Genetic Evaluation of Beef Fertility in Ireland

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1. Introduction

Genetic evaluation for female fertility, and inclusion of female fertility in breeding objectives is, by now, the norm in most dairy populations (Miglior *et al.*, 2005). Genetic evaluation for fertility in Irish dairy cattle is changing in 2011 with the following modifications:

1) number of parities included in the evaluation is increasing from 3 to 5 parities
2) the predictor traits of body condition score, angularity, foot angle and udder depth are being replaced by calving to first service interval and number of services
3) genetic parameters are being updated since last estimated in 2005 (Pool *et al.*, 2005)
4) Length of contemporary groups changed from 182 days to 70 days
5) Adjustment for heterogeneity of variances based on herd-year.

Genetic evaluations for beef performance as well as both dystocia and perintal mortality are currently undertaken in Ireland in a combined dairy and beef genetic evaluation. Despite the pertinent fertility traits in dairying and beef being identical in Ireland, a combined dairy and beef genetic evaluation for fertility is not sensible for several reasons:

1) herd-size in beef herds is, on average, smaller than herd size in dairy herds, which has implications for contemporary group size
2) predictor traits available (e.g., type traits and farmer scored traits) differ between dairy and beef populations
3) the associations among fertility traits and between predictor traits and fertility traits are likely to differ between the two production systems.

Therefore, the objective here was to put in place a national genetic evaluation system for female fertility for beef cattle in Ireland. Evaluation of male fertility in Ireland (Berry *et al.*, 2011) will still be across both dairy and beef cattle.

2. Materials and Methods

2.1 Data

Calving dates from 1,632,941 cows totaling 5,127,232 calving events between the years 2002 and 2010 were available from 45,480 beef herds. Fertility traits defined were age at first calving (AFC), calving interval (CI), survival to next lactation (SURV), and calving in the first 42 days of the calving season (CALV42), a trait especially important in seasonal calving herds. CALV42 was defined separately in primiparae and pluriparae and is identical to that defined in dairying (Berry *et al.*, 2007) although it is not actually used in the dairy genetic evaluation. The start of the calving season was defined as the first calving date, within herd, when five cows calved within the subsequent 14 days. The end of the calving season was defined as the last calving, within herd, which was not followed by a subsequent calving within 21 days. Only calving seasons between 35 and 200 days in length were retained and each calving season had to have at least 5 and 10 calving events for primiparae and pluriparae, respectively. Survival was defined as whether or not a cow survived from lactation *i* to lactation *i*+1. A cow was assumed not to have survived lactation *i* if she did not have a calving record for lactation *i*+1 and the difference between the cow's last recorded calving date was >800 days from the last recorded calving date for that herd or if the cow was slaughtered or died on farm within 400 days of calving in parity *i*. Insemination data was not considered in the genetic evaluation of beef fertility because of the low usage of AI in beef herds.

Unlike dairy genetic evaluations for fertility, where contemporary group for pluriparae traits are defined as herd-year-season of calving within each parity, in the beef genetic evaluations contemporary groups for CI, SURV and CALV42 in pluriparae were defined across parities. Contemporary group for AFC and CALV42 in primiparae were based on the herd-year-season of service resulting in the subsequent calving. The algorithm used to define herd-year-season was identical to that used in dairying (Berry *et al.*, 2007). The number of records included in the estimation of genetic parameters are detailed in Table 1.

Information was also available on 20 linear type traits, animal price and live-weight (McHugh *et al.*, 2011a), carcass traits (Pabiou *et al.*, 2011) and dystocia. In 2008 the Irish Department of Agriculture launched a new voluntary participation scheme for Irish beef herds called the Animal Welfare, Recording and Breeding Scheme for Suckler Herds. A component of the scheme involved the farmer subjectively recording docility on a scale of 1 (docile) to 5 (aggressive) at weaning; animal quality at weaning, assessed subjectively by the farmer, was also scored on a scale of 1 (very poor) to 5 (very good). Animals were only scored once during their lifetime. Both traits were considered as predictors of fertility.

2.2 Estimation of genetic parameters

Variance components for all reproduction traits were estimated using animal models in ASREML (Gilmour *et al.*, 2009). Calving interval, CALV42 in pluriparae and survival were all analysed using a repeatability animal model. Covariance components among the reproduction traits themselves and between the reproduction traits and the other performance traits were estimated using a series of bivariate sire linear mixed models. The exceptions were calving difficulty and maternal weaning weight where a sire-maternal grandsire model were fitted. Among the pluriparae fertility traits where multiple records per animal existed, a permanent environmental covariance was also estimated. Fixed effects included in the model for all reproduction traits were contemporary group, a general heterosis term and a general recombination loss term; parity was included in the model for the analysis of CI, CALV42 and SURV.

With the exception of farmer scored animal quality and docility, the fixed effects included in the models for the other traits have been described elsewhere (Crowley *et al.*, 2010; McHugh *et al.*, 2011a; Pabiou *et al.*, 2011). Contemporary group(s) was included in the model as a fixed effect for all traits and gender was included when more than one gender was included in the analysis but not implicitly assumed within the definition of contemporary group. Age at the time of the relevant event (e.g., slaughter), heterosis and recombination loss were also included in all models, where significant ($P<0.05$) as continuous variables with non-linear associations were also tested; interactions between age and gender were also investigated where gender was also included in the model as a main effect. Where significant ($P<0.05$) parity of the dam was also included in the model. For cow BW and price, fate post-calving and days since calving were included as class effects; for cow carcass traits days since last calving was included in the model.

The pedigree of each animal was traced back to the base population and founder animals were allocated to breed groups (n=11) based on breed. The pedigree file consisted of 1,015,250 individuals.

3. Results and Discussion

Cows calved for the first time at over 30 months of age with a mean calving interval thereafter of 384 days. With the exception of the moderate heritability for age at first calving of 0.31, the heritability of the reproduction traits were ≤0.06 (Table 1).

Irrespective of whether evaluated by trained assessors on live animals or based on mechanical grading of carcass conformation, greater genetic merit for muscularity was generally associated with reduced CALV42 and longer CI (Table2). This is substantiated by the genetic correlations of both price and weanling quality with reproductive performance (Table 2 & 3) since moderate to strong genetic correlations have previously been reported between increased muscularity and greater animal price (McHugh *et al.*, 2011b) as well as there being a very likely strong contribution of muscularity to a farmer's perception of weanling quality. All of these traits, with the possible exception of weanling quality, are relatively independent of live-weight; animal price is independent of animal live-weight since live-weight was included as a covariate in the statistical model. Therefore, because of the genetic correlation between live-weight and reproductive performance, the unfavorable genetic effect of selection for muscularity on reproductive performance can be exacerbated further by simultaneously selecting for increased live-weight or growth rate.

Few beef studies have attempted to quantify the genetic associations between calving difficulty and reproductive performance. Roughsedge *et al.* (2005) reported genetic correlations between both direct and maternal calving difficulty and AFC, CI and lifespan. Although the standard errors of the correlations were large (i.e., sometimes up to 1) and the correlations sometimes differed by breed there was a general tendency for a negative or close to zero genetic correlation (-0.23 to 0.03) between AFC and direct calving difficulty. With the exception of the Simmental breed, the genetic correlation between maternal calving difficulty and AFC was positive (0.07 to 0.12). These are directly opposite to the correlations observed in the present study although the standard errors reported by Roughsedge *et al.* (2005) do not imply that their estimates were different to those in the present study. The genetic correlations reported by Roughsedge *et al.* (2005) between maternal calving difficulty and CI were positive or close to zero (-0.05 to 0.38) agreeing with the positive genetic correlation between maternal calving difficulty and CI in the present study (0.32; Table 3) as well as the positive genetic correlation of 0.49 between calving difficulty and CI in Asturianna de los Valles beef cattle (Gutiérrez *et al.,* 2007).

4. Conclusions

Consistent with dairy cattle in Ireland (Berry *et al.,* 2007), low heritability estimates exist for reproduction traits in beef cows. Several potential predictor traits, genetic correlated with reproductive performance most of which are already routinely available at no extra cost, were identified. Selection for terminal traits may have undesirable consequences for female fertility.

5. References

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Table 1. Number of records (N), mean and standard deviation, and heritability (h^2) and repeatability (r^2) estimates for the reproduction traits.

Trait	N	Mean	h^2	r^2
Age at first calving (days)	64380	936	0.31 (0.02)	
CALV42 - Heifers (%)	40671	0.91	0.06 (0.01)	
CALV42 - Cows (%)	106419	0.82	0.008 (0.003)	0.06 (0.005)
Calving interval (days)	101864	384	0.02 (0.004)	0.05 (0.007)
Survival (%)	104117	0.85	0.02 (0.003)	0.02 (0.003)

Table 2. Genetic correlations (standard errors in parenthesis) between live-weight, price, and carcass traits and reproduction.

		CALV42			
Trait	AFC	Heifers	Cows	CI	Survival
Cow live-weight	-0.05 (0.12)	-0.34 (0.21)	-0.13 (0.26)	0.54 (0.19)	-0.33 (0.20)
Cow price	0.09 (0.12)	0.05 (0.21)	0.27 (0.23)	-0.02 (0.19)	-0.15 (0.19)
Cow carcass weight	0.11 (0.06)	-0.04 (0.12)	-0.13 (0.16)	0.34 (0.12)	0.26 (0.12)
Cow carcass conform.	0.06 (0.05)	0.00 (0.10)	-0.18 (0.14)	0.19 (0.11)	0.08 (0.11)
Cow carcass fatness	0.18 (0.07)	0.07 (0.14)	0.37 (0.17)	-0.44 (0.13)	0.18 (0.14)
Weaning weight (Dir)	-0.08 (0.06)	-0.16 (0.11)	-0.34 (0.16)	0.39 (0.10)	0.46 (0.09)
Weaning weight (mat)	0.35 (0.07)	0.41 (0.13)	0.20 (0.15)	-0.21 (0.09)	0.01 (0.09)
Weaning price	-0.05 (0.08)	0.16 (0.14)	-0.86 (0.13)	0.64 (0.09)	0.26 (0.11)
Post-weaning weight	0.09 (0.07)	0.21 (0.14)	-0.21 (0.18)	0.70 (0.07)	0.44 (0.09)
Post-weaning price	0.01 (0.06)	-0.37 (0.11)	-0.70 (0.12)	0.50 (0.08)	0.51 (0.07)
Progeny carcass weight	-0.07 (0.05)	0.04 (0.10)	-0.05 (0.15)	0.22 (0.11)	0.26 (0.12)
Progeny carc. conform.	0.01 (0.05)	0.04 (0.09)	-0.15 (0.15)	0.29 (0.11)	0.26 (0.11)
Progeny carcass fat	0.06 (0.05)	0.17 (0.12)	0.14 (0.16)	-0.31 (0.12)	0.06 (0.13)

Table 3. Genetic correlations (standard errors in parenthesis) with reproduction for calving dystocia, and both docility and quality of the weanling subjectively assessed by the farmer.

	Dystocia			
Trait	Direct effect	Maternal effect	Weanling docility	Weanling quality
Age at first calving	0.28 (0.06)	-0.22 (0.08)	0.46 (0.07)	-0.33 (0.08)
CALV42 -Heifers	-0.20 (0.11)	0.13 (0.14)	-0.51 (0.13)	-0.44 (0.13)
CALV42 - Cows	-0.80 (0.15)	0.18 (0.13)	-0.45 (0.19)	-0.54 (0.21)
Calving interval	0.18 (0.13)	0.32 (0.12)	0.16 (0.15)	0.44 (0.15)
Survival	-0.06 (0.13)	-0.65 (0.11)	-0.15 (0.17)	0.28 (0.17)