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Genetic and phenotypic relationships between milk protein percentage, reproductive performance and body condition score in New Zealand dairy cattle

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ABSTRACT

Recent research from the Australian In-Calf and New Zealand Monitoring Fertility projects have demonstrated that low milk protein percentage in early lactation is phenotypically linked to poor reproductive performance. The purpose of this study was to quantify the phenotypic and genetic relationship between body condition score (BCS), protein percentage (and other milk production traits) and the reproductive measures used to predict the female fertility breeding value in New Zealand's Animal Evaluation System: probability of mating in the first 21 days of a herd's mating period (PM21) and the probability of having a calf born to AI (CAI). Data on 99,870 first lactation cows, recorded as part of Livestock Improvement's and Ambreed's progeny test schemes were used for both a phenotypic analysis and to estimate genetic parameters. Effects of breed, heterosis, BCS, protein percentage and dairy conformation were statistically significant in logistic regression analyses on both CAI and PM21. Genetic correlations between protein percentage and PM21 and CAI were 0.18 and 0.20 respectively and genetic correlations of BCS and PM21 and CAI were 0.48 and 0.38 respectively. These results show that selection for protein percentage is unlikely to have a large effect on reproductive performance, while BCS is a promising tool to aid in selection for improved fertility.

Keywords: body condition score; protein percentage; fertility; dairy cow.

INTRODUCTION

Both the In-Calf project in Australia (Morton, 2000; Fahey *et al.*, 2003) and the Monitoring Fertility project in New Zealand (Z. Xu, personal communication) have reported a strong favourable relationship between protein percentage and fertility. Yet there is little information available in current literature on the genetic correlation between protein percentage and fertility. As current selection policies in Holstein populations, in particular, have tended to focus on the yield of protein as opposed to percentage, it is important to investigate whether a strong genetic correlation exists, as this would have implications for current breeding programmes.

Body condition score (BCS) has been proposed as a proxy for energy reserves (Fox *et al.*, 1999). Although subjective, it is currently the only practical and inexpensive method of evaluating the body energy stores of large numbers of cattle. There is interest in the potential use of BCS in breeding programmes, both in its own right and as a selection tool for improving fertility (e.g. Pryce *et al.*, 2000; Kadarmideen and Wegmann 2003; Lassen *et al.*, 2003).

There were two parts to this study, a phenotypic analysis and a genetic analysis. The phenotypic analysis was to investigate the phenotypic relationship of a number of factors that include BCS and protein percentage, in relation to two measures of reproductive performance. The two measures of reproductive performance are the traits which are the basis of the Animal Evaluation Unit's

(AEU) fertility breeding value: probability of being mated in the first 21 days of mating after the planned start of mating (PM21) and the probability of giving birth to a calf by AI (CAI) (Harris and Montgomerie, 2001). The phenotypic analysis will give an insight into the relationship between reproductive performance and a number of explanatory variables after noise factors, such as herd-year-season and sire are taken into consideration. Genetic parameters were estimated for BCS, milk volume, milk fat and protein percentages and two AEU fertility traits. These parameters are required for the design of future breeding schemes for dairy cattle improvement.

MATERIALS AND METHODS

Data

Data were collected on first lactation cows in herds that participated in either Livestock Improvement's or Ambreed's progeny testing schemes (SPS) or participated in linear type classification from the 2000/01 through 2002/03 seasons. Two BCS measurements were taken in the SPS herds, the first when live weights were recorded and the second at the time of linear type classification. In the non-SPS herds, one BCS measurement was taken at the time of linear type classification. BCS was recorded visually on a 1 to 9 scale, where 1 is emaciated and 9 is obese. Additional data on 270-day milk yield traits including lactation average milk fat and protein percentages, traits other than production (TOP; predominantly related to the visual appearance of cows)

and cow fertility, breed and pedigree information were extracted from the Livestock Improvement national database. Breed proportions of the cow, dam and sire were available in 16ths which allowed both the calculation of breed, and heterosis effects (Koch *et al.*, 1985). The data set contained a total of 99,870 cows, of which, 54,635 had information on CAI.

Phenotypic analysis

Logistic regression was used (SAS JMP, 2002). The response variables were PM21 and CAI. The effects fitted in the regression model included covariates for percent NZ Holstein Friesian (NZHF), overseas HF (OSHF), Jersey breed (JR), percent NZHFxJR, percent NZHFxOSHF and percent OSHFxJR heterosis, linear and quadratic effects of age at calving, 270 day lactation yield deviation for milk (milk), average lactation protein percent (protein %), average lactation milk fat percent (fat %), liveweight, BCS, stature, capacity, dairy conformation and udder overall score. Age at calving was fitted to remove the effects of heifer mating performance on subsequent reproductive performance and the data were pre-adjusted to remove the effects of contemporary group (herd-year-season) and sire. Body condition score, liveweight and the type traits was pre-adjusted to day 100 of lactation to remove the effect of stage of lactation.

Genetic analysis

The same data set was used in both the genetic analysis and the phenotypic analysis. A multivariate analysis was undertaken with a single observation per cow for each trait. Where cows had two measurements recorded the first BCS measurement was used in the analysis. Heritabilities, genetic and phenotypic correlations, and fixed effects were estimated by restricted maximum likelihood (REML) with a multivariate linear sire model including a sire-maternal grandsire relationship matrix using the average information algorithm of Johnson and Thompson (1995). Two analyses were done, the first was a multivariate analysis that included milk yield, average fat %, average protein %, BCS and PM21 and the second analysis used a subset of the first data set, but included CAI as an additional trait.

The model for each analysis included fixed effects for herd-year-season, covariates for NZHF, OSHF and JR breed effects, percent NZHFxJR, percent NZHFxOSHF and percent HFxJR heterosis, linear and quadratic effects of age at calving. The model for BCS included a linear and quadratic fixed effect for stage of lactation at the time of measurement.

RESULTS

Phenotypic analysis

The overall means for PM21 and CAI were 81% and 68% respectively. All the breed and heterosis effects regressed on PM21 were highly significant ($P < 0.001$) in the logistic regression analyses. Other highly significant effects included protein percentage, liveweight, capacity, udder overall, dairy conformation and BCS at day 100 of lactation. In the logistic regression analysis on CAI, the following were significant at the $P < 0.0001$ level: NZHF, JR, 270 day milk yield deviation, protein %, dairy conformation and BCS. Other significant effects at the $P < 0.05$ included: NZHFxJ, OSHFxJ. In contrast to the regression on PM21, OSHF and OSHFxNZHF heterosis were not statistically significant in the logistic regression analysis on CAI.

TABLE 1: Probabilities of PM21 and CAI of NZHF, OSHF and Jersey and their first crosses.

| | PM21 | CAI |
|-----------------------------------|------|------|
| NZHF | 0.84 | 0.73 |
| OSHF | 0.67 | 0.61 |
| JR | 0.86 | 0.72 |
| NZHFxJ (1 st cross) | 0.89 | 0.75 |
| OSHFxJ (1 st cross) | 0.88 | 0.70 |
| NZHFxOSHF (1 st cross) | 0.82 | 0.65 |

PM21: Probability of a cow to be mated in the first 21 days of mating; CAI: probability of a cow to have a calf born to AI (CAI); NZHF: New Zealand Holstein-Friesian; OSHF: overseas Holstein-Friesian; JR: Jersey

The probability of PM21 and CAI at different levels of the effects were calculated by converting the logistic regression estimate back to the observed scale. Table 1 shows the probability of PM21 and CAI for the purebred and first-cross cows. The crossbred cows exhibit heterosis for reproductive performance, with their average probabilities being above the average of the means of their parent breeds. First-cross NZHFxOSHF show only a 2% reduction in PM21 compared to purebred NZHF, while the difference between the two purebreds (NZHF and OSHF) is 17%. The same is not true for the CAI, as NZHFxOSHF only show a 4% advantage over the purebred OSHF. In general, the lower reproductive performance of the OSHF relative to NZHF or Jersey cows supports previous estimates summarised by Harris and Kolver (2001).

Table 2 shows the difference in the average probability of PM21 and CAI for the cows in the top 10% compared to cows in the bottom 10% for the significant factors in each model. There is a clear advantage in high phenotypic BCS, with a 9% and 10% advantage in PM21 and CAI for cows in the top 10% for BCS compared to the bottom 10% for BCS (Table 2). The difference in PM21

and CAI between the top and bottom 10% for protein percent was 9% and 11% respectively. Note, the differences in the average probability shown in Table 2 are not independent because the factors are correlated and the differences can not simply be added to get estimates for cows in the top 10% compared to the bottom 10% for two or more factors.

TABLE 2: Probability of a cow to be mated in the first 21 days of mating (PM21) and probability of a cow to have a calf born to AI (CAI) of the top 10% and bottom 10% of the population for covariates that were statistically significant in the logistic regression analysis.

| Covariates | PM21 | | CAI | |
|--------------------|------------|---------|------------|---------|
| | Bottom 10% | Top 10% | Bottom 10% | Top 10% |
| BCS | 0.77 | 0.86 | 0.64 | 0.74 |
| Protein % | 0.77 | 0.86 | 0.64 | 0.73 |
| Milk yield | N.S. | N.S. | 0.69 | 0.67 |
| Live weight | 0.83 | 0.78 | N.S. | N.S. |
| Capacity | 0.76 | 0.83 | N.S. | N.S. |
| Udder overall | 0.85 | 0.81 | N.S. | N.S. |
| Dairy conformation | 0.79 | 0.82 | 0.67 | 0.72 |

N.S. Not statistically significant

BCS: Body condition score

Genetic analysis

Genetic parameter estimates are presented in Table 3. The heritability estimates of BCS and production traits ranged between 0.20 and 0.52, while the heritability estimates of fertility traits were less than 0.05. Heritabilities of fertility traits were similar to those reported by Harris and Winkelman (2000) and the heritability estimate of BCS is consistent with Harris (2002). Heritabilities of BCS from other countries where BCS is recorded as part of a national recording scheme are also of similar magnitude (Pryce *et al.*, 2000; Kadarmideen and Wegmann, 2003; Lassen *et al.*, 2003).

Genetic correlations between milk yield and fat percentage and protein percentage were negative and

large. The genetic correlation between BCS and milk yield was not significantly different from zero, genetic correlations between BCS and fat percentage and protein percentage were also small. The milk production data were 270-day yields, therefore effects of BCS on lactation length will not be shown, genetic correlations with actual yield may have given different results. Of the genetic correlations between milk, fat percentage, protein percentage and BCS, and the fertility traits, the smallest correlations were with protein percentage, closely followed by fat percentage. Milk yield was moderate in size and negatively correlated with PM21 and CAI (-0.25 and -0.21 respectively), while the largest positive genetic correlations, with the fertility traits, were with BCS (0.48 and 0.38).

In all phenotypic and genetic analyses, the effect of contemporary group was removed, so cows with higher BCS, both genetically and phenotypically, tend to be the ones with better fertility.

DISCUSSION

The phenotypic analysis confirms research by Morton (2000), Fahey *et al.* (2002) and Z. Xu (personal communication) in showing that protein percentage is a good phenotypic indicator of fertility. However, using the same large data set in both genetic and phenotypic analyses, the genetic correlation between protein percentage and fertility (as defined in our study as PM21 and CAI) is weak. Thus genetic selection for or against protein percentage is unlikely to have an effect on fertility. In contrast, the genetic correlation and phenotypic relationship between BCS and both PM21 and CAI is strong, confirming results from studies (e.g. Pryce *et al.*, 2000; Veerkamp *et al.*, 2001; Dechow *et al.*, 2002; Berry *et al.*, 2003), that BCS may be a useful selection criterion for fertility, as well as being a good phenotypic indicator. Calculations on response to selection indicate that single-trait selection on BCS will achieve 96% of the response in fertility, compared to single-trait selection on fertility.

TABLE 3: Values for genetic parameters estimated from the data set; heritabilities on the diagonal, genetic correlations below diagonal, phenotypic above (standard errors in parentheses)

| | Milk | Fat% | Protein% | BCS | PM21 | CAI |
|------------------|--------------------|--------------------|--------------------|--------------------|----------------------|----------------------|
| Milk | 0.35 (0.02) | -0.439 (0.003) | -0.443 (0.003) | -0.062 (0.004) | -0.026 (0.003) | -0.014 (0.005) |
| Fat% | -0.60 (0.02) | 0.48 (0.02) | 0.646 (0.003) | 0.14 (0.004) | 0.061 (0.003) | 0.046 (0.005) |
| Protein% | -0.61 (0.02) | 0.69 (0.02) | 0.52 (0.02) | 0.077 (0.004) | 0.038 (0.004) | 0.031 (0.005) |
| BCS | -0.066 (0.04) | 0.12 (0.04) | 0.10 (0.04) | 0.20 (0.01) | 0.107 (0.003) | 0.070 (0.004) |
| PM21 | -0.25 (0.05) | 0.19 (0.05) | 0.18 (0.05) | 0.48 (0.05) | 0.049 (0.005) | 0.126 (0.004) |
| CAI ¹ | -0.21 (0.09) | 0.32 (0.09) | 0.20 (0.09) | 0.38 (0.10) | 0.74 (0.10) | 0.020 (0.005) |

PM21: Probability of a cow to be mated in the first 21 days of mating; CAI: probability of a cow to have a calf born to AI (CAI); BCS: body condition score.

¹Genetic parameters for CAI estimated using a smaller data set that included animals with a second calving date.

Whereas, single-trait selection for protein percentage will only achieve 58% of the selection response in fertility. The reason for the relationship between protein percentage and fertility has been hypothesised to be mediated by energy balance (Fahey *et al.*, 2003). It appears that cows that are in negative energy balance are likely to have low phenotypic protein percentages. Thus a strong genetic correlation between protein percentage and fertility is not necessarily expected. Correspondingly, the genetic correlation between BCS and protein percentage reported here was low (0.10).

The genetic correlation between BCS and 270-day milk yield was close to zero, indicating that selection for volume will have little effect on BCS. This contradicts most recent studies from outside New Zealand, where the genetic correlation between BCS and yield traits are statistically significant. For example Pryce *et al.* (2000) reported a genetic correlation between BCS and milk yield of -0.51 and Veerkamp *et al.* (2001) estimated it as -0.31 . This could be because in New Zealand little or no emphasis has been placed on angularity or dairyness in national breeding objectives, whereas in many other countries there has been some selection for dairyness. Dairy character and body condition score are genetically related traits in the linear type evaluation systems operated in most countries. An alternative hypothesis could be that a genotype by environment interaction exists. In high production systems, typical of those used in Europe, cows are able to sustain production through mobilising BCS. In New Zealand production systems, cows are able to eat enough pasture with little effect on BCS, management policies over years may have had an effect as those cows that maintain BCS also become pregnant again. It is worth noting, that if milk yield was not adjusted to 270-days of lactation-length, the relationship between milk yield and BCS may have been quite different to the results presented here. Current guidelines in New Zealand recommend drying cows off to allow sufficient time to achieve target BCS at calving (Macdonald and Penno, 1998). Thus, cows of higher BCS might be expected to have longer lactation lengths

To conclude, these results show that selection for protein percentage is unlikely to have a large effect on reproductive performance in the New Zealand dairy cow population. However, genetic correlations between BCS and fertility measures, show that BCS is a promising tool to aid in selection for improved fertility. At a farm management level, the phenotypic analysis shows that cows with low protein percentage and/or low BCS are at risk of poor fertility.

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