Dairy cattle breeding objectives combining production and non-production traits for pasture based systems in Ireland

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SUMMARY

The objectives of this study were: 1) to estimate genetic (co) variances among body condition score, body weight, milk production, linear type traits and fertility, and 2) to investigate the presence of genotype by environment interactions for milk production, body condition score, and body weight, in Irish grass based seasonal calving herds.

Genetic parameters were estimated from a potential 8928 primiparous and multiparous Holstein-Friesian cows over two years (1999 and 2000). Heritability estimates for body condition score (BCS) and body weight (BW) were found to be moderate to high; estimates ranged from 0.27 to 0.51 for BCS, and from 0.39 to 0.61 for BW. Heritability estimates for BCS change and BW change at different stages of lactation were all less than 0.11. Heritability for the linear type traits varied from 0.11 to 0.43. Phenotypic and genetic correlations between BCS and BW at the same stage of lactation were all close to 0.50 indicating that approximately 25% of the genetic and phenotypic variation in BW may be attributed to differences in BCS. Genetic correlations between BCS and milk yield tended to be negative (-0.14 to –0.51) and genetic correlations between BW and milk yield were close to zero (-0.07 to 0.09). However, the genetic correlations between BW adjusted for differences in BCS were positive (0.15 to 0.39). Genetic correlations between BCS and the fertility traits investigated were all favourable, indicating that cows with a superior genetic merit for BCS are on average likely to be served sooner, receive less services and have higher pregnancy rates. The genetic correlations between linear type traits and milk yield indicate that selection for milk production has resulted in taller, deeper cows that tend to be more angular and have less body condition. Genetically these cows are predisposed to inferior reproductive efficiency. Moderate genetic correlations were found between some of the linear type traits investigated and somatic cell count.

A comparison of BCS, as recorded by Teagasc personnel (scale 1-5) and Holstein herd-book classifiers (scale 1-9) indicated consistency between the two sources. Phenotypic and genetic correlations of 0.54 and 0.86, respectively, were observed between the two measurement sources on the same animals.

Genotype by environment interactions, were found for milk yield across different silage quality environments, and for BCS across different herd-year milk yield, concentrate, grazing severity and silage quality environments.
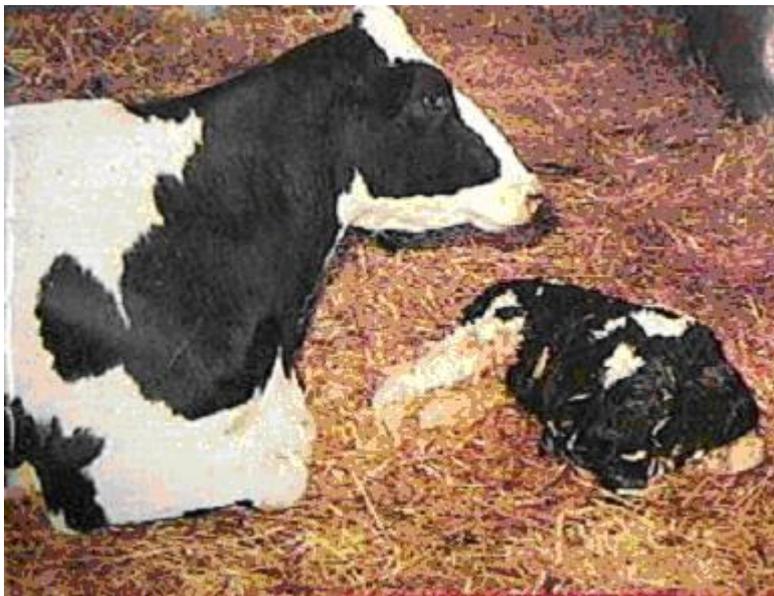
INTRODUCTION

Infertility in dairy cattle represents a problem of increasing importance world-wide (Hoekstra et al., 1994; Pryce and Veerkamp, 2001). Survival from first to second lactation in Irish milk recorded dairy herds has dropped from 80% in 1993 to 73% in 1999, while calving interval has extended from 389 to 395 days over the same period (Irish Cattle Breeding Statistics, 2001). This reduction in reproductive efficiency has been largely attributed to the aggressive breeding programs within the Holstein-Friesian population for increased milk production. The decline in fertility has resulted in more diversified breeding goals being established, with many countries now incorporating functional traits that reflect fertility/survivability as well as production traits. Although progress towards increased milk production may be reduced overall economic efficiency is increased.

The low heritability of traits like fertility, coupled with the long time interval required to collect sufficient data for genetic evaluation, means that there is interest to identify traits that may act as genetic indicators of improved fertility. Indicator traits should be 1) easily measurable, 2) measurable early in life, and 3) possess a moderate to strong genetic correlation with fertility. Potentially interesting indicator traits for fertility include body condition score (BCS), body weight (BW) and linear type traits. Several researchers have reported moderate heritability estimates for BCS and BW (Pryce *et al.*, 2001; Veerkamp *et al.*, 2001) and have documented moderate genetic correlations between fertility with BCS and BW (Moore *et al.*, 1992; Veerkamp *et al.*, 2000). Most of these estimates are based on single measurements on a small number of animals at different stages of lactation. Less is known about the genetics behind BCS or BW change during lactation, or how best to incorporate traits such as BCS or BW into a selection index. The existence of significant genotype by environment interactions may indicate the necessity of more sophisticated models/methods of estimating breeding values to account for this phenomenon.

The objectives of this study were: 1) to estimate genetic (co) variances among body condition score, body weight, milk production, linear type traits and fertility, and 2) to investigate the presence of genotype by environment interactions for milk production, body condition score, and body weight, in Irish grass based seasonal calving herds. The results may indicate the suitability of BCS, BW and/or other linear type traits as potential indicator traits of fertility.

MATERIALS AND METHODS

Data

The data comprised 80 spring-calving dairy herds (76 commercial and 4 research), with a potential 8,928 primiparous and multiparous Holstein-Friesian cows available for inclusion in data analysis. The data were recorded during 1999 and 2000; 4,402 cows had records in both years of the study. Herd size ranged from 30 to 240 cows. The key factors in herd selection were: (1) spring-calving, (2) high standard of recording, (3) at least the sire and maternal grand sire known for the majority of cows in the herd, (4) participation in A4 milk recording (once every 4 weeks). Each herd participated in the Dairy Management Information System (Dairy-MIS) (Crosse, 1986). The Dairy Management Information System is a recorder-based computerised system collecting detailed stock, farm inputs, production, and reproduction information on a monthly basis.

Pedigree information

Pedigree information was accumulated for all cows on the study. In total 48% were herd-book-registered with Holstein UK and Ireland (HUKI). For 92% of these cows it was possible to obtain four generations of ancestry on the paternal side, whereas 66% of cows had four generations of ancestry on the maternal side. For those cows not registered with HUKI, sire and maternal grand sire were obtained from the Dairy-MIS. For these herds the paternal ancestry and maternal grand sire ancestry was provided by HUKI to the same level as for the pedigree cows. The proportion of North American Holstein-Friesian genetics (NAHF) for each sire/maternal grand sire contained in the data set was also provided by HUKI. The proportion of NAHF for the individual cows in the study was calculated as 0.5*sire plus 0.25*maternal grand sire, assuming that maternal grand dams had zero NAHF. The latter was assumed because the proportion of NAHF was unknown for most maternal grand-dams. The proportion of NAHF was available for all sires in the data set, however, it was only available for 50% of maternal grand sires and was assumed to be zero as these bulls were available pre-1980 and were not present in the data set - (personal communication Matt Winters HUKI).

Body condition score, body weight and milk production

Trained Teagasc personnel visited the farms up to nine times annually. Visits were carried out at two and a half, to four weekly intervals, with visits being more frequent in early lactation. During each visit all cows in

the herd were recorded for BCS and BW. Body weight was recorded electronically, using portable weighing scales and the Winweigh software package. The scales were calibrated weekly against permanent scales in Moorepark Research Centre and were calibrated again with known weights on arrival at each farm. Body condition score, recorded simultaneously using the Winweigh software package, was on a scale of 1 (thin) to 5 (fat) with increments of 0.25 (Lowman *et al.*, 1976). Only records between calving and 350 days post partum were included in the analysis for BCS and BW.

Milk production records for each cow were obtained from the Irish Dairy Recording Co-operative. A single somatic cell count (**SCC**) figure per lactation was derived as the natural logarithm of the arithmetic mean of monthly SCC test day records. No restriction was placed on the number of SCC tests per lactation so as to avoid any selection bias against cows culled for high SCC in early lactation. The resulting distribution of the logarithm of SCC was normal.

Linear Type traits

As part of the study all primiparous cows were assessed for linear type traits in both years of the study. Five different classifiers from Holstein UK and Ireland (**HUKI**) scored 17 traits on each cow and two supplementary traits (temperament and ease of milking) were supplied to the classifier by the farmer. In this study 'type traits' refer to these 19 traits. Each trait was classified on a scale of one to nine, inclusive, according to biological extremes. Before analysing this data differences between classifiers in their range of scoring was accounted for by adjusting each of the 17 type traits by the ratio of the standard deviation of each field officer to the mean standard deviation of all field officers (Brotherstone, 1994); neither temperament nor ease of milking were re-scaled. In total 2,256 primiparous cows were assessed between 51 and 223 days in milk.

Fertility

Five fertility variables similar to those used internationally (Grosshans et al., 1997; Veerkamp et al., 2001) were calculated: interval to first service (**IFS**), interval from first service to conception (**FSCO**), pregnancy rate to first service (**PRFS**), number of services per cow (**NS**), and pregnant 63 days after the start of the breeding season (**PR63**). In total 8,315 cows had identified first service records. The start of the breeding season for each herd was defined as the first service date recorded in that herd; start of breeding dates were available for both years of the study. All cows in the study were determined to be pregnant or not by rectal palpation of the entire herd at least 56 days after the end of the defined breeding season. No cognisance of further losses beyond this point were taken.

Environmental descriptors

For the investigation of genotype by environment interactions only 66 herds that had detailed management information were included in the analysis. Four environmental variables pertaining to the nutritional management of each herd in 1999 and 2000 were investigated. These were herd-year mean milk yield, concentrate supplementation level, grazing severity and silage quality. Herd-year mean milk yields were calculated as the mean lactation milk yield for each herd in both years of the study; herd-year mean milk yield varied from 3,362 to 5,904 kg. The average level of concentrate supplementation offered per cow in each herd for both years of the study was obtained from the DairyMIS system; concentrate feeding level varied from 163 to 1,700 kg per annum. Grazing measurements were recorded once per week, up to 15 times in total, during the breeding season on 61 of the 66 farms. The measurements were post-grazing sward surface height using a sward stick and pre-grazing DM yield as described by O'Donovon et al.

(2002). At each visit 20 post-grazing sward surface height measurements were taken at random from the most recently grazed paddock and the average height was calculated. Pre-grazing DM yield was estimated for the paddock next in the grazing rotation. The paddock in which the pre-grazing yield was estimated was grazed within 12-24 hours of the visit. The weekly estimates of post-grazing sward surface height and pre-grazing DM yield were subsequently averaged to give a single post-grazing sward surface height record per herd per year and a single pre-grazing DM yield record per herd per year. Subsequently, a single grazing severity figure per herd-year was calculated by adjusting the post-grazing sward surface height of each herd-year for differences in the pre-grazing DM yield for each herd-year using a simple linear regression; the residuals of the regression were subsequently taken to indicate the grazing severity practised in each herd-year. Silage samples were taken from each farm to determine the quality of forage offered during the winters prior to the 1999 and 2000 grazing seasons. Each silage clamp on each farm was sampled at 40 to 100 days after ensiling using a silage core to take a 3 cm diameter sample from the top to the bottom of the clamp, at three points. Prior to chemical analysis the silage samples were dried at 40 ºC for 48 hours in an oven with forced air circulation. The subsequent oven dried samples were analysed for in-vitro dry matter digestibility. Silage UFL values ranged from 0.66 to 0.89 UFLs/kg DM.

Genetic parameter estimation

The genetic parameters of interest were the heritability of individual traits and the genetic correlations between traits. The observed performance of an animal (it's phenotypic value) for any given trait is a function of its genetic value for that trait together with the environmental effect and random noise. The heritability (h^2) for a trait represents the contribution of the genetic variation as a proportion of the total phenotypic variation for the trait. Its value ranges from 0 to 1. A higher heritability indicates that a larger proportion of the differences observed on farms is due to the differences in genetic background of the animals. A genetic correlation illustrates the genetic relationship between the true breeding values for two traits. Values range from –1 to +1. Genetic coefficients of variation (CVg, calculated as the genetic standard deviation divided by the mean multiplied by 100) give an indication of the genetic variation present for a trait. The genetic coefficients of variation allow comparisons, in terms of genetic variation, to be drawn between traits that are measured on different scales.

Genetic parameters were estimated by Restricted Maximum Likelihood using both ASREML (Gilmour et al., 2003) and the variance component estimation suite (Neumaier and Groeneveld, 1998). An animal model was used in all analyses. Fixed effects in the models included herd-year-month of calving, parity, NAHF, days in milk, days conceived, calving to the start of the breeding season and calving to the end of the breeding season, where appropriate. As well as a random animal effect, a random permanent environmental effect was fitted both within and between years where appropriate.

Smoothing spline curves with four knot points were fitted to milk yield, BCS and BW data for each lactation to model the effect of days in milk (DIM). This facilitated the extrapolation of test day records of interest and, for example, cumulative lactation milk yield for periods of interest. Body condition score and BW at days 5, 60, 120, 180 and BCS at day 240 were also extrapolated in this fashion.

Multivariate (MT) analyses were performed between BCS, BW and milk yield at the different DIM which were extrapolated from the smoothing splines. Body condition score, BW and milk yield at different DIM were treated as separate traits. Additive genetic, permanent environmental and residual (co)variances within and between traits were estimated; heritability estimates were subsequently calculated from the additive genetic, permanent environmental and residual variances. The MT analyses were subsequently extended to included a fertility trait. This facilitated the estimation of genetic correlations between BCS, BW and milk yield at different DIM with fertility.

Multivariate analyses were also performed on the raw data for BCS, BW and milk yield without any pre-adjustment using splines. All lactation records with a valid spring-calving date were included in the analyses. A total of 81,313, 91,937 and 100,458 records were included in the analyses for BCS, BW and milk yield, respectively. The interval from calving to 350 days post partum was divided into seven blocks, each fifty days in length; for milk yield, calving to 300 days post partum was divided into six blocks. Each block was subsequently treated as a different trait and included in the MT analyses; residual covariances between blocks were set to zero. Each MT analysis was further extended to include a fertility trait; this allowed the estimation of the genetic correlations between BCS, BW and milk yield at different stages of lactation with each of the fertility traits.

Multivariate analyses were also performed to determine the relationship between the various type traits with themselves and subsequently with milk yield, BW, fertility and SCC. Firstly, three separate multivariate analyses were undertaken within the related linear type traits themselves – the body related traits (stature, chest width, body depth, angularity, rump angle, rump width and body condition score), the udder related traits (fore udder attachment, rear udder height, udder support, teat placement side view, teat placement

rear view and teat length), and the feet and miscellaneous traits (rear legs side view, foot angle, locomotion, temperament and ease of milking). Subsequently, correlations between each group of related type traits with all other traits were estimated singly by including the trait of interest in the multivariate analysis and the additive genetic and residual covariance matrices recalculated.

Covariance functions provide an alternative of treating longitudinal traits (e.g., BCS, BW and milk yield) measured at different stages of lactation as separate traits with a correlation structure between them. The use of covariance functions avoids over simplification (repeatability model) or over parameterisation (multivariate analysis). Covariance functions can readily be estimated from random regression models (RRM).

A random regression model (RRM) was applied to all records from cows with a valid spring-calving date to estimate a covariance function for BCS, BW and milk yield across DIM. The model was similar to that previously used in the MT analyses except that the random additive genetic component and permanent environmental component within years were both modeled using a set of orthogonal polynomials across DIM. A random permanent environmental effect across years was also included in the model of analysis. The order of polynomial fitted was consistently the same for both the additive genetic and permanent environment components. The criteria set down to obtain the most parsimonious covariance function were: 1) the likelihood test of two nested models were compared; 2) the eigenvalues of the additive genetic and permanent environmental covariance matrix were calculated; 3) the estimated variances from the RRM were visually compared to the MT analyses on the raw data; and, 4) the residual variances estimated for each order increase in the RRM were compared against each other. Similar to the MT analyses on the raw data, the residual variances were estimated within the seven blocks (six blocks for milk yield), each fifty days in length, from day 0 to day 350 of lactation (day 0 to day 300 for milk yield). Residual covariances between blocks were assumed to be zero and are therefore likely to have entered the additive genetic and permanent environmental components.

The RRM was extended to include a fertility trait. However, it was only possible to estimate the between-year permanent environmental variance for the fertility trait while both the within-year and the between-year permanent environmental variance was estimable for the longitudinal trait in the MT and RRM analyses. To overcome this, the residual variance of the fertility trait was set to zero, thus the residual variance of the fertility trait entered the within-year permanent environmental component; this facilitated a within-year permanent environmental correlation structure between the fertility trait and the longitudinal trait. Between-years permanent environmental (co) variances were also estimated.

The existence of GxE interactions was investigated across different herd-year milk production, concentrate feeding levels, grazing severity and silage quality environments. The additive genetic variance across environments was modelled using a random regression. Each environmental parameter was divided as evenly as possible into five blocks. Residual and permanent environmental variances were estimated within block; residual correlations between blocks were set to zero and the permanent environmental correlations between blocks were set to unity. A MT analyses was also used to investigate the existence of GxE interactions across different herd-year milk production environments; genetic (co)variances were estimated across three groups, split as evenly as possible, based on herd-year milk production. Residual correlations between groups were again set to zero and the permanent environmental correlations between groups were set to unity.

Selection index methodology was used to determine the accuracy of selection on various breeding objectives with alternative selection indexes across different sized half-sib daughter progeny groups. The accuracy of the breeding value for PR63 was calculated over different sized half-sib daughter groups, with three alternative selection indexes: (a) PR63; (b) average BCS; and (c) PR63 + average BCS. A second analysis was performed whereby the breeding objective was BW and the alternative selection indexes investigated included either BW or a range of linear type traits.

RESULTS

Heritability estimates
The heritability for BCS ranged from 0.27 (240 DIM) to 0.46 (50-100 DIM) when estimated using multivariate analyses; heritabilities estimated from a cubic random regression model varied from 0.39 (0 DIM) to 0.51(112 DIM). Body weight tended to exhibit higher heritabilities; heritability estimates for BW at different stages of lactation varied from 0.39 (0 DIM) to 0.61 (294 DIM) across all models used. Heritability estimates for BCS change (0.02 to 0.10) and BW change (0.03 to 0.09) were lower than those reported for the levels of BCS and BW. Heritabilities estimated for milk test-day yield using either multivariate or random regression models varied from 0.19 to 0.26 and 0.26 to 0.44, respectively. For cumulative milk yield heritability estimates varied from 0.26 to 0.29. Cumulative fat and protein yield expressed higher

heritabilities (0.44 and 0.32, respectively). The heritability estimates obtained for the body related type traits were largest (0.24 to 0.43). Heritability estimates for the udder type traits varied from 0.11 to 0.38 while heritability estimates for the feet and legs related type traits varied from 0.14 to 0.19. Heritability estimates of the type trait scored by the individual farmers (ease of milking and temperament) were lowest (0.11 to 0.12). These results suggest that the accuracy of selection for BCS, BW and/or type traits will be similar to that for milk yield over the same progeny group sizes. Heritability estimates for the fertility traits were all less than 0.03; The heritability for SCC in this study varied from 0.06 to 0.08.

First service conception rate and PRFS both showed a coefficient of genetic variation of greater than 10%; the coefficient of variation for BCS, BW and milk production were all less than 7% with the exception of cumulative fat yield (9.1%). Of the type traits analysed the largest genetic variation existed for the body related type traits; the coefficient of genetic variation for the body related type traits were all greater than 14%.

Genetic correlations
Among body condition score, body weight and linear type traits

Genetic correlations between BCS values obtained at different stages of lactation varied from 0.66 to 1.00. Similarly, genetic correlations between BW at different stages of lactation varied from 0.84 to 1.00. However, there was a significant change in genetic variance for both traits within lactations. These results suggest that the use of repeated observations for either of these traits will have little effect on increasing the accuracy of selection and thus imply that a repeatability model with lactation stage as a fixed effect might describe the data adequately. Adjustment for heterogeneous variances is advised when breeding value estimation for BCS/BW is based on field data recorded at different stages of lactation, which is likely under Irish circumstances. The phenotypic correlations between BCS and BW at the same stage of lactation ranged from 0.40 to 0.55, while the genetic correlations ranged from 0.35 to 0.50. Therefore around 16-30% of the phenotypic variation and 12-25% of the genetic variation in BW is due to differences in BCS, and vice versa.

A strong negative genetic correlation existed between angularity and BCS (scale of 1-9) (-0.84) while a strong positive genetic correlation existed between chest width and BCS (0.77). Genetic correlations between stature, chest width, body depth, rump angle, rump width, and BCS (scale 1-9) with average BW were all moderate to strongly positive (Table 1) indicating that taller, wider, deeper and fatter cows tended to be heavier. Genetic correlations between BW and the udder and leg related type traits were all near zero with the exception of fore udder attachment (0.40) and rear legs, side view (0.21). The moderate to strong genetic correlations between most of the body type traits and average BW is expected given that the body type traits reflect an element of size of the animal. Ahlborn and Dempfle (1992) reported a genetic correlation between stature and BW of 0.92. The accuracy of selection on BW with a progeny group size of 50 half-sib daughters was 0.79 when the index included stature, chest width and rump width; this compares to an accuracy of 0.90 when the index included body weight alone also with a progeny group size of 50. Hence, the inclusion of BW within a selection objective for Ireland may be achievable through the use of linear type traits as predictors of BW.

The phenotypic and genetic correlations between BCS measured by Teagasc personnel (scale 1-5) with BCS measured by the Holstein UK and Ireland classifiers (scale 1-9) were 0.54 and 0.86, respectively. Hence, BCS assessed by the two different sources on the two different scales are genetically very similar traits.

Traits	MILK	BW	IFS	NS	PRFS	PR63	SCC
Stature	0.42	0.63	-0.33	0.67	-0.64	-0.44	-0.09
	(0.050)	(0.015)	(0.075)	(0.106)	(0.200)	(0.100)	(0.078)
Chest width	0.24	0.80	-0.51	0.45	-0.44	-0.06	-0.39

Table 1. Genetic correlations (SE in parenthesis) between the linear type traits with milk yield, BW, IFS,

	(0.044)	(0.026)	(0.104)	(0.080)	(0.112)	(0.077)	(0.135)
Body depth	0.36	0.68	-0.17	0.76	-0.75	-0.49	-0.06
	(0.050)	(0.024)	(0.086)	(0.094)	(0.157)	(0.101)	(0.111)
Angularity	0.48	-0.10	0.37	0.26	-0.24	-0.48	0.33
	(0.045)	(0.035)	(0.083)	(0.170)	(0.215)	(0.107)	(0.075)
Rump angle	0.24	0.29	-0.83	-0.31	0.31	0.42	-0.42
	(0.081)	(0.037)	(0.079)	(0.171)	(0.170)	(0.102)	(0.104)
Rump width	0.46	0.74	-0.53	0.80	-0.80	-0.22	-0.40
	(0.058)	(0.040)	(0.104)	(0.107)	(0.122)	(0.122)	(0.103)
Body condition score	-0.153	0.50	-0.53	0.13	-0.14	0.35	-0.57
	(0.055)	(0.024)	(0.109)	(0.116)	(0.122)	(0.056)	(0.099)
Fore udder attachment	0.32	0.40	-0.52	0.36	-0.38	0.17	-0.253
	(0.133)	(0.075)	(0.119)	(0.079)	(0.090)	(0.066)	(0.082)
Rear udder attachment	0.48	0.22	0.36	0.433	-0.29	-0.26	-0.158
	(0.086)	(0.087)	(0.146)	(0.060)	(0.104)	(0.073)	(0.086)
Udder support	0.36	0.12	0.02	0.225	-0.15	0.12	0.45
	(0.108)	(0.114)	(0.126)	(0.085)	(0.154)	(0.113)	(0.110)
Udder depth	-0.05	0.10	-0.57	0.236	-0.31	0.20	-0.07
	(0.090)	(0.061)	(0.058)	(0.059)	(0.103)	(0.046)	(0.057)
Teat placement, rear view	0.51	-0.01	0.38	-0.285	0.30	0.08	-0.28
	(0.066)	(0.056)	(0.107)	(0.033)	(0.067)	(0.056)	(0.041)
Teat placement, side view	0.36	-0.05	0.57	-0.303	0.45	-0.12	0.06

	(0.044)	(0.035)	(0.091)	(0.045)	(0.087)	(0.060)	(0.055)
Teat length	-0.14	-0.23	0.28	0.019	0.30	0.03	0.31
	(0.064)	(0.085)	(0.126)	(0.083)	(0.060)	(0.096)	(0.075)
Rear leg, side view	0.21	0.21	-0.86	0.05	0.36	0.02	0.67
	(0.060)	(0.063)	(0.113)	(0.088)	(0.123)	(0.075)	(0.102)
Foot angle	0.08	-0.02	0.84	0.01	-0.38	-0.30	-0.53
	(0.068)	(0.077)	(0.060)	(0.095)	(0.138)	(0.072)	(0.127)
Locomotion	0.21	0.04	0.71	0.42	-0.32	0.16	-0.28
	(0.093)	(0.077)	(0.132)	(0.093)	(0.259)	(0.133)	(0.180)
Temperament	0.44	-0.02	0.74	0.23	-0.35	0.08	-0.42
	(0.077)	(0.086)	(0.176)	(0.178)	(0.281)	(0.095)	(0.178)
Ease of milking	0.69	0.36	-0.18	0.36	-0.16	-0.15	0.24
	(0.060)	(0.104)	(0.248)	(0.149)	(0.212)	(0.098)	(0.170)

Body condition score, body weight, linear type traits and milk yield

Genetic correlations between BCS and milk yield imply that genetic selection for milk yield alone will reduce BCS. A biological interpretation of this antagonistic correlation is the apparent relationship of BCS with energy balance and tissue mobilization. A reduction in genetic merit for BCS as a consequence of selection for higher milk yields may have deleterious effects on the subsequent fertility of the animal. Also, because body tissue reserves act as a biological buffer for milk synthesis, a continued reduction in genetic merit for BCS may in time become the major limiting factor in response to selection for increased milk production. Genetic correlations between BW and milk production were all close to zero (-0.07 to 0.09). However, after adjustment of BW for differences in BCS all genetic correlations became positive (0.15 to 0.39) and are in agreement with previous genetic correlations between milk production and body "size".

The genetic correlations between all type traits (except BCS, udder depth and teat length) with milk yield were all positive (Table 1). This likely reflects past emphasis on "good type" within Holstein breeding programs. The outcome is taller, wider, deeper cows which tend to be more angular and have less body condition. Genetic improvement for increased milk production has been in tandem with improved udder score; tighter fore udder attachments and shallower udders. The moderate genetic correlation between milk production and teat position indicates that selection on milk yield is likely to result in teats that are closer together from the rear view, yet further away from a side view, the latter possibly reflecting udder capacity. However, close teats may have practical implications for efficient milking routine, especially with robotic milking systems.

Body condition score, body weight, linear type traits and fertility

Genetic correlations between BCS and fertility traits were all favourable. This indicates that cows with a superior genetic merit for BCS had shorter IFS, required a lower NS, had higher PRFS and had a greater probability of being pregnant 63 days after the start of breeding. Changes in the genetic correlations between BCS at different stages of lactation with fertility were minimal. Genetic correlations estimated with the cubic RRM between BCS with IFS ranged from –0.47 to –0.31 and between BCS with NS ranged from –0.34 to -0.17. Genetic correlations estimated with the RRM between BCS and PR63 ranged from 0.15 to 0.40 (Figure 1), while the genetic correlations between BCS and PRFS ranged from 0.15 to 0.38 This indicates that using BCS as a predictor of fertility is relatively insensitive to when during the lactation BCS is assessed and may be attributable to the strong genetic correlation between BCS at different stages of lactation.
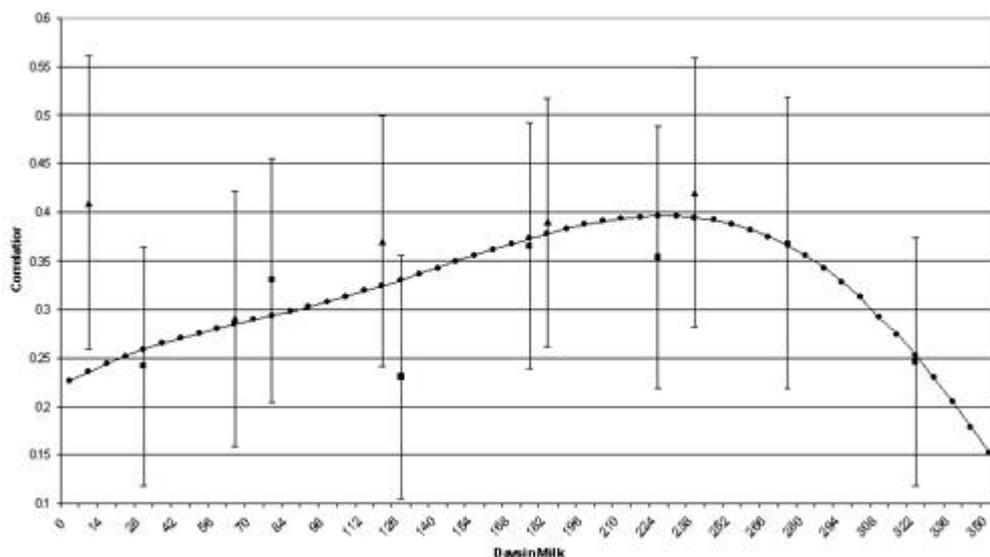

Figure 1. *Genetic correlations between body condition score and pregnant 63 days after the start of breeding estimated using either a smoothing spline (▲), a multivariate analysis of the raw data (■) or a random regression model (●). Also included in the vertical bars is one standard error of the correlations.*

Figure 2 illustrates the advantage of including BCS in a selection index when the breeding objective is PR63. The inclusion of only PR63 in the selection index served as a better predictor (based on the

accuracy of the selection index as a representation of the selection goal) of PR63 in the selection objective than the inclusion of only average BCS in the index when the number of daughters with records was greater than 18 daughters per sire. However, a combined index of PR63 and BCS consistently produced a more accurate estimate of the breeding value for PR63 up to 100 daughters per sire than an index with only PR63.
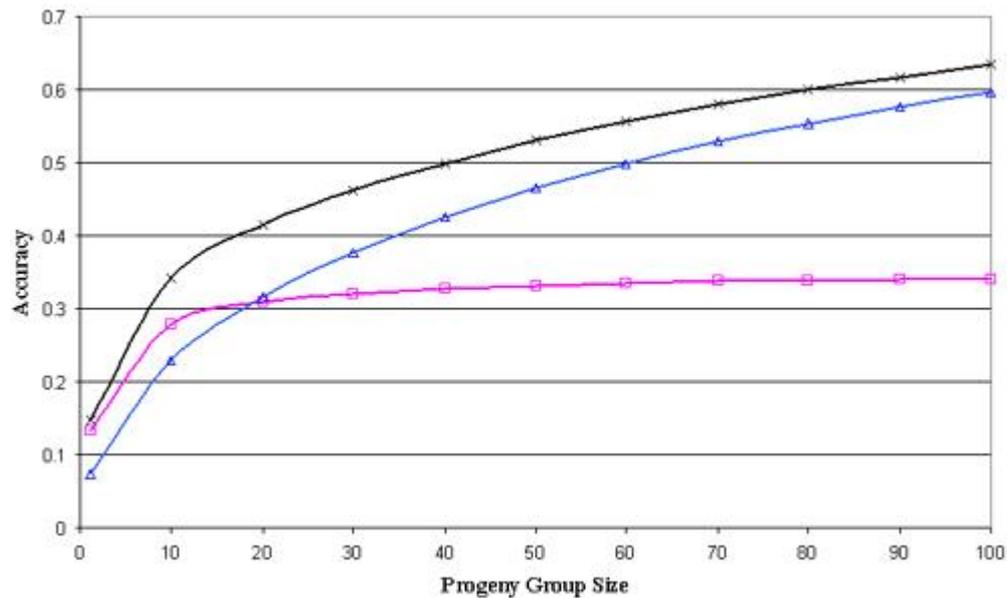

Figure 2. *Accuracy of breeding value of PR63 as a function of progeny group size for daughters that have records for either PR63 (△), BCS (□), or PR63 + BCS (x).*

The genetic correlations between BW and a range of fertility traits indicated that although cows with higher BW had shorter IFS, they required more services, had reduced PRFS and reduced PR63. The magnitude of the correlation estimated with the cubic RRM ranged from –0.69 to –0.51 between BW with IFS and from 0.34 to 0.38 between BW with NS. Genetic correlations estimated with the RRM between BW and PR63 varied from –0.22 to –0.12 (Figure 3) while correlations between BW and PRFS ranged from –0.52 to -0.45.
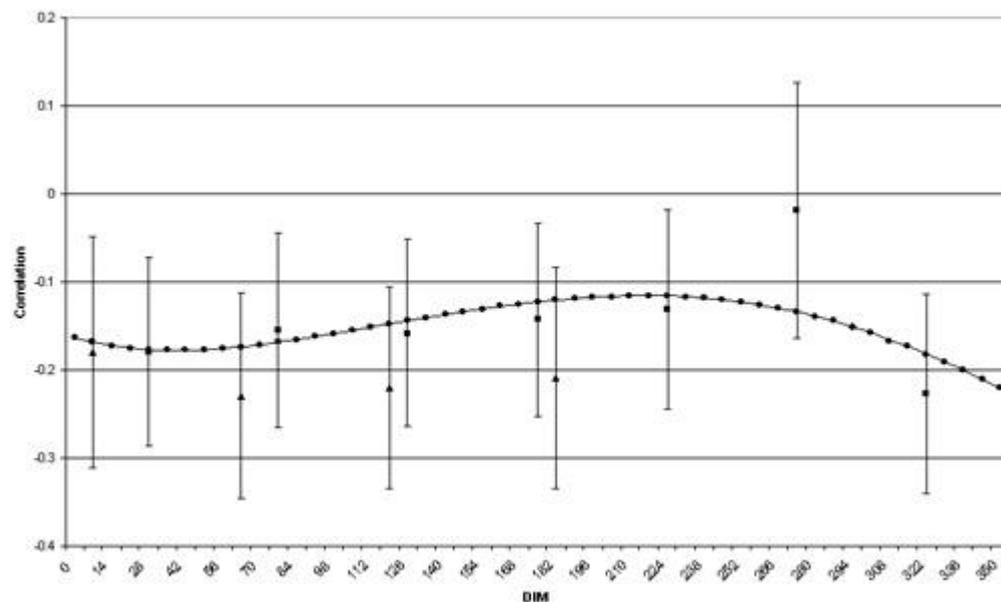

Figure 3. *Genetic correlations between body weight and pregnant 63 days after the start of breeding estimated using either a smoothing spline (▲), a multivariate analysis of the raw data (■) or a random regression model (●). Also included in the vertical bars is one standard error of the correlations.*

In agreement with most international studies the genetic correlations between milk yield and fertility were generally antagonistic. There was a tendency for the correlations between milk yield and IFS to be slightly favourable (negative) but never significantly different from zero. The pattern of change in correlations over the lactation suggests that selection for higher peak milk yields will have a more pronounced deleterious effect on pregnancy rates in the current lactation than selection for higher milk yield in late lactation. This may be attributed to an exacerbation of negative energy balance in early lactation due to the inability of feed intake to provide the increased energy required for each incremental increase in milk yield, consequently resulting in poorer fertility. The magnitude of the correlation estimated with the cubic RRM ranged from 0.08 to 0.35 between milk yield with IFS and from 0.28 to 0.58 between milk yield with NS. Genetic correlations estimated with the RRM between milk yield and PR63 varied from –0.30 to 0.09; the correlations were all negative after day seven of lactation. Genetic correlations between milk yield and PRFS ranged from –0.70 to -0.24 (Figure 4). Based on the genetic parameters in the present study selection for an increase of 10 kg in milk yield at day 112 compared to day 259 of lactation will intensify the depression in PRFS by an additional three percentage units. Therefore it appears that to minimise the effect of genetic selection for increased lactation milk yield on fertility within the same lactation, greater emphasis should be placed on milk yield in late lactation rather than increases in milk yield in early lactation i.e. increase persistency, with fertility or other related traits also included in the breeding objective. However, the effect of selection for increased milk yield in late lactation on fertility in the subsequent lactations must be first assessed.
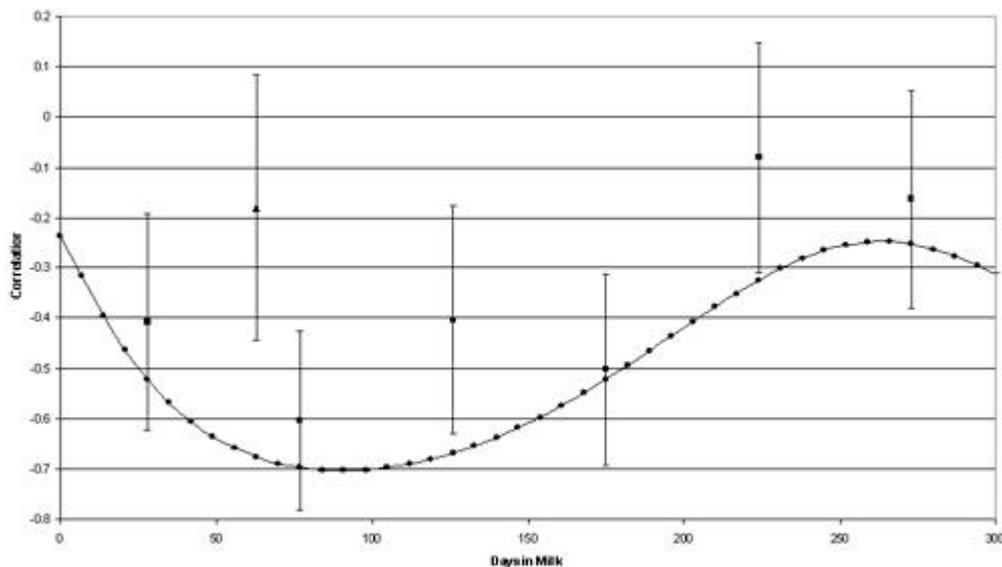

Figure 4. *Genetic correlations between milk yield and pregnant to first service estimated using either a smoothing spline (▲), a multivariate analysis of the raw data (■) or a random regression model (●). Also included in the vertical bars is one standard error of the correlations.*

Genetically taller, wider, deeper more angular cows with high pins tended to express lower genetic merit for PRFS and PR63; these animals also tended to require more NS (Table 1). Cows with genetically tighter fore udders and higher, shallower udders with stronger support also tended to express lower PRFS and require more NS. Similarly, cows with shorter teats that were further apart from a rear view but closer together from a side view had inferior PRFS and required more NS. Sires of daughters that had straighter rear legs with steep foot angles tended to produce daughters that were served later and had inferior PRFS. Genetic correlations between temperament and ease of milking with fertility were generally not significantly different from zero

Linear type traits and somatic cell count

Wider, less angular cows with more body condition and lower pins tended to have lower SCC (Table 1). Cows with tighter fore udder attachments and stronger udders with shorter, closer teats also tended to have lower SCC levels. The positive genetic correlation between SCC and teat length (0.31) is stronger than a previous estimate (0.20) in primiparous cows (Rogers *et al.,* 1991). The increased SCC in cows with longer teats may be due to longer teats being more prone to injury from housing, handling and milking. The strongest absolute genetic correlation with SCC involved udder support (0.45) indicating that animals with genetically stronger supported udders were genetically predisposed to higher lactation average SCC levels. The direction of the relationship between udder support and SCC agrees with Pryce *et al.* (1998).

Genotype by environment interactions

A genotype by environment (GxE) occurs when the performances of different genotypes are not equally affected by different environments. Genotype by environment interactions may involve either changes in the relative magnitude of variances across different environments (scaling effect) and/or it may involve genetic correlations between the "same trait" in different environments being significantly less than unity (re-ranking effect). Significant re-ranking of individuals across environments may suggest a possible advantage of separate breeding programs within the different environments or the requirement of more sophisticated models/methods of genetic evaluations to account for this phenomenon. In this study a GxE interaction for milk yield was only observed across different silage quality environments. Genotype by environment interactions for BCS were observed across all environments, and for BW change, across different concentrate levels and silage quality environments. These were associated with changes in genetic variance (a three fold increase in the genetic standard deviation for BCS change in early lactation over the different silage quality environments) and/or genetic correlations between the "same trait" being significantly different from unity (correlations as low as –0.60 were found between extreme milk production environments for BCS change in early lactation). The lack of significant GxE for milk yield across most environments may be due to a buffering effect due to increased mobilisation of body tissue (BCS) (and/or increased intake) to meet energy demands for milk production.

Nevertheless, the implementation of separate breeding programs within different environments will depend not only on the evidence of re-ranking between the environments but the possible economic benefit of a separate breeding program. This will be a function of the expected genetic gain achievable in comparison to the importation of genetics from an alternative environment. The change in genetic gain between environments is a function of the genetic correlation between the environments (assuming similar selection intensities, similar accuracies of selection and similar genetic variances in both environments). However, similar accuracies of selection may not be achievable in both environments; accuracy of selection will be lower in the environment with the smaller progeny group sizes assuming the same heritability in both environments. The majority of the genetic correlations estimated in this study between the "same trait" in different environments varied from 0.70 to 0.99 (with the exception of the BCS/BW change traits). Robertson (1959) suggested that only genetic correlation less than 0.80 were of biological significance.

CONCLUSIONS AND IMPLICATIONS

- Based on the similar heritability estimates between BCS, BW, type traits and milk yield observed in the present study, the accuracy of selection for BCS, BW and/or type traits will be similar to selecting on milk yield over the same progeny group sizes. Therefore genetic selection for BCS, BW or type is possible.

- Heritability estimates for fertility were lower indicating that larger progeny group sizes would be required to achieve the same accuracy of estimated breeding values as for traits of higher heritability. However, some fertility traits expressed larger genetic variation; accurate identification of animals on the favourable side of the distribution will result in fruitful genetic improvement in fertility.

- The use of repeated BCS and BW records within lactation has little effect on the accuracy of selection. A repeatability model for BCS and BW is therefore more feasible with adjustment for stage of lactation and heterogeneity of variances. Body condition score is currently assessed by Holstein herd-book classifiers on all first lactation animals in farms participating in the linear type classification scheme.

- Genetic selection for milk yield alone will reduce BCS, increase body size, have no effect on BW, and have a deleterious effect on fertility Therefore, more balanced breeding objectives which incorporate functional traits as well as production traits will result in optimal economic gains.

- Genetic selection for increased BCS will improve genetic merit for fertility and somatic cell count. Therefore attention should also be given to published estimated breeding values of sires for BCS (i.e., sires with a positive breeding value for BCS are favourable)

- The possibility exists for the use of linear type traits as predictors of BW, fertility and SCC within a national breeding objective. Currently BCS, angularity, foot angle and udder depth are used as predictors of calving interval and survival within the economic breeding index; increased accuracy of selection on new traits in the economic breeding index such as udder health may be achieved using linear type traits.

- Genotype by environment interactions existed for BCS across all environments and BW change across different concentrate feeding levels and silage quality environments. Appropriate adjustment for GxE interactions should therefore be investigated in the genetic evaluation of BCS in Ireland.

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