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Genetic Parameters for Milkability from the First Three Lactations in Fleckvieh

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Abstract

Test-day records for average flow rate (AFR) from the routine dairy recording from Bavarian Fleckvieh cows were analysed. Two data sets with observations on approximately 20,000 cows each were sampled from the total data set. For the estimation of variance parameters a two-step approach was applied. In a first step multiple-trait REML analyses were carried out. For each of the first three lactations six time periods with up to 33 days were defined. An algorithm for iterative summing of expanded part matrices was applied in order to combine the estimates. In the second step covariance functions for additive genetic variances and non-genetic animal variances were derived using second-order Legendre polynomials plus an exponential term. Estimates of test-day heritability for AFR ranged from .21 to .40, and were largest in lactation 1. For lactations 1 and 3, heritabilities decreased considerably towards the end of lactation. Genetic correlation estimates within lactation decreased as the distance between DIM increased. Genetic correlations between corresponding DIM in the three lactations were generally large, ranging from .80 to .99. The largest estimates were found between DIM from lactations 2 and 3. Results from this study suggest that including AFR data from second and third lactations in genetic evaluation systems could improve accuracy of genetic selection.

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1. Introduction

According to a description of National genetic evaluation systems (Interbull, 2007) several countries have implemented a breeding value estimation for workability. This trait group includes milking speed and (milking) temperament. In most countries milking speed is subjectively scored by farmers, and only one observation per cow is available. In Italy and Germany (Bavaria), where milking speed is recorded with a milk meter that calculates flow rates during milking, cows can have repeated observations.

In genetic evaluation systems related to milk production, e.g., milk yield, fat yield, protein yield, and somatic cell count, observations from the first, second, and third lactation are often considered as different traits. In studies including milking speed data from several lactations a fixed parity effect was fitted in the model (Bagnato et al., 2003; Zwald et al., 2005). In the joint genetic evaluation in Austria and Germany (Baden-Wuerttemberg, Bavaria) for somatic cell count and milking speed a multiple trait model with five traits is applied: somatic cell count from lactations 1 to 3, average flow rate (**AFR**) from Austria and Baden-Wuerttemberg, and AFR from Bavaria. Only AFR from lactation 1 is considered, even though in Bavaria AFR from all lactations is available for approximately 75% of the cows.

Objective of this study was to estimate genetic parameters for AFR in the first three lactations via a two-step approach, deriving covariance functions (**CF**) based on multiple trait REML estimates.

2. Materials and Methods

Data for this study included test-day records on Fleckvieh cows from Northern Bavaria, recorded from 1999 to 2007. The data were from the routine dairy recording, where AFR was derived based on threshold flow rates (Worstorff et al. 1992). Depending on the recording method (two milkings per day or alternative milking) one or two observations per test-day were available. Two data sets with records from herds larger than average were sampled. These data sets included 630,000 (583,000)

AFR observations on 22,700 (20,400) cows. On average, each cow had 27.8 (28.6) observations. Data were edited with respect to age at calving, days in milk (8 to 305), and number of observations per herd test-day. Cows were required to have at least one observation in the first lactation. These edits left 18,719 (16,937) cows in the data sets. For each cow, seven generations of paternal pedigree information and two generations of maternal pedigree information were added. Only informative ancestors were kept so that the total number of animals in the relationship matrix was 46,216 (40,725).

For the estimation of variance parameters a two-step approach was applied (Mäntysaari, 1999). In a first step multiple-trait REML analyses were performed to get estimates for several time periods within the first three lactations, whereas in the second step covariance functions (Kirkpatrick et al., 1990) were fitted.

Lactations were divided into periods which were considered to be different traits. 18 time periods (DIM 8-20, 31-63, 64-96, 130-162, 196-228, 275-305 in lactations 1, 2, and 3, respectively) were defined. The first time period in each lactation included only 13 days in order to obtain precise information about the beginning of lactation. If two milkings per cow and test-day were available, the one where the component sample was taken remained in the data. Preliminary studies revealed that AFR from morning milkings and AFR from evening milkings can be considered to be the same trait, even though AFR from morning milkings is slightly larger (uneven milking intervals). To improve normality of AFR, a square root transformation was applied.

For each data set numerous multiple trait analyses with two, three, and four traits were carried out for various combinations of the time periods in order to fill the 18 x 18 matrix of parameter estimates. To account for selection, each analysis included at least on time period from the first lactation. In the models, fixed effects of herd x year and calving year x calving month were included. Days in milk and age at first calving were linear covariates. Components of variances were estimated by REML using an average information algorithm implemented in the DMU package (Madsen and Jensen, 2000). Estimates were combined applying an algorithm for iterative summing of expanded part matrices (Mäntysaari, 1999).

In the second step CF for additive genetic variances ($\Phi K_a \Phi'$) and non-genetic animal variances ($\Phi K_p \Phi' + D$) were derived. In the derivation second-order Legendre polynomials plus an exponential term were used in Φ to get an order of fit with rank 12 in the coefficient matrices K_a and K_p (Emmerling et al., 2002).

3. Results and discussion

Due to the definition of time periods, fewest observations were in the first period (DIM 8-20) of each lactation (Table 1). As could be expected, the number of observations decreased towards the end of lactations (cows drying off) as well as across lactations (cows being culled). While AFR tended to be higher for data set 2, pattern of AFR within and across lactations was very similar for both data sets. At the beginning of lactations, AFR in lactations 2 and 3 was considerably higher than in lactation 1. However, the decrease of AFR towards the end of lactation was less pronounced in lactation 1. In time periods 5 and 6, AFR in lactation 1 was actually higher than in later lactations. The degree of udder filling plays an important role in milk ejection (Bruckmaier, 2001). Towards the end of lactation milk production of cows from different lactations is rather similar (Table 1), but in general, first lactation cows likely have smaller udders than later lactation cows. Early in lactation, AFR in lactation 3 was larger than in lactation 2, but in later time periods there was almost no difference. The pattern of the shapes of AFR curves was very similar to those of milk production traits and somatic cell count. The curve in lactation 1 was different from the curves in lactations 2 and 3, which were almost identical.

In general, estimates of variances for the two data sets agreed very well. Heritability estimates for time periods were almost identical in lactation 2 as well as in lactation 3, while in lactation 1 they were larger for data set 2. Estimates of genetic correlations between time periods within and across lactations were slightly larger for data set 2. Since the estimates, and especially the pattern of estimates within lactations, were so similar, and since the data sets were sampled from the same population, the estimates from both data sets were combined before the iterative summing of expanded part matrices was applied.

For lactation 1, estimates of heritability (h^2) for AFR from multiple trait analyses after iterative summing ranged from .27 to .39 (Figure 1). The estimates from the first time period and the last time period, respectively, were considerably smaller than those from mid-lactation. Analysing data from the same population with a fixed regression model, Sprengel et al. (2000) found h^2 estimates of .25 for first lactation AFR. In our study, data were from a larger time span (nine years vs. three years) and, therefore, aside from the model applied, a better structure of the data might explain the larger estimates. Ilahi et al. (2004) reported h^2 estimates for milk flow of above .40, and those by Gäde et al. (2006) were above .50. Heritabilities assumed in national genetic evaluation systems for subjectively scored milking speed tend to be smaller, ranging from .16 to .32 (Interbull, 2007).

Range of h^2 estimates for time periods was smaller in the second and in the third lactation, respectively. For most time periods, heritabilities from lactations 2 and 3 were very similar. Only at he end of lactation h^2 in lactation 3 was smaller than in lactation 2. During mid-lactation heritabilities were largest for lactation 1. Estimates of genetic variances (not presented in detail) were of the same magnitude for all lactations. In lactations 1 and 3, respectively, genetic variance decreased towards the end of lactation, while it increased in lactation 2.

Test-day h^2 estimates based on the derived full-rank CF are shown in Figure 1. Except for the first part of lactation 2, the combination of second-order Legendre polynomial and an exponential term proved to be a sufficient fit. Assuming 10 test-days per lactation resulted in lactation heritabilities of .46 for lactation 1, .44 for lactation 2, and .41 for lactation 3, respectively.

Estimates of genetic correlations (r_a) for AFR from multiple trait analyses after iterative summing ranged from .65 to .99 (Table 2). Within lactation, r_a estimates between time periods were very similar for all lactations. Estimates of r_a were always larger for adjacent time periods than for time periods further apart. A similar pattern could be observed for r_a estimates between time periods across lactations. Those estimates were largest between time periods from lactations 2 and 3, and they tended to be slightly larger between time periods from lactations 1 and 2 than between time periods from lactations 1 and 3.

In order to illustrate the genetic correlation structure estimates of r_a between DIM 20, 150, and 280, respectively, and other DIM over the course of lactation 1 are presented in Figure 2. Genetic correlations decreased as the distance between DIM increased. The curve for DIM 150 shows that this tendency was more pronounced towards the beginning of lactation than towards the end of lactation. Figure 3 shows that estimates of r_a between corresponding DIM in the three lactations were smallest early in lactation. The estimates were fairly stable during mid-lactation and, somewhat surprisingly, hardly decreased towards the end of lactation. The largest estimates of r_a were found between DIM from lactations 2 and 3, with even the estimates early in lactation as well as late in lactation above .96. Estimates between DIM from lactations 1 and 2 were slightly larger than between DIM from lactations 1 and 3.

4. Conclusions

Heritability estimates for AFR in lactation 1 were larger than in later lactations. This agrees with results from numerous studies on other traits, where lactations were considered to be different traits (milk production traits, somatic cell count). Estimates of genetic correlations between test-days within and across lactations were generally larger than for those traits. Test-day heritabilities and the genetic correlation structure suggest that including AFR from the second and third lactation in a breeding value estimation could result in a more accurate genetic selection. The correlation structure also indicates that applying a rank reduction to the CF (Emmerling et al., 2002) might lead to a considerable reduction of the number of equations per animal. This would decrease the computational demands and, therefore, make the further development of the already existing genetic evaluation system for somatic cell count and milkability more feasible.

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Table 1. Number of observations and means for milk yield per milking and AFR.

Lactation	DIM	Data set 1			Data set 2		
		Records	Milk yield per milking	AFR	Records	Milk yield per milking	AFR
1	8 - 20	5484	10.9	1.93	5147	10.9	1.96
	31 - 63	15325	11.6	1.91	13995	11.8	1.94
	64 - 96	15319	11.2	1.88	13977	11.4	1.92
	130 - 162	14673	10.1	1.82	13522	10.3	1.86
	196 - 228	13990	9.1	1.75	12864	9.3	1.79
	275 - 305	9607	7.9	1.65	8804	8.1	1.70
2	8 - 20	4129	14.2	2.08	4000	14.5	2.12
	31 - 63	10809	14.3	2.07	10048	14.6	2.13
	64 - 96	10526	13.2	2.00	9813	13.5	2.06
	130 - 162	9799	11.2	1.86	9121	11.5	1.92
	196 - 228	8900	9.6	1.72	8290	9.8	1.77
	275 - 305	5263	7.6	1.54	4926	7.7	1.59
3	8 - 20	2443	14.9	2.12	2318	15.1	2.18
	31 - 63	6351	15.2	2.10	5885	15.5	2.17
	64 - 96	6194	14.0	2.02	5659	14.3	2.09
	130 - 162	5676	11.8	1.86	5243	12.1	1.93
	196 - 228	5057	9.9	1.72	4654	10.2	1.78
	275 - 305	2991	7.6	1.51	2779	7.9	1.58

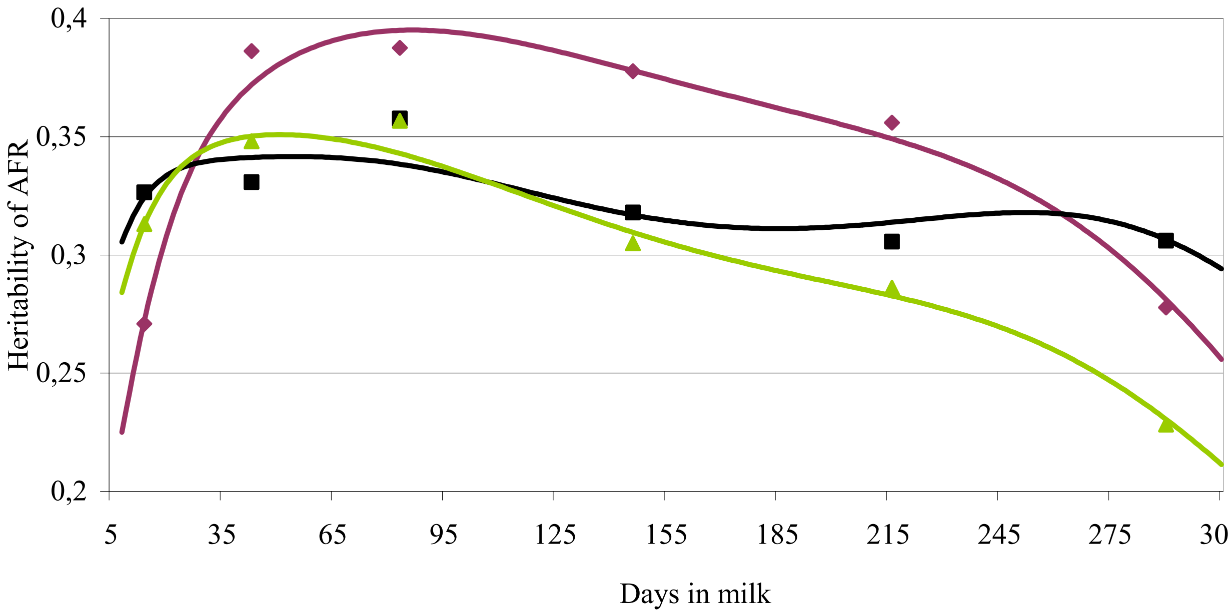

Figure 1. Heritability estimates for test-day AFR during lactations (lines: estimates derived by covariance functions (1st lactation: —; 2nd lactation: —; 3rd lactation: —); symbols: estimates from multiple trait analyses after iterative summing (1st lactation: ♦; 2nd lactation: ■; 3rd lactation: ▲)).

Table 2. Estimates of genetic correlations from multiple trait analyses after iterative summing for AFR in the first three lactations

Lactation		1						2						3					
	DIM	8-20	31-63	64-96	130-162	196-228	275-305	8-20	31-63	64-96	130-162	196-228	275-305	8-20	31-63	64-96	130-162	196-228	275-305
1	8 – 20		.95	.93	.88	.84	.79	.92	.92	.89	.83	.77	.65	.86	.88	.87	.82	.72	.65
	31 - 63			.99	.96	.91	.84	.96	.97	.95	.89	.80	.69	.92	.92	.91	.85	.75	.69
	64 - 96				.99	.95	.89	.97	.98	.97	.93	.86	.76	.94	.95	.95	.90	.81	.76
	130 - 162					.98	.94	.96	.99	.99	.97	.91	.84	.95	.97	.97	.95	.88	.84
	196 - 228						.98	.92	.96	.97	.98	.96	.91	.91	.96	.97	.97	.94	.91
	275 - 305							.86	.91	.94	.97	.99	.96	.85	.92	.94	.97	.98	.96
2	8 - 20								.98	.98	.94	.85	.73	.98	.97	.97	.92	.81	.75
	31 - 63									.99	.96	.89	.79	.97	.99	.98	.94	.85	.81
	64 - 96										.98	.92	.82	.97	.99	.99	.97	.89	.85
	130 - 162											.97	.90	.94	.98	.99	.99	.95	.92
	196 - 228												.96	.85	.91	.94	.98	.99	.97
	275 - 305													.72	.81	.84	.91	.97	.97
3	8 - 20														.98	.97	.93	.82	.77
	31 - 63															.99	.97	.89	.84
	64 - 96																.98	.92	.87
	130 - 162																	.97	.94
	196 - 228																		.98
	275 - 305																		

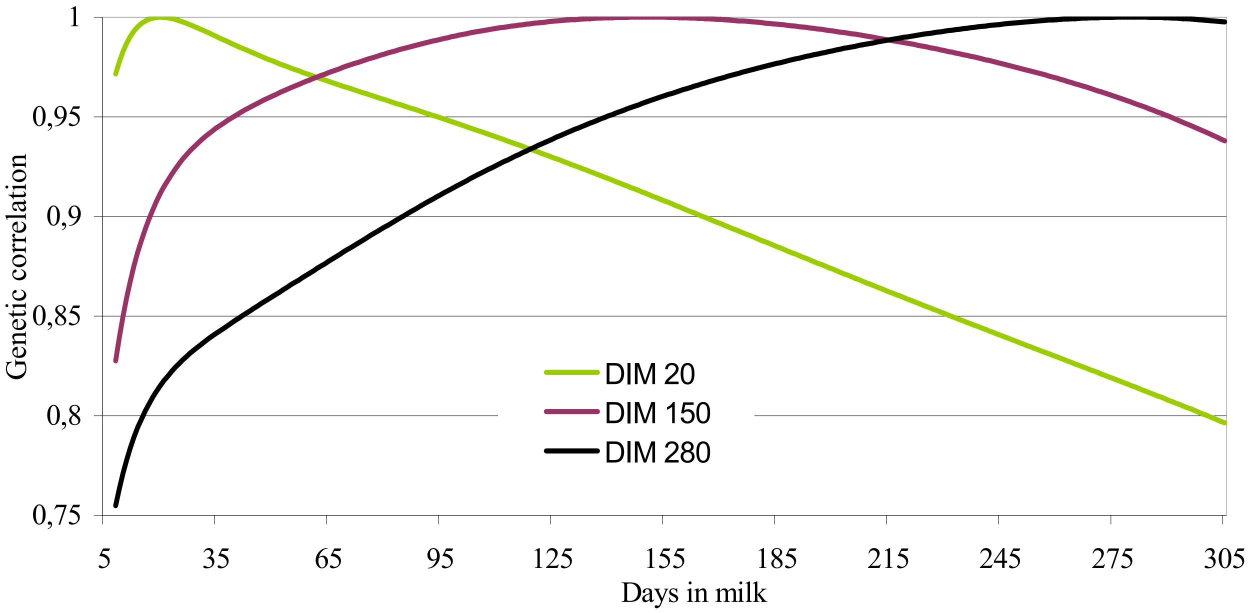

Figure 2. Genetic correlation estimates for AFR between DIM 20, 150, and 280, respectively, and other DIM over the course of lactation 1.

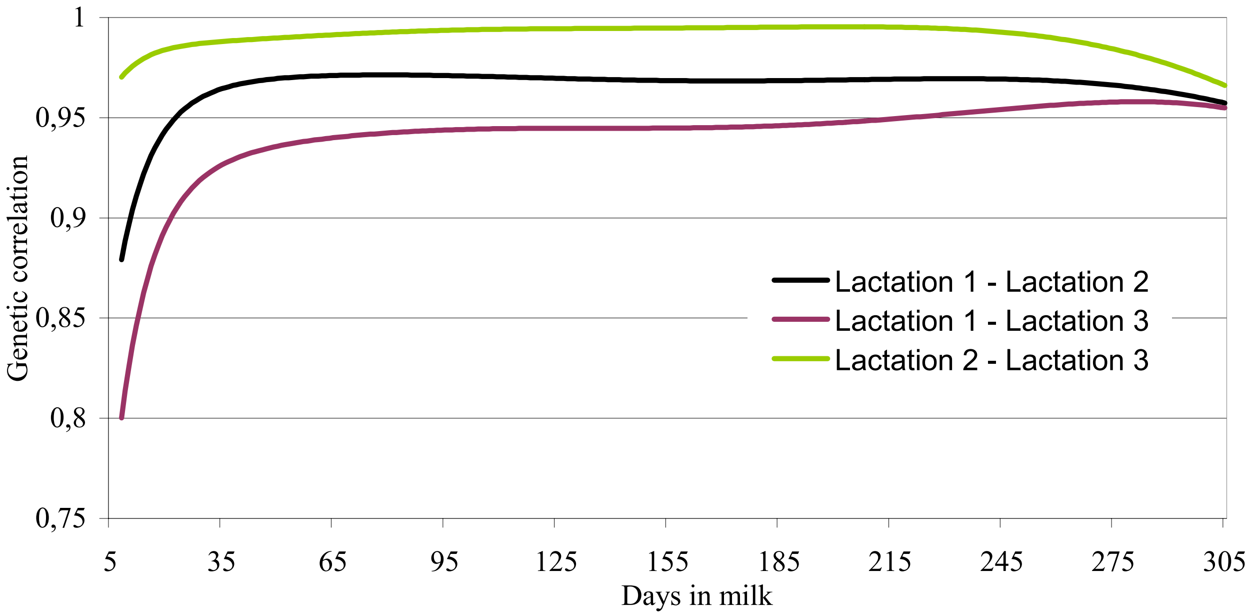

Figure 3. Genetic correlation estimates for AFR between corresponding DIM of two lactations.