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Evaluating sire effects on cow fertility: Timed AI and repeat-breeder dairy cows

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ABSTRACT

In this single herd observational study, there is investigation of the effects of 81 sires (with 11,424 artificial inseminations) on conception rates in 1790 Holstein cows for 5 years. Sires were catagorized based on the published sire conception rate (SCR) into different sire fertility groups (low, average and high fertility sires). The performance of different-sire fertility groups was assessed in timed artificial insemination (TAI) and repeat-breeder (RB) cows. With this aim, two logistic regression models with sire, inseminator, cow, and lactation random effects were applied to data on pregnancies assessed at days 30 and 70 post-insemination. Fixed effects of sire fertility group, sire breed, cow-fertility status, insemination type, postpartum problems, milk yield, temperature humidity index, and year were evaluated. Results from the analysis indicated there was a significant individual sire effect on conception rates, and large heterogeneity in values for this variable among sires. Results indicate that SCR could be assessed to predict low fertility sires reasonably well, and the predicted probabilities for pregnancy per AI (P/AI) at 30 and 70 days post-insemination for high fertility sires were consistent for the most part with values for the SCR. The sire breed did not affect conception rates at days 30 and 70 post-insemination nor its interactions with insemination type (estrous detection AI (EDAI) compared with TAI) and cow-fertility status (RB compared with non-RB). Predicting response probabilities for sires with at least 100 inseminations in each insemination group resulted in greater conception probabilities in cows in which there was EDAI than those in the TAI group.

1. Introduction

The profitability of dairy herds is greatly affected by cow reproduction. Many factors affect fertility in dairy herds (Buckley et al., 2003; Garcia-Ispierto et al., 2007a; 2007b) and among these are sire-related factors. Results of previous studies have indicated there are substantial sire effects on conception rate. For example, Lopez-Gatius et al. (2005) and Nagamine and Sasaki (2008) reported individual sire effects on conception rate of Holstein cows.

The quality of insemination dose is important in the reproductive performance of dairy herds. Semen doses from high fertility sires provide a great number of spermatozoa with the capacity for fertilization as indicated by there being more accessory sperm per

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embryo when there is use of semen for insemination from these sires. Furthermore, with the use of semen from these sires there is development of embryos with a greater quality (Saacke, 2008). In addition, the use of semen from highly fertile bulls result in a greater conception rate in the herd and, therefore, there is a greater reproductive performance. Lower fertility sires may produce semen of lesser quality that when used for AI results in a lesser conception rate and greater animal culling rate in the herd, negatively affecting herd profitability. Practically, semen suppliers are responsible for the processing of semen in ways that assure high-quality semen for artificial insemination (AI). This process consists of many sub-processes, including, but not limited to; selecting sires, post-thawing semen evaluation, eliminating doses that have a relatively greater probability of there being detrimentally impacted fertility if this semen is used for AI (DeJarnette et al., 2004; Vincent et al., 2012). In addition to the laboratory evaluation of semen doses, the fertility after AI-sires is also evaluated in the field using either cow non-estrous-return rate (estimated relative conception rate; ERCR) or sire conception rate (SCR) (Kuhn et al., 2008; Kuhn and Hutchison, 2008). In the past, field evaluation of AI-sires were restricted to the first insemination, but recently it has been extended to include multiple insemination records and published as SCRs (Kuhn et al., 2008). Such SCRs are computed based on a large amount of data using a mixed-effects model with many variables, including cow and sire factors being considered (Kuhn et al., 2008; Kuhn and Hutchison, 2008). In recent years, dairy producers have begun to consider the published sire fertility data as a second criterion for sire selection to improve herd fertility (Amann and DeJarnette, 2012).

Even though there is the use of different insemination types in estimating the published SCR including timed artificial insemination (TAI), the SCR value does not provide information about sire performance when there is TAI nor provide information about sire fertility in repeat-breeder (RB) cows. The TAI is a commonly applied program on dairy farms to reduce estrous detection efforts and increase the submission rate for insemination. It is more efficient to AI cows in which time of ovulation has been induced in a short period of time, which enables the insemination of cows around the time of ovulation (Stevenson, 2016). Because sperm cells of lowly fertile sires have shorter periods of viability in the reproductive tract of females than the semen from highly fertile sires (Hockey et al., 2010), the fertility of these sires may be improved with the use of TAI (Macmillan and Watson, 1975; Batista et al., 2016). The effects of TAI and the different time intervals between GnRH injection and insemination on sire fertility have been studied. For example, Cornwell et al. (2006) investigated the effect of time of GnRH treatment relative to the time of insemination on fertility for sires with average and high published ERCRs, whereas TAI effects have been evaluated by Batista et al. (2016).

In practice, Holstein cows have lesser reproductive efficiency, which may be due to the great emphasis on milk production for many years in this breed (Gonzalez-Recio et al., 2006). Using sires from different breeds may lead to improvements in the conception rates of these cows. Holstein cows can be bred using semen from sires of different breeds to enhance hybrid vigor of crossbred offspring (Buckley et al., 2014). For example, Holstein cows inseminated with semen from Gyr bulls have greater conception rates than Holstein cows inseminated with semen from Holstein sires (Pegorer et al., 2007). Even though there are a large number of studies that deal with the conception rate and herd fertility, little research has been conducted to assess the association between the published SCR and herd fertility. Also, sire effects on conception rate with use of TAI and in RB cows have not been evaluated to any great extent and further investigation is needed to further assess the importance of these two variables on conception rate. In the present study, there is evaluation of individual sire effects and sire factors on the conception rate while accounting for the hierarchical structures of the data.

The specific objectives of the present study were: firstly, to assess the effect of individual sire and its factors on the conception rate in Holstein cows while taking into account the data structure and non-sire predictors. Secondly, there was assessment of fertility when there is use of semen from sires in cows with TAI and in RB cows by predicting the response probabilities.

2. Materials and methods

2.1. Animals and herd management

Data were extracted from the database of Al-Kassem farm, Ismailia desert road, Egypt. Briefly, the Al-Kassem farm has a strict registration system and uses AfiFarm software (Afimilk Ltd. Kibbutz Afikim, Israel) to obtain detailed data at animal and farm levels, such as data for reproductive and production variables, as well as data for general health status. Cows were fed *ad libitum* a total mixed ration formulated according to the NRC (National Research Council, 2001), and had free access to water. All cows were housed in free stall paddocks and supplied with shelters and a cooling system including fans and water sprinklers. Furthermore, cows were vaccinated against all endemic infectious diseases.

2.2. Insemination and pregnancy diagnosis

Cows were inseminated either after estrous detection (EDAI) or TAI with an obligatory waiting period before the first AI of 60 days. The EDAI was performed by monitoring cow activities using a pedometer system (AfiTag, Afimilk Ltd, Kibbutz Afikim, Israel), and cows that had obvious behaviorial symptoms of estrus were inseminated within 8–16 h after these behaviors were detected. Different TAI programs (synchronization of time of ovulation among cows) such as Presynch-Ovsynch, Double-Ovsynch, Ovsynch, and CIDR-Ovsynch were applied to cows at the time of first postpartum insemination. Non-pregnant cows that had not expressed symptoms of behavioral estrus were treated to induce a resynchronized expression of estrus with use of either Ovsynch or CIDR-Ovsynch. For a detailed description of the treatment regimens used for synchronization of times of ovulation among cows these have been previously described (Abdalla et al., 2017). Furthermore, the gynecological examination of cows was performed at either the time of AI or pregnancy diagnosis. Non-pregnant cows after three inseminations were subjected to an ultrasonic examination and if no clinical problems were diagnosed, those cows were considered as typical RB animals. Repeat-breeder cows were not treated for

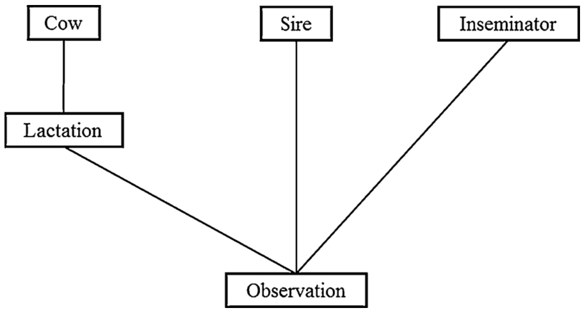

Fig. 1. Classification diagram for pregnancy per AI 30 (P/AI 30) and 70 (P/AI 70) data structure as used in the models.

control of timing of estrus during an intervening estrous cycle before the next insemination. Data for a maximum of seven inseminations per cow were included in the final data set.

Semen doses from six semen suppliers mostly from Europe and the USA, were used to conduct this study. The number of sires per semen supplier was 43, 20, 12 sires from the first three suppliers and six sires from the other suppliers (two from each supplier). The SCR was recorded at the time of straw purchasing and was available for the majority of sires. Only one semen supplier had a data set for both the SCR and star systems simultaneously. The fertility of these sires was evaluated based on the published SCR (range from -6.8 to 5.1) and if a sire had no published SCR, this sire was classified as a non-rated sire. Sires were grouped based on the published SCR into three different fertility classifications (low: < -1, average: ≥ -1 and ≤ 1, and high: >1). The published SCR mean per group was -2.7, -0.05, and 2.4 for low, average, and high fertility sires, respectively. All sires had a SCR reliability of $\geq$ 86% and a minimum of 1500 inseminations when the SCR was published. Furthermore, sperm motility was evaluated based on assessments of three doses from each given batch of semen, and in all batches of semen used in the study there was a sperm motility of $\geq$ 50%.

Cows for which there was a non-return of estrus were ultrasonically assessed for pregnancy diagnosis at 31 $\pm$ 2 days post-insemination, and pregnancy per AI at 30 days post-insemination (P/AI 30) was determined. Furthermore, the pregnancy status was reassessed by rectal palpation at 71 $\pm$ 2 days post-insemination, and pregnancy per AI at 70 (P/AI 70) was reevaluated.

2.3. Data description

The data used in the current study were structured in five hierarchical levels (Fig. 1). The least level consisted of 11,424 inseminations. These inseminations were nested in 3544 lactations (second level) of 1790 cows (third level). Cows and lactations were cross-classified by sires (forth level) and inseminators (fifth level). The total numbers of sires and inseminators were 81and 27; respectively. The dichotomous variables of pregnancies per AI at 30 (P/AI 30) and 70 days (P/AI 70) post-insemination were the response variables.

The investigated explanatory variables were sire ID, sire-fertility group, sire breed, cow ID, lactation number, postpartum problems, insemination number, days in milk (DIM) at insemination, 305-milk yield, insemination type, cow-fertility status, year, inseminator and temperature humidity index (THI) at month of insemination. The data for distributions of categorical variables are shown in Table 1.

2.4. Statistical modeling and data analysis

2.4.1. Bayesian estimation and inference

To account for the hierarchical structure of the data set, Bayesian Markov Chain Monte Carlo (MCMC) techniques were used for estimating model parameters. The Bayesian analyses were conducted using the MLwiN software version 2.26 using the same prior distributions and similar MCMC diagnostic tools as previously described (Elghafghuf et al., 2014a; 2014b). Medians of posterior distributions were considered as parameter estimates and computed based on 100,000 samples after discarding the first 20,000 (burn-in) samples. The 95% credible intervals (CrI) were used as a tool to assess the significance of single-parameter effects in the Bayesian analysis. The effect (based on odds ratio, OR) is considered non-significant if one lies in the CrI. The Deviance Information Criteria (DIC) (Spiegelhalter et al., 2002) was used as a tool for model selection in Bayesian inference.

2.4.2. Descriptive statistics and simple associations

Descriptive analyses were conducted for all variables for assessing distributions, identifying missing values, and detecting invalid observations. The associations between explanatory variables were evaluated to detect possible collinearity. Because the Bayesian model with full hierarchical structure was impractical and time consuming for variable selection, the unconditional associations between the two response variables (P/AI 30 and P/AI 70) and explanatory variables were estimated in a non-Bayesian framework using logistic models with cow and lactation as random effects. The two models assumed a zero-mean normal distribution for the random effects and independent error structures within lactation. The functional forms of continuous variables were assessed using Lowess smoothing graphs, and if necessary a quadratic term was included in the model.

Table 1
Descriptive statistics for explanatory variables used in the analyses of pregnancy per AI 30 (P/AI 30) and 70 (P/AI 70).

Explanatory Variables*	Number of Sire/Cow	Number of inseminations	P/AI 30 proportion	P/AI 70 proportion
Sire variables				
Sire breed				
0: Holstein	73	9865	0.303	0.243
1: Non-Holstein	8	1559	0.345	0.270
Sire fertility group				
1: Low	13	1882	0.259	0.200
2: Average	25	4807	0.332	0.268
3: High	18	3226	0.307	0.253
4: Non-rated	25	1509	0.366	0.224
Total	81	11424	0.309	0.247
Non-sire variables				
Postpartum problems				
0: No	948	5965	0.325	0.265
1: Yes	842	9459	0.291	0.227
Insemination type				
0: EDAI	533	4709	0.309	0.252
1: TAI	1257	6715	0.308	0.243
Cow-fertility status				
0: Non-RB	1466	7795	0.317	0.249
1: RB	324	3629	0.291	0.242
Temperature humidity index				
1: < 65	477	2880	0.380	0.306
2: 65- < 70	578	2947	0.361	0.293
3: 70- < 75	488	2735	0.273	0.222
4: ≥75	247	2862	0.216	0.163
Year				
1: 1st	529	1423	0.360	0.304
2: 2nd	326	2096	0.318	0.246
3: 3rd	306	2637	0.335	0.253
4: 4th	297	2517	0.297	0.229
5: 5th	332	2751	0.261	0.226
Continuous variables				
305-milk yield			Mean (SD)	Mean (SD)
Pregnant			9.45 (1.89)	9.39 (1.93)
Non-pregnant			9.68 (1.83)	9.69 (1.82)

* Sire fertility group, sires classified according to the published sire conception rate; EDAI, estrous detection AI; TAI, timed AI; RB, repeat breeder (cows inseminated more than three times).

2.4.3. Multivariable model building

All variables were detected to be significant at a liberal *P*-value of 0.20 in the unconditional association analyses, for both the P/AI 30 and P/AI 70 outcomes, were included in the multivariable logistic model with random cow and lactation effects. A stepwise backward strategy with a *P*-value of 0.10 was used as variable inclusion criterion prior the assessment of variable interactions (Elghafghuf et al., 2014a; 2014b). The two-way interactions between variables retained in the model were assessed; significant interactions between variables (at a level of 0.05) were retained in the model along with the main effects. During the variable selection process, the non-significant variables were returned to the model and reassessed for confounding. A change of ≥ 20 % in the coefficient estimates was considered as a criterion for identifying potential confounders. During model building, sire fertility group was modeled in two different ways, as a categorical variable (low, average, high, non-rated) and as a continuous variable based on the published SCR. All data manipulation, descriptive statistics, and frequents analyses during the model-building processes were conducted using Stata 15 (StataCorp, 2017).

2.4.4. Bayesian model analysis

The data structure was accounted for in the final models (for P/AI 30 and P/AI 70) by including cow, lactation, sire ID and inseminator as cross-classified random effects. Each model included all variables found significant for each response variable in the multivariable model-building processes. Because the data sets had multiple cross-classified hierarchal levels, the final models were estimated using MCMC techniques assuming independent error structures within lactation. Variables that did not contribute to the model fit (assessed based on the DIC values) after accounting for correlations within sires and inseminators were not included in the final models.

The fixed effects were interpreted based on the values of odds ratio and at a 95% CrI, while the interpretation of random effects was based on the variance components for each variable on the log-odds scale as well as the estimated residuals with 95% confidence intervals (CI). Furthermore, the response probability was computed for some groups.

Table 2
Parameter estimates for explanatory variables used in the analyses of pregnancy per AI 30 (P/AI 30) and 70 (P/AI 70) data: the median, standard deviation (SD), and tail probability (*P*) of posterior distributions with 95% credible intervals (CrI) using two logistic regression models with four cross-classified random effects (cow, lactation, sire, and inseminator).

Predictor/Parameter*	P/AI 30				P/AI 70			
	Median	SD	*P*	CrI	Median	SD	*P*	CrI
Post-partum problem								
Yes vs. No	−.135	.059	.011	(−.250, −.020)	−.208	.069	.001	(-.344, -.073)
Insemination type								
TAI vs. EDAI	−.222	.054	.000	(−.328, −.116)	−.260	.061	.000	(−.382, −.141)
Cow-fertility status								
RB vs. Non-RB	.446	.065	.000	(.320, .572)	.781	.082	.000	(.619, .944)
305-milk yield	−.103	.017	.000	(−.136, −.070)	−.160	.020	.000	(−.199, −.122)
Temperature humidity index								
65- < 70 vs. < 65	−.100	.073	.086	(−.242, .043)	−.056	.081	.239	(−.214, .101)
70- < 75 vs. < 65	−.495	.095	.000	(−.683, −.312)	−.466	.104	.000	(−.671, −.261)
≥75 vs. < 65	−.967	.098	.000	(−1.16, −.777)	−1.01	.111	.000	(−1.23, −.796)
Year								
2nd vs. 1st	−.175	.135	.101	(−.435, .094)	−.349	.154	.013	(−.643, −.043)
3rd vs. 1st	−.097	.148	.258	(−.387, .197)	−.415	.172	.009	(−.747, −.072)
4th vs. 1st	−.077	.154	.307	(−.380, .226)	−.234	.175	.093	(−.571, .104)
5th vs. 1st	−.731	.150	.000	(−1.03, −.442)	−.606	.171	.000	(−.946, −.277)
Constant (intercept)	−.293	.159	.030	(−.614, .013)	−.663	.182	.000	(−1.03, −.323)
Cow variance	.456	.077	–	(.317, .618)	.556	.103	–	(.371, .774)
Lactation variance	.575	.100	–	(.388, .783)	1.11	.176	–	(.783, 1.48)
Sire variance	.159	.045	–	(.092, .278)	.203	.058	–	(.117, .343)
Inseminator variance	.076	.071	–	(.012, .278)	.077	.069	–	(.016, .271)

* EDAI, estrous detection AI; TAI, timed AI; RB, repeat breeder (cows inseminated more than three times); *P*, Tail probability of the posterior distribution (analogous to *P*-value).

3. Results

3.1. Descriptive analysis

The P/AI 30 and P/AI 70 percentages in the present study were 30.9% (3,526/11,424) and 24.7% (2,818/11,424), respectively. The mean number of inseminations for all sires was 141 with 10th and 90th percentiles of 13 and 346, respectively. The data for distributions of each level of the investigated categorical variables and descriptive statistics of the continuous variables are in Table 1. The percentages of P/AI 30 and P/AI 70 were different, and varied across sire fertility groups from 25.9% to 33.2% and 20% to 26.8%, respectively. These percentages were slightly different between Holstein and non-Holstein sires. In RB cows, the conception rate within each sire fertility group varied from 21.9% (low) to 31.2% (average) for P/AI 30 and between 17.3% (low) to 26.6% (high) for P/AI 70. As well, the percentages of P/AI 30 and 70 in RB cows were 28.9% (P/AI 30) and 24.1% (P/AI 70) for Holstein sires, and 30.7% (P/AI 30) and 24.8% (P/AI 70) for other sires.

3.2. Multivariable model analyses

The fixed effects in the final models for P/AI 30 and P/AI 70 included postpartum problems, insemination type, cow-fertility status, 305-milk yield, year, and THI. The effects of cow, lactation, sire, and inseminator were modeled as cross-classified random effects using the two final models. Median, standard deviation, and 95% CrI from posterior distributions of the final model parameters are presented in Table 2.

3.2.1. Effect of sire

The effect of individual sire was modeled as a random effect. The sire-level variance (measured on the log-odds scale) was estimated at 0.159 (95% CrI; 0.092, 0.278) and 0.203 (95% CrI; 0.117, 0.343) for P/AI 30 and P/AI 70, respectively. This indicates that the variation between sires was larger for P/AI 70 than for P/AI 30. When all the fixed-effect variables in the final models were set at the reference values and the random effects at zero (the mean of random effects), the predicted probabilities of P/AI 30 and P/AI 70 and 95% CIs were estimated at $\exp(-0.293)/1 + \exp(-0.293) = 0.427$ ($95\,\%\,\mathrm{CI} = \pm 1.96\sqrt{0.159} - 0.293$; 0.255, 0.620) and 0.340 (95% CI; 0.176, 0.555) for P/AI 30 and P/AI 70, respectively.

Furthermore, the estimated residuals for sire random effects and standard errors were extracted from the two final models. These data for these estimated residuals are depicted in Figs. 2 (P/AI 30) and 3 (P/AI 70) along with 95% CIs. As expected, the results indicate sires with a few inseminations had greater CIs than those with a large number of inseminations. Furthermore, eight sires in P/AI 30 analysis (Fig. 2) and seven in P/AI 70 analysis (Fig. 3) had residuals of greater than the mean (zero) of random sire effects. The residuals of seven and nine sires, however, were less than the mean for P/AI 30 and P/AI 70, respectively. The rest of sire

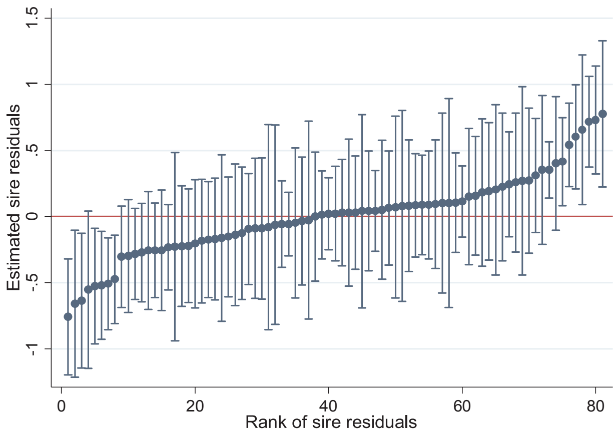

Fig. 2. Caterpillar plot for sire random effects based on the final model of pregnancy per AI 30 (P/AI 30); Y-axis is the estimated residuals for sire, x-axis is the rank of sire residuals; Vertical lines represent the 95% CI for the estimated residuals.

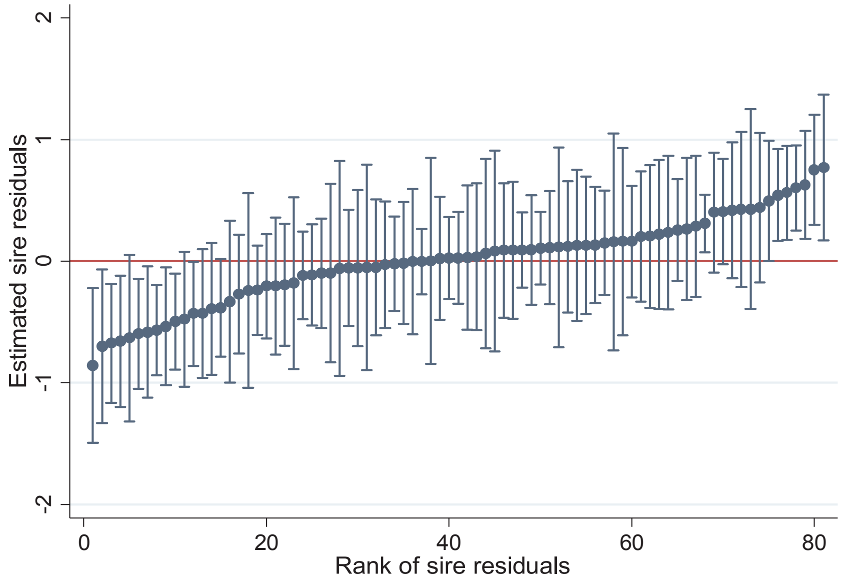

Fig. 3. Caterpillar plot for sire random effects based on the final model of pregnancy per AI 70 (P/AI 70); Y-axis is the estimated residuals for sire, x-axis is the rank of sire residuals; Vertical lines represent the 95% CI for the estimated residuals.

residuals were not different from the mean because the zero value lies within the CIs.

The probabilities of the response variables (P/AI 30 and P/AI 70) were predicted for 12 sires that had at least 100 inseminations in each of the EDAI and TAI insemination types. The data for these response variables are included in Table 3. The predicted probabilities of P/AI 30 and P/AI 70 for these sires were computed for the two insemination type groups (EDAI and TAI) based on the final models assuming non-RB cows had no postpartum problems that affected conception, had average milk production, were in the 5th production year, and were inseminated when there was a THI of <65. Other random-effects variables in the model such as cow, lactation, and inseminator were set at the mean (zero). The results indicate the predicted probabilities were always larger for P/AI 30 than for P/AI 70 for both EDAI and TAI groups, which is expected because the P/AI 70 must be less than or equal P/AI 30 due to embryonic losses. Such predicted losses varied from 7.4% (Sire 6, Table 3) to 24.6% (Sire 3) in cows where there was EDAI and between 10.2% and 27.6% in cows where there was TAI for the same sires. For both the P/AI 30 and P/AI 70 analyses, the predicted response probabilities were always greater in cows where there was EDAI as compared with TAI.

3.2.2. Non-significant effects of sire breed and fertility group

There was no effect of the sire breed nor fertility group when the two model analyses were conducted for P/AI 30 and P/AI 70. Adding these variables to the two models did not improve the model fit nor substantially change the coefficient estimates of other variables in the models, therefore, the data for these variables were removed from the final models. The estimated ORs for the effects of average and high fertility groups, before data for fertility group was removed from the final P/AI 30 model, compared with the low fertility group were estimated, respectively, to be 1.213 (95% CI; 0.858, 1.728) and 1.182 (95% CI; 0.814, 1.694). In contrast, the

Table 3

Predicted probabilities of pregnancy per AI 30 (P/AI 30) and 70 (P/AI 70) displayed by insemination type for 12 sires that had more than 100 inseminations in each group; Predicted probabilities computed based on the final models of P/AI 30 and P/AI 70, where all fixed-effects variables were set at the reference values except for year (set at the 5th production year) and insemination type; Random effects other than sire effect were set at the mean (zero).

Sire	Fertility group*	Number of inseminations	Type of insemination	Predicted response probability	
				P/AI 30	P/AI 70
1	1	104	EDAI	0.213	0.161
		186	TAI	0.178	0.129
2	1	203	EDAI	0.273	0.224
		230	TAI	0.231	0.182
3	1	203	EDAI	0.183	0.138
		208	TAI	0.152	0.110
4	2	375	EDAI	0.338	0.277
		540	TAI	0.291	0.228
5	2	211	EDAI	0.287	0.239
		238	TAI	0.244	0.195
6	2	131	EDAI	0.352	0.326
		116	TAI	0.303	0.272
7	2	257	EDAI	0.253	0.219
		524	TAI	0.214	0.178
8	3	123	EDAI	0.178	0.146
		223	TAI	0.147	0.117
9	3	162	EDAI	0.424	0.330
		185	TAI	0.371	0.276
10	3	161	EDAI	0.382	0.339
		188	TAI	0.331	0.284
11	3	185	EDAI	0.253	0.200
		155	TAI	0.213	0.162
12	3	158	EDAI	0.269	0.235
		257	TAI	0.227	0.192

* 1, low; 2, average; 3, high fertility sires; EDAI, estrus detection AI; TAI, timed AI.

ORs for sire fertility group when the P/AI 70 analysis was conducted were estimated to be 1.428 (95% CI; 0.972, 2.041) and 1.368 (95% CI; 0.906, 2.008) for average and high fertility groups, respectively. Similarly, the ORs of P/AI 30 and P/AI 70 for Holstein relative to non-Holstein sires after accounting for the other risk factors in the model were estimated to be 1.046 (95% CrI; 0.730, 1.594), and 2.702 (95% CrI; 0.740, 13.45), respectively.

Furthermore, the interactions between sire fertility group and cow-fertility status, fertility group and insemination type; and sire breed and cow-fertility status were not significant when the two analyses were conducted. These results indicate that the effects of sire fertility group did not depend on insemination type nor cow-fertility status.

3.2.3. *Effect of non-sire factors*

Because the focus in the present study was on the effect of sire factors, the effects of non-sire variables were taken into account in the final models but were not evaluated in detail. The non-sire variables that affect the risk of P/AI 30 and P/AI 70 included: postpartum problems, insemination type, cow-fertility status, 305-day milk yield (measured in thousand liters and centered at a mean of 9613), temperature humidity index, and production year. The non-sire random effects included in the final models were cow, lactation, and inseminator. The data for estimated effects of non-sire variables are presented in Table 2. Overall, the results indicate there is a consistency with what was previously reported in terms of the effects of these variables. Furthermore, results from the present study indicate there is a substantial variation among cows, lactations, and inseminators. Accounting for such variation substantially improved the model fit.

4. Discussion

Consistent with results from previous studies, pregnancy rates on days 30 and 70 post-insemination varied by sire in the present study. Individual sires had marked effects on establishing and sustaining pregnancy up to day 70 post-insemination. Similar results were reported previously (Sarder, 2006; Kasimanickam et al., 2008; Nagamine and Sasaki, 2008). There were differences in pregnancy rates among sires although strict quality control procedures were applied by semen suppliers to ensure fertility was consistent and reliable when semen marketed by these enterprises was used for AI. There are many factors that affect sire fertility. Some of these factors are difficult to control and may not be measurable. In the present study, there was modelling of the effect of individual sire as a random effect (i.e., effect of sire was estimated as a distribution not as a fixed value). This was to take into account unobserved effects that occurred due to the clustering in the data. There was a large magnitude of heterogeneity among sires in the present study, which may be attributable to the differences in semen (Attia et al., 2016), sperm cell capacity to reach the fertilization site (Nadir et al., 1993), or acidic and basic sperm protein balance (Somashekar et al., 2015). Ortega et al. (2018) reported that the reduced fertilization capacity of low-fertility sires is multifactorial and includes sperm fertilizing capacity, preimplantation embryonic development, and development of the embryo and placenta after conceptus elongation and pregnancy recognition. Furthermore, Haugan et al. (2007) reported that there was a lesser probability of conception when there was use of semen that had been stored for a relatively long compared with a relatively shorter period. Other factors, such as the expression of some sperm function regulating genes (Han and Peñagaricano, 2016), proportion of non-compensable seminal traits (Saacke et al., 2000), or sperm mid-piece length (Shahani et al., 2010) may also result in substantial variation in P/AI among sires. All these factors are likely to affect the establishment of pregnancy.

There were no effects in the present study of sire fertility groups (low, average, high) on P/AI 30 and P/AI 70, although the variable was categorized based on the published SCR. The descriptive data indicated low-fertility sires had a lesser P/AI 30 percentage than average-fertility and high-fertility sires by about 7% and 5%, respectively. Similar results were reported by Cornwell et al. (2006)where sires with estimated relative conception rates ≥ 3 or = -1 had similar P/AI 40 percentages. Furthermore, the results from the present study indicate there is a question about how dependable the published SCR is for selecting sires for improving herd conception rate. Semen suppliers often update the SCR when new data become available. For example, Cornwell et al. (2006) reported that the ERCR for five (out of six) sires changed within a 6 month period. One of these sires had a change of three points. Findings in the present study indicate that seven sires had a P/AI 30 that was less than the average, and three of these were classified based on the published SCR as high-fertility sires.

Furthermore, there was no significant difference in P/AI 30 and 70 between Holstein and non-Holstein sires. This may be due to the limited amount of data for non-Holstein sires in the present study. These findings are consistent with results reported by Kasimanickam et al. (2006). Results of other studies indicate sires from different breeds have different sperm cell structure and kinetics (Söderquist et al., 1996; Hoflack et al., 2007; Shahani et al., 2010). The developmental competence of hybrid zygotes (or embryos) was greater than that of purebred zygotes (Boediono et al., 2003; Lazzari et al., 2011).

In the present study, there was an attempt to assess interactions between sire fertility group and insemination type (EDAI and TAI), but there were no interaction effects. This indicates the effects of sire fertility group do not depend on insemination type. Abdel-Azim (2010) reported that use of TAI did not improve the P/AI for low fertility sires, while, Batista et al. (2016) reported that use of TAI had an effect on sire fertility without referring to the rank of sire fertility. In the present study, the failure to observe pregnancy improvements with the use of TAI compared with EDAI may be attributable to the optimum timing of insemination in the EDAI group as a result of using the pedometer system. Another possible issue is the assignment of cows to a synchronization program without assessing the estrous cyclicity, which may result in an estrous synchronization failure and inseminating of non-estrous cyclic cows at the time of TAI.

In the present study, the P/AI 30 and P/AI 70 models were used to generate response probabilities for P/AI 30 and 70 at fixed values for variables in the models. In this regard, the response probabilities for P/AI 30 and P/AI 70 within the EDAI and TAI groups for sires that had at least 100 inseminations in each group were predicted. When other variables in the model were set at the reference values, the predicted probabilities were greater for both the P/AI 30 and 70 responses in EDAI compared to TAI groups for 12 sires that had ≥ 100 inseminations in each group. These patterns were also observed in the data for most of the twelve sires, although P/AI 30 and P/AI 70 proportions were computed without taking other factors into account. Findings in the present study indicated the SCR variable effectively ranked low-fertility and most high-fertility sires. The predictions of P/AI 30 and 70 for low-fertility and high-fertility sires were consistent with the raw data, although predictions were computed for one scenario (at reference values). Furthermore, predicting the response probabilities of P/AI 30 and P/AI 70 indicated there was a large variation among sires in the loss rate of embryos, which was consistent with findings in many previous studies [e.g., Lopez-Gatius et al. (2005) and Pegorer et al. (2007)]. Assessments of effects on these variables was beyond the scope of the present study and may be worthy of further investigation.

Data from the present study indicate there was an increase of about 9% in P/AI 30 and P/AI70 percentages for high and average fertility sires in RB cows, however, there was no effect of interactions between sire fertility group and cow fertility status. It was suspected that the use of semen from high fertility sires may improve the fertility of RB cows due the fact that sperm cells from these bulls have a greater capacity to penetrate artificial mucus and to fertilize oocytes in vitro (Al Naib et al., 2011), as well as a more substantial membrane functional status and acrosomal membrane integrity (Correa et al., 1997). The analyses of P/AI 30 and P/AI 70 indicated there was a larger variation in fertility as a result of number of lactations than as a result of cow and sire effects. The analyses also accounted for between-inseminator variation that resulted in improvements in the model fit. The random-effect variances were larger in the P/AI 30 model than in the P/AI 70 analysis, and between-lactation variance was about twice as great for P/AI 70 compared to P/AI 30 data. The later finding indicates that pregnancy rates within the same lactation at day 70 are more similar than pregnancy rates at day 30 post-insemination.

5. Conclusion

Two logistic regression models with sire, inseminator, cow, and lactation random effects were fitted to the pregnancy data at days 30 and 70 post-insemination. The results indicate there are individual sire effects on conception rates, and a great magnitude of heterogeneity among sires. Sire factors such as sire fertility group and sire breed, however, did not affect P/AI 30 nor P/AI 70. Furthermore, there were no significant effects of interactions between sire fertility group and insemination type, and sire fertility group and cow-fertility status. After accounting for model variables, predicting response probabilities for a subset of sires provided evidence that there was a greater probability of cows where EDAI occurred than in cows where there was TAI.

Declaration of Competing Interest

All authors declare that no conflict of interest could be perceived as prejudicing the impartiality of the research reported.

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