

EFFECT OF CULLING ON THE ESTIMATES OF GENETIC CORRELATION BETWEEN MILK YIELD AND LENGTH OF PRODUCTIVE LIFE IN DAIRY CATTLE

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SUMMARY

The objective of this study was to study the effect of voluntary culling on the estimates of phenotypic and genetic correlations between milk and productive life.

Additive genotypes and phenotypes for milk yield and fertility in the first three lactations were simulated for 40000 cows, the daughters of 400 sires. In each lactation cows below a certain level for fertility were culled (involuntary culling) and the rest were ranked on milk yield and a certain proportion was culled (voluntary culling). Involuntary culling was around 15% and 30% of the cows entering the lactation, for the 1st and later lactations, respectively. In the base situation, voluntary culling was 15%, 5% and 10% of all cows starting the 1st, 2nd and 3rd lactations, respectively. Several alternatives with decreasing voluntary culling (10%, 5%, and 0% in 1st lactation and no voluntary culling in any lactation) were studied. Length of productive life was measured as the number of lactations (1-4).

The estimates of genetic correlation between milk yield in 1st lactation and length of productive life decreased from 0.77 for the base situation to -0.47 for the alternative without any voluntary culling. The implication of the results is that in a real data set, one could expect a favorable genetic correlation between milk yield in 1st lactation and length of productive life if there is at least some voluntary culling for milk yield.

INTRODUCTION

The length of productive life in dairy cattle, measured as the time from 1st calving to culling or death, is determined by several factors. First, there may be cases of disease or disorders that are so severe that the cow does not survive. These certainly are a part of what is called *involuntary culling*. However, there are less severe situations, such as mastitis, sterility or low fertility that can also be considered reasons for involuntary culling. Beard and James (1993) defined involuntary culling as when a cow is sufficiently poor for a trait that she is culled regardless of the performance of her herdmates.

Given the involuntary culling there is also culling of cows due to low milk production or *voluntary culling*. A cow with high milk yield in relation to its herdmates, will not be voluntarily culled and will have a longer productive life. If both milk yield and productive life are measured in the same animals, one might expect voluntary culling to contribute to a positive phenotypic and genetic correlation between the traits. This was also found to be the case when the traits milk and productive life were studied algebraically or by simulation (e.g. Essl, 1989; Strandberg, 1991; Dekkers, 1993; Strandberg, 1994).

In the studies above, length of productive life was considered to be a trait with genetic background in itself. In this article, however, length of productive life is constructed from the traits behind voluntary and involuntary culling. The objective of this study was to study the effect of voluntary culling on the estimates of phenotypic and genetic correlations between milk and productive life.

MATERIAL AND METHODS

Additive genetic values for milk yield and fertility in the first 3 lactations (MILK1,...,FERT3) were simulated for 400 unrelated sires as: $\mathbf{a}_s = \mathbf{L}'_1 \mathbf{x}_1$, where \mathbf{a}_s is a (6x1) vector of additive genetic values for the 6 traits, \mathbf{x}_1 is a (6x1) vector of (pseudo-)random normal deviates with mean zero and variance unity ($\mathbf{x}_1 \sim N(0,1)$), and \mathbf{L}'_1 is a (6x6) lower triangular matrix resulting from a Cholesky decomposition of \mathbf{V}_a , the additive genetic variance-covariance matrix, such that $\mathbf{V}_a = \mathbf{L}'_1 \mathbf{L}_1$. For each sire the phenotypic values for each of 100 daughters were created as: $\mathbf{p} = 0.5\mathbf{a}_s + 0.5\mathbf{a}_d + \mathbf{r} + \mathbf{e}$, where $\mathbf{a}_d = \mathbf{L}'_2 \mathbf{x}_2$ (additive genetic values for the dam), \mathbf{r} is the vector of components due to Mendelian segregation, $\mathbf{r} = \mathbf{L}'_3 \mathbf{x}_3 \sqrt{0.5}$, and the vector of environmental deviations \mathbf{e} was created as $\mathbf{e} = \mathbf{L}'_4 \mathbf{x}_4$, where \mathbf{L}'_4 is a lower triangular matrix resulting from a Cholesky decomposition of \mathbf{V}_e , the environmental variance-covariance matrix, such that $\mathbf{V}_e = \mathbf{L}'_4 \mathbf{L}_4$, and \mathbf{x}_2 , \mathbf{x}_3 , and \mathbf{x}_4 are vectors of random normal deviates. Heritabilities, genetic and phenotypic correlations are shown in Table 1.

In each lactation there was first involuntary culling and then voluntary culling. As a simplification, involuntary culling was here restricted to fertility, whereas in a real situation other traits would be considered as well. Voluntary culling was on milk yield. Cows culled in one lactation had information from that and previous lactations but not from the following lactations. Cows below a phenotypic value of -1.036 and -0.524 for fertility in the 1st and later lactations, respectively, were culled. These values correspond to 15% and 30% involuntary culling, respectively, when the mean phenotypic value was zero and the standard deviation unity. Several alternatives of voluntary culling were studied. In the first alternative, 15%, 5% and 10% of all cows starting a lactation were culled voluntarily in the three lactations, respectively. In the three next alternatives the voluntary culling in 1st lactation decreased to 10%, 5%, and 0%, respectively. In the fifth alternative there was no voluntary culling in any lactation. Involuntary culling was identical for all alternatives.

Table 1. Heritabilities for (on diagonal) and genetic (above diagonal) and phenotypic correlations (below diagonal) among the simulated traits

Trait	Simulated trait					
	MILK1	MILK2	MILK3	FERT1	FERT2	FERT3
MILK1	0.3	0.9	0.8	-0.3	-0.3	-0.3
MILK2	0.5	0.2	0.9	-0.2	-0.3	-0.2
MILK3	0.5	0.5	0.2	-0.2	-0.2	-0.3
FERT1	-0.2	-0.1	-0.1	0.04	0.6	0.5
FERT2	-0.2	-0.1	-0.1	0.05	0.05	0.2
FERT3	-0.2	-0.1	-0.1	0.05	0.05	0.07

Length of productive life (PL) for each cow was measured as number of lactations (1-4). PL was analyzed together with milk or fertility in 1st lactation using a multiple-trait sire model:

$$y_{ij} = \mu + s_i + e_{ij}$$

where for each trait μ is the mean, s_i is the random effect of the i th sire, and e_{ij} is the random residual associated with the observation ij . Genetic parameters were estimated using the program DMU (Jensen and Madsen, 1992) which applies a derivative-free method to achieve restricted maximum likelihood estimates.

RESULTS

Table 2. Estimates of genetic (r_g) and phenotypic (r_p) correlations between milk yield or fertility in 1st lactation and length of productive life. Also, estimates of heritability (h^2) for length of productive life

	Voluntary culling in lactation 1			No voluntary	
	15%	10%	5%	0%	culling
r_g (MILK1-PL)	0.77	0.65	0.46	-0.01	-0.47
r_p (MILK1-PL)	0.29	0.20	0.08	-0.10	-0.21
r_g (FERT1-PL)	0.21	0.34	0.52	0.82	0.98
r_p (FERT1-PL)	0.29	0.34	0.39	0.49	0.50
h^2 (PL)	0.06	0.06	0.04	0.04	0.04

DISCUSSION

Voluntary culling had a substantial effect on the estimates of genetic correlation between MILK1 and PL (Table 2). There was a favorable genetic correlation between milk yield and PL as long as there was any voluntary culling at all in the 1st lactation. Estimates in the literature have usually ranged from 0.4 to 0.9 (see Strandberg (1991) for review) so the values found here for 5-15% of voluntary culling in 1st lactation seem quite reasonable. The phenotypic correlation was affected in a similar manner but the range between the two extremes was smaller.

Heritability estimates for PL or similar traits have usually been fairly low, around 5%, which was similar to the estimates in this study. Note that this heritability was found even though there was no genetic variation created for PL *per se*.

The negative correlation between MILK1 and PL when there was no voluntary culling was due to the unfavorable correlation between milk and fertility (Table 1), which in turn had a strong correlation to PL (Table 2). The correlation between FERT1 and PL increased with decreasing voluntary culling. This decreasing influence of milk also showed up as a tendency for the heritability of PL to decrease from 0.06 to 0.04.

Essl (1989), Strandberg (1991), Dekkers (1993) and Strandberg (1994) also found that as the influence of milk yield on productive life increased, so did the heritability estimate for productive life and the genetic correlation between milk yield and productive life. These studies all considered productive life to be a trait with genetic and phenotypic values. The

phenotypic value for productive life was considered to be unaffected by voluntary culling, and thus not equal to the value actually observed. Voluntary culling was then simulated as a regression of productive life on milk yield, i.e. the higher the milk yield the more was added to give the actually observed productive life. It seems that both that approach and the one used in this study give similar results.

It seems quite likely that one would find a positive genetic correlation between milk yield in 1st lactation and productive life in a real-life data set, if there is at least some voluntary culling based on milk yield in 1st lactation. This correlation, however, is valid only within generation. Let's look at a simplified situation where selection is only for milk yield. Milk is assumed to be uncorrelated with the traits causing involuntary culling. A sire with a good breeding value for milk yield has daughters that have a long productive life. Looking at the high positive genetic correlation with PL, one would expect that selection for milk yield would also give a positive response in PL. However, in the next generation we still decide to cull the same proportion due to low production, and productive life will be unchanged. If we have more traits the situation becomes more complicated and needs to be investigated in more detail, but the general conclusion should still hold: the estimated genetic correlation between milk yield and productive life does not correctly predict the selection response in productive life.

ACKNOWLEDGEMENTS

The authors would like to thank Just Jensen and Per Madsen for the use of their program DMU.

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