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Genetic analysis of atypical progesterone profiles in Holstein-Friesian cows from experimental research herds

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ABSTRACT

The objective of this study was to quantify the genetic variation in normal and atypical progesterone profiles and investigate if this information could be useful in an improved genetic evaluation for fertility for dairy cows. The phenotypes derived from normal profiles included cycle length traits, including commencement of luteal activity (C-LA), interluteal interval, luteal phase length. and interovulatory interval. In total, 44,977 progesterone test-day records were available from 1,612 lactations on 1,122 primiparous and multiparous Holstein-Friesian cows from Ireland, the Netherlands, Sweden, and the United Kingdom. The atypical progesterone profiles studied were delayed cyclicity, prolonged luteal phase, and cessation of cyclicity. Variance components for the atypical progesterone profiles were estimated using a sire linear mixed model, whereas an animal linear mixed model was used to estimate variance components for the cycle length traits. Heritability was moderate for delayed cyclicity (0.24 ± 0.05) and C-LA (0.18 ± 0.04) but low for prolonged luteal phase (0.02 ± 0.04), luteal phase length (0.08 ± 0.05), interluteal interval (0.08 ± 0.14), and interovulatory interval (0.03 ± 0.04). No genetic variation was detected for cessation of cyclicity. Commencement of luteal activity, luteal phase length, and interovulatory interval were moderately to strongly genetically correlated with days from calving to first service (0.35 ± 0.12, 0.25 ± 0.14, and 0.76 ± 0.24, respectively). Delayed cyclicity and C-LA are traits that can be important in both genetic evaluations and management of fertility to detect (earlier) cows at risk of compromised fertility. Delayed cyclicity and C-LA were both strongly genetically correlated with milk yield in early lactation (0.57 ± 0.14 and 0.45 ± 0.09, respectively), which may imply deterioration in these traits with selection for greater milk yield without cognizance of other traits.

Key words: dairy cow, progesterone profile, fertility, genetic parameter

INTRODUCTION

Good reproductive performance is important for both economic and ethical reasons; for example, cow welfare and consumer preferences (Berglund, 2008). Reproductive performance affects milk production, breeding costs, and both voluntary and involuntary culling, all of which affect the profitability of a dairy herd (Plaizier et al., 1997). Female fertility in dairy cows has deteriorated for several decades, although this decline has now been halted in most populations (e.g., Philipsson, 2011). Suboptimal fertility has been reported worldwide in many dairy populations, particularly in Holstein-Friesian (**HF**) populations subjected to strong genetic selection for milk production (Rodriguez-Martinez et al., 2008). Reproductive and management factors contributing to the deterioration in the overall fertility phenotype may include poor return to cycling postpartum, poor expression of estrus, as well as inappropriate timing of insemination (Friggens and Chagunda, 2005; Crowe, 2008; Walsh et al., 2011). Dobson et al. (2008) documented that the percentage of animals that stand to be mounted and the duration of standing heat have decreased during the last 30 to 50 yr, whereas the number of silent heats has increased with increasing milk production.

An estrus cycle, which averages 21 d (range 18–24 d), is defined as the period initiated by an increase in progesterone (**P4**) above a threshold value and subsequently terminated with the next decrease below the threshold P4 value. The estrus cycle constitutes 3 phases: (1) the onset of the estrus cycle, (2) the follicular phase, and (3) the luteal phase (Friggens and Chagunda, 2005). To obtain a 1-yr calving interval, cow cyclicity should resume at least 60 d postpartum (Walsh et al., 2011). Early resumption of ovarian cyclicity postpartum facilitates a greater number of estrus

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cycles before insemination which, on average, increases the likelihood of subsequent conception (Darwash et al., 1997a). Relative to multiparous cows, primiparous cows have, on average, a greater incidence of delayed interval postpartum to first ovulation (Tanaka et al., 2008). Opsomer et al. (2000) documented a greater increase in delayed resumption of ovarian activity and more prolonged luteal phases in cows with clinical endometritis. Royal et al. (2002a) reported that cows with a genetically longer interval to the start of the first cycle; that is, commencement of luteal activity (**C-LA**), had a longer calving to first service interval (**CFS**) and a longer calving interval (**CInt**). A later start of ovulation and longer CFS and CInt will likely decrease the total milk production per cow and herd profitability.

Because of the low heritability of traditional fertility measurements (e.g., calving interval, nonreturn rates, conception rates) in dairy cows (Veerkamp et al., 1998), achieving rapid genetic gain for fertility can be difficult. A likely contributing factor to the low fertility traits is environmental effects (e.g., voluntary waiting period, poor heat detection) not properly accounted for in the statistical methods. Therefore, using more detailed phenotypes based on the biology of the animal itself, less prone to random environmental influences, may result in improved heritability estimates and, if genetically correlated with fertility traits in national breeding goals, could be used to increase genetic gain. Moreover, some of these detailed phenotypes may themselves have economic values.

Endocrine fertility traits, including P4-based fertility measures such as C-LA, can offer a more objective and accurate measurement of the ovarian activity in dairy cows (Petersson et al., 2006a) with 3 to 4 times higher heritability than traditional fertility measures (Petersson et al., 2006a; Berry et al., 2012). To obtain reliable measures of P4 profiles, frequent collection of individual cow P4 information is required. A limiting factor is the high cost of collecting P4 data from individual animals (Berry et al., 2012). Recently developed automated inline tools for progesterone sampling and analysis, such as Herd Navigator (DeLaval, Tumba, Sweden) can predict the reproductive status of a cow and can also handle vast amounts of data (Friggens and Chagunda, 2005). These tools may have the potential to be more cost effective for producers replacing the manual collecting of P4 information.

Deviations from a normal estrus cycle, termed atypical P4 profiles, have been associated with compromised fertility (Bulman and Wood, 1980; Royal et al., 2002a). Reduced pregnancy rate in dairy cows has been associated with repeated atypical P4 profiles (Royal et al., 2000). McCoy et al. (2006) showed that any atypical P4 profile delayed CFS and calving interval compared with normal P4 profiles. Finally, atypical P4 profiles were reported to be a major contributing factor to reduced conception rate (Darwash et al., 1998).

The incidence of atypical P4 profiles has increased in recent years which could be due to, for example, an increased proportion of delayed cyclicity (Royal et al., 2000; Petersson et al., 2006a). In earlier studies, Opsomer et al. (1999) reported that the most common atypical P4 profiles were delayed cyclicity and prolonged luteal phase, which together constituted 21.5% of all profiles and 88% of all atypical P4 profiles, whereas cessation of cyclicity was much less common. Factors reported to be associated with type of profile by Petersson et al. (2006a) include calving season, calving year group, parity, milk production, and BCS. Severe negative energy balance after calving in first-lactation cows can cause a later onset of the ovulation (Petersson et al., 2006b).

Few studies documented the genetic variation in P4-based measures of fertility such as C-LA (Royal et al., 2002b; Petersson et al., 2007; Berry et al., 2012), but to our knowledge there are no studies of the genetic variation in other measures describing normal and atypical P4 profiles, with the exception of Royal et al. (2002a), who reported a heritability estimate for prolonged luteal phase in the first postpartum estrus cycle. The objective of this study, therefore, was to estimate genetic parameters for measures of normal and atypical P4 profiles in HF cows and to investigate if this information could be useful to improve genetic evaluations for fertility.

MATERIALS AND METHODS

Animals

Data were collected from 4 research herds in 4 countries: (1) Jälla, Swedish University of Agricultural Sciences (Sweden) between 1987 and 2011; (2) Teagasc, Moorepark (Ireland) between 2001 and 2004; (3) Scotland's Rural College (United Kingdom; **UK**) between 2003 and 2005; and (4) Wageningen UR Livestock Research (the Netherlands) between 1991 and 1998, and 2003 and 2004. Detailed management information on each of the herds are provided elsewhere (Petersson et al., 2006a; Horan et al., 2005; Pollott and Coffey, 2008; and Veerkamp et al., 2000, respectively).

Across populations, phenotypic data were available from 1,618 lactations from 1,126 primiparous and multiparous HF cows. The cows were in their first to sixth lactation. Table 1 summarizes the information available from each of the 4 research herds.

Cows were coded as pregnant at first service if they had (1) no second service, (2) were not diagnosed as