

Genetic Correlations among Detailed Reproductive Traits, Traditional Reproductive Traits and Milk Production in Irish Dairy Cows

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ABSTRACT: The objectives of this study were to estimate genetic parameters of detailed reproductive traits and to estimate genetic correlations between these traits and both traditional reproductive traits and milk production. Detailed reproductive traits, derived from ultrasound examination of the reproductive tract, included resumed cyclicity, cystic structures, multiple ovulation, embryo loss, and uterine score (1 to 4 based on the uterine environment). Data were available on 208,962 records from 88,288 dairy cows. Variance components and genetic correlations were estimated using repeatability animal/sire models. Heritability estimates for the detailed reproductive traits ranged from 0.001 (embryo loss) to 0.07 (cyclicity). Genetic correlations among the detailed reproductive traits varied from 0.05 to 0.74, between the detailed reproductive traits and traditional reproductive traits from 0.04 to 0.89 and between the detailed reproductive traits and production from 0.01 to 0.49, suggesting higher milk production was associated with poorer reproductive performance.

Key words: correlation; production; fertility.

INTRODUCTION

The broadening of breeding goals to include generally low heritability functional traits has prompted the necessity to identify approaches to improve the accuracy of selection for these traits in order to retain producer confidence in using breeding goals to identify genetically elite animals. Although genomic selection is improving the accuracy of selection it does not explain all of the genetic variance, so therefore, there is still the requirement of higher heritability predictor traits. Novel reproductive traits that may be less influenced by management could be more heritable and assuming that sufficient genetic variation remains, genetic gain for reproductive performance could be improved. Detailed reproductive traits, such as commencement of luteal activity, have already been shown to be more heritable and be phenotypically and genetically correlated with traditional reproductive traits levels (Berry et al. (2014)). Furthermore, most national breeding goals include aggregate reproductive phenotypes such as calving interval which is a combination of the ability of a cow to return to cyclicity post-calving, undergo normal uterine involution, express estrus, and conceive and successfully establish pregnancy. The influence of such breeding strategies on the individual detailed components of reproductive performance (e.g., return to cyclicity, uterine involution) is unclear and therefore, selection for the individual reproductive components may result in more rapid genetic gain for overall reproductive performance.

Additionally, although the antagonistic genetic correlations between milk production and traditional reproductive traits have been well established (Berry et al. (2014)), few studies have attempted to relate genetic merit for milk production with detailed reproductive traits, especially using field data. The objectives of this study were to estimate genetic parameters of detailed reproductive traits derived from ultrasound examination of the reproductive tract of dairy cows and to estimate the genetic correlations among detailed reproductive traits, traditional reproductive traits and milk production.

MATERIALS AND METHODS

Data were available from Irish Cattle Breeding Federation (ICBF) database on ultrasound examination records of the reproductive tract, individual cow 305-day milk production, calving events and insemination data. Pedigree information, breed composition and cow parity information were also available.

Detailed reproductive traits. Five detailed reproductive traits were derived from the ultrasound examination of the reproductive tract. Resumption of cyclicity was defined by the presence (CYCLE=1) or absence (CYCLE=0) of a non-cystic corpus luteum (CL) on the ovaries at the time of examination. Multiple ovulation was defined as the presence of one CL (MULTI=0) or ≥ 2 CLs (MULTI=1) on one or both ovaries at the time of examination. Cystic structures were defined as the presence (CYST=1) or absence (CYST=0) of a cystic structure on the ovaries at time of examination. Embryo loss was assumed to have occurred if an embryo was deemed to be unviable at the time of examination or if a cow was determined pregnant at ultrasound examined but failed to calve at the estimated calving date \pm gestational age of embryo/fetus at examination days (LOSS=1); if a cow calved at the estimated calving date embryo loss was assumed not to have occurred (LOSS=0). If a subsequent calving date were not yet available (i.e. estimated calving dates in 2014) then embryo loss was set to missing. Uterine score was measured on a: 1 to 4 scale based on the tone of the uterine wall, the size of the lumen, and the quantity of fluid present in the uterus of non-pregnant cows. Uterine score (UTERUS) was defined as 1) little or no fluid (< 2 mm) with normal tone and normal lumen, 2) small quantity of fluid (2mm-5mm) with normal tone and slightly enlarged lumen, 3) large quantity of fluid (5mm-60mm) with moderately flaccid tone and enlarged lumen and 4) very large quantity of fluid (> 60 mm) with a flaccid tone and very enlarged lumen. Where subsequent calving interval were available, only records with calving intervals

between 300 and 600 days were retained; where no subsequent calving interval was available, only ultrasound records that occurred less than 600 days postpartum were retained.

Traditional reproductive traits. Six traditional reproductive traits were generated: 1) calving interval (CIV), 2) calving to first service interval (CFS), 3) pregnant to first service (PRFS), 4) number of inseminations (NS), 5) pregnant within 42 days of breeding season (PREG42) and 6) submission rate in the first 21 days of the breeding season (SR21). PREG42 was determined if a cow conceived in first 42 days of the herd's breeding season (PREG42=1) or not (PREG42=0). SR21 was defined as a cow presented for insemination (SR21=1) or not (SR21=0) in the first 21 day of the breeding season. Only CFS between 10 and 250 days were retained. Only CIV records between 300 and 600 days were retained; the exception was where an insemination occurred within 150 days postpartum, then CIV was then restricted to between 300 and 800 days

Milk production traits. Milk production data included individual cow milk (MILK), protein (PROT) and fat (FAT) 305-day yields and somatic cell count (SCC). Milk fat concentration (FAT%), protein concentration (PROT%) and Fat to protein ratio (FPR) were calculated. Somatic cell count was normalized to somatic cell score (SCS) by taking the natural log of SCC. Only lactations between 100 and 400 days in length were retained.

Data edits. Only animals with a known sire were retained. Contemporary groups of herd-year-season of calving for each trait were defined separately, grouping animals together, within herd, that have calving dates in close proximity. Herd-year-seasons that contained less than five animals were removed from the analysis. Parity 5 to 10 was grouped together as parity 5+ and parity greater than 10 were removed from the data. After edits, there were 111,420 ultrasound records from 50,354 cows across 75,524 lactations, 2,601,717 calving events from 1,136,022 cows across 2,574,363 lactations and 1,703,391 insemination records from 764,374 cows across 1,076,780 lactations. A random sample of contemporary groups within each of the traditional reproductive traits and milk production traits were selected to result in a dataset with approximately 60,000 records for each trait.

Data analysis. Variance components were estimated using repeatability animal models and genetic correlations were estimated using a series of bivariate repeatability sire models in ASREML (Gilmour et al. (2009)). Fixed effects included in all models were parity, heterosis and recombination loss coefficient of the dam and contemporary group; animal was included as a random effect. Stage of lactation (0-14, 15-39, 40-84, 85-149 and 150-300 days postpartum) was also included as a fixed effect for CYCLE, MULTI, CYST and UTERUS.

Results And Discussions

Heritability estimates. Heritability of the detailed reproductive traits (Table 1) was similar to the traditional reproductive traits (<0.05) with the exception of CYCLE that had a heritability of 0.07. However, this is lower than what has been previously reported for detailed reproductive

traits such as commencement of luteal activity (Royal et al. (2002)) and anovulation (Bamber et al. (2009)). The heritability of embryo loss in the present study was also lower (0.003) than previously reported heritability (Bamber et al. (2009)). The greater heritability estimates in other populations may be due data in these studies originating from controlled environments where less environmental variance may exist and accuracy of recording such as pedigree and environment effects may be superior. Despite the low heritability of the detailed reproductive traits there were considerable genetic standard deviations, for example 8% for cycling and 0.09 difference in uterine score. The heritability of the traditional reproductive traits in the present study ranged from 0.001 to 0.06 corroborating previously reported heritability estimates for traditional fertility traits (Berry et al. (2014)). Similarly, the heritability of the production traits in the present study (0.21 to 0.37) are in line with previously reported heritability estimates (Veerkamp et al. (2001)).

Table 1. Number of records (n), mean incidence (μ), heritability estimates (h^2 ; standard errors in parenthesis) repeatability (t; standard errors in parenthesis) and genetic standard deviation (σ_g) of the detailed reproductive traits.

	n	μ	σ_g	h^2	t
CYCLE	49,622	0.87	0.08	0.07 (0.009)	0.23 (0.008)
MULTI	23,846	0.10	0.04	0.03 (0.008)	0.05 (0.012)
LOSS	58,517	0.05	0.01	0.003 (0.002)	0.003 (0.002)
CYST	54,101	0.03	0.01	0.002 (0.002)	0.05 (0.007)
UTERUS	48,997	1.39	0.09	0.02 (0.005)	0.09 (0.008)

Genetic correlations. Genetic correlations among the detailed reproductive traits are in Table 2. The standard errors meant none of the correlations were different from zero with the exception that a greater likelihood of cycling was associated with an inferior uterine score. Early resumption of cyclicity is generally accepted as beneficial to reproductive performance, however, it has been shown that early ovulation has delayed uterine involution (Heppelmann et al. (2013)). Therefore, the association observed in the present study may reflect the increase in cycling and therefore, progesterone levels, inhibiting the ability of the uterus to eliminate bacteria and return to normal postpartum and may question any recommendation for selection for early post-partum cyclicity without also considering uterine health in the breeding goal.

Table 2. Genetic correlations (standard errors in parenthesis) among detailed reproductive traits

	LOSS	CYST	UTERUS
CYCLE	0.000(0.00)	0.12(0.36)	0.26(0.12)
MULTI	0.64(0.46)	0.47(0.40)	0.34(0.16)
LOSS		0.74(0.54)	0.00(0.00)
CYST			-0.05(0.40)

Table 3. Genetic correlations (standard errors in parenthesis) between detailed reproductive traits and traditional reproductive traits.

	CYCLE	MULTI	LOSS	CYST	UTERUS
CIV	-0.67 (0.45)	0.07 (0.27)	0.000 (0.00)	-0.12 (0.99)	0.19 (0.24)
CFS	-0.41 (0.15)	0.15 (0.23)	0.49 (0.27)	-0.60 (0.53)	-0.01 (0.18)
PRFS	0.46 (0.24)	0.06 (0.15)	-0.89 (0.34)	-0.94 (0.62)	-0.11 (0.26)
NS	-0.49 (0.22)	0.27 (0.24)	0.33 (0.46)	0.99 (0.64)	0.33 (0.23)
PREG42	0.59 (0.24)	-0.12 (0.17)	-0.64 (0.43)	0.13 (0.74)	-0.25 (0.23)
SR21	0.89 (0.14)	0.32 (0.21)	-0.99 (0.54)	0.60 (0.82)	-0.01 (0.21)

Genetic correlations between the detailed reproductive traits and traditional reproductive traits are in Table 3. CYCLE was negatively correlated with the CIV, CFS and NS and positively correlated with PREG42, PRFS and SR indicating that, despite the unfavorable associated previously alluded to between CYCLE and UTERUS, genetic predisposition to CYCLE is favorably associated with traditional reproductive performance such as shorter CIV and improved pregnancy rates. These correlations are similar to previous reports of shorter CIV in animals with earlier commencement of luteal activity post-partum (Royal et al. 2002). LOSS was positively correlated with CFS and negatively correlated with PREG42, PRFS and SR indicating that embryo loss had an unfavorably associated with reproductive performance, increasing the interval to first service and reducing pregnancy rates and submission rates. With the exception of UTERUS and NS, MULTI and UTERUS were not genetically correlated with the traditional reproductive traits.

The genetic correlations between the detailed reproductive traits and milk production (Table 4) are similar to reported correlations between traditional reproductive traits and the milk production (Berry et al. (2014)). Antagonistic (i.e., negative) correlations existed between CYCLE and milk, fat and protein yield while positive correlations existed with milk fat and protein percent. Increased milk and fat yield was also associated with an increase in the occurrence of multiple ovulations. This indicates cows of superior genetic merit for milk production had superior genetic merit for MULTI and inferior genetic merit for CYCLE. Royal et al. (2002) reported a negative correlation between commencement of luteal activity and milk production showing further evidence that as milk production increases there is a unfavorable impact on fertility, especially cyclicity.

Table 4. Genetic correlations (standard errors in parenthesis) between detailed reproductive traits and milk production.

	CYCLE	MULTI	LOSS	CYST	UTERUS
MILK	-0.35 (0.12)	0.25 (0.18)	0.18 (0.31)	-0.07 (0.28)	-0.03 (0.15)
FAT	-0.26 (0.12)	0.23 (0.19)	0.10 (0.30)	-0.19 (0.29)	-0.10 (0.15)
PROT	-0.17 (0.13)	0.05 (0.19)	-0.49 (0.28)	-0.30 (0.29)	-0.02 (0.15)
FAT%	0.21 (0.10)	0.01 (0.17)	-0.15 (0.28)	-0.08 (0.20)	-0.05 (0.15)
PROT%	0.14 (0.10)	-0.16 (0.17)	-0.49 (0.28)	-0.10 (0.26)	0.06 (0.15)
FPR	0.06 (0.33)	0.07 (1.23)	-0.00 (0.00)	-0.21 (0.70)	-0.34 (0.24)
SCS	-0.49 (0.18)	0.14 (0.26)	0.59 (0.33)	0.44 (0.36)	-0.04 (0.21)

Conclusion

Heritability estimates for the detailed reproductive traits were low. The heritability for CYCLE was slightly greater than traditional reproductive traits, however, was still lower than previously reported heritability estimates for detailed reproductive traits for cyclicity. Both CYCLE and LOSS were moderately correlated with the traditional reproductive traits. Furthermore, moderate antagonistic correlations between the detailed reproductive traits and milk production are comparable to the correlations that exist between traditional reproductive traits and milk production.

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