Correlated Selection Responses in Fertility after Selection for Increased Protein Yield or Against Mastitis in a Norwegian Red Selection Experiment

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Introduction

There are antagonistic genetic relationships between milk production and female fertility in dairy cattle (e.g. Roxström et al. (2001); Andersen-Ranberg et al. (2005)), while favorable genetic correlations have been found between clinical mastitis (CM) and fertility (Kadarmideen et al. (2000); Andersen-Ranberg and Heringstad (2006); Heringstad et al. (2006)). Correlated selection responses in female fertility, in opposite directions, can therefore be expected after selection for increased milk production and selection against mastitis, respectively. A Norwegian selection experiment with two groups selected for high protein yield (HPY) and low CM frequency (LCM), provide the necessary data to calculate such correlated responses in female fertility. Large genetic differences in mastitis resistance have been reported from this selection experiment. After 5 cow generations the genetic difference between the two selection groups was 10 %-units CM (Heringstad et al. (2007)). The genetic difference in 305 day protein yield was 25 kg. The objective of this study was to estimate correlated responses in female fertility after selection for increased protein yield in HPY and selection against mastitis in LCM.

Material and methods

Selection Experiment. The selection experiment started in 1989 and includes 9 herds, each with approximately the same number of cows in the two selection groups HPY and LCM (Heringstad et al., 2007). Proven sires from the Norwegian Red active breeding program are used as sires. Each year the 2-4 best proven sires for the given trait (protein yield or mastitis) are selected among the 120-130 progeny tested Norwegian Red bulls. Thus, the experiment is based on single trait selection of sires pre-selected for Norwegian Red breeding objective. All cows present in the herds when the selection experiment started, that were mated with one of the defined sires and produced a daughter that made a first lactation record were defined as belonging to cow generation 0. Their daughters were defined as cow generation 1 and so on. Cows born in the same year may therefore belong to different cow generations.

Data and Prediction of Breeding Values. Data were from the Norwegian Dairy Herd Recording System, and fertility EBVs for cows were from the September 2009 routine

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genetic evaluation of Norwegian Red (Larsgard, 2008). The traits included were non-return rate within 56 days (NR56) for heifers, first lactation cows, and 2nd and 3rd lactation cows, calving interval between 1st and 2nd calving (CI), and interval from calving to first insemination (CFI) for first lactation cows, and for 2nd and 3rd lactation cows. A total of 5,001 cows from the selection experiment had fertility EBVs, of which 2,806 were HPY and 2,195 were LCM cows. A total of 68 sires used in HPY and 57 sires used in LCM were present in the data.

Selection Responses. Genetic trends for the two selection groups were obtained by plotting mean EBV per cow generation, for cow generations 0 to 6. Cows in later cow generations were excluded from the genetic trend calculations because there were too few animals. Permutation tests, where cows were assigned randomly to 2 groups, were used to test whether the mean EBV in the two selection groups were significantly different. For each trait 10,000 permutations were performed, and the differences between mean EBV in the 2 randomly assigned groups were computed per cow generation. The observed differences in mean EBV between HPY and LCM were then compared to the differences in mean EBV from the permutations.

Results and discussion

The overall genetic trend for NR56 in heifers (Figure 1, left) was relatively flat for HPY, while mean EBV increase with cow generation for LCM. After 6 cow generations the genetic difference between HPY and LCM cows was 2.5 %-units NR56. The overall genetic trends for NR56 in cows were decreasing for HPY and were flat or slightly increasing for LCM, resulting in a genetic difference after 6 cow generations of about 2 %-units NR56 (Figure 1).

![Figure 1: Mean EBV for non-return rate within 56 days (NR56) in heifers and 1st lactation cows per cow generation for cows selected for high protein yield (HPY) and low clinical mastitis (LCM)](image)

Mean EBV for CI per cow generation (Figure 2, left) indicates a genetic difference of about 4 days between HPY and LCM after 6 cow generations. This is mainly a result of genetic improvement in the LCM group, where there has been a favorable decreasing trend for CI. The correlated responses for CFI were less clear (Figure 2). In 1st lactation cows, the genetic difference of 1-2 days CFI found in generation 1-5 was reduced to 0 in generation 6. The genetic trends for CFI in 2nd and 3rd lactation cows were flat and partly overlapping in the
two selection groups, and there were no indications of genetic differences between LCM and HPY for this trait.

Figure 2: Mean EBV for calving interval (CI) and interval from first calving to first insemination (CFI) per cow generation for cows selected for high protein yield (HPY) and low clinical mastitis (LCM).

Permutation tests were used to test whether the observed differences between selection groups were significantly different. Table 1 gives the observed difference in mean EBV between HPY and LCM per cow generation for the 6 fertility traits together with the maximum differences in mean EBV from the permutation tests. Except for CFI in 2nd and 3rd lactation cows, NR56 in heifers in cow generation 2, and CI and CFI in cow generation 6; all differences between HPY and LCM, from cow generation 1 onwards, were larger than the maximum value from the permutation tests (Table 1). Observed differences far outside the range from the permutation test imply that the observed differences are unlikely to have occurred by chance.

Table 1: Observed difference in mean EBV between LCM and HPY (obs) per cow generation and maximum difference (absolute value) from permutation tests (max) for non-return rate within 56 days for heifers (NR56-0), 1st lactation cows (NR56-1), and 2nd and 3rd lactation cows (NR56-2), calving interval (CI), and interval from calving to first insemination for 1st lactation cows (CFI-1) and 2nd and 3rd lactation cows (CFI-2).

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*Bold number indicates observed value outside the range of the permutation test.

Permutations tests showed significant genetic differences between LCM and HPY for all fertility traits except CFI for 2nd and 3rd lactation cows. LCM cows were in general
genetically better for fertility than HPY cows, with higher NR56 in heifers and cows, shorter CI and shorter CFI in 1st lactation. The genetic differences after 6 cow generations were 2.5 %-units NR56 in heifers, 2 %-units NR56 in cows, and 4 days CI. No difference was found for CFI in 2nd and 3rd lactation.

When interpreting these results it should be kept in mind that sires used in the selection experiment were selected among progeny tested Norwegian Red sires and were thus pre-selected for the Norwegian Red breeding objective, which have had a strong emphasis on fertility over the past 30 years. Sires used in the HPY group were therefore on average better for fertility than if they were selected for increased milk production only.

Our findings of correlated selection responses for female fertility after selection for increased protein yield were in general in agreement with previous studies (Bonczek et al. (1992); Kelm et al. (2000)). This is the only selection experiment involving direct selection against clinical mastitis, and our study is therefore the first to report genetic change in female fertility as a correlated response after selection against mastitis.

Previous studies (Heringstad et al., 2007; 2008) have shown that selection for high protein yield resulted in unfavorable correlated selection responses in resistance to clinical mastitis as well as other diseases and lactation mean SCS in HPY, while the side effects of selection against mastitis in LCM includes increased resistance to other diseases and reduced lactation mean SCS. These together with results of the present study demonstrate that while selection only or mainly for milk production results in genetic deterioration of health and fertility, selection against mastitis can be viewed as indirect selection for more robust cows, with genetic improvement of health and fertility as correlated responses.

References