# Genetic Relationships between Milk Yield, Somatic Cell Count, Mastitis, Milkability and Leakage in Finnish Dairy Cattle Population

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**Abstract**

Heritabilities and genetic and phenotypic correlations were estimated for subjectively scored milkability and leakage, clinically recorded mastitis, somatic cell score (SCS) and milk production using data from Finnish sire sampling program, health and milk recording system. Four sets of data were analyzed using multi-trait REML included in DMU-package with sire model. The data consisted of 23,854 Finnish Ayrshire (FAY) and 10,720 Finnish Hostein-Friesian (FHF) cows. Records of clinically recorded mastitis, SCS and milk production for three first lactation were used. Observations of milkability and leakage were collected from first calving cows.

The estimated heritabilities for clinically recorded mastitis were low (0.01 - 0.02). The heritability estimate of leakage was 0.08. For milkability, heritability estimates were 0.24 for FAY and 0.16 for FHF. The heritabilities of SCS varied between 0.14 and 0.23.

The phenotypic correlations were low (-0.11 - 0.29). The genetic correlations between milkability, leakage and SCS were from moderate to high positive (0.22 - 0.89). Genetic correlations between milkability and clinically recorded mastitis were negative or almost zero (-0.50 - 0.02). The genetic correlation among udder health traits was moderatly (0.31 - 0.49). The milkability and leakage were not genetically correlated with milk production. The clinically recorded mastitis had an antagonistic relationship with milk production ($r_g$ = 0.31 - 0.49).

In general, these results indicate that milkability is an optimum trait, because selection for faster milking cows increases leakage and SCS and selection for slower milking cows increases clinical mastitis. In addition milkabililty is not correlated with milk production.

## 1. Introduction

Many functional traits as milking speed and leakage have importance in everyday management of dairy herd. Milking speed affects straight to working time and leaking is very unhygienic. Milking speed accounts more than 50 % of routine work at dairy herd (Blake and McDaniel, 1978). Milking speed and leaking has been found to be connected to mastitis and high somatic cell account (Moore et al., 1983; Trede and Kalm, 1989; Geer et al., 1988; Klemetsdal et al., 1992; Jørstad et al., 1989).

Mastitis causes great economic losses at dairy farm, mainly from reduced milk production, lower milk quality premium and increased cost of replacement, labor and veterinary service. According to Finnish Milk Recording System 33.2% of culling was due to udder health problems (Association of Rural Advisory Centres 1996).

In Finland milking speed is measured subjectively by farmer. The comparison is done under classes 1 to 5. The heritability estimates of subjectively scored milkability in Finnish dairy population was 0.20 (Juga et al., 1996). Others find

heritability estimates of subjectively scored milking between 0.11 and 0.21 (Meyer and Burnside, 1987; Erf et al., 1992; Lawstuen et al., 1989). The milk leakage is recorded as a yes or no trait. The observed frequencies of the milk leakage in the different populations vary 0 - 24% (Geer et al., 1988; Schukken et al., 1990; Slettbakk et al., 1995; Juga et al., 1996). The leakage is routinely recorded at least in Norway, Sweden and Finland. The heritability estimates of leakage were near 0.10 (Steine, 1988; Juga et al., 1996).

The heritability estimates of clinical recorded mastitis from field data are low (Emanuelson et.al., 1988; Pösö and Mäntysaari, 1996). The somatic cell count (SCC) has been routinely used as an indicator trait for udder health in many countries. SCC has moderately high heritability (Emanuelson et al., 1988; Weller et al., 1992; Pösö and Mäntysaari, 1996). The SCC is often transformed into logarithmic scale (referred as SCS) because of better statistical properties of SCS.

The objective of this study was to estimate genetic (co)variance components of milkability, leakage, somatic cell score and milk production.

## 2. Material and methods

### *2.1. Data*

The data of milkability and leakage were sampled in 1997 by Finnish Animal Breeding Association. The udder health treatments data were extracted from Finnish system for recording health data. These data were merged with somatic cell score and 305-d milk production data from Finnish Milk Recording System.

The edited data consisted of 23,854 Finnish Ayrshire (FAY) and 10,720 Finnish Holstein-Friesian (FHF) cows from different geographical regions in Finland (Pohjois-Savo and Pohjois-Karjala). Cows had calved between 1991 and 1996. Milkability was scored on a scale from 1 to 5 by farmer. Milk leakage and clinical mastitis were recorded as binomial traits. The period of registration for clinical mastitis was within 7 days before calving to 150 days after calving. If the cow had been treated for clinical or chronic mastitis by veterinarian or culled because of the udder problems, it was assumed to be diseased. The others were considered to be healthy. Somatic cell score (SCS) was expressed as a geometric mean of log-transformed somatic cell count (SCC) from bimonthly test days. Records for three first lactations were used as observation of clinical recorded mastitis, SCS and milk production.

The number of sires in FAY breed was 637 and in FHF breed 232; each sire averaged 37 daughters in FAY breed and 46 daughters in FHF breed. The herd-year was classified to two year periods and first parity was separated from second and third parity. The number of herd-years was 8025 in FAY and 4788 in FHF for first parity and 13,441 in FAY and 7861 in FHF in total. The information in FAY breed was collected by 137 AI-technicians and in FHF breed by 124 AI-technicians.

### *2.2. Statistical methods*

The genetic parameters were analysed with DMU-package using multiple-trait AI-REML for five traits (Jensen et al., 1997). Analyses were carried out using sire model for first lactation data.

The model for trait (i = 1, 2) was

$$y_i = \mathbf{X}_i\mathbf{b}_i + \mathbf{Z}_{hi}\mathbf{h}_i + \mathbf{Z}_s\mathbf{s}_i + \mathbf{e}_i \qquad (1)$$

and the model for trait (i=3,4,5) was

$$\mathbf{y}_i = \mathbf{X}_i\mathbf{b}_i + \mathbf{Z}_{hi}\mathbf{h}_i + \mathbf{Z}_s\mathbf{s}_i + \mathbf{e}_i \qquad (2)$$

where

- $\mathbf{y}_i$ (i=1,2) is the vector of $N_i$ observation of milkability or leakage of the daughters
- $\mathbf{y}_i$ (i=3,4,5) is the vector of $N_i$ observation of clinical mastitis, SCS and milk production of the daughters for irst lactation
- $\mathbf{b}_i$(i=1,2) is the vector of fixed effects including the technician who collected the information
- $\mathbf{b}_i$(i=3,4,5) is the vector of fixed effects including calving age (1-7), calving year-season (1-31)
- $\mathbf{h}_i$ is the vector of random herd-year effects with $V(h_i) = \mathbf{I}\ \sigma_{hi}^2$
- $\mathbf{s}_i$ is the vector of random sire effects with $V(s_i) = \mathbf{A}\ \sigma_{si}^2$
- $\mathbf{e}_i$ is the vector of random residual effects with $V(e_i) = \mathbf{I}\ \sigma_{ei}^2$

$\mathbf{X}_i$, $\mathbf{Z}_{hi}$ and $\mathbf{Z}_{si}$ are the incidence matrices that link effects $\mathbf{y}_i$

The assumed covariances between traits where $cov(s_i,s_k) = A\,\sigma_{sisk}^2$, $cov(e_i,e_k) = I\,\sigma_{ee'}^2$ and $cov(s_i,e_i) = cov(h_i,e_k) = cov(h_i,s_k) = 0$ with (i and k=1,2,3,4,5).

Clinical mastitis, SCS, milk production were collected for three lactations. The following repeatability model was assumed to compute (co)variance components. Analyses were carried out bivariatly using sire model. The model (1) was used for milkability and leakage (i=1,2).

The model for clinical mastitis, SCS and milk production was (i=3,4,5)

$$\mathbf{y}_i = \mathbf{X}_i\mathbf{b}_i + \mathbf{Z}_{hi}\,\mathbf{h}_i + \mathbf{Z}_{pi}\mathbf{p}_i + \mathbf{Z}_{si}\,\mathbf{s}_i + \mathbf{e}_i \qquad (3)$$

where

$\mathbf{y}_i$ = is the vector of $N_i$ observation of clinical mastits, SCS or milk production of the daughters for first, second or third lactation

$\mathbf{b}_i$ is the vector of fixed effects including calving age (1-21), calving year-season (1-31)

$\mathbf{X}_i$, $\mathbf{b}_i$, $\mathbf{h}_i$, $\mathbf{Z}_s$ and $\mathbf{e}_i$ are the same as in model (1) and (2)

$\mathbf{p}_i$ is the vector of random permanent environmental effects of daughters

$\mathbf{Z}_p$ is the incidence matrix that links permanent environmental effects to $\mathbf{y}_i$

The assumed covariances between traits where $cov(s_i,s_k) = \mathbf{A}\,\sigma_{sisk}^2$, $cov(e_i,e_k) = \mathbf{I}\,\sigma_{ee}^2$ and $cov(s_i,e_i) = cov(p_i,s_k) = cov(h_i,p_k) = cov(h_i,s_k) = cov(p_i,e_k) = 0$ with (i and k=3,4,5).

## 3. Results and discussion

Means and standard deviations of the observations are presented in Table 1. The frequency of the leakage was almost 9%, which was moderate compared to the frequencies in the literature (Geer et al., 1988; Steine, 1988). The frequencies of udder health treatments were much lower than the total mastitis rate in Finland, because the recording period in this study was only 150 d after calving.

Heritability estimates and genetic and phenotypic correlations are given in Tables 2-5. The heritability estimates of milkability in FAY and FHF were 0.24 and 0.16, respectively, which is in very good agreement with estimates of subjectively scored milkability found in the literature (Erf et al., 1992; Lawstuen et al., 1988; Meyer and Burnside, 1987), even milkability is scored as a farmer's impression of cow's milking speed from the first calving to first insemination.

Leakage and clinical mastitis are measured on farms as an all- or none trait on farms. The heritability estimate of leakage for both breeds was 0.08. Clinical mastitis had lowest heritability estimates of the udder healt traits which varying between 0.01 - 0.02 in different analyses. The results agreed well with literature values (Pösö and Mäntysaari, 1996; Emanuelson et al., 1988). SCS had heritability estimates between 0.14 - 0.23. FHF had higher estimates for heritability of SCS than FAY.

The estimated repeatability of clinical mastitis in FAY was hardly greater than estimated heritability. FHF had repeatability estimates of clinical mastitis about 0.2. The estimated repeatability of SCS was about 0.43 in both breeds.

The phenotypic correlations among traits were low. The estimated genetic correlations between milkability and leakage were high: in both breeds, namely 0.65 in FAY and 0.89 in FHF. This means that selecting for bulls and cows with faster milking speed will increase the frequency of milk leaking cows.

The subjectively scored milkability and leakage were not genetically correlated with milk production. The estimated genetic correlation between udder health traits and milkability and leakage did not show the same trend. The faster milking and leaking cows had greater SCS and less clinical mastitis, which agreed well with the correlations found by Lund et al. (1994).

## 4. Conclusion

Milkability has been regarded as an optimum trait, which means that neither slow nor very fast cows are wanted. This study supports this opinion, because selection of slow milkers increase mastitis treatments and selection of fast milkers increases SCS.

Some results show that selection for higher milk production will increase milking speed (Miller et. al., 1976; Trede and Kalm, 1989). We did not find connection between milk production and subjectively scored milkability and leakage. The relationship between milk production and udder

health was antagonistic, however. The negative correlation should be kept in mind when selecting for milk production so that the selection would not increase udder health problems.

The udder health traits are included into Finnish total merit index of dairy cattle, but milkability and leakage are not. The information of these functional traits has been made available for individual breeders to be used in within herd breeding planning. They are frequently used by breeder's in corrective mating. Genetic trend of milkability has been stabled under all years. However, current breeding goal results in positive selection response in udder health.

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Table 1. Number of observations, means and standards deviations of milkability, leakage, clinically recorded mastitis, somatic cell score and milk production of FAY and FHF.

| | 1st lactation | | | 2nd lactation | | | 3rd lactation | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Mean | SD |
| **FAY** | | | | | | | | | |
| Milkabiliy | 23,854 | 2.94 | 0.81 | | | | | | |
| Leakage | 23,854 | 8.9 | | | | | | | |
| Mastitis | 23,854 | 7.8 | | 10,249 | 7.9 | | 4434 | 8.6 | |
| SCS | 23,854 | 4.26 | 0.93 | 10,941 | 4.12 | 0.92 | 4763 | 4.07 | 0.91 |
| Milk | 23,849 | 5887 | 1082 | 10,921 | 6908 | 1292 | 4786 | 7355 | 1401 |
| **FHF** | | | | | | | | | |
| Milkability | 10,720 | 3.10 | 0.78 | | | | | | |
| Leakage | 10,720 | 8.7 | | | | | | | |
| Mastitis | 9,977 | 10.9 | | 4609 | 10.3 | | 1984 | 11.6 | |
| SCS | 10,720 | 4.54 | 0.95 | 4932 | 4.37 | 0.94 | 2132 | 4.29 | 0.92 |
| Milk | 10,716 | 5996 | 1127 | 4922 | 6944 | 1342 | 2132 | 7523 | 1429 |

[1]Frequency (as a percentage).

Table 2. Estimates of heritabilities, genetic and phenotypic correlations in milkability, leakage, incidence of clinically recorded mastitis, somatic cell score (SCS) and milk production in first lactation FAY. (Standard errors of estimates are in the parenthesis).

| | Milkability | Leakage | Mastitis | SCS | Milk |
|---|---|---|---|---|---|
| Milkability | **0.24** | 0.65 (0.046) | -0.11 (0.098) | 0.57 (0.045) | -0.03 (0.052) |
| Leakage | 0.29 | **0.08** | -0.16 (0.112) | 0.22 (0.069) | -0.03 (0.064) |
| Mastitis | 0.02 | 0.03 | **0.02** | 0.31 (0.090) | 0.53 (0.090) |
| SCS | 0.09 | 0.07 | 0.06 | **0.15** | 0.06 (0.056) |
| Milk | 0.06 | 0.01 | 0 | -0.07 | **0.37** |

$h^2$ on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal.

Table 3. Estimates of heritabilities, genetic and phenotypic correlations in milkability, leakage, incidence of clinically recorded mastitis, somatic cell score (SCS) and milk production in first lactation FHF. (Standard errors of estimates are in the parenthesis).

| | Milkability | Leakage | Mastitis | SCS | Milk |
|---|---|---|---|---|---|
| Milkability | **0.16** | 0.89 (0.045) | -0.20 (0.183) | 0.50 (0.072) | 0.11 (0.086) |
| Leakage | 0.28 | **0.08** | -0.36 (0.187) | 0.36 (0.090) | -0.04 (0.099) |
| Mastitis | -0.02 | 0.11 | **0.01** | 0.48 (0.160) | 0.31 (0.180) |
| SCS | 0.11 | 0.08 | 0.02 | **0.23** | -0.05 (0.082) |
| Milk | 0.24 | 0.08 | -0.02 | -0.18 | **0.43** |

$h^2$ on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal.

Table 4. Estimates of heritabilities, genetic and phenotypic correlations in milkability, leakage, incidence of clinically recorded mastitis, somatic cell score (SCS) and milk production in FAY. Udder health traits and milk production were recorded for three lactations. (Standard errors of estimates are in the parenthesis).

| | Milkability | Leakage | Mastitis | SCS | Milk |
|---|---|---|---|---|---|
| Milkabilty | | | 0.02 (0.085) | 0.54 (0.046) | 0.03 (0.052) |
| Leakage | | | 0.10 (0.010) | 0.24 (0.068) | -0.01 (0.008) |
| Mastitis | 0 | 0.03 | **0.02** | 0.48 (0.077) | 0.49 (0.075) |
| SCS | 0 | 0.04 | 0.07 | **0.14** | 0.08 (0.006) |
| Milk | 0.06 | 0.05 | 0 | -0.11 | **0.32** |

$h^2$ on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal.

Table 5. Estimates of heritabilities, genetic and phenotypic correlations in milkability, leakage, incidence of clinically recorded mastitis, somatic cell score (SCS) and milk production in FHF. Udder health traits and milk production were recorded for three lactations. (Standard errors of estimates are in the parenthesis).

| | Milkability | Leakage | Mastitis | SCS | Milk |
|---|---|---|---|---|---|
| Milkability | | | -0.50 (0.18) | 0.48 (0.073) | 0.13 (0.085) |
| Leakage | | | -0.60 (0.209) | 0.37 (0.010) | -0.06 (0.101) |
| Mastitis | 0 | 0 | **0.01** | 0.50 (0.166) | 0.31 (0.206) |
| SCS | 0.10 | 0.07 | 0.04 | **0.19** | 0.08 (0.055) |
| Milk | 0.06 | 0.02 | -0.01 | -0.01 | **0.40** |

$h^2$ on the diagonal, genetic correlations above the diagonal and phenotypic correlations below the diagonal.