

Updated Genetic Parameters for Holstein Reproductive Traits Using More Recent Data

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INTRODUCTION

Canadian model for female reproductive traits includes 16 fertility and calving performance traits, defined separately for heifers and mature cows. Co-variance components and genetic parameters of this model were estimated in 2005, using data on approximately 50,000 Holstein cows that were born in 1997 - 2002 (Jamrozik et al., 2005b). Parameters of any genetic evaluation model should be re-estimated periodically, when changes are made to the model or the way that the data is generated; or in general, to account for time trends for the traits in the population. Reproductive performance traits in Canada might have been a subject of genetic and environmental changes in the last 15 years. Methods have recently been developed to utilize pregnancy confirmation data for more timely calculation of First Service to Conception phenotypes (Jamrozik and Kistemaker, 2016).

Objectives of this research were therefore:

1. to estimate genetic parameters for sixteen reproductive traits for the Holstein breed using the recent data and pregnancy check calculated First Service to Conception,
2. to compare new estimates with the currently used parameters.

MATERIAL AND METHODS

Fertility and calving traits were: age at first insemination (**AFS**), days from calving to first insemination (**CTFS**), number of services (**NS**), first service non-return rate (**NRR**) to 56 days, days from first service to conception (**FSTC**), calving ease (**CE**), stillbirth (**SB**), gestation length (**GL**), and calf size (**CZ**). Continuous, interval traits (AFS, CTFS, FSTC and GL) were expressed in days. Stillbirth was defined as 0 (dead) or 1 (alive calf). Non-return rate was coded 1 when there was no subsequent insemination between 15 to 56 days following the first service and 0 otherwise. Ordered, categorical traits (CE and CZ) were subjectively scored in four classes (CE from 1 to 4 and CZ from 0 to 3) with 1 corresponding to unassisted calving (CE) and 0 describing small calf size (CZ).

February 2016 official Holstein extracts for reproductive performance and pregnancy confirmation data were used. Data for missing FSTC was generated by using pregcheck data as described in Jamrozik and Kistemaker (2016). Data on parities 1 (heifers) to 6 only was used. Time edits were applied to eliminate censored records for animals that were born or calved recently. Only cows with records born in years 1997-2012 were used. First insemination of heifers occurred in years 1998-2014, calving years were 1999-2015. Other requirements included: age at first calving had to be greater than 18 months, AFS between 274 and 639 days, CTFS between 14 and 244 days. Number of services (NS) was assigned to 10 when the actual NS was greater than 10.

For the purpose of estimating genetic parameters further restrictions were needed. Subset of the data of a smaller size (approximately 10% of the total records after edits) was generated,

by a random sampling of herds with at least 200 records from Ontario and Quebec and with no restrictions on conception rates for bulls and herds. Descriptive statistics for each trait are shown in Table 1. All cows were required to have a heifer record. Records for each calving were only included if a cow had records on all preceding calvings. Sequential edits on missing traits within parity (traits ordered in their sequence of occurrence as in Table 1) were also employed to account for selection biases and to facilitate computations. Total number of cows with data was 120,644 and the total number of records (each calving treated as separate record) was equal to 281,166. Distribution of records by parity is given in Table 2. Fertility records up to 6th calving were present in the selected data. Heifer records, however, constituted 42.9% of the total data. Total number of animals in pedigrees was 344,047. Number of service sire by year of insemination classes and number of sires of calf were 13,983 and 7972, respectively.

The overall model was a multiple-trait animal model (same model as used in 2005) that included all sixteen traits with specific linear models for a given trait. Single trait models for particular traits are listed below in a simplified scalar notation. For heifer traits there were:

$$\begin{aligned}
 \text{AFS} &= \text{RYM} + \text{HY} + \text{A} + \text{E}, \\
 \text{NRR} &= \text{RYM} + \text{HY} + \text{Mf} + \text{SS} + \text{T} + \text{A} + \text{E}, \\
 \text{NS} &= \text{RYM} + \text{HY} + \text{Mf} + \text{A} + \text{E}, \\
 \text{FSTC} &= \text{RYM} + \text{HY} + \text{Mf} + \text{A} + \text{E}, \\
 \text{GL} &= \text{RYM} + \text{HY} + \text{MfX} + \text{SC} + \text{A} + \text{E}, \\
 \text{CE} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{E}, \\
 \text{SB} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{E}, \\
 \text{CZ} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{E}.
 \end{aligned}$$

Similarly, for cow traits:

$$\begin{aligned}
 \text{NRR} &= \text{RYM} + \text{HY} + \text{ApMf} + \text{SS} + \text{T} + \text{A} + \text{PE} + \text{E}, \\
 \text{NS} &= \text{RYM} + \text{HY} + \text{ApMf} + \text{A} + \text{PE} + \text{E}, \\
 \text{CTFS} &= \text{RYM} + \text{HY} + \text{ApMp} + \text{A} + \text{PE} + \text{E}, \\
 \text{FSTC} &= \text{RYM} + \text{HY} + \text{ApMf} + \text{A} + \text{PE} + \text{E}, \\
 \text{GL} &= \text{RYM} + \text{HY} + \text{ApMpX} + \text{SC} + \text{A} + \text{PE} + \text{E}, \\
 \text{CE} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{PE} + \text{E}, \\
 \text{SB} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{PE} + \text{E}, \\
 \text{CZ} &= \text{RYM} + \text{HY} + \text{AcMcX} + \text{SC} + \text{A} + \text{PE} + \text{E},
 \end{aligned}$$

where genetic and environmental factors were:

RYM	Region by Year of birth by Month of birth (12 classes)	- fixed effect,
HY	Herd by Year of birth	- random effect.
Mf	Month of first insemination	- fixed,
MfX	Month of first insemination by sex of calf (3 classes)	- fixed,
AcMcX	Age at current calving by month of current calving by sex of calf by parity	- fixed,
ApMp	Age at previous calving by month of previous calving by parity	- fixed,
ApMf	Age at previous calving by month of first	- fixed,

	insemination by parity	
ApMpX	ApMp by sex of calf by parity	- fixed,
A	Animal additive genetic effect	- random,
SS	Service sire by year of insemination	- random,
SC	Sire of calf	- random,
PE	Permanent environment	- random,
T	AI technician	- random,
E	Error term	- random.

Details on the covariance structure for the random effects of the model as well as methods for the estimation process (i.e. Bayesian methods with Gibbs sampling) can be found in Jamrozik et al. (2005a). Estimates of covariance components and genetic parameters were obtained as posterior means of 200,000 samples (after burn-in). Co-variance components and genetic parameters (will further be labeled as **NEW**) were compared with the 2005 parameters (further denoted as **OLD**).

RESULTS AND DISCUSSION

Phenotypic means for the OLD (1998 - 2004) and the NEW (1998 - 2014) data were very similar (Table 1). Differences between samples were statistically non-significant for all traits. Estimates of phenotypic variance and ratios with respect to the total variance for additive genetic (heritability), RYS:H (or HY), PE, SS, T, SC and E variances are shown in Table 3 for the OLD and NEW data. Both sets of estimates were similar for the total variance; with slightly smaller variation for interval traits (FSTC and CTFS) for the NEW data. Partition of variance, however, was different between estimates for some traits. Age at first service was the trait with the largest differences between OLD and the NEW data. Heritability of AFS decreased from 9.4% to 5.2% with the NEW data, and the herd variance increased (from 42% to 52%). This resulted in a significant decrease of the residual variance for this trait. Heritabilities for other traits with the NEW data were in general smaller than the current official values. Calving ease, SB in heifers, and CZ in heifers and cows had slightly higher proportion of additive genetic in the overall variance. Sire of cow relative variances also decreased for calving traits which resulted in a decrease of the direct effect heritability for these traits. Although the new estimates of heritability for fertility traits were smaller than the current official estimates, they seemed to be more in line with estimates for other Holstein populations (i.e. Germany, Italy, France, DNS, Netherlands, Great Britain).

Estimates of genetic, herd-year, PE, SC, and residual correlations are presented in Tables 4 – 8. Genetic correlation between heifers and cows for fertility traits dropped with the use of the NEW data. The opposite trend was observed for the calving performance traits. No evident pattern of changes was shown by correlations between fertility and calving traits. Correlations among PE effects for later parities traits were characterized by relatively larger posterior SD (results not shown), thus the direction and magnitude of changes between OLD and the NEW were more erratic. The magnitude of correlations among sire of calf effects increased in general for all calving performance traits.

Changes in rankings of animals and estimates of their breeding values are expected, in general, when the new estimates of genetic parameters are used in genetic evaluation. Those

should not be extreme for the Canadian reproductive performance model with the new parameters, given the scale of changes in co-variance components. Lower heritability for fertility traits should result in a better stability of evaluation (i.e. smaller impact of additional phenotypic data on proofs). Similarly, smaller genetic correlations between parities (heifers versus cows) for these traits should also lessen the impact of the earlier data on consecutive evaluations.

Comparison of estimates using the data with and without FSTC calculated using pregnancy confirmation data showed virtually no impact of pregcheck generated FSTC phenotypes on genetic parameters (results not shown). This indicated that the subsequent calving verified FSTC and FSTC obtained via pregnancy check data can be jointly used as a single trait in the genetic evaluation model.

CONCLUSIONS AND RECOMMENDATIONS

The new, more relevant, genetic parameters should be used in the genetic evaluation for female reproductive traits in Canadian dairy populations. In agreement with the current strategy, Holstein estimates are recommended to be used for all other breeds. The impact on bull proofs should be quantified as well as the stability study should be performed before the official implementation of the new parameters.

REFERENCES

Jamrozik, J., J. Fatehi, G.J. Kistemaker, and L.R. Schaeffer. 2005a. Estimates of genetic parameters for Holstein female fertility – sixteen traits. Research Report to the GEB, March 2005, pp. 14.

Jamrozik, J., J. Fatehi, and L.R. Schaeffer. 2005b. Models for fertility traits with random herd-year effects: estimates of genetic parameters for Holsteins. Research Report to the GEB, November 2005, pp. 6.

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Table 1: Descriptive statistics of the data

Parity	Trait		Number of records	Mean	SD	Min	Max
First	AFS	OLD	53,158	499.7	53.6	275	639
		NEW	120,644	491.5	55.5	275	639
	NRR	OLD	53,158	0.74	0.44	0	1
		NEW	120,641	0.74	0.44	0	1
	NS	OLD	53,093	1.64	1.09	1	10
		NEW	120,632	1.56	0.94	1	10
	FSTC	OLD	29,907	16.3	31.4	0	206
		NEW	116,954	18.5	34.1	0	206
Later	GL	OLD	29,907	279.6	6.1	240	300
		NEW	96,867	279.0	6.1	240	300
	CE	OLD	29,907	1.63	0.71	1	4
		NEW	96,867	1.60	0.68	1	4
	SB	OLD	27,643	0.90	0.30	0	1
		NEW	95,886	0.89	0.31	0	1
	CZ	OLD	27,418	2.03	0.60	0	3
		NEW	94,457	2.00	0.58	0	3
	NRR	OLD	41,092	0.57	0.49	0	1
		NEW	160,522	0.55	0.50	0	1
	NS	OLD	37,409	2.14	1.50	1	10
		NEW	160,502	2.13	1.37	1	10
	CTFS	OLD	35,474	87.1	29.4	16	244
		NEW	160,485	83.3	27.7	14	244
	FSTC	OLD	16,124	32.5	44.4	0	206
		NEW	156,264	37.8	47.9	0	206
	GL	OLD	16,124	280.5	6.3	240	300
		NEW	135,392	279.9	6.4	240	300
	CE	OLD	16,124	1.41	0.59	1	4
		NEW	135,392	1.40	0.58	1	4
	SB	OLD	15,416	0.96	0.19	0	1
		NEW	134,924	0.95	0.22	0	1
	CZ	OLD	15,371	2.16	0.64	0	3
		NEW	133,935	2.17	0.58	0	3

Table 2: Distribution of records by parity number

Parity		Number of records
1	OLD	53,158
	NEW	120,644
2	OLD	24,989
	NEW	77,366
3	OLD	10,927
	NEW	44,455
4	OLD	4046
	NEW	23,197
5	OLD	1010
	NEW	10,972
6	OLD	120
	NEW	4532

Table 3: Estimates (posterior means) of phenotypic variance and ratios (%) with respect to phenotypic variance for additive genetic (h^2), herd ($herd^2$), permanent environment (pe^2), sire of calf (sc^2), service sire (ss^2), technician ($tech^2$) and residual (e^2) variances

Parity	Trait	Breed	Total variance	h^2	$herd^2$	pe^2	sc^2	ss^2	$Tech^2$	e^2
First	AFS	OLD	2830.6	9.4	41.6					49.0
		NEW	3072.6	5.2	52.1					42.7
	NRR	OLD	0.19	3.0	2.2			0.1	0.4	94.4
		NEW	0.19	1.5	2.1			0.2	0.8	96.4
	NS	OLD	1.19	3.4	3.5					93.0
		NEW	0.89	2.3	3.7					94.0
	FSTC	OLD	1455.9	3.3	3.5					93.2
		NEW	1207.2	2.1	4.1					93.8
	GL	OLD	38.7	19.2	1.3		7.0			72.5
		NEW	37.8	16.9	2.9		7.2			73.0
	CE	OLD	0.48	12.1	14.5		1.8			71.6
		NEW	0.46	12.5	15.0		0.9			71.6
	SB	OLD	0.09	5.6	1.6		0.5			92.3
		NEW	0.10	7.1	1.8		0.1			91.0
	SZ	OLD	0.35	9.4	9.7		3.5			77.4
		NEW	0.33	10.5	12.0		2.7			74.8
Later	NRR	OLD	0.24	3.9	2.6	0.5		0.1	0.4	92.3
		NEW	0.25	2.7	2.1	0.7		0.2	0.6	93.8
	NS	OLD	2.2	7.7	2.5	0.2				89.6
		NEW	1.9	6.0	2.8	2.1				89.1
	CTFS	OLD	864.0	7.1	21.4	3.4				68.1
		NEW	766.9	6.2	20.5	2.3				71.0
	FSTC	OLD	2940.4	7.7	3.1	0.2				88.9
		NEW	2460.8	5.3	3.1	1.5				90.0
	GL	OLD	39.9	16.4	1.5	2.2	6.4			73.5
		NEW	43.0	15.5	1.4	0.7	6.4			76.0
	CE	OLD	0.33	8.5	15.3	0.6	1.6			74.0
		NEW	0.34	7.5	15.0	2.0	0.7			74.9
	SB	OLD	0.03	2.3	0.5	1.5	0.3			95.3
		NEW	0.05	1.4	0.5	1.0	0.1			97.1
	CZ	OLD	0.39	6.2	15.0	1.2	2.6			74.9
		NEW	0.33	8.8	10.6	1.2	2.2			77.2

Table 4: Estimates (posterior means*100) of genetic correlations (above diagonal) and herd correlations (below diagonal)

Parity/Trait			First								Later							
			AFS	NRR	NS	FSTC	GL	CE	SB	CZ	NRR	NS	CTFS	FSTC	GL	CE	SB	CZ
First	AFS	OLD NEW		30 20	-16 0	-5 10	-31 -15	-6 -6	-2 9	-33 -33	15 12	-8 0	27 33	-2 10	-14 -2	-4 -1	0 7	-29 -25
	NRR	OLD NEW	39 44		-86 -84	-68 -69	-8 -9	-20 -4	18 14	-19 -11	59 57	-54 -50	26 25	-51 -46	8 -12	-8 8	4 -1	10 0
	NS	OLD NEW	-19 -16	-74 -76		92 93	4 14	14 2	-23 -7	18 15	-67 -54	67 57	-13 -4	63 57	-7 23	1 -7	-21 -5	-12 6
	FSTC	OLD NEW	-15 -15	-66 -67	95 94		1 13	13 3	-40 -9	17 18	-67 -47	70 55	-6 6	67 59	-5 22	-3 -6	-33 -9	-14 8
	GL	OLD NEW	25 28	-13 17	-3 -13	-4 -16		20 21	-4 -2	41 47	2 -5	-5 9	-11 -3	-6 9	81 87	18 21	5 -9	51 44
	CE	OLD NEW	-12 -17	-14 -8	11 3	11 2	7 0		-54 -48	58 50	-26 -20	30 28	9 14	32 27	13 15	78 88	-12 -26	45 35
	SB	OLD NEW	7 27	24 18	-41 -23	-39 -25	2 2	-14 -11		-23 -10	41 30	-52 -39	-13 -10	-53 -37	3 -2	-33 -27	36 64	-8 5
	CZ	OLD NEW	-19 -19	-21 -19	12 9	14 8	-38 -9	16 20	-18 -15		-26 -16	22 21	-10 6	20 20	36 45	41 40	-17 -6	70 88
Later	NRR	OLD NEW	31 28	50 59	-24 -43	-24 -38	-22 14	-23 -12	15 9	-19 -12		-90 -88	-3 14	-83 -78	17 -5	-14 -11	34 21	6 -5
	NS	OLD NEW	-24 -14	-63 -58	64 61	63 57	16 -15	12 3	-19 0	16 4	-80 -84		20 18	97 96	-16 10	22 21	-36 -32	-6 8
	CTFS	OLD NEW	31 33	33 38	-21 -22	-26 -21	18 14	-1 -8	17 12	3 -6	76 72	-62 -52		27 31	-2 -2	13 14	-22 -22	5 10
	FSTC	OLD NEW	-18 -9	-54 -46	65 54	68 57	9 -15	6 -1	-20 -4	17 3	-63 -69	96 92	-50 -44		-15 10	25 20	-37 -31	-6 8
	GL	OLD NEW	1 14	11 23	-35 -27	-46 -30	15 36	35 13	-26 5	-32 -14	11 19	-33 -30	4 12	-40 -28		18 14	16 -2	57 48
	CE	OLD NEW	0 -2	-13 -8	5 3	2 0	-3 4	78 74	10 15	9 8	-8 -8	-2 2	11 -2	-6 -1	11 7		-5 -18	46 32
	SB	OLD NEW	5 16	30 35	-25 -32	-33 -41	-24 -7	-22 -10	33 38	6 4	6 2	-4 15	24 18	1 7	-16 1	-13 0		6 10
	CZ	OLD NEW	-2 1	1 -7	-2 7	-4 3	-5 -10	19 15	-13 -7	55 65	-5 -10	7 10	-4 -2	8 6	1 -11	11 5	-47 -17	

Table 5: Estimates (posterior means*100) of permanent environmental correlations

Trait/Breed		NS	CTFS	FSTC	GL	CE	SB	SZ
NRR	OLD	-52	55	53	-54	-7	7	-12
	NEW	-59	49	-37	-27	-26	37	-16
NS	OLD		0	14	44	65	28	13
	NEW		7	92	15	29	-51	10
CTFS	OLD			65	18	47	2	13
	NEW			31	13	16	-2	-10
FSTC	OLD				-35	25	-19	-12
	NEW				-2	30	-58	5
GL	OLD					44	3	31
	NEW					19	-1	12
CE	OLD						44	38
	NEW						-18	-5
SB	OLD							28
	NEW							6

Table 6: Estimates (posterior means*100) of sire of calf correlation

Parity/Trait			First				Later			
			GL	CE	SB	CZ	GL	CE	SB	CZ
First	GL	OLD		23	-16	20	83	35	-10	30
		NEW		36	-18	34	98	40	-10	44
	CE	OLD			-48	78	21	62	-28	65
		NEW			-71	94	36	90	-46	92
	SB	OLD				-44	-11	-30	50	-37
		NEW				-69	-17	-65	69	-64
Later	CZ	OLD					23	54	-22	75
		NEW					35	88	-43	96
	GL	OLD						39	-3	38
		NEW						41	-7	46
	CE	OLD							-20	66
		NEW							-44	91
	SB	OLD								-13
		NEW								-37

Table 7: Estimates (posterior means*100) of residual correlations for first parity traits

Trait	Breed	NRR	NS	FSTC	GL	CE	SB	CZ
AFS	OLD	0	-1	-1	8	0	-1	0
	NEW	0	-2	-1	5	0	-1	0
NRR	OLD		-59	-49	7	0	0	2
	NEW		-65	-52	4	0	0	1
NS	OLD			90	-1	1	-1	-1
	NEW			86	-1	0	0	-2
FSTC	OLD				-1	1	-1	-1
	NEW				0	-1	0	-2
GL	OLD					6	8	16
	NEW					4	7	18
CE	OLD						-17	25
	NEW						-14	24
SB	OLD							-8
	NEW							-5

Table 8: Estimates (posterior means*100) of residual correlations for later parities traits

Trait	Breed	NS	CTFS	FSTC	GL	CE	SB	CZ
NRR	OLD	-52	4	-44	7	1	-1	-1
	NEW	-57	3	-48	5	0	-1	0
NS	OLD		-6	92	-4	1	-2	2
	NEW		-7	87	-5	1	0	0
CTFS	OLD			-6	-1	-1	0	-1
	NEW			-7	-1	0	0	-1
FSTC	OLD				-2	1	-1	2
	NEW				-4	1	0	0
GL	OLD					3	11	13
	NEW					2	15	23
CE	OLD						-13	13
	NEW						-11	14
SB	OLD							2
	NEW							7