Estimation of lifespan breeding values in the UK and their relationship with health and fertility traits

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Abstract

In the UK BVs for herd life are currently predicted from a bivariate BLUP analysis of lifespan, measured in lactations, and a phenotypic index of the type traits most closely related to it. The type traits included in the index are foot angle (rg=0.22), fore udder attachment (rg=0.63), udder depth (rg=0.14) and teat length (rg=0.44). Lifespan PTAs are combined with production PTAs in the UK's Profitable Lifetime Index (£PLI= -0.03*PTAMilk+0.6*PTAFat+4.04*PTAProt+38*PTALifespan). The economic value of lifespan (£38 per lactation) was calculated using a dynamic programming model by improving survival from lactation 1 to 4 by 1%, through a reduction in involuntary culling. Most of the benefit comes from a higher average level of production, as the herd age structure is more mature, and from a lower replacement cost. Selection using £PLI is expected to have an annual economic benefit of 5.9% over selection on production only. Including lifespan in the index may already be beneficial in terms of slowing down the rate of increase in incidence of health disorders and decline in fertility when selection is for production alone, so further analysis concentrated on the associations between lifespan and more direct measures of health and fertility. Calving interval was considered a measure of fertility, as calving dates are generally well recorded in most herds. Body condition score is recorded as part of the linear type classification scheme operated by Holstein UK and Ireland. Genetic correlations were inferred from the regression of daughter performance on sire PTAs for lifespan and were equal to -0.44 with calving interval, -0.11 with condition score, -0.22 with mastitis and -0.27 with lactation average SCC records. Thus cows with lower SCC, lower condition score and shorter calving intervals last longer in the herd. Future development of £PLI will include traits such as fertility and mastitis, either measured directly or using correlated traits, such as linear type scores, condition scores etc.

1. Introduction

Lifespan (LS) is defined here as the number of lactations a cow completes, or is expected to complete prior to culling. LS is either the number of lactations completed where a culling date is known, or a prediction based on average survival probabilities from lactation to lactation (Brotherstone et al., 1997). Breeding values (BVs) for herd life are currently predicted from a bivariate BLUP analysis of LS, measured in lactations, and a phenotypic index of the type traits most closely related to it (udder depth, teat length, fore udder attachment and foot angle). Most voluntary culling is assumed to be for production, with the decision being made on a within herd basis. As we are interested in lifespan free from any association with production, BVs are calculated after adjusting for deviations from within herd mean milk yield. A full explanation of the methdology to predict LS breeding values is given in Brotherstone et al. (1998). Young bulls' PTAs will be based mainly on information from their daughters' linear type traits and their ancestors' genetic merit for survival. As survival records accumulate on a bull's daughters the emphasis will gradually shift to these in his LS PTA. A bull with a PTA of +0.5 for LS will have daughters that survive on average a half lactation more than the national average, which is currently 3.6 lactations. PTAs for LS range between -0.4 and +0.6.

The Animal Data Centre (ADC) currently provide genetic evaluations for production traits, LS and somatic cell count (SCC). Two indexes are also available: PIN which is a production only index and £PLI (Profitable Lifetime Index). In PIN Predicted Transmitting Abilities (PTAs) of milk, fat and protein have the following economic values: -0.03, 0.6, 4.04. The weightings take into account the expected higher value of protein compared to fat (relative values of 1.5:1 are assumed), the extra feed costs resulting from increased production, the extra transport and cooling costs of high volume, low solids milk, and the cost of leasing extra quota to match the higher production of daughters of high genetic merit bulls. £PLI includes milk, fat and protein weighted by the same economic weights in addition to PTAs for LS.

The economic value of LS (£38 per lactation) was calculated using a dynamic programming model by improving survival from lactation 1 to 4 by 1%, through a reduction in involuntary culling. Most of the benefit comes from a higher average level of production, as the herd age structure is more mature, and from a lower replacement cost (Stott, 1994). Selection on £PLI is expected to lead to about 5.9% extra response in margins compared to selection on PIN value, which is based on production alone.

Including LS in the index may already be beneficial in terms of slowing down the rate of increase in incidence of health disorders and decline in fertility when selection is for production alone. Here, we aim to investigate the relationship between LS and some direct measures of health and fertility.

1.1 Calving interval

In the UK, several milk recording organisations (MROs) record insemination dates as part of their standard service. The final insemination date provides a date for the start of the dry period and a due to calve date. Some MROs also provide an additional optional service for monitoring within herd fertility which requires all service dates to be recorded. Therefore national UK data consists of a mixture of all insemination dates, some insemination dates and just the insemination date leading to the pregnancy. Incomplete service information makes measures calculated using service dates unreliable.

Calving interval (CI) defined as the number of elapsed days between two consecutive calvings is more likely to be recorded accurately, as all herds need to record calving dates. We expect therefore that of all the measures of fertility available on a large number of animals (which is a pre-requisite for national genetic evaluations), calving interval is the least likely to be affected by data quality issues.

1.2 Somatic Cell Count (SCC)

Genetic evaluations of SCC are currently available in the UK, details of parameter estimates are given in Mrode et al. (1998). SCC is likely to be included in future versions of £PLI as a predictor of mastitis. There are problems with including SCC in its own right as its economic value is dependent on bulk tank means (Veerkamp et al., 1998).

1.3 Condition Score (CS)

CS is used to obtain a quick and simple assesment of body fat cover. Successive measures of condition score (CS) may be a useful indicator of energy balance as the shortfall in energy obtained from food is believed to come from mobilisation of body tissue reserves (Veerkamp, 1998).

2. Material and methods

Available data comprised phenotypic CI, mastitis and LS records and PTAs for LS, SCC and CS.

CI data were obtained from Holstein UK and Ireland (HUKI; formerly HFS) from 1996 to 1998. Calving dates were recorded by HUKI on:

a) receiving a complete lactation record from the milk recording organisation.

b) receiving an incomplete lactation record (if a cows moved herd, died, culled etc).

c) a calf born or registered .

Mastitis records for first lactation heifers were from UK Livestock Services from 1994 to 1998. The same data editing procedure was used as by Pryce et al. (1997). Briefly, UKLS record a disease incidence date and an identification code for that disease. Herd-years were selected where at least one occurrence of any disease had been recorded. The mastitis data was coded as 0/1 (where 1 was at least one occurrence of mastitis within a lactation).

Phenotypic LS records were obtained from the ADC, as were PTAs for both LS and SCC (see Mrode et al., 1998, for details of national evaluations for SCC). PTAs for CS were from an analysis by Jones et al., 1999, which modelled the shape of the CS curve at both the phenotypic and the genetic level with a cubic polynomial. CS PTAs averaged over the lactation (CSA) and CS PTAs in month one of lactation (CS1) were used in the regression analysis.

Genetic correlations were inferred from regressions of daughter phenotypic records for CI and mastitis on sire PTAs for LS, and from the regression of daughter phenotypic records for LS on sire PTAs for SCC and CS. Sire PTAs with a minimum reliability of 65% for all traits were used.

All statistical models included herd-year and month of calving as fixed effects, calving age as a covariate.

The genetic correlation (rg) was calculated using the regression estimate b and the genetic standard deviation (SDa) for each trait (using estimates from Brotherstone et al., 1997; Pryce et al., 1997; .Mrode et al., 1998; Jones et al., 1999).

Expected responses to selection using PIN and £PLI were calculated using published genetic parameter estimates (from the UK) and correlations with LS estimated in the present study. Economic values are those currently used in PIN and £PLI. It was assumed that each sire would have 75 daughters.

3. Results

Regression coefficients and genetic correlations inferred from these estimates are presented in Table 1. Genetic correlations with LS ranged between -0.11 (CSA) and -0.44 (CI). Genetic correlations with mastitis and SCC were -0.22 and -0.27 respectively.

Table 1. Number of daughter records (n_x), number of sires (n_s), regression coefficients ($b_{LS,x}$) and genetic correlation estimates with LS

Trait (x)	N_x	n_s	b	$rg_{LS,x}$
CI	16886	517	-7.1	-0.44
CSA	100259	150	-0.09	-0.11
CS1	100259	150	-0.20	-0.23
Mastitis	9649	75	-0.02	-0.22
SCC	144153	310	-1.38	-0.27

Table 2 gives the consequences of one standard deviation of selection on both indices. Selection for PIN (production only) leads to an increase in CI, mastitis and SCC and a decrease in CS. LS remains unchanged, as expected. Selection for £PLI results in an increase in LS, but CI, mastitis and SCC would continue to increase, albeit at a slower rate than selection using PIN.

Table 2. Consequences of one standard deviation of selection on PIN and £PLI in units of measurement

	PIN	£PLI
Milk	234	217
Fat	10.5	9.8
Protein	7.6	7.1
LS	0	0.12
CI	1.4	0.8
CS	-0.024	-0.025
Mastitis	0.008	0.005
SCC	0.02	-0.002

4. Discussion

Estimating genetic correlations through genetic regressions of phenotypic records on sire PTAs was used in preference to estimating genetic correlations using animal model REML for several reasons. PTAs for LS are estimated using data from the national population and thus include information from many more animals than were available in the data sets used here, PTAs were also required to have a minimum reliability of 0.65. Phenotypic LS records include the number of lactations a cow completes (a qualifying lactation is 200 days) or is expected to complete, thus, a cow that fails to complete her second lactation would have a LS score of 1 and a missing CI. CI and LS are confounded in this instance. Moreover as genetic evaluations are available for LS and in turn the index £PLI, it is of value to investigate the consequences of selection on this index on other traits of importance.

Genetic correlations of LS with CI, Mastitis and SCC were moderate in size (>-0.2) and in the expected direction. Cows with shorter calving intervals, lower SCCs and fewer incidences of mastitis are more likely to last longer in the herd. Thus selection for LS is likely to be beneficial in terms of cow health and fertility. The genetic correlation between LS and average CS was -0.11, the direction is such that thinner cows are expected to live longer (although the relationship is not strong). It is possible that there may be some preferential treatment for daughters of dairy-like bulls to be kept longer and at the phenotypic level farmers may keep thinner cows in the belief that they will yield more than fatter cows, or because a higher sale price could be achieved for fatter cows.

There are relatively few published studies on the genetic relationship between survivability and health and fertility traits. Rogers et al. (1998) used sire PTAs of productive life (PL) from the USA and PTAs for SCC and mastitis from Denmark and Sweden to investigate the genetic relationship between udder health and survivability. The genetic correlation between PTAs for productive life from the USA and SCC from Denmark and Sweden (adjusted for reliabilities) were 0.06 and 0.36 respectively (higher values represent lower SCC). Genetic correlations between PL and clinical mastitis in Denmark and Sweden were 0.28 and 0.56 respectively. Again, the positive sign is because high PTAs for mastitis are desirable. These results, are similar to ours, although we found a stronger relationship between LS and SCC. Rogers et al. (1998) also reported that quadratic regressions of clinical mastitis from Denmark and from Sweden were not significant indicating that the genetic relationship between clinical mastitis and PL is linear.

The expected responses to selection presented in Table 2, show that selection for production only (PIN) leads to an increase in calving interval and an increase in mastitis and SCC. Selection for £PLI would result in a modest reduction in genetic progress in production, but the decline in health and fertility would continue at a slower rate than when selection was for PIN. There may be additional benefit from expanding the breeding goal to include more of the costs of production directly. Mastitis, predicted using SCC is likely to be included in £PLI shortly and fertility is an area in which we are devoting our current research efforts.

A limitation with CI as a measure of fertility is that it is only available after a cow has calved for a second time, which makes it of limited use in progeny testing schemes where information is required from either the early part of lactation or preferably using information from juveniles. Of greater concern is that CI is only available for the most fertile animals, as only they will actually calve for a second time. Data imputation techniques to predict a cow's CI from information from relatives, the cows own production level etc. should in part resolve this problem, but more research is needed into techniques to do this.

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References

Brotherstone, S., McManus, C.M. and Hill, W.G. (1990). Estimation of genetic parameters for linear type traits in Holstein Friesian dairy cattle. *Livestock Production Science*, 26: 177-192.

Brotherstone, S., Veerkamp, R.F. and Hill, W.G. (1997). Genetic parameters for a simple predictor of the LS of Holstein-Friesian dairy cattle and its relationship to production. *Animal Science* 65: 31-37.

Brotherstone, S., Veerkamp, R.F. and Hill, W.G. (1998). Predicting breeding values for herdlife of Holstein Friesian dairy cattle from LS and type. *Animal Science* 67: 405-412.

Jones, H.E., White, I.M.S. and Brotherstone, S. (1999). Genetic evaluation of Holstein Friesian sires for daughter condition score changes using a random regression model. *Animal Science* 68: 467-476.

Groeneveld, E. (1996). REML VCE a multivariate multi model restricted maximum likelihood (co)variance component estimation package version 3.2 User's guide.

Mrode, R.A., Swanson, G.J.T. and Winters, M.S. (1998). Genetic parameters and evaluations for somatic cell counts and its relationship with production. *Animal Science* 66: 567-576.

Pryce, J.E., Veerkamp, R.F. Thompson, R., Hill, W.G. and Simm, G. (1997). Genetic aspects of common health disorders and measures of fertility in Holstein Friesian dairy cattle. *Animal Science*. 65: 353-360.

Rogers, G.W., Banos, G., Sander Nielsen, U., Philipsson, J. (1998) Genetic correlations among somatic cell scores, productive life, and type traits from the United States and udder health measures from Denmark and Sweden. *Journal of Dairy Science* 81: 1445-1453.

Stott, A.W. (1994) The advantage of longevity in the dairy cow. *Journal of Agricultural Economics* 45: 113-122.

Veerkamp, R F (1998). Selection for economic efficiency in dairy cattle using information on liveweight and feed intake: a review. *Journal of Dairy Science* 81: 1109-1119.

Veerkamp, R.F. and Brotherstone, S. (1997). Genetic correlations between linear type traits, food intake, live weight and condition score in Holstein Friesian dairy cattle. *Animal Science* 64: 385-392.

Veerkamp, R.F., Stott, A. W., Hill, W.G. and Brotherstone, S (1998). The economic value of somatic cell count payment schemes for UK dairy cattle breeding programmes. *Animal Science* 66: 293-298.