef bulls were assumed to be unrelated to dairy cows. Data edits consisted of keeping the most recent 4 yr of data, removing herds with fewer than 80% of matings via AI, and removing herd-year contemporary groups with conception rates <10% or >90% to exclude herds that only reported successful breedings and other outliers. Cow lactations 1 through 5 were included. A separate analysis was conducted on heifers because inseminations of heifers was considered a different trait (Kuhn et al., 2006b). Heifers are not included in the national phenotypic evaluation system of SCR. A maximum of 7 conventional-semen breeding services were allowed for each cow. All breeds of dairy cows were required to have a minimum standardized milk yield of at least 4,536 kg (10,000 pounds) to eliminate lactations involving injury, health, or other unrecorded problems (Kuhn and Hutchison, 2008). Cows were placed into 1 of 2 groups based on the interval between subsequent breedings, referred to as the cow's short cycle: those breeding between 10 and 17 d and those breeding more than 17 d after the previous breeding. A subsequent insemination within 10 d replaced the prior record. Cows with breedings <18 d apart may indicate an abnormal estrus cycle and result in a lower CR (Kuhn et al., 2008). Cows <2 yr of age and service sires <1 yr of age were removed; cows >8 yr of age were rounded down to 8 yr; ages remaining were rounded to nearest year. Service-sire age was combined into 3 groups (1 to <4, 4 to <7, and ≥7 yr). Service sires >12 yr of age were rounded down to 12 yr. All confirmed breedings (failure or success) within these parameters were included. Failure was assigned if another reproductive code event was subsequently reported (i.e., breeding, heat, or diagnosis of "not pregnant"). The service was coded as a success if insemination resulted in conception confirmed by pregnancy check or resulting calf date. Subsequent inseminations ≥10 d after breeding were evaluated as new observations and accounted for by the insemination service number. Inclusion of multiple services and the expanded service sire term as a predictor increased the accuracy of predictions by 16% compared with using only first services and service sires (Kuhn and Hutchison, 2008). No embryo transfer or sexed semen breedings were included. Publishable bulls were required to have ≥100 total matings, ≥10 matings in the most recent 12 mo, and breedings in at least 5 herds.

In addition to the beef service-sire mating records, purebred Holstein insemination records were obtained from the National Cooperator Database for comparison of cow and heifer CR when mated to different breeds of bulls.

Model and Analysis

A SCR model was constructed using the factors proposed by Kuhn et al. (2008). In addition to factors characterizing the service bull, cow CR were estimated with nuisance variables using BLUP90IOD2 (Tsuruta et al., 2001), an iteration-on-data software for large data sets, under the following model:

$$y = HYSPR + YrStMo + lact + serv + ageGrp_{cow} + milkGrp + ShrtCycl + \beta_1(F_{bull}) \text{ and } \beta_2(F_{mating}) + ageGrp_{sire} + StudYr + SSR + PE_{cow} + a_{cow} + e,$$

where y was the binary outcome of the breeding (0 = failure, 1 = success). Categorical fixed effects included cow's herd-year-season-parity-registry status group ($HYSPR$), year-state-month of mating group ($YrStMo$), cow's lactation number ($lact$), the insemination service number ($serv$), cow's age rounded to the nearest year ($ageGrp_{cow}$), standardized milk yield of the cow in 6 groups ($milkGrp$), and cow's short cycle group ($ShrtCycl$). The coefficients β_1 and β_2 of the covariate effects for service-sire inbreeding (F_{bull}) and mating inbreeding (F_{mating}) were set to zero as pedigree information was unavailable. Random effects included the age of the bull into 3 groups ($ageGrp_{sire}$), year of mating combined with AI organization to account for changes in semen processing and transport as well as AI technicians' skills at the dairy ($StudYr$), the residual service-sire effect (SSR), cow's genetic ability to conceive (a_{cow}), permanent environmental effect of the cow (PE_{cow}), and residual (e). The cow's genetic effect $a_{cow} \sim N\left(0, \mathbf{A}\sigma_a^2\right)$, where $\mathbf{A}$ is the pedigree relationship matrix for cows and $\sigma_a^2 = 0.005327$ is the additive genetic variance for cows. The remaining random effects, $ageGrp_{sire}$, $StudYr$, SSR, PE_{cow}, and e, were considered noncorrelated, with variances $\sigma_{ageGrp}^2 = 0.000143$, $\sigma_{StudYr}^2 = 0.000110$, $\sigma_{SSR}^2 = 0.000535$, $\sigma_{PEcow}^2 = 0.005327$, and $\sigma_e^2 = 0.196970$, respectively. Variance components were obtained from the literature (Kuhn et al., 2004). The categorical service sire–related factors $ageGrp_{sire}$ and $StudYr$ were fit as random effects. Kuhn et al. (2008) reported that fitting these 2 effects as fixed effects resulted in substantial bias; however, when fit as random effects, accuracy improved with no bias. The SSR captured all residual variation including any genetic component of the sire.

Sire conception rate predictions were obtained by summing the effects for factors related to bull fertility, with no genetic component for the sire, as follows (Kuhn et al., 2008):

$$Predict\ SCR,\ \% = \left[\beta_1\left(F_{bull}\right) + \beta_2\left(F_{mating}\right) + ageGrp_{sire} + StudYr + SSR\right] \times 100.$$

Again, given that pedigree information was unavailable, the solution for the linear regression for service sire (β_1) and mating inbreeding (β_2) were set to zero. Therefore, for the beef service-sire SCR evaluation, our equation was reduced as follows:

$$Predict\ SCR,\ \% = \left[ageGrp_{sire} + StudYr + SCR\right] \times 100.$$

The final phenotypic evaluation was expressed as a percentage by subtracting the bull's within-breed predicted SCR from the breed's mean SCR. A bull with an average SCR has a 0.0% SCR; a bull with an SCR 4.0% is expected to have a 4% higher CR than an average bull and 8% higher CR than a bull with an SCR of −4.0%.

Reliabilities (R) for SCR were obtained using the method described by Norman et al. (2008), where R = $n/(n + 260)$, and n is the number of inseminations. The constant 260 was derived from the sum of the cow's genetic effect, permanent environmental effect of the cow, and residual variance divided by all random effects in the expanded service sire term: $\left(\sigma_a^2 + \sigma_{PEcow}^2 + \sigma_e^2\right) / \left(\sigma_{ageGrp}^2 + \sigma_{StudYr}^2 + \sigma_{SSR}^2\right)$.

RESULTS AND DISCUSSION

Insemination Records

Preliminary results revealed the total number of inseminations per breed pairing found in a 2015 evaluation versus a 2019 evaluation before applying edits (Table 1); the number of breedings in 2019 was more than 2-fold greater; that is, 277,952 versus 111,515. Table 2 displays the number of inseminations in the 2019 evaluation after edits, the number of bulls used for matings, and the resulting number of publishable bulls. A total of 268,174 inseminations occurred between 158,166 cows from 7 different dairy breeds and 3,022 bulls from 37 different beef breeds. The breeds of dairy cows included Holstein, Jersey, Crossbred Dairy, Brown Swiss, Ayrshire, Guernsey, and Milking Shorthorn. In decreasing order of mating frequency, bull breeds included Angus, Charolais, Gelbvieh, Hereford polled, Crossbred Beef, Limousin, Brahman, and 30 others. Angus bulls sired 255,801 (95.4%) of the inseminations; within the Angus-sired breedings, 233,379 (91.2%) were matings to a Holstein cow, limiting further multi-breed evaluations. The 233,379 mating records were between 1,344 Angus service sires and 163,919 Holstein cows. The number of bulls used among all beef breeds was expected to be substantially higher; however, only bulls with properly recorded NAAB codes could be evaluated. Further evaluation was restricted to Angus, the only beef breed with a sufficiently large recorded population in the data to enable accurate predictions. The Angus-sired breedings were compared with purebred Holstein evaluations. The calculations for each breeding pair, Holstein cow with Angus sire ($\mathbf{HO_c/AN_b}$), Holstein cow with Holstein sire ($\mathbf{HO_c/HO_b}$), Holstein heifer with Angus sire ($\mathbf{HO_h/AN_b}$), and Holstein heifer with Holstein sire ($\mathbf{HO_h/HO_b}$), were evaluated separately due to large differences in total number of inseminations. The HO_c/HO_b breeding pairs had >328-fold more than the others.

Currently, the closest trait available from the American Angus Association related to bull fertility is scrotal circumference. Table 3 shows the 10 publishable Angus bulls with the highest number of inseminations to Holstein cows in the past 4 yr. The number of weaning weight and scrotal circumference progeny records were obtained from the American Angus Association EPD Pedigree Search website (American Angus Association, 2019). Combined, the 10 bulls had a total of 108,771 matings, but few (3,614) progeny scrotal circumference records.

Nuisance Variables

Nuisance variables that affect breeding outcomes but are not related to sire fertility have to be accounted for in the model to improve accuracy and reduce bias in SCR evaluations (Kuhn et al., 2008). Among those

Table 1. Frequency of inseminations between beef bull and dairy cow breeds before edits, 2012–2015 versus 2016–2019

	Dairy cow breed							
Beef bull breed	Holstein	Jersey	Crossbred Dairy	Brown Swiss	Ayrshire	Guernsey	Milking Shorthorn	Total
Angus								
2016–2019	241,759	11,528	11,081	460	169	64	52	265,113
2012–2015	100,686	4,600	—	212	186	34	58	105,950
Charolais								
2016–2019	2,452	97	94	2	3	2	8	2,658
2012–2015	557	2	—	4	3	—	—	566
Gelbvieh								
2016–2019	317	2,118	52	64	—	1	1	2,553
2012–2015	190	2,069	—	72	—	—	—	2,331
Hereford, polled								
2016–2019	2,007	23	25	14	5	4	3	2,081
2012–2015	1,642	21	—	8	4	6	—	1,681
Crossbred Beef								
2016–2019	1,340	224	15	—	—	—	—	1,579
2012–2015	539	150	—	—	1	—	—	690
Limousin								
2016–2019	1,055	117	39	2	1	1	—	1,215
2012–2015	141	68	—	—	—	—	—	209
Brahman								
2016–2019	401	297	57	5	—	1	—	761
2012–2015	46	—	—	—	—	—	—	46
Braford								
2016–2019	293	—	—	—	—	—	—	293
2012–2015	1	—	—	—	—	—	—	1
Chianina								
2016–2019	163	3	2	1	—	—	—	169
2012–2015	1	—	—	—	—	—	—	1
Brahmousin								
2016–2019	16	—	—	—	—	—	—	16
2012–2015	1	—	—	—	—	—	—	1
Kobe (Wagyu)								
2016–2019	4	—	—	—	—	—	—	4
2012–2015	8	—	—	—	—	—	—	8
Chiangus								
2016–2019	1	—	—	—	—	—	—	1
2012–2015	—	—	—	3	—	—	—	3
Other								
2016–2019	1,343	104	55	1	—	4	2	1,509
2012–2015	—	—	—	—	—	—	—	—
Total								
2016–2019	251,151	14,511	11,420	549	178	77	66	277,952
2012–2015	104,014	6,910	—	299	194	40	58	111,515

Table 2. Frequency of matings, bulls, and publishable bulls involved in specific breed combinations in 2019 after data edits

	Dairy cow breed							
Beef bull breed	Holstein	Jersey	Crossbred Dairy	Brown Swiss	Ayrshire	Guernsey	Milking Shorthorn	Total
Angus								
Inseminations[1]	233,379	11,138	10,577	441	165	59	42	255,801
Bulls[2]	1,344	301	411	112	62	34	24	2,288
Publishable bulls[3]	122	7	14	—	—	—	—	143
Charolais								
Inseminations	2,440	97	94	2	3	2	8	2,646
Bulls	108	14	19	2	3	2	4	152
Publishable bulls	2	—	—	—	—	—	—	2
Gelbvieh								
Inseminations	309	2,095	51	64	—	1	1	2,521
Bulls	45	6	13	3	—	1	1	69
Publishable bulls	—	—	—	—	—	—	—	—
Hereford, polled								
Inseminations	1,931	13	23	13	5	4	3	1,992
Bulls	115	9	12	7	4	4	3	154
Publishable bulls	2	—	—	—	—	—	—	2
Crossbred Beef								
Inseminations	1,239	216	15	—	—	—	—	1,470
Bulls	7	1	3	—	—	—	—	11
Publishable bulls	1	1	—	—	—	—	—	2
Limousin								
Inseminations	1,017	116	39	2	1	1	—	1,176
Bulls	36	7	2	1	1	1	—	48
Publishable bulls	1	—	—	—	—	—	—	1
Brahman								
Inseminations	339	215	57	4	—	1	—	616
Bulls	65	11	6	1	—	1	—	84
Publishable bulls	—	—	—	—	—	—	—	—
Braford								
Inseminations	292	—	—	—	—	—	—	292
Bulls	2	—	—	—	—	—	—	2
Publishable bulls	1	—	—	—	—	—	—	1
Chianina								
Inseminations	156	2	2	1	—	—	—	161
Bulls	24	2	2	1	—	—	—	29
Publishable bulls	—	—	—	—	—	—	—	—
Brahmousin								
Inseminations	8	—	—	—	—	—	—	8
Bulls	4	—	—	—	—	—	—	4
Publishable bulls	—	—	—	—	—	—	—	—
Kobe (Wagyu)								
Inseminations	4	—	—	—	—	—	—	4
Bulls	1	—	—	—	—	—	—	1
Publishable bulls	—	—	—	—	—	—	—	—
Chiangus								
Inseminations	1	—	—	—	—	—	—	1
Bulls	1	—	—	—	—	—	—	1
Publishable bulls	—	—	—	—	—	—	—	—
Other								
Inseminations	1,325	101	55	—	—	4	1	1,486
Bulls	140	18	15	—	—	4	1	178
Publishable bulls	—	—	—	—	—	—	—	—
Total								
Inseminations	242,440	13,993	10,913	527	174	72	55	268,174
Bulls	1,892	370	483	127	70	47	33	3,022
Publishable bulls	129	8	14	—	—	—	—	151

[1]Number of inseminations between beef specific beef bull breed and dairy cow breed.

[2]Number of bulls involved in inseminations.

[3]Number of publishable beef bulls.

Table 3. The 10 publishable Angus bulls with the highest number of inseminations in the past 4 yr to Holstein cows for sire conception rate, along with their total number of weaning weight (WW) and scrotal circumference (SC) progeny records as of August 2019

Registration number	Year of birth[1]	Name	Total matings,[1] n	WW progeny records,[2] n	SC progeny records,[2] n
ANUSA000017667190	2013	KONZA	25,217	69	8
ANUSA000016150299	2008	THUNDER	20,634	1,382	140
ANUSA000016767407	2010	WALKER	15,446	102	11
ANUSA000017264260	2011	PROFIT DRIVEN	14,550	91	14
ANUSA000017076135	2011	HORIZON	13,073	453	62
ANUSA000017718786	2013	EMPIRE	4,729	54	4
ANUSA000016761484	2010	IRISH	4,632	1,569	241
ANUSA000017256285	2011	GOLD RUSH	4,256	46	6
ANUSA000015832750	2007	RIGHT ANSWER	3,176	7,680	1,750
ANUSA000017031465	2011	COMRADE	3,058	6,287	1,378

[1]Year of birth and total matings were obtained from the Council on Dairy Cattle Breeding National Cooperators Database.

[2]Number of WW and SC progeny records were obtained from the American Angus Association.

variables, the ones that had the greatest impact on phenotypes were year-state-month of mating group, which varied from −0.508 to 1.152, and cow's herd-year-season-parity-registry status group, which varied from −0.727 to 0.940. We observed that CR was greatest for initial lactations (lactation 1, average CR = 35.68%) and decreased with each subsequent lactation (lactation 5, average CR = 29.79%). Conception rate decreased as cow age increased. Cows ≥8 yr old had, on average, CR 17 percentage points lower than 2-yr-old cows. Additionally, cows with cycles ≥18 d had a larger average CR (33.87%) compared with cows with subsequent breedings between 10 and 17 d (22.57%). We expected cows with shorter intervals between breedings to result in a lower CR because of possible atypical estrus cycles, misinterpreted heats, or errors in record keeping (Kuhn et al., 2008). The nuisance variable with the least impact was insemination service number, ranging from 0.17 for seventh service to 0.20 for third service.

Cow Conception Rate

Table 4 shows that mean CR of all breeding pairs did not differ considerably. Holstein sires resulted in a higher CR for both Holstein cows and heifers (differences of 0.52 and 2.38 percentage points, respectively). Mean conception rates of cows and heifers were significantly different when mated to Angus versus Holstein bulls ($P < 0.05$). The total number of Holstein and Angus sires mated to Holstein cows and heifers was 16,745 and 12,572, respectively. Evaluating CR by sire breed in ANOVA resulted in residual degrees of freedom 16,743 for cows and 12,570 for heifers. Given such a large sample size, very small mathematical differences are expected to be significant. The lower CR for dairy cows mated to Angus sires could be attributed to scenarios in which beef sires are used on problem breeders. This is supported by the higher average mean service number observed for Holstein cows and heifers mated to Angus bulls; significant differences ($P < 0.01$) of 0.91 were observed for both scenarios.

Service Sire Fertility-Interdependent Factors

According to Norman et al. (2008), excluding the service sire residual component, service sire age had the largest influence on SCR of dairy bulls, whereas service-sire inbreeding and expected inbreeding of resulting embryo had a very small impact, and omitting those 2 effects did not considerably affect sire rankings. The SCR in Angus decreased from 0.4 to 0.1 and to −0.5% when bull age changed from 1 to <4, 4 to <7, and ≥7 yr, as shown in Table 5. Norman et al. (2015) found similar results when evaluating dairy bulls; bull age had a positive effect on SCR from 1.3 to 5.5 yr of age but decreased thereafter. A total of 68 different

Table 4. Frequency of breedings between Angus and Holstein bulls when bred to Holstein cows and heifers in August 2019, as well as mean and standard deviation of conception rate (CR) and number of services

Model[1]	Inseminations, n	Bulls, n	Dams, n	CR, % (mean ± SD)	Service number (mean ± SD)
HO_c/AN_b	233,379	1,344	163,919	33.77 ± 47.30	3.04 ± 1.78
HO_c/HO_b	14,474,142	15,401	4,344,070	34.29 ± 47.47	2.13 ± 1.38
HO_h/AN_b	19,437	443	15,971	52.96 ± 49.91	2.83 ± 1.56
HO_h/HO_b	2,261,250	12,129	1,535,943	55.34 ± 49.71	1.92 ± 1.19

[1]HO_c = Holstein cow, HO_h = Holstein heifer, AN_b = Angus bull, HO_b = Holstein bull.

Table 5. Best linear unbiased predictor solutions as % for service sire age groups effect, 1 (1 to <4 yr), 2 (4 to <7 yr), and 3 (≥7 yr) of Angus bulls mated to Holstein cows

Service sire age group	Solution, %	Bulls,[1] n	Matings, n
1	0.400	81	6,553
2	0.139	257	95,535
3	−0.549	627	109,884

[1]Bulls counted in each age group to which they contributed.

StudYr combinations were formed from 26 different AI organization over 4 yr of insemination, with solutions ranging from −0.5 to 0.8%. Variation was also observed in SSR, where solutions for 630 bulls ranged from −5.0% to 4.5%.

Sire Conception Rate

Sire conception rate in Angus ranged from −5.1 to 4.4, with an average close to zero and standard deviation (SD) of 1.75%. Norman et al. (2008) reported SD of 2.37% for SCR over several dairy breeds. In 2015, this number was slightly lower (i.e., 2.08%) after CDCB began paying for data extraction and bulls from all AI organizations were included (Norman et al., 2015).

Each bull's SCR prediction is a deviation from the sire and dam breed group's base average. Table 6 shows the SCR summary statistics for Holstein cows and Angus sires, as well as all other purebred dairy breeds evaluated for SCR. The SCR summary statistics for all purebred matings were obtained from published evaluation summaries on the CDCB website (CDCB, 2019). The SCR for HO_c/AN_b had more publishable bulls (116) than the currently evaluated Brown Swiss, Ayrshire, Guernsey, and Milking Shorthorn breeds, and also had a higher mean number of matings per bull (1,574) than those breeds. Mean SCR reliability was 64.5% for the 116 Angus publishable bulls, with a maximum reliability of 99% based on 25,217 breedings. Because reliability of SCR is based on the number of inseminations, the SCR for Angus bulls was not as high as for Holstein bulls that had, on average, 3 times more matings. In this case, the extra matings provided an advantage of 18 points in reliability for the Holstein bulls. As beef bulls are more frequently used, the reliability of beef SCR is expected to increase in the near future.

Figure 1 shows the distributions of publishable bull's SCR predictions. All pairings show predictions that are approximately normally distributed with mean of zero as expected, except for panel (b) HO_c/HO_b, which graphs more than 8 times the number of publishable bulls than the other 3 groups combined. We expect purebred matings between HO_c/HO_b to experience the most selection, which could be causing the distribution to be skewed to the left.

When using beef semen on dairy cows and heifers, knowledge of fertility and ranking of beef bulls is important to ensure pregnancies, especially because problem breeders are usually the candidates to be bred to beef bulls. Traits related to growth and carcass composition, as well as fertility, should be of interest for future research. This is because crossbred calves are used for beef production, and the demand for premium, high-grade beef is rapidly increasing. Some beef cattle associations in the United States are developing special indices for bulls that are bred to dairy cows to improve carcass yield and quality in crossbred animals (S. Miller, Angus Genetics Inc., St. Joseph, MO; personal communication).

CONCLUSIONS

The number of matings of beef bulls to dairy cows has more than doubled in the past 4 yr. This increase indicates the importance of beef bull fertility within

Table 6. Sire conception rate (SCR) summary statistics for Holstein cows bred to Angus bulls (HO_c/AN_b) and all purebred breeds evaluated for SCR, based on August 2019 evaluation data from the Council on Dairy Cattle Breeding

			SCR, %				Reliability, %	
Model[1]	Publishable bulls, n	Mean matings/bull, n	Mean	SD	Minimum	Maximum	Mean	Maximum
HO_c/AN_b	116	1,574	0.005	1.75	−5.1	4.4	64.49	99.00
HO_c/HO_b	1,707	4,847	0.000	1.89	−18.2	4.2	86.30	99.00
JE_c/JE_b	219	2,148	0.001	1.82	−6.4	4.1	75.68	99.00
BS_c/BS_b	47	689	−0.004	2.16	−4.5	3.9	64.68	91.00
AY_c/AY_b	8	498	0.000	1.39	−2.0	2.9	58.25	84.00
GU_c/GU_b	12	482	−0.008	2.28	−5.7	2.8	62.33	81.00
MS_c/MS_b	2	251	0.000	0.60	−0.6	0.6	49.00	51.00

[1]Ayrshire (AY_c), Brown Swiss (BS_c), Guernsey (GU_c), Holstein (HO_c), Jersey (JE_c), and Milking Shorthorn (MS_c) cows mated to Angus (AN_b), Ayrshire (AY_b), Brown Swiss (BS_b), Guernsey (GU_b), Holstein (HO_b), Jersey (JE_b), and Milking Shorthorn (MS_b) bulls.

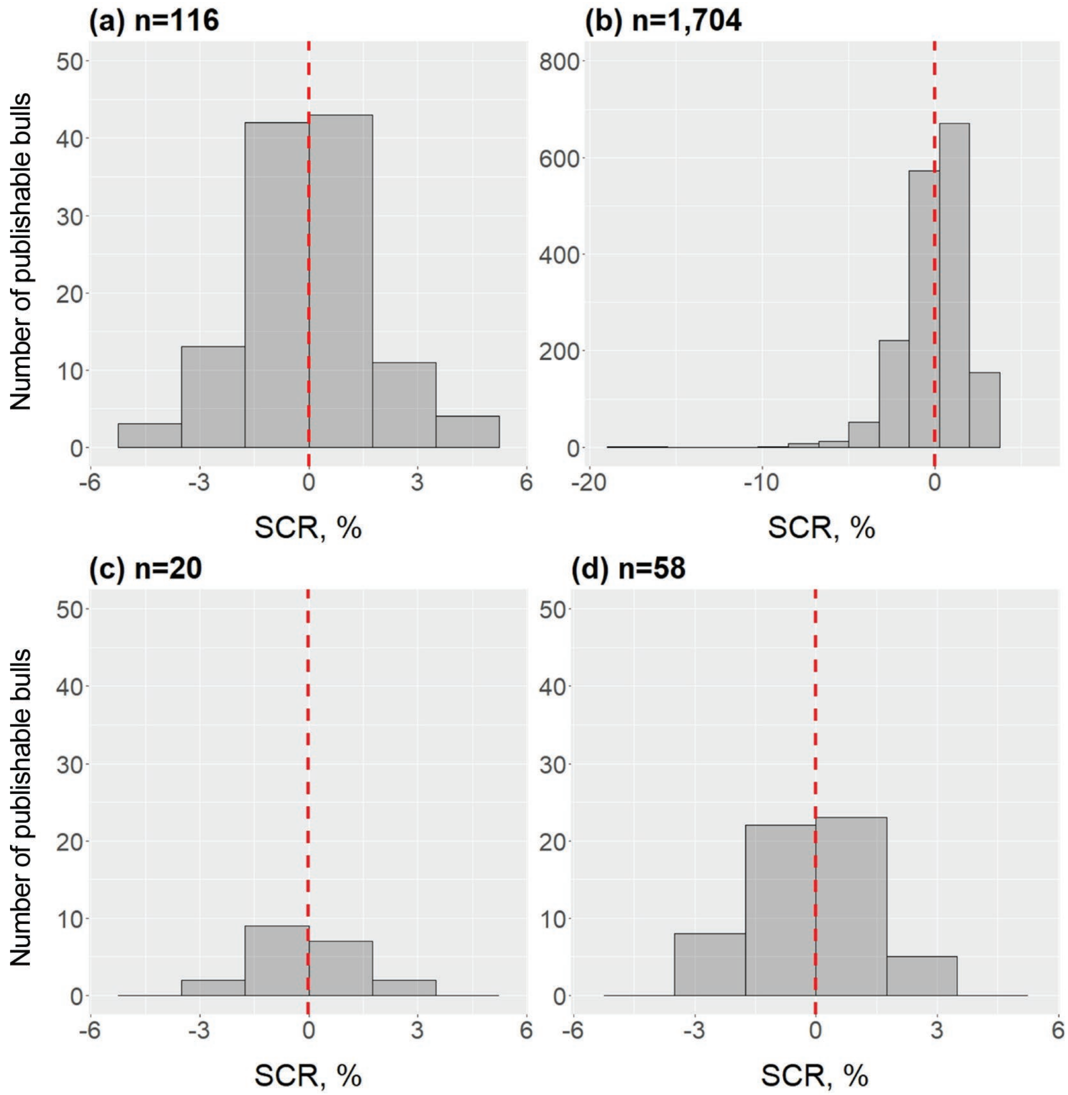

Figure 1. Sire conception rate (SCR) prediction distribution for (a) publishable Angus bulls mated to Holstein cows, (b) publishable Holstein bulls mated to Holstein cows (y-axis differs by 16-fold), (c) publishable Angus bulls mated to Holstein heifers, and (d) publishable Holstein bulls mated to Holstein heifers.

the dairy industry. Most of the matings, 87.0%, were of Angus bulls mated to Holstein cows. When Angus bulls are ranked by SCR, dairy producers are provided with better information about the fertility of each bull when mated to a dairy cow or heifer. The CR of Holstein cows by Holstein and Angus sires does not greatly differ; therefore, mating beef bulls to dams not producing replacement heifers will result in more valuable crossbred calves for beef output. As more beef-on-dairy insemination records become available, further research can be conducted to test for fertility across the breeds as well as to investigate whether the reduced Angus-sired CR in heifers is caused by service number differences or other effects.

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ORCIDS

T. M. McWhorter https://orcid.org/0000-0002-6158-5669
H. D. Norman https://orcid.org/0000-0002-0555-5764
J. B. Cole https://orcid.org/0000-0003-1242-4401
G. C. Fok https://orcid.org/0000-0001-8853-2885
D. A. L. Lourenco https://orcid.org/0000-0003-3140-1002
P. M. VanRaden https://orcid.org/0000-0002-9123-7278