



Genetic parameters of production traits in automatic and conventional milking systems

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ABSTRACT

Milk recordings of 1297 animals from 23 farms with automatic (AMS) and 20555 animals from 616 farms with conventional milking systems (CMS) were analysed. The data was collected within the years 2001 – 2003. Recordings were available for milk-kg, fat and protein content from the first three test days of each cow after calving. Genetic parameters between AMS and CMS recordings for each single test day and with a fixed regression test day model were calculated. Heritabilities of the three test days were in an expected range from .182 and .418. Genetic correlations were high with values near 1 for milk-kg and fat-%. Values for protein-% ranged between .760 and .881.

Heritabilities for the fixed regression test day model with all three test days as repeated measures were for milk-kg .242 (AMS) and .201 (CMS), for fat-% .316 (AMS) and .254 (CMS) and for protein-% .202 (AMS) and .337 (CMS). Genetic correlations between AMS and CMS were 1.00 (milk-kg), .999 (fat-%) and .994 (protein-%). It can be concluded, that under this model no genetic difference can be found between AMS and CMS. Therefore genotype by environment interaction between automatic and conventional milk recording systems is irrelevant for milk yield and fat percentage and small for protein percentage.

INTRODUCTION

Dairy production in Europe is based on strict economic limits. Falling prices for milk force the farmers to invest in cost reducing technologies and to make the herd management more efficient. Milking robots used for automatic milking systems (AMS) eventually are an effective way to reduce the production costs by reducing the number of workers involved in the production system. These milking systems also have positive effects on the animals, by increasing the average number of milkings per day, which is a decision of the cow and no longer of man.

The different numbers of milkings and other features of AMS raise the question, if AMS and conventional milking systems (CMS) can be directly compared. Especially for breeding value estimation, the new milking system needs to be tested for additional effects. Environmental effects are already included in the breeding value estimation, but if a performance from AMS is a different trait than from CMS, the whole breeding value estimation needs to be adapted for the new milking technologies. Most of the selection decisions are made on base of conventional milking systems. It has to be investigated, if the correlated response in AMS-performance is satisfying in comparison to direct selection on AMS.

Differences between AMS and CMS performances are frequently reported. Phenotypic comparisons between AMS and CMS somatic cell counts (SCC) show a significant lower SCC in AMS systems (BERGLUND et al., 2002). In case of assuming different traits for AMS and CMS the milk quality can be different in the two systems and needs to be considered in the selection process.

The aim of this study was to estimate genetic parameters of AMS and CMS milk recordings.

MATERIAL AND METHODS

Milk recordings of 1297 cows from all 23 farms with AMS and 20555 cows from 616 representative farms with CMS were analysed. The data were collected within the years 2001-2003. Recordings were available for milk-kg, fat and protein content and somatic cell count (SCC) from the first three test days of each cow after calving. SCC was used as log10 of SCC.

Table 1 shows means and standard deviations of the three test days in each milking system.

Table 1: Means and standard deviation of the milk recordings for each test day and milking system

		$\bar{x}$ (CMS)	s (CMS)	$\bar{x}$ (AMS)	s (AMS)
Test day 1	milk-kg	26.5	5.46	23.2	6.07
	fat-%	4.29	0.79	4.20	0.78
	protein-%	3.23	0.29	3.26	0.28
	SCC	4.95	0.52	4.96	0.51
Test day 2	milk-kg	28.36	5.70	27.86	6.19
	fat-%	3.88	0.59	3.84	0.61
	protein-%	3.17	0.25	3.20	0.25
	SCC	4.81	0.48	4.86	0.47
Test day 3	milk-kg	27.46	5.77	27.77	6.24
	fat-%	3.90	0.62	3.87	0.64
	protein-%	3.30	0.26	3.30	0.25
	SCC	4.83	0.48	4.87	0.49

The three test days make two different statistical models possible. The first model treated the test day records as different traits. Genetic parameters for each test day record were calculated separately. The model included following effects:

$$y_{ijk} = H_i + S_j + b_1 \cdot ca_k + b_2 \cdot ci_k + a_k + e$$

where:

y_{ijk}	=	phenotypical performance of each animal
H_i	=	fixed effect of the herd i
S_j	=	fixed effect of the season j
b_1	=	regression coefficient on age of first calving
ca_k	=	age of first calving of cow k
b_2	=	regression coefficient on calving interval
ci_k	=	calving interval of cow k
a_k	=	random effect of the animal
e	=	residual effect

The analysis were calculated in bivariate runs, considering the same trait in AMS and CMS systems.

The second model treated the three successive test days as repeated measurements of the same trait. The model was set up in analogy to the test day model with fixed regression lactation curves.

$$y_{ijklm} = HTD_i + AYS_j + \sum b_{k;j} * x_k + c_l + a_l + e$$

with:

y_{ijklm}	=	phenotypical performance of each animal
HTD_i	=	fixed effect of the herd test-day
AYS_j	=	fixed effect of age of first calving * calving year * calving season
$b_{k;j}$	=	fixed regression coefficients of the WILMINK lactation curve on days in milk m nested within age*year*season class j
x_j	=	days in milk
c_l	=	random effect of the cow l
a_l	=	random animal effect of cow l
e	=	residual effect

Variance components were estimated with the program VCE4 (GROENEVELD, 1997)

RESULTS AND DISCUSSION

Before the genetic analysis least-square-means of the performance in AMS and CMS were calculated to investigate the differences between the two systems without misleading influences. Table 2 shows least-squares-means of the investigated traits in CMS and AMS

Table 2: Least-squares-means for milk-kg, fat-%, protein-% and SCC of the three test days in the two different milking systems and significance level of the test for difference

Trait	CMS	AMS	p
Milk-kg 1	26.22	28.21	n.s.
Milk-kg 2	28.04	31.56	< 0.08
Milk-kg 3	27.10	32.96	n.s.
Fat-% 1	4.30	3.80	< 0.01
Fat-% 2	3.90	3.50	n.s.
Fat-% 3	3.95	2.89	< 0.07
Protein-% 1	3.23	3.18	n.s.
Protein-% 2	3.17	3.02	n.s.
Protein-% 3	3.30	2.85	< 0.07
SCC 1	4.95	4.84	n.s.
SCC 2	4.81	4.73	n.s.
SCC 3	4.87	3.92	< 0.04

n.s. = $p(\text{CMS}=\text{AMS}) > 0.1$

It can be shown that there are only few significant differences between the performances with AMS and CMS. For milk-kg only the second test day shows a small significant difference, the two other test days do not show influences of the milking system. The result of SCC in the different milking systems is of a special interest, because it is often argued, that the milking robots produce more udder diseases and therefore higher cell counts. It can be shown with this large data set, that there are no significant influence on the SCC because of the milking system. Only the SCC in test day 3 show a small significant difference in favour of AMS. Although differences in SCC are not high significant, AMS shows lower SCC than CMS in all three test days.

Table 3 shows estimated heritabilities and genetic correlations for the four traits in each test day.

Table 3: Heritabilities (on the diagonal) and genetic correlations (above diagonal) for the milk production traits between automatic and conventional milking systems in test day 1 to 3

		Test day 1		Test day 2		Test day 3	
		AMS	CMS	AMS	CMS	AMS	CMS
Milk	AMS	.182	1.00	.153	.999	.281	.996
	CMS		.127		.105		.260
Fat-%	AMS	.219	1.00	.297	1.00	.418	.893
	CMS		.172		.243		.338
Protein-%	AMS	.156	.760	.287	.851	.186	.881
	CMS		.206		.348		.389
SCC	AMS	.045	.854	.046	1.00	.127	.718
	CMS		.070		.089		.090

Estimated heritabilities for milk-kg are in all test days for AMS higher than for CMS. Estimates for test day 3 are higher than for the first two test days. Genetic correlations between AMS and CMS are close to one, decrease in later test days.

For fat-% heritabilities for AMS are higher than in CMS, as been found for milk-kg. The estimates for test day 3 are higher than for test day 1 and 2. Genetic correlations between AMS and CMS are 1 for test day 1 and 2, for test day 3 lower with a value of .893, which is still in a high range.

For protein-% heritabilities for AMS are lower than for CMS. Between the test days, h^2 for AMS is at test day 2 the highest value and decreases for test day 3, for CMS it increases with the test days. Genetic correlations between AMS and CMS are lower than for fat-% and show the lowest value (.760) for test day 1 and the highest value (.881) for test day three.

Genetic parameters of SCC for AMS are lower than CMS in test day 1 and 2, in test day three h^2 for AMS is higher than for CMS. All heritabilities are at a lower level than for the production traits. Genetic correlations between AMS and CMS show no specific trend for the test days. The estimated value for test day 2 is the highest (1.0) followed by test day 1 (.854) and test day 3 (.718). The genetic correlation between AMS and CMS in test day 3 for SCC is the lowest value, which was estimated in this analysis.

Table 4 shows the results of the genetic parameter estimation with fixed lactation curves.

Table 4: Heritabilities (on the diagonal) and genetic correlations (above the diagonal) for milk production traits in automatic and conventional milking systems with all test days as repeated measurements. Repeatabilities are in brackets.

		AMS	CMS
Milk-kg	AMS	.242 (.549)	1.00
	CMS		.201 (.515)
Fat-%	AMS	.316 (.371)	.999
	CMS		.245 (.407)
Protein-%	AMS	.202 (.341)	.994
	CMS		.337 (.558)
SCC	AMS	.113 (.482)	.723
	CMS		.070 (.447)

Heritabilities for milk-kg and fat-% are for AMS higher than for CMS. For protein-% h^2 for CMS is higher than for AMS. For SCC the heritability for AMS is higher than in CMS, but on a lower level than for milk-kg and fat-%. The genetic correlations between AMS and CMS are 1 and close to 1 for the production traits and .723 for the SCC.

Two different statistical models were assumed to consider the last two models in the breeding value estimation process for Holstein-cattle in Germany. The model with repeated measurements and assumed fixed lactation curve was used to regard all performances as repeated measurements of the same trait. Therefore only one heritability could be calculated for each trait. Estimated heritabilities were in a range to confirm former estimations. The national evaluation system for Holstein cattle in Germany (VIT, 2001) used heritabilities for a breeding value estimation of .228 - .295 for milk, .179 - .254 for fat-% and .202 - .248 for protein-%. The estimated heritabilities in this paper are very similar to these parameters used in practical breeding schemes.

The heritabilities in the model assuming the performances at each test-day as different trait shows lower values than in the repeatability model. This is based on the estimation of the phenotypic variance on three repeated measurements, which reduces the residual variance component and has a positive effect on the heritability.

The genetic parameters of the model assuming each test day as different trait can be compared with the heritabilities used in a random regression test day model in the German Holstein population. In this model, heritabilities based on each day are calculated. The actual breeding value estimation model in Germany uses estimated heritabilities, that confirm the results in this paper. It can also be shown, that the parameters increase with the first test days, as shown on the results of this data set.

The aim of this study, however, was not to reconfirm estimated genetic parameters, but to estimate the genetic correlation between milk performances in automatic and conventional milking systems.

The genetic correlations between AMS and CMS are for all production traits high, with values up to 1. No genetic correlation was lower than .70. This result shows the close relationship between milk performances in AMS and CMS. It has to be assumed, that there is no genetic difference between these milk production traits and therefore it is correct to treat them as the same trait. The parameters confirm a study by MULDER et al. (2003).

If AMS and CMS would be two different traits, the selection on AMS would cause a correlated response in CMS and vice versa. The need of treating both systems different can be compared in calculating the proportion between direct and correlated genetic response in selecting on AMS and CMS. The two assumed traits are connected through their genetic correlation. High genetic correlations cause a high correlated response. It can be shown, that under given breeding situations the correlated response in AMS while selecting on CMS is as high as the direct response in AMS while selecting AMS traits.

The high genetic correlations between AMS traits and CMS traits lead to the conclusion, that these traits do not have to be treated as different traits. They should be treated as the same trait. Not taking AMS or CMS for the definition of milk recording traits into account, does not lead to a bias in the breeding value estimation. Therefore the actual system can be used and does not have to be changed.

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