

Genetic Analysis of Evaluations for Female Fertility with Production Included

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Introduction

Most countries have reported unfavourable consequences on reproductive traits of selecting primarily for milk yield. This has led to the inclusion of fertility traits in the national breeding indices of many countries in the last 5 years or so. However, the majority of genetic evaluation systems for fertility do not include milk yield. One of the arguments is that fertility will be included in national indices that already incorporate production traits; therefore there is no need for such multivariate analysis. However, the evaluations for fertility that exclude production might be biased and therefore selection for fertility might not be optimum in the national index. De Jong (2007) reported that including milk production resulted in 10 to 20% increase in estimated genetic trend for fertility traits. In a study involving a series of bivariate analyses, Sewalem and Kistemaker(2008) reported that including milk has no effect on the trend for non-return rate at day 56 (NR56) but increased trends on calving to first service and first service to conception. However, the correlation between NR56 and milk test day (MTD) they reported was low at -0.13. Their study seems to indicate that the influence of milk could depend on the number of fertility traits included in the multivariate analysis. In addition, milk yield is easily recorded in most countries and could be utilised as an earlier predictor of fertility traits in a multivariate analysis. The accuracy of such earlier prediction of fertility from milk yield has never been reported.

This study evaluates the effect of including milk in fertility evaluations in a bivariate involving NR56 and MTD and a multivariate analysis involving NR56, MTD, calving interval (CI), days to first service (DFS) and number of services observed that resulted in a calf (NSO). Evaluations for NR56 were partitioned to quantify the contributions of

milk yield deviations (YD) to cow trends and milk daughter yield deviations (DYD) to bull trends from both analyses. The accuracy of milk yield as an early predictor of fertility in the multivariate analyses was examined in a reduced data set in which NR56 records have been deleted for the daughters of young bulls.

Materials and Methods

The data for the UK official genetic evaluation for March, 2009 was utilised for this study. It consisted of records for cows born from 1989 to 2006 and there were 1,958,783; 2,631,371; 2,294,359; 2,288,529; 1,793,331 observations for CI, MTD, DFS, NR56 and NSO respectively. An animal model was used for the analysis with fixed effects of herd-year season, month of calving and linear and quadratic effects of age at calving and of days in milk for MTD only. The heritabilities for CI, MTD, DFS, NR56 and NSO used in this study were 0.033, 0.329, 0.035, 0.019 and 0.022 and the genetic correlation of MTD with CI, DIF, NR56 and NSO were 0.27, 0.49, -0.25 and 0.058 respectively. A series of 4 analyses were carried out; a univariate of NR56 (UNI), bivariate analysis of NR56 and MTD (BIV), multivariate of NR56, MTD, CI, DFS and NSO (MUL1) and a second multivariate run with MTD excluded (MUL2). In all cases, only evaluations for NR56 were examined and reported. In the BIV and multivariate analyses, there were 342842 cows which had no records for NR56 but had observations for other traits but were included in these analyses, to evaluate the genetic trend for NR56 in these cows relative to cows with NR56 records. The estimated breeding value (EBV) for NR56 for cows were partitioned as $EBV_{NR56} = W1(PA) + W2(YD)$, where W's were appropriate weights and PA is parent average. The percentage contribution of the YD of each trait to the rate of change in NR56 for cows was computed to determine the relative importance of milk.

Correspondingly, NR56 EBV for bulls were partitioned as $EBV_{NR56} = W1(PA) + W2(DYD)$. Then the percentage contribution of the DYD of each trait to the rate of change in NR56 for bulls was computed. In an attempt to estimate the accuracy of MTD as a earlier predictor of NR56 in a multivariate analysis, NR56 records were deleted for 92,553 daughters of 460 bulls born in 2000 onwards to produce a reduced data set. Then univariate analysis of NR56 (UNIR), bivariate analysis of NR56 and MTD (BIVR), multivariate analysis of NR56, MTD, CI, DFS and NSO (MUL1R) and with MTD (MUL2R) excluded were carried out with the reduced data set. Evaluations for NR56 from the full data were then regressed on the parent averages from the reduced data for the 460 bulls and 92,553 cows to determine the effect of including milk on predictive ability of the models.

Results and Discussion

The inclusion of milk yield generally increased the genetic trend in cows and bulls for NR56 both in the bivariate and multivariate analyses (Table 1 and Figures 1 and 2).

This was more pronounced in cows with the trend from the UNI being 84 % of that from the BIV, while the trend from MUL2 being 65% of that from MUL1. The correlation between cow NR56 evaluations from the UNI and BIV was 0.95 but was lower at 0.93 between MUL1 and MUL2. A similar difference in trends between the UNI and the BIV was observed for cows with only milk records in the bivariate analysis (Figure 3) but the correlation between both evaluations dropped to 0.93.

In the case of cows with records for MTD and NR56 in the BIV, the YD of MTD contributed 17% of the observed genetic trend in NR56 while it was 22 % for cows with only MTD records in the BIV. The corresponding figure for the DYD of MTD was 23% for bulls. The relative contribution of the YD of MTD reduces in MUL1 with more fertility traits analysed. For cows with NR56 records in MUL1, the percentage of the trend in NR56 contributed by the YD of MTD was 14% compared with 17% for cows with no NR56

records. The contribution of the DYD of MTD to the trend for NR56 was 20% for bulls. Thus the relative contribution of milk YD to NR56 genetic trends reduces as more fertility traits were included.

The reliability of cows for NR56 in the BIV increased on average by 2% with a maximum increase of 10% compared with UNI. Corresponding average increase in cows with only MTD in the BIV was 3% with a maximum increase of 15%.

The increase in genetic trend with the inclusion of milk is less pronounced in bulls in the BIV analysis, with the correlation between EBV from the UNI and BIV being 0.97 for bulls with at least 50 daughters. However, the average increase in the reliability of bull EBVs in the BIV compared with the UNI was 11%. For instance for bulls with at least 50 daughters in the UNI, an increase in daughters by at least 10%, and 11-30% from milk records increased reliability by 11, and 14% respectively.

The increased genetic trend represented an overestimation of genetic trend for NR56 when milk is not included in the analysis and would seem to indicate a upward bias. This is similar to the results reported by De Jong (2007) and Sewalem and Kistemaker (2008) for some fertility traits.

The correlations between evaluations from the UNI and UNIR and BIV and BIVR for the 92,553 cows with NR56 records deleted in the reduced data set were 0.82 and 0.87 respectively. Corresponding estimates for the 460 bulls were 0.75 and 0.80. However the regressions of evaluations from full data set on the reduced data for the cows were 0.713 for the univariate analysis and 0.788 for bivariate analysis. Corresponding estimates for bulls were 0.908 and 0.930. This indicates a better predictive ability of EBV for NR56 for young bulls and cows with no NR56 records with the inclusion of MTD. This was accompanied in the case of cows with a mean increase in reliability of 5% for cows and 8% for bulls for including milk yield. In the multivariate analysis, the correlations of EBV between MUL2 and MUL2R and MUL1 and MUL1R for the 92,553 cows were 0.91 and 0.95

respectively. Similar estimates were obtained for bulls. The regressions of EBV from MUL2 on MUL2R and MUL1 on MUL1R for the cows were 0.889 and 0.947. The estimates for bulls that correspond to these were 0.894 and 0.917 respectively.

While the predictive ability of the multivariate model was better than the univariate and bivariate analyses, the inclusion of milk resulted in further increase. However, the increase in average reliability was only 3% for cows but higher at 14% for bulls. It however demonstrates the added advantage of including milk in multivariate analysis of fertility traits in young bulls with limited fertility data.

Conclusion

The exclusion of milk yield always resulted in over prediction of the genetic trend for fertility

traits both in univariate and multivariate fertility models. The contribution of the YD or DYD of milk to the genetic trend for NR56 varied from 13 to 23%. Secondly, the inclusion of milk yield resulted in increased accuracy of both bulls and cow evaluations. The inclusion of milk resulted in the increased predictive of multivariate models for fertility traits and especially in young bulls or cows with limited fertility information.

References

- De Jong, G. 2007. Usage of predictors for fertility in the genetic evaluations, application in the Netherlands. *Interbull report*.
- Sewalem, A. & Kistemaker, G. 2008. Including production in female fertility evaluations. *Interbull Bulletin* 38, 44-47.

Table 1. Genetic trend for NR56 (days/year).

	Univariate		Bivariate		Multivariate	
	Cows	Bulls	Cows	Bulls	Cows	Bulls
No milk	-0.00182	-0.00151			-0.00197	-0.00136
With Milk			-0.00217	-0.00177	-0.00302	-0.00227



