

Genetic Parameters for Endocrine Fertility Traits from In-line Milk Progesterone Records in Dairy Cows

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ABSTRACT: In-line milk progesterone records (n = 163,145) collected from June 2009 through November 2013 for 2,274 lactations of Holstein-Friesian cows in 12 commercial herds in the Netherlands were analyzed for commencement of luteal activity (CLA), luteal activity during first 60 days in milk (LA60), proportion of samples with luteal activity (PLA), interval from commencement of luteal activity to first service, length of first luteal phase, and number of inter-ovulatory intervals before first service. Heritability (0.13, 0.10, and 0.05) and repeatability estimates (0.26, 0.21, and 0.16) were greatest for CLA, PLA and LA60, respectively, compared with other traits. Genetic correlations were 0.96 to 0.99 between these traits. This study shows that in-line P4 records can be used to define and explore several heritable endocrine fertility traits that can be used in genetic improvement of fertility by selection.

Keywords: in-line progesterone; cow fertility; genetics

Introduction

Although milk progesterone (P4) levels have been widely accepted as valid indicators to assess fertility in dairy cows (Darwash et al. (1999); Royal et al. (2002)), their application in routine genetic evaluation schemes has been constrained by the high cost associated with collecting these measures in sufficient number of samples per cow. Until recently, methods to measure milk P4 level were manual and labor intensive. However, P4 level measuring technology has advanced to allow in-line systems to instantly measure milk P4 level (Friggens and Chagunda (2005)). In these systems, milk is automatically sampled, P4 level measured, and recorded. Hence, more animals can be sampled at an economically feasible cost, making it possible to have sufficient endocrine fertility traits for use in routine genetic evaluations. To use endocrine fertility traits from in-line milk P4 records in genetic improvement of fertility, the first step will be to examine whether these traits have sufficient genetic variation. Most studies on characterization of heritable endocrine fertility traits have, however, been based on manual P4 records (Darwash et al. (1997); Royal et al. (2000); Petersson et al. (2007)).

The aim of this study was to define and estimate genetic parameters for endocrine fertility traits from in-line progesterone records.

Data and quality control. Milk progesterone records (n = 237,133) collected from June 2009 through November 2013 were available for 2,684 Holstein-Friesian cows from 13 commercial dairy herds in the Netherlands, that use the Herd Navigator in DeLaval milking systems.

Most cows were sampled from 27 days in milk (DIM) to 175 DIM, with a mean sampling duration of 148 days. Milk P4 samples were taken on average every 2 days, with 25 percent of samples taken at an interval of 1 day or less, and 75 percent at an interval of 4 days or more. A mean total of 67 P4 records were available per lactation. Editing and linking P4 records to calving data resulted in 3,745 lactations of 2,377 cows with 215,993 P4 records. In total, 9 % of P4 records and 11 % of cows were lost after editing. Two sets of quality control (QC) criteria were applied to P4 records (herd and lactation level QC). At the herd level, to reduce sampling variation due to different start and end dates of P4 sampling per herd, a lactation was retained if a) the interval from calving to start of herd P4 sampling was ≤ 25 days, and b) the interval from calving to end of herd P4 sampling was ≥ 60 days. At the lactation level, to reduce sampling variation due to difference in start of P4 sampling per lactation, P4 samples taken before 25 DIM per lactation were excluded, and lactations for which P4 sampling started after 35 DIM were excluded. After quality control, 163,145 (76%) P4 records of 2,417 (65%) lactations for 1,822 (77%) cows were retained.

Defining endocrine fertility traits. For each lactation, the following traits were defined (illustrated in Figure 1): a) Commencement of luteal activity (CLA; indicator I, Figure 1), defined as the difference between day of calving and first day on which milk P4 level was elevated (≥ 5 ng/ml); b) Commencement of luteal activity to first service (CLAFS; indicator II) as the interval from the first day of elevated P4 level (≥ 5 ng/ml) fitting the luteal activity criteria, to day of first service; c) Luteal activity during first 60 days in milk (LA60) as the presence (LA60 = 1) or absence (LA60 = 0) of luteal activity during the first 60 DIM; d) Proportion of samples with luteal activity (PLA) as number of P4 records with luteal activity (P4 level ≥ 5 ng/ml), divided by total number of P4 records per lactation, e) Length of first luteal phase (LPL1; indicator III) as the interval from the first day of elevated P4 level (≥ 5 ng/ml), to last consecutive day of elevated P4 level (≥ 5 ng/ml). Length of first inter-luteal interval (ILI1; indicator IV), and length of first inter-ovulatory interval (IOI1; indicator V) were defined, but were found to have no genetic variation, thus were excluded from further analysis. Number of estrus cycles before first service (IOIFS) refers to the number of complete estrus cycles before first service. The IOI is an objective measure of estrus cycle length and was used to define IOIFS.

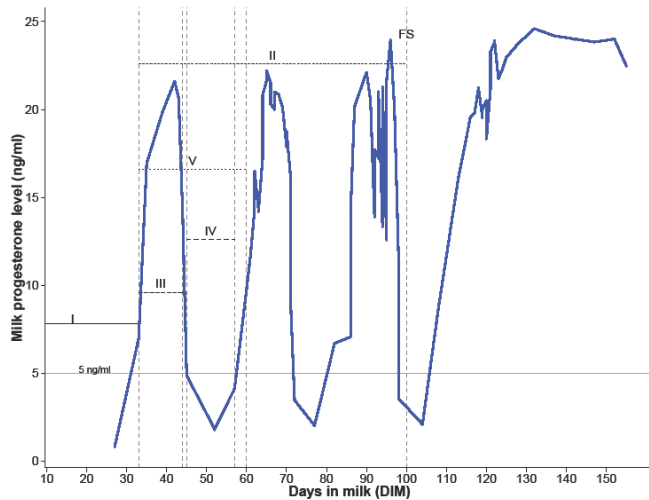


Figure 1 : Milk progesterone level over days in milk used to define endocrine fertility traits in dairy cows.

I (CLA) = Commencement of luteal activity.

II (CLAFS) = Commencement of luteal activity to first service.

III (LPL1) = Length of first Luteal phase.

IV (ILI1) = Length of first inter-luteal interval.

V (IOI1) = Length of first inter-ovulatory interval.

FS = First service.

Line at 5 ng/ml represents threshold for luteal activity.

Statistical analysis. Data was analyzed with linear mixed models in ASREML (Gilmour et al. (2009)). Model fixed effects were: herd-year-season classes, parity (1 to 6), calving age (in months) and percentage of Holstein genes (PCH). Calving age and PCH were fitted as fixed regression nested within parity. Model random effects were animal genetic and permanent environmental effect. CLA was log transformed before fitting the model. Final data with defined endocrine fertility traits and pedigree information, used in genetic analysis consisted of 2,274 lactations of 1,552 cows from 12 herds. Pedigree data (n= 5,5758) consisted of 406 paternal and 1238 maternal half-sib groups, over 9 generations.

Results and Discussion

Genetic parameters. Summary statistics for all traits analyzed are in Table 1, together with heritability and repeatability estimates. Mean CLA (38.6 days) was greater than reported by previous studies, but with a similar standard deviation. Mean CLA of 29.5 days, with a standard deviation of 16.8 days was reported by Veerkamp et al. (2000), while Royal et al. (2002), reported a mean CLA of 29.4 days, with standard deviation of 18.4 days. One reason for this mean difference might be due to the restriction of excluding P4 records sampled before 25 DIM (lactation QC) applied in this study.

Table 1. Number of observations (n), overall means, standard deviation (s.d), heritability (h^2), repeatability (r) and standard errors (s.e) for commencement of luteal activity (CLA), luteal activity during first 60 days in milk (LA60), proportion of samples with luteal activity (PLA), commencement of luteal activity to first service (CLAFS), length of first luteal phase (LPL1), and number of inter-ovulatory intervals before first service (IOIFS)

Trait	n	Mean	s.d	h^2	s.e	r	s.e
CLA	2229	38.49	18.28	0.13	0.05	0.26	0.04
LA60	2274	0.87	0.33	0.05	0.04	0.16	0.04
PLA	2274	0.57	0.30	0.10	0.04	0.21	0.04
CLAFS	1401	60.80	41.16	0.04	0.04	0.12	0.06
LPL1	1077	12.63	11.12	0.03	0.05	0	0
IOIFS	1401	0.74	1.17	0.04	0.04	0.12	0.05

Heritability estimates varied from 0.03 to 0.13, and repeatability from 0 to 0.26, but were generally higher for CLA, LA60, and PLA. Heritability of CLA (0.13) was lower than estimates of up to 0.16 reported in other studies (Veerkamp et al. (2000); Royal et al. (2002); Petersson et al. (2007)), but similar to the estimate reported by Berry et al. ((2012)). Similarly, heritability for PLA (0.10) was lower than has been reported by Petersson et al. ((2007)). However, all previous studies have been based on manual progesterone (P4) records, which might explain the difference.

Genetic correlations among traits were generally stronger than their respective phenotypic correlations, but were in general of the same sign (Table 2). The traits CLA, LA60, and PLA, were more strongly correlated with each other, both genetically (0.96 to 0.99) and phenotypically (0.71 to 0.82) than other traits.

Table 2. Genetic[¶] and phenotypic[#] correlations, and standard errors[§] of commencement of luteal activity (CLA), luteal activity during first 60 days in milk (LA60), proportion of samples with luteal activity (PLA), commencement of luteal activity to first service (CLAFS), length of first luteal phase (LPL1), and number of inter-ovulatory intervals before first service (IOIFS)

Trait	CLA	LA60	PLA	CLAFS	LPL1	IOIFS
CLA		-0.82	-0.77	-0.29	-0.16	0.18
		<i>0.01</i>	<i>0.01</i>	<i>0.03</i>	<i>0.03</i>	<i>0.03</i>
LA60	-0.96		0.71	0.25	0.11	0.00
	<i>0.06</i>		<i>0.01</i>	<i>0.03</i>	<i>0.03</i>	<i>0.03</i>
PLA	-0.99	0.99		0.26	0.41	-0.18
	<i>0.06</i>	<i>0.10</i>		<i>0.03</i>	<i>0.03</i>	<i>0.03</i>
CLAFS	0.03	0.00	0.60		0.22	0.27
	<i>0.48</i>	<i>0.50</i>	<i>0.41</i>		<i>0.04</i>	<i>0.03</i>
LPL1	-0.30	-0.48	0.41	0.62		-0.05
	<i>0.58</i>	<i>1.08</i>	<i>0.45</i>	<i>0.71</i>		<i>0.04</i>
IOIFS	0.77	-0.97	-0.89	-0.09	0.25	
	<i>0.49</i>	<i>0.82</i>	<i>0.56</i>	<i>0.85</i>	<i>0.79</i>	

[¶]Genetic correlations (below diagonal).

[#]Phenotypic correlations (above diagonal)

[§]Standard errors (below correlation estimates, in italics).

Conclusion

We showed that in-line progesterone records can be used to define and explore several endocrine fertility traits in dairy cows. These traits have sufficient genetic variation, and because availability of sufficient records per animal and on sufficient number of animals is no longer a limitation, in-line progesterone records provide the potential to use endocrine fertility traits for genetic improvement of fertility by selection in genetic evaluation schemes.

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Literature Cited

- Berry, D. P., J. W. Bastiaansen, R. F. Veerkamp et al. (2012). *Animal*. 6: 1206-1215.
- Darwash, A. O., G. E. Lamming and J. A. Woolliams. (1997). *J. Dairy Sci.* 80: 1227-1234.
- Darwash, A. O., G. E. Lamming and J. A. Woolliams. (1999). *Animal Sci.* 68: 333-347.
- Friggens, N. C. and M. G. G. Chagunda. (2005). *Theriogenology*. 64: 155-190.
- Gilmour, A. R., B. R. Cullis and R. Thompson. (2009). ASReml, release 3.0.
- Petersson, K.-J., B. Berglund, E. Strandberg et al. (2007). *J. Dairy Sci.* 90: 427-434.
- Royal, M. D., A. O. Darwash, A. P. E. Flint et al. (2000). *Animal Sci.* 70: 487-501.
- Royal, M. D., J. E. Pryce, J. A. Woolliams and A. P. F. Flint. (2002). *J. Dairy Sci.* 85: 3071-3080.
- Veerkamp, R. F., J. K. Oldenbroek, H. J. Van Der Gaast and J. H. J. V. D. Werf. (2000). *J. Dairy Sci.* 83: 577-583.