

Genetic Parameters of Atypical Progesterone Profiles in Holstein-Friesian Cows using Data from Four European Experimental Research Herds

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ABSTRACT: Compromised fertility is a major problem in dairy herds. An objective way to classify estrus cycles is to analyze milk progesterone. The objective of this study was to estimate genetic parameters for measures of normal estrus cycles, delayed cyclicity, prolonged luteal phases and cessation of cyclicity in 1122 Holstein-Friesian cows with 1618 lactations. The heritability was moderate for delayed cyclicity (0.24) and commencement of luteal activity (0.23), but was low for prolonged luteal phase (0.02), luteal phase length (0.09) and inter-ovulatory interval (0.06). Little and no genetic variation was detected for inter-luteal interval and cessation of cyclicity, respectively. Moreover, delayed cyclicity and commencement of luteal activity were strongly genetically correlated with milk yield in early lactation (0.57 ± 0.14 and 0.63 ± 0.09 , respectively) which may imply a deterioration of these traits with selection for higher milk yield.

Keywords: dairy cow, progesterone profile, fertility, genetic parameters

Introduction

Because of the low heritability of traditional fertility measurements 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 animal itself, less prone to random environmental influences, may result in improved heritability estimates and, if genetically correlated to fertility traits in the 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 progesterone (P4) based fertility measures such as commencement of luteal activity (CLA), can offer a more objective and accurate measurement of the ovarian activity in dairy cows (Petersson et al. (2006)) with documented 3-4 times greater heritability than traditional fertility measures (Petersson et al. (2006); Berry et al. (2012)).

The objective of this study 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 the genetic evaluation of fertility. We quantified the genetic variation in atypical P4 profiles and compared with the genetic variation in the traditional fertility traits.

Materials and Methods

Animals. Data were collected from HF cows producing in four research herds: 1) A Swedish research herd, Swedish University of Agricultural Science (Sweden) between 1987 to 2011, 2) Teagasc, Moorepark (Ireland) between 2001 to 2004, 3) the Scottish Agricultural College (United Kingdom, UK) between 2003-2005, and 4) the Netherlands, data were collected from Wageningen UR Livestock Research between 1991 to 1998 and 2003 to 2004.

Milk sampling. In Sweden and the Netherlands milk samples for progesterone were collected and analyzed twice weekly. After ovarian cyclical activity was detected, sampling in the Swedish herd was reduced to once weekly until first AI. In the Netherlands P4 was sampled and analyzed twice weekly for the first 100 d of lactation. In both Ireland and the UK, milk was sampled and analyzed three times per week, until 26 d after first AI in Ireland and until the first 140 d in the lactation in UK. The progesterone concentration was determined in whole milk in all four populations. Data on milk yield and milk composition was used to calculate kilograms of ECM (Sjaunja et al. (1990)) produced from calving to first service.

Progesterone profiles as a measure of cyclicity. The generated P4 profiles were used to derive early P4 based fertility measurements. Progesterone concentrations were plotted using the SAS software (SAS Institute Inc. 9.2 (2012)) against days postpartum to first service to establish individual profiles. These were classified into four different categories based on a modified definition given by Opsomer et al. (2000) and Petersson et al.

(2006); 1) normal profile, 2) delayed cyclicity, 3) prolonged luteal phase, and 4) cessation of cyclicity. Each normal profile was divided into four phases named cycle length traits; CLA, inter-luteal interval (**ILI**), luteal phase length (**LPL**), and inter-ovulatory interval (**IOI**).

Records of calving data, services, lactations and pregnancy data were used to calculate traditional fertility measures such as calving to first service (**CFS**, n=1096).

Statistical analysis. A total of 1612 lactations from 1122 HF cows from Ireland (n = 168), the Netherlands (n = 582), Sweden (n = 224) and UK (n = 148) were analyzed for atypical P4 profiles and 1618 lactations from 1126 HF cows were analyzed for the cycle length traits. For the atypical P4 profiles the influence of various fixed and random effects of sire were determined with a mixed linear sire model, and for cycle length traits the influence of various fixed and random effects of the cow were determined with a mixed linear animal model. Variance components were estimated with the DMU-package (Madsen and Jensen (2007)). Genetic correlations were estimated between the atypical P4 profiles and CFS and kilograms of ECM from calving to first service with a sire model, and for cycle length traits with an animal model using the DMU-package (Madsen and Jensen (2007)). The models applied were:

$$y_{ijklm} = \mu + P_i + Y_j + S_k + \beta_l + e_{ijklm}$$

$$y_{ijklmn} = \mu + P_i + Y_j + S_k + \beta_l + pe_m + e_{ijklmn}$$

where y_{ijklmn} was the analyzed trait, μ was the overall mean, P_i parity within country, Y_j calving year within country, S_k calving season within country, β_l the cow in the animal model and the sire in the sire model. The permanent environment effect, pe_m , was between lactations of the cow in the sire model, and within lactations of the cow in the animal model. Pedigree information of each animal was tracked back at least four generations and approximately 6000 animals were included.

Results and Discussion

Population statistics. The prevalence of atypical P4 profiles in the present study (30.2%) was similar to an earlier study from Sweden (29.6%; Petersson et al. (2006)), but lower than reported for HF cows in Belgium (49%; Opsomer et al. (2000)) and France (46%; Cutullic et al. (2011)). The definition of atypical profiles nonetheless differs between studies. Moreover, the present study included data from four countries differing in

genetic ancestry, production systems, experimental treatments as well as different sampling years.

The proportion of atypical P4 profiles was explained by a higher prevalence of prolonged luteal phase (14.9%) than for delayed cyclicity (11%) and cessation of cyclicity (5.8%). This did not agree with Petersson et al. (2006) who showed a higher incidence of delayed cyclicity for the Swedish cows while Royal et al. (2000) reported that prolonged luteal phase was the most common atypical P4 profile in HF cows (16.8%), while for British Friesians this incidence was only 6.4%.

Mean CLA in the present study was 31.9 d (SD=17.5) and one to four days shorter than documented in other populations (Horan et al. (2005); Cutullic et al. (2011); Berry et al. (2012)), but longer than reported by Darwash et al. (1997) and Veerkamp et al. (2000) who reported a mean CLA of 28.7 d and 29.5 d, respectively. Mean LPL and ILI for all observations were 18.7 d (SD=10.4) and 5.0 d (SD=3.2), respectively. Mean IOI for normal profiles was 22.8 d (S.D=10.5) which is similar to i.e. the 22.3 d (Royal et al. (2000)) reported elsewhere.

Genetic parameters. To our knowledge, this is the first study to document genetic variation for atypical P4 profiles, with the exception of prolonged luteal phase in the first estrus cycle post-partum which Royal et al. (2002) stated to be 0.13 ± 0.06 in UK HF cows. Significant genetic variation was detected in the present study for delayed cyclicity which warrants further investigation to improve genetic evaluations for fertility in dairy cows. Since reproduction failure is one of the main reasons for culling (Ahlman et al. (2011)), P4 based fertility measures facilitates earlier and more direct physiological approaches for measuring reproduction performance, less influenced by preferential treatment. The earlier the producer can detect an atypical P4 profile the easier it may be to detect cows with compromised fertility and to treat them accordingly thereby possibly reducing calving interval and involuntary culling rates.

Heritability estimates (Table 1) were moderate for delayed cyclicity (0.24) and CLA (0.23), and ranged from 0.00 to 0.09 for prolonged luteal phase, cessation of cyclicity, ILI, LPL and IOI. Delayed cyclicity and CLA are very close traits and had similar heritability and relatively low SE. Both traits therefore expressed genetic variation and may be included in the breeding program for improved fertility. The heritability for CLA in the present study was greater than in earlier studies where heritability estimates of between 0.13 (Berry et al. (2012)) and 0.16 (Veerkamp et al. (2000));

Royal et al. (2002) and Petersson et al. (2007) were documented.

Table 1. Estimated heritability (h^2) and genetic correlation (SE in parenthesis) between the atypical P4 profiles, cycle length traits, and calving to first service and milk production

Trait	h^2	Genetic correlation	
		CFS ^{&}	ECM ^{&}
Delayed	0.24 (0.05)	-0.14 (0.19)	0.57 (0.14)
Prolonged	0.02 (0.04)	0.42 (0.56)	-0.60 (0.54)
CLA ^{&}	0.23 (0.08)	0.33 (0.11)	0.63 (0.09)
LPL ^{&}	0.09 (0.03)	0.42 (0.11)	0.10 (0.10)
IOI ^{&}	0.06 (0.09)	0.71 (0.16)	0.22 (0.15)

[&]CLA= commencement of luteal activity, LPL= luteal phase length, IOI=inter-ovulatory interval, CFS = Calving to first service, ECM=kg ECM from calving to first service.

Genetic correlations between type of atypical P4 profiles and type of estrus length traits with CFS and kilogram ECM from calving to first service are shown in Table 1. Standard errors of the estimates were generally large. The large standard errors are probably due to the relatively small dataset and/or the weak genetic links between the traits, as well as the relatively low heritability of the trait. As no genetic variation was detected for cessation of cyclicity and ILI they were not included in the estimation of genetic correlations.

High milk production in early lactation were strong genetically associated with delayed cyclicity profiles ($r=0.57\pm 0.14$) and CLA ($r=0.63\pm 0.09$) and moderate genetically associated with longer IOI ($r=0.22\pm 0.15$). A long CLA was genetically associated with a longer CFS and longer calving interval which is in agreement with results by Royal et al. (2002) and Berry et al. (2012). Moreover, CFS was genetically associated with a longer LPL, CLA and IOI (0.42 ± 0.11 , 0.33 ± 0.11 and 0.71 ± 0.16 , respectively). To reduce IOI and CFS, it is important that cows begin cycling earlier after calving.

Conclusion

The genetic variation in CLA and delayed cyclicity observed in the present study suggests both traits could be useful indicators for fertility. Moreover, these measurements were strongly genetically correlated with milk yield in early lactation which may imply deterioration in these traits if not considered in breeding goals that also include selection for higher milk yield.

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