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Estimating genetic parameters for fertility in dairy cows from in-line milk progesterone profiles

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ABSTRACT

The aim of this study was to define endocrine fertility traits from in-line milk progesterone (P4) records and to estimate genetic parameters for these traits. Correlations of classical fertility (calving interval and calving to first service) and milk production traits with endocrine fertility traits were also estimated. In-line milk P4 records ($n = 160,952$) collected from June 2009 through November 2013 for 2,273 lactations of 1,561 Holstein-Friesian cows in 12 commercial herds in the Netherlands were analyzed for (the log of) the number of days from calving till commencement of luteal activity (lnC-LA), proportion of samples between 25 and 60 d in milk with luteal activity (PLA), presence or absence of luteal activity for a cow between 25 and 60 d in milk, interval from commencement of luteal activity to first service (CLAFS), first luteal phase length, length of first interluteal interval, and length of first interovulatory interval. Milk P4 records were sampled, on average, every 2 d. Genetic parameters were estimated using a mixed linear animal model. Heritability estimates (\pm SE) of endocrine fertility traits were 0.12 ± 0.05 for lnC-LA, 0.12 ± 0.05 for PLA, and 0.11 ± 0.06 for CLAFS, and their repeatability estimates were 0.29 ± 0.04 , 0.21 ± 0.04 , and 0.15 ± 0.06 , respectively. The genetic correlation of lnC-LA with PLA was -0.91 ± 0.06 and with CLAFS was -0.56 ± 0.25 . The genetic correlations of lnC-LA were 0.26 ± 0.33 with calving interval and 0.37 ± 0.21 with calving to first service. Genetic correlations of the milk production traits with lnC-LA ranged from 0.04 to 0.18 and 0.07 to 0.65 with classical fertility traits. The phenotypic correlations of all endocrine fertility traits with milk production traits were close to zero (0.01 to 0.07). This study shows that

in-line P4 records can be used to define and explore several heritable endocrine fertility traits in dairy cows and might help in selection for improved fertility.

Key words: dairy cow, fertility, in-line progesterone, heritability

INTRODUCTION

Fertility is an important component of herd production efficiency because each additional estrus cycle that does not result in a planned pregnancy adds to the cost of dairy farming. The negative effect of fertility on production efficiency is often reflected in increased number of inseminations per conception, higher involuntary herd replacement, high cost of veterinary intervention, and longer calving intervals. In addition to these negative effects, subfertility can affect the rate of genetic gain in other traits of economic importance.

Genetically improving fertility by selection with classical traits such as interval from calving to first service (CFS), calving interval (CInt), or days open is complicated by the low heritability of these traits (Jansen, 1985; Berry et al., 2003). These low heritabilities ($h^2 < 0.1$) may be explained by the fact that classical fertility traits are highly influenced by farm management decisions and poor recording practices (Hayes et al., 1992; Campos et al., 1994; Marti and Funk, 1994). For instance, a planned extended CInt will delay CFS not because a cow has a late start of cyclic activity, but because of the farmer's decision on when to inseminate, which results in large residual variance and low heritability estimates. Further indications that commercial farm management and recording might affect heritability estimates for classical fertility traits is the fact that larger heritability estimates ($h^2 = 0.13$, for days open and CFS) have been estimated from records collected on an experimental farm under controlled management (Pryce et al., 1997). This low heritability of classical fertility traits makes it difficult to discriminate fertile genotypes at the cow level and, consequently, makes selection less effective.

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Endocrine fertility traits have been suggested as alternative indicators for fertility in dairy cows because they more directly reflect a cow's physiology (Bulman and Lamming, 1978; Lamming and Darwash, 1998; Darwash et al., 1999). For example, the interval from calving to first ovulation as determined by progesterone (P4) levels in milk could be used as a direct indicator of a cow's ability to return to luteal activity after calving, instead of an indirect indicator such as CFS. Several studies have revealed that endocrine fertility traits yield higher heritability estimates than classical fertility traits. Notably, for the interval from calving to commencement of luteal activity (C-LA), heritability estimates of 0.16 to 0.28 have been found, which is larger than for classical fertility traits (Darwash et al., 1997a; Veerkamp et al., 1998; Petersson et al., 2007). Furthermore, examination of phenotypic correlation of C-LA with classical fertility traits revealed that early reestablishment of cyclic activity in postpartum cows increases the probability of an early insemination after calving, shortens the interval from calving to conception, increases conception rate, and reduces the number of services per conception (Darwash et al., 1997b). These results further suggest that early reestablishment of cyclic activity is an important prerequisite for high fertility. In addition to C-LA, Darwash et al. (1997a) confirmed that milk P4 profiles could provide several objective heritable endocrine fertility traits. For example, corpus luteum competence and interluteal interval (ILI) were highly correlated with conception rate. Similarly, (Petersson et al., 2006) showed that endocrine fertility traits have moderate repeatability (0.14–0.16), suggesting more influence by the cow itself compared with classical fertility traits.

Although milk P4 levels have been widely accepted as valid indicators of fertility in dairy cows (Bulman and Lamming, 1978; Lamming and Darwash, 1998; Royal et al., 2002a), 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 labor intensive. They often entailed manually taking several milk samples per cow, analyzing, and recording the results. However, P4 level-measuring technology has advanced to allow in-line systems to instantly measure milk P4 level (Friggens et al., 2008). In these systems, milk is automatically sampled, P4 level is measured, and results are recorded. Hence, more animals can be sampled at a lower 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. Moreover, it will be important to know the correlation of in-line endocrine fertility traits with other traits included in the selection index before use in genetic improvement. To the best of our knowledge, no study has attempted to characterize heritable endocrine fertility traits in dairy cows from in-line milk P4 records. The aim of the current study was to define endocrine fertility traits from in-line milk progesterone records and estimate genetic parameters for these traits and their genetic correlations with classical fertility and milk production traits.

MATERIALS AND METHODS

In-line Milk Progesterone Records and Filtering Criteria

Milk P4 records ($n = 226,188$) collected from June 2009 through November 2013 were available for 2,514 Holstein-Friesian cows from 12 commercial dairy herds in the Netherlands. Milk sampling, measuring, and recording of P4 level was performed by the Herd Navigator (HN, DeLaval International, Tumba, Sweden). The HN is a management tool for dairy herds which samples and analyzes several milk constituents automatically during milking. One function of the HN is to monitor reproductive performance of cows by sampling and analyzing milk P4 level. This function is based on a bio-model that controls automatic in-line sampling, measuring, and recording of milk P4 level at varying intervals during a cow's estrus cycle (Friggens et al., 2008). Progesterone record files from each herd consisted of 4 variables: (1) herd number, (2) cow identification, (3) sampling date and time, and (4) sample value (P4 level in ng/mL). These records were accompanied by corresponding data files with information on calving dates, parity, and data files with insemination dates. Linking of P4 records to calving data resulted in 3,648 lactations of 2,340 cows with 213,877 P4 records. In total, 5% P4 records and 7% of cows were edited out after linking because their corresponding calving information was not available. Most cows were sampled from 27 to 176 DIM, with a mean sampling duration of 149 d. Milk P4 samples were taken on average every 2 d, with 25% of samples taken at an interval of less than 1 d and 75% at an interval of less than 4 d.

Two sets of filtering criteria (FC) were applied to P4 records: herd-level FC and lactation-level FC. At the herd level, 2 criteria were applied. The management tool is recent and most herds installed the tool at a certain date when not all sampled cows were at the start of their lactation; therefore, a lactation was retained if

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