CAN MILK PROTEIN PERCENTAGE OR YIELD SERVE AS INDICATOR OF FERTILITY (CALVING INTERVAL) IN DAIRY CATTLE?

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SUMMARY

Data on milk yield traits, survival from first to second lactation and calving interval (CI) were analysed to estimate the relationships among them and determine whether the reliability of estimated breeding values (BVs) for CI could be increased from multi-trait analyses. The data consisted of 87,942 first parity cows which were daughters of 1679 sires. The genetic correlations of milk, protein and fat yield with CI were unfavourable (0.4 to 0.5) and were not influenced by stage of lactation while environmental correlations were slightly higher (~0.05) towards the end of the lactation (181 to 210 days) than at the beginning of the lactation (6 to 91 days). Protein percentage was favourably correlated both genetically (at the beginning) and environmentally (throughout the lactation) with CI. However, the genetic correlation between CI and protein % was slightly weaker than between CI and other milk yield traits. Consequently, protein % did not improve the reliability of estimated BVs for CI whereas milk yield resulted in a modest increase.
Keywords: Fertility, milk yield traits, genetic and environmental correlation.

INTRODUCTION

Improving fertility genetically is frustrated by the lack of suitable heritable traits that can be used as selection criteria. Analyses of fertility data collected from 168 commercial dairy herds in Australia (DRDC, 2000) showed that fertility (6-week in-calf rate, 21-week in-calf rate, 3-week submission rate, first insemination conception rate) of dairy cows was strongly positively associated with protein percent in the first 120 days of lactation. For example, 6-week in-calf rate varied from 52% in cows with protein % of 2.75 or less to 67 % in cows with over 3.5% protein (DRDC, 2000). Genetic analysis of the InCalf data showed that the genetic correlation (r_g) between protein % in the first 150 days of lactation and pregnancy rate (occurrence of pregnancy at anytime after calving - PR) was 0.41±0.12 (unpublished results). The r_g between PR and other milk yield traits was unfavourable (-0.02 for milk yield (MY), -0.26 for fat yield (FY), -0.05 for fat %) but all the estimates were not different from zero, probably due to small data size. The r_g between protein yield (PY) and PR was 0.16±0.16 (unpublished results). Others working on fertility of dairy cattle have reported that the correlation between all yield traits and conception rate was unfavourable although less antagonistic for PY than for MY (Boichard and Manfredi, 1994). The objective was to report the genetic and environmental relationship between CI and MY traits including protein percent in a large population of cows based on milk recording data. A secondary objective was to determine if a joint analysis of CI with protein % or other milk yield traits would increase reliability of BVs for CI.

MATERIALS AND METHODS
Data were extracted from the Australian Dairy Herd Improvement Scheme (ADHIS) database as described by Haile-Mariam *et al.* (2003a). Briefly the data consisted of test-day MY, FY, PY, survival (coded 1 if the cow survived the next lactation or zero otherwise - Surv) and calving data of Holstein-Friesian cows. Cows that calved between January 1993 and June 1999, sired by bulls in artificial insemination service, were included in this study. From this dataset, sires with fewer than 3 daughters were deleted. In the final dataset the average number of daughters per sire was 52, and about 8 % of the sires had more than 100 daughters. The total number of sires with daughters was 1679 and the total number of cows was 87,942. Mean yields and percentages by test days and the number of cows with test records are shown in Table 1.

Data on MY traits in test 2 (31-60 days in milk (DIM), representing early lactation) and 7 (181-210 DIM, representing late lactation) were analysed with calving interval and survival. Fixed effects included in the model for test-day MY, FY, PY and protein % were herd-test day, year-season of calving and age at test and days in milk (as a covariate). In addition the fixed effects of month of calving and herd-year-season of calving were fitted for CI and Surv. The random effect of sire was fitted for all traits. To examine if the relationship between CI and MY traits was affected by stage of lactation the data on CI and Surv were analysed with MY or protein % at test 1 (6-30 days), 2, 3 (61-90 days) and 7. CI's in the range of 300 through 730 days were considered valid. If CI's were not within the above range or if the fate of a cow at the end of the lactation was not known, then that cow was included in the analyses with a missing record for the trait concerned. All analyses were performed using the ASREML software (Gilmour *et al.* 2000). Additive genetic relationships through sires were considered and all sires had at least a known sire and over 80% of the sires had known dam. The total number of animals with pedigree information was 3575. Reliability of BVs for CI from each analysis was computed.

Table 1. Mean milk yield, protein yield and protein % at the first (6-30 DIM), second (31-60 DIM), third (61-90 DIM) and seventh (181-210 DIM) test.

Trait	No. of records	Milk yield kg	Protein %	Fat %
First test	48232	21.5(5.2)[+]	3.10(0.30)	3.82(0.68)
Second test	68558	22.9(5.3)	2.96(0.25)	3.56(0.59)
Third test	69317	22.2(5.2)	3.0(0.26)	3.55(0.57)
Seventh test	64713	16.9(5.1)	3.16(0.26)	3.94(0.61)

[+] Values in parenthesis are standard deviations.

RESULTS AND DISCUSSION
MY was highest and protein % was lowest at the second test (Table 1). The h^2 values for all traits were similar to those reported in Haile-Mariam *et al.* (2003a). Protein % was favourably genetically correlated with CI particularly at the beginning of the lactation and the correlation decreased with stage of lactation (Table 2). Genetic correlations (r_g) between CI and MY traits were moderately unfavourable and generally similar to reports where lactational MYs are analysed (Brotherstone *et al.* 2002; Haile-Mariam *et al.* 2003a). In contrast to r_g, environmental correlations (r_e) were less antagonistic early in lactation than late in lactation because cows with long CI are also more

persistent. The r_g between protein % and CI was more favourable at the beginning of the lactation and near zero at the end of the lactation (Table 2). On the other hand, r_e remained the same ($\sim$ –0.05) throughout the lactation. At test 1 where the r_g was the highest, the total phenotypic correlation (r_p) between CI and protein % was -0.05 and in the case of MY at test 2 where the correlation was the highest, the r_p was 0.03. The r_p between PR and protein % in the InCalf data was 0.05 (unpublished). The sightly higher r_g at the beginning of the lactation compared to that at the end may be related to the effect of negative energy balance on both fertility and protein %. Others working at phenotypic level have identified a decline in fat percentage early in lactation as a good indicator of fertility status in dairy cattle (Vries and Veerkamp 2000).

Table 2. Genetic (r_g) and environmental (r_e) correlations between CI and milk yield trait or protein % at different stage of the lactation.

Traits	r_g	R_e
Protein % at test 1	-0.27±0.09	-0.04±0.0[+]
Protein % at test 2	-0.19±0.09	-0.06±0.0
Protein % at test 3	-0.16±0.09	-0.06±0.0
Protein % at test 7	-0.04±0.09	-0.04±0.0
Milk yield at test 1	0.46±0.08	0.02±0.0
Milk yield at test 2	0.47±0.08	0.02±0.0
Milk yield at test 3	0.44±0.08	0.01±0.0
Milk yield at test 7	0.41±0.08	0.07±0.0
Protein yield at test 2	0.45±0.08	0.0±0.0
Protein yield at test 7	0.43±0.08	0.05±0.0
Fat yield at test 2	0.49±0.08	0.0±0.0
Fat yield at test 7	0.49±0.08	0.04±0.0

[+] Standard errors approximated to zero.

Table 3. Average reliability (rel) for CI when analysed alone, with Surv and milk yield traits

Traits	Mean rel	Animals with rel > 0.3
CI alone	0.21	505(14%)[+]
CI & Surv	0.22	624(17%)
CI, Surv & MY (4 tests)	0.26	1089(30%)
CI, Surv & MY (2 tests)	0.26	1056(30%)
CI, Surv & P% (4 tests)	0.23	688(19%)
CI, MY & FY (2 tests each)	0.26	1061(30%)
CI, MY & P% (2 tests each)	0.26	1041(29%)
CI, Surv, PY (2 tests)	0.25	975(27%)

[+] Values in parenthesis are proportion of animals with reliability above 0.3.

A multi-trait genetic evaluation of fertility based on CI, Surv, calving to first service, first service non-return and insemination rate was recommended (Haile-Mariam *et al.* 2003b). Currently only

10% of Australian dairy herds provide insemination data to ADHIS. Thus, genetic evaluation of fertility is largely based on CI despite its shortcomings (MacGregor and Casey, 1999). CI is the most widely recorded fertility trait and is reasonably (genetically) correlated with other fertility traits even in seasonal calving herds (Haile-Mariam *et al.* 2003b). Heritabilities for CI and Surv are low (~ 0.05) and the information on these traits is available a year later than mating data. Consequently the reliabilities of estimated BVs for fertility are often low, particularly for young bulls in the progeny-testing program.

The average reliability of estimated BVs for CI of all animals and the number of animals that have estimates with reliability of above 0.3 based on a combination of traits are shown in Table 3. These results show that analysis of MY at about peak yield together with CI and Surv will help to improve reliability by about 4% compared to evaluation based on CI and Surv only. Computed reliabilities also showed that including more than one test-day record does not have advantages over using only a single-test record. Because of the slightly lower correlation between CI and protein %, the average increase in reliability was 1% compared to an analysis based on CI and Surv. However, since improving protein % is economically important in dairy herds, the relationship between protein % and fertility needs further study. The feasibility of improving fertility and protein % simultaneously is of particular interest. Although the h^2 for protein % is higher than for other MY traits, its coefficient of variation is relatively low. This may limit genetic progress when selecting for protein %.

Research to introduce genetic evaluation for fertility has also focussed on other indicator traits such as body condition score and progesterone profile (Veerkamp *et al.* 2000). In Australia, the h^2 of condition score was low (~ 0.13 to 0.15) (Sjollema 2002) and the r_g with fertility traits needs to be estimated. In populations where the h^2 of body condition scores was higher (~0.38) than in Australia, its r_g with fertility traits was high (0.4 to 0.6). Angularity was also considered as a one of the suitable indicators of fertility (Pryce *et al.* 2000). The approximate r_g between angularity and fertility traits was moderately unfavourable (~0.3) (Haile-Mariam *et al.* 2003b) suggesting that it can also be used to improve the reliability of BV for fertility traits.

CONCLUSION

In conclusion, the r_g between CI and MY was unfavourable and slightly stronger (0.4 to 0.5) than between CI and protein % which was favourable (-0.27 to –0.04). The results from this study suggest that any of the MY traits can be analysed with fertility traits and that this will result in a modest increase in reliability of estimated BVs. Analysis of CI with survival may help to account for any bias due to culling for fertility but its importance in improving reliability is less than that of MY.

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