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Development of a test day model for milk sheep and goats under unfavourable structural conditions in Germany

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1. Introduction

Milk sheep and goats have an important tradition in Germany and they are worldwide known for their excellent performances. The main dairy sheep breed is the German Milk sheep which excels in good growth, precocity, high fertility and milk performance. In dairy goats the German Fawn and White Goat represent about 70% of the whole population and 90% of the dairy breeds.

The population sizes are rather small counting about 21.000 Milk sheep and 100.000 dairy goats with about 5.000 and 10.000 registered herd book animals. Out of these, about 1.850 milk sheep and 5.000 dairy goats are annually performance tested (Astruc et al., 2002a; ICAR, 2002, BDZ, 2001). Milk production contributes a main part to the goat and sheep farmers' income. Therefore, an efficient breeding programme could contribute to maintain such farms and conserve these breeds. Currently, each of the 12 goat and 15 sheep breeding societies in Germany has its own breeding programme. In most cases they are based on herd mate comparisons.

The performance tests comprise the following trait complexes: Milk performance (150-days-performance for milk sheep, 240-days-performance for dairy goats), exterior, udder and reproduction. The appraisal of functional traits like exterior and udder is carried out subjectively and inconsistently between breeding societies. Milk performance, however, objectively recorded and results registered at the Milk Recording Organisations as well as the exchange of breeding animals between herds and breeding societies fulfil basic requirements for a common breeding value estimation. The positive genetic trends reported for milk performance traits in different dairy sheep and goat breeds (e.g. Astruc et al. 2002b, Montaldo and Manfredi, 2002) encourage the present endeavours in Germany towards a joint breeding value estimation.

First estimates of genetic parameters based on a lactation model for important German goat breeds are reported by Rikabi et al. (2003) for Saxony and Dolezal et al. (2003) for Lower Austria. The estimates of Bömkes et al. (2004a,b) separately for the German White and Fawn goats, are based on a fixed regression test day model taking test day records from all parities into account. For Milk sheep estimates on the basis of a fixed and random regression test day model (Horstick et al., 2001, 2002) do exist.

The objective of this paper is to give an overview of the available goat data in Germany followed by the estimation of genetic parameters for a random regression test day model of first lactation data via a two step approach (Mäntysaari, 1999).

2. Materials and methods

Two main problems regarding a joint German breeding value estimation currently exist. First the quality of data and identification and second the structure of data. The problem of different identification systems between herd book societies impede the traceability of genetic links, and the inconsistent identification between herd book societies and their appendant Milk Recording Organisations reduce the data considerably. The unfavourable herd structure with mainly small herds and the restricted relationship structure with use of selected males in natural service only within herds hamper genetic evaluations.

2.1 Data structure:

For the analysis of the goat data about 300.000 test day records from about 17.000 animals recorded between 1987 and 2003 were considered. The data were obtained from six German breeding societies. However, only half of the data could be selected for the estimation of genetic parameters mainly because of identification problems (table 1).

Tab. 1: Amount of delivered test day data compared to the prepared data from different breeding societies

Breeding society	**Delivered test day data**		**Prepared test day data**	
	test day records	animals	test day records	animals
Bavaria	194.722	9.694	72.899	3.796
Berlin-Brandenburg	5.033	438	4.574	390
Baden-Wuerttemberg	67.721	4.438	33.624	2.376
Mecklenburg-Western Pomerania	220	17	220	17
Saxony	19.673	1.684	13.798	1.144
Westphalia	15.160	1.102	5.605	500
Total	302.529	17.373	130.720	8.223

The performance data include the breeds German Fawn goat (73.1%), German White goat (19.7%), Saanen (3.8%), Toggenburger (2.7%) as well as in small proportions Thuringian Waldziege, Anglo Nubian and Alpine (< 1%).

Five and more records per animal and lactation represent about 86% of the whole data set, where 8 (22.3%) and 9 (19.9%) test day records per animal and lactation are most frequent.

For about 62% of the recorded animals both parents are known, while for about 27% any pedigree information is lacking (table 2). Genetic links between herd book societies could only be traced for Berlin-Brandenburg, Saxony and Mecklenburg-Western Pomerania who use the same herd book programme.

Table 2: Pedigree information of animals

No. animals with known sire and dam	5.090
No. animals with only known sire	619
No. animals with only known dam	329
No. animals without pedigree information	2.185

In the data set the lactation numbers 1 to 10 were considered. Analyses of phenotypic data will be done separately for the lactation numbers 1, 2, 3 to 6 and 7 to 10. Table 2 shows the number of test day records within these four classes.

Table 2: Number of test day records for milk yield, protein and fat percentage and somatic cell score

Lactation number	**No. of test day records**			
	Milk yield	Protein %	Fat %	Somatic cells
1	36.144	36.063	35.999	27.638
2	30.657	30.600	30.526	22.714
3-6	55.409	55.290	55.152	37.924
7-10	7.923	7.901	7.901	3.651

2.2 Estimation of genetic parameters:

Genetic parameters are derived by a two step approach (Mäntysaari, 1999) where in the first step multiple trait parameters were estimated for different lactation periods and in the second step covariance functions were derived based on the parameters from the first step. The estimation of genetic parameters is presented in this paper for the first lactation traits milk, fat and protein yield.

2.2.1 Multiple trait parameters

Genetic parameters are estimated for six time periods of the 1st lactation in one six trait run per biological trait using the computer programme VCE4, version 4.25 (Groeneveld, 1998). The following statistical model was used:

$$y_{ijkl} = \text{BS-B-HYM}_i + \text{LS}_j + \text{animal}_k + e_{ijkl,},$$

where

y_{ijkl}: test day observation for milk, fat and protein yield ;

BS-B-HYM_i: fixed effect of Breeding-Society-Breed-Herd-Year-Month of test date i (i=1, ... , 277);

LS_j: fixed effect of litter size at lambing j (j=1, 2, ≥3)

animal_k: random additiv genetic effect of the animal k (k= 1, 2, ... 33.916);

e_{ijkl}: random residual effect of observation ijkl.

For the fixed effect Breeding-Society-Breed-Herd-Year-Month of test date only classes containing at least 4 records are considered.

2.2.2 Derivation of the covariance functions

Based on the matrices G_0 for the additive genetic (co)variances and R_0 for the residual (co)variances out of step one, covariance functions were derived. A full rank covariance function that exactly reproduces the estimated additive genetic covariance matrix G_0 can be written as $G_0 = \Phi\ K_a \Phi^T$, where Φ is a 6 by 6 matrix of polynomial covariables and K_a represents the coefficients of the covariance function (CF). A rank reduction of the CF can be achieved by using fewer polynomial covariables in Φ (Kirkpatrick et al., 1990). Then K_a can be solved through the generalized least squares inverse of Φ (Tijani et al., 1999). Here, the derivation of CF with rank 3 is chosen, where Φ includes second order normalized Legendre polynomials (intercept, linear and quadratic term).

R_0 can be considered as $R_0 = \Phi K_p \Phi^T + I\sigma_e^2$, where K_P represents CF coefficients for non-genetic animal effects and σ_e^2 the measurement error variance (Van der Werf *et al.*, 1998). An Expectation Maximization (EM) algorithm (Mäntysaari, 1999) was applied to fit the CF to the residual (co)variance matrix R_0. Dimension of CF K_p with rank 3 is achieved by using same polynomials as for the derivation of K_a.

3. Results

Figure 1 shows the average daily milk yield per week over all lactations. The performances range from 1.5 to 3.5 kg milk according lactation stage and lactation number from the 1st to the 40th week of lactation. The curves show a maximum at about the second month of lactation. Milk yield increases from the 1st until the 6th lactation and thereafter declines again to the level of the 2nd lactation. Somatic cell numbers (figure 2) start at a level of about 700.000 at the beginning of the 1st lactation and increase until the end (2.000.000). Their level increases in later lactations where they surpass 3.000.000 at the end of the lactations 7-10.

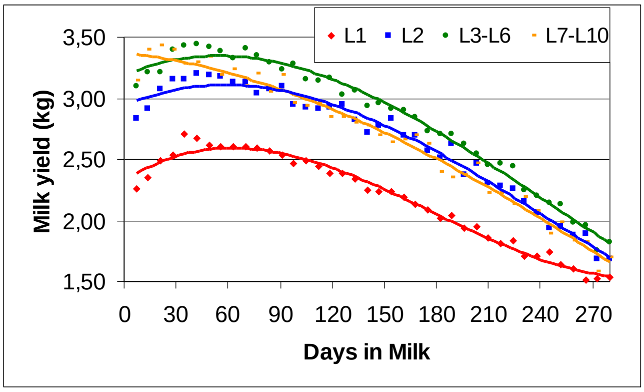

Figure 1: Milk yield curves for lactation numbers 1, 2, 3-6 and 7-10

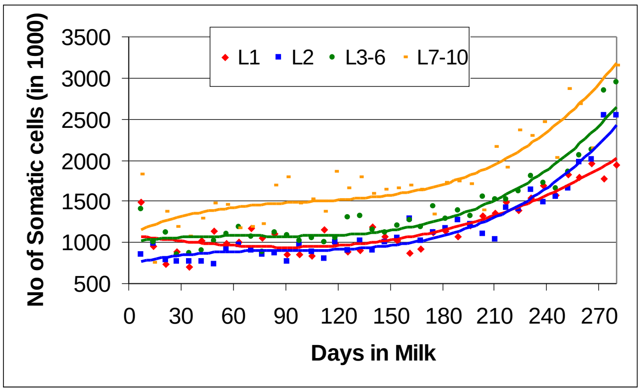

Figure 2: Somatic cell count curves for lactation numbers 1, 2, 3-6 and 7-10

Fat and protein content (figures 3 and 4) vary from about 3.0 and 2.9% to 4.5 and 3.8 %, respectively, showing a minimum at the 4th month of lactation.

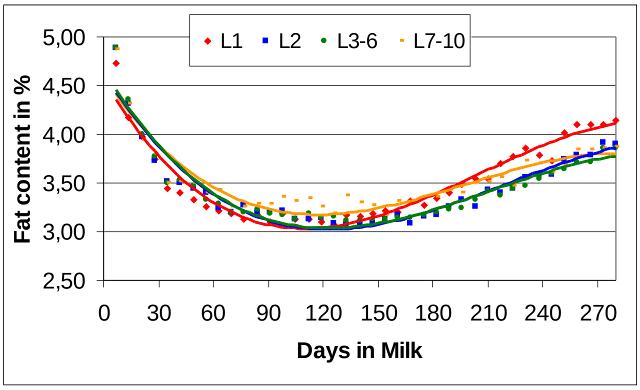

Figure 3: Fat content curves for lactation numbers 1, 2, 3-6 and 7-10

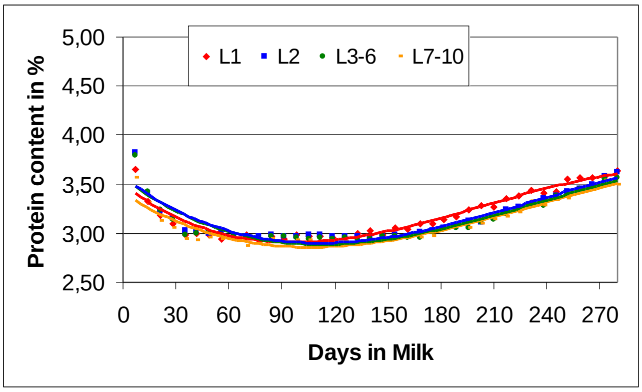

Figure 4: Protein content curves for lactation numbers 1, 2, 3-6 and 7-10

Fat and protein yield (figures 5 and 6) show a pattern similar to the milk yield with regard to the differences between lactations. As fat content is higher than protein content, the levels of fat yield are also higher, varying between 60 and 105g compared to 55 to 105g for protein yield.

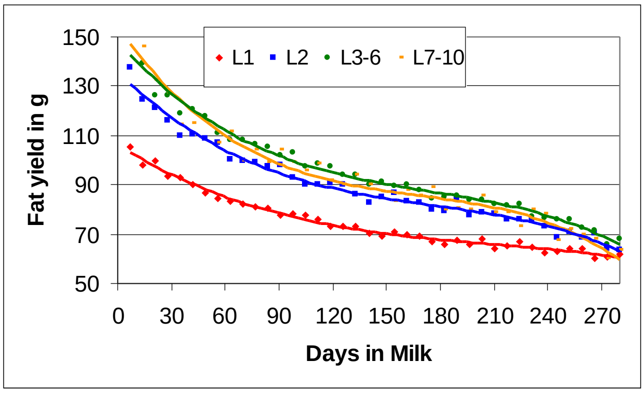

Figure 5: Fat yield curves for lactation numbers 1, 2, 3-6 and 7-10

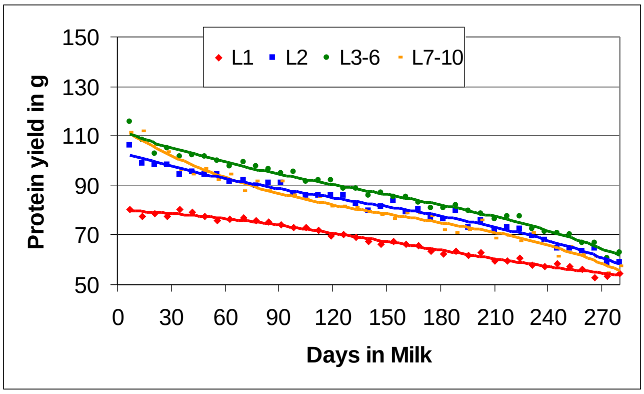

Figure 6: Protein yield curves for lactation numbers 1, 2, 3-6 and 7-10

Table 4 shows the means and standard deviations for the traits considered for the breeding value estimation from the 31st to the 300th day of lactation in 30 day periods. Six time periods (days in milk: 31-60, 61-90, 91-120, 151-180, 181-210 and 241-270) were selected for the estimation of genetic parameters.

Table 4: Means and standard deviations for milk yield, fat and protein content and yield from the 31st to the 300th day in milk in 30 days periods during the 1st lactation

Period (days in milk)	Number of test records N	Milk yield (kg) $\bar{x}$ SD	Fat content (%) $\bar{x}$ SD	Protein content (%) $\bar{x}$ SD	Fat yield (g) $\bar{x}$ SD	Protein yield (g) $\bar{x}$ SD
31- 60	2468-2476	2.45 (0.94)	3.00 (0.30)	3.31 (0.67)	80.6 (35.3)	73.2 (28.4)
61- 90	2461-2469	2.40 (0.93)	2.99 (0.28)	3.14 (0.64)	74.7 (31.7)	71.3 (27.5)
91-120	2501-2518	2.24 (0.89)	3.00 (0.30)	3.09 (0.71)	68.9 (31.3)	67.0 (26.4)
121-150	2547-2567	2.12 (0.83)	3.01 (0.30)	3.11 (0.77)	63.4 (24.6)	64.8 (28.3)
151-180	2342-2363	1.98 (0.81)	3.09 (0.32)	3.21 (0.80)	62.8 (28.1)	61.0 (24.2)
181-210	2120-2131	1.80 (0.83)	3.25 (0.38)	3.44 (0.92)	60.3 (29.1)	57.7 (26.0)
211-240	1897-1901	1.65 (0.77)	3.39 (0.49)	3.76 (1.10)	54.9 (24.6)	59.9 (29.6)
241-271	1207-1209	1.47 (0.72)	3.55 (0.48)	4.11 (1.22)	57.9 (29.0)	51.2 (24.4)
271-300	610- 612	1.45 (0.71)	3.62 (0.55)	4.12 (1.24)	51.4 (24.1)	57.9 (30.1)

Tables 5 to 7 show the estimated heritabilities and genetic and phenotypic correlations out of the multiple trait estimations runs for milk, fat and protein yield. Heritability values for milk yield for five 30 day periods (table 5) vary from 0.25 to 0.33, while the period from 181-210 days in milk sticks out with a value of 0.41. Also the correlations between this time period and others are rather low and difficult to interpret.

Table 5: Heritabilities (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) with standard errors for Milk Yield (MY) for the selected time periods of the 1st lactation

	MY31-60	MY61-90	MY91-120	MY151-180	MY181-210	MY241-270
MY31-60	**0.33**±.05	0.84±.06	0.80±.06	0.88±.06	0.58±.09	0.75±.09
MY61-90	0.66	**0.32**±.05	0.67±.08	0.91±.05	0.13±.11	0.67±.09
MY91-120	0.61	0.69	**0.28**±.05	0.92±.04	0.55±.10	0.95±.06
MY151-180	0.52	0.62	0.64	**0.25**±.04	0.36±.10	0.90±.06
MY181-210	0.39	0.47	0.48	0.55	**0.41**±.06	0.60±.10
MY241-270	0.42	0.44	0.48	0.51	0.47	**0.32**±.07

Heritabilities for protein yield (table 6) vary from 0.28 to 0.35 in the first 5 time periods, while at the end of the lactation (241-270 days in milk) a value of 0.47 is estimated, due to a relatively low residual variance in this period. Correlations between neighboured time periods are generally rather low and biologically not plausible.

Table 6: Heritabilities (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) with standard errors for Protein Yield (PY) for the selected time periods of the 1st lactation

	PY31-60	PY61-90	PY91-120	PY151-180	PY181-210	PY241-270
PY31-60	**0.34**±.06	0.80±.07	0.65±.08	0.80±.08	0.63±.11	0.50±.09
PY61-90	0.61	**0.34**±.05	0.41±.09	0.76±.06	0.13±.12	0.58±.08
PY91-120	0.55	0.62	**0.35**±.05	0.89±.06	0.67±.09	0.73±.11
PY151-180	0.48	0.57	0.61	**0.28**±.04	0.52±.10	0.79±.10
PY181-210	0.35	0.44	0.45	0.52	**0.33**±.06	0.48±.13
PY241-270	0.37	0.41	0.44	0.48	0.46	**0.47**±.07

The trend for the estimated heritabilities for fat yield (table 7) varies from 0.28 (beginning of lactation) to 0.48 (end of lactation), while a very low value (0.16) is estimated for the period from 151 to 180 days in milk. In this stage genetic variance is at a minimum ($66.8g^2$) and the residual variance at a maximum ($346.6g^2$). Genetic correlations of zero are estimated between the second and third time period and between the second and fifth period, respectively, which are biologically not plausible.

Table 7: Heritabilities (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) with standard errors for Fat Yield (FY) for the selected time periods of the 1st lactation

	FY31-60	FY61-90	FY91-120	FY151-180	FY181-210	FY241-270
FY31-60	**0.28**±.06	0.56±.09	0.52±.10	0.73±.09	0.74±.08	0.41±.14
FY61-90	0.54	**0.34**±.06	-0.05±.10	0.41±.11	0.03±.12	0.33±.13
FY91-120	0.44	0.50	**0.42**±.05	0.84±.06	0.36±.09	0.47±.11
FY151-180	0.41	0.42	0.44	**0.16**±.04	0.25±.15	0.37±.14
FY181-210	0.31	0.35	0.38	0.47	**0.36**±.05	0.37±.11
FY241-270	0.23	0.25	0.30	0.29	0.38	**0.48**±.06

Table 8 shows the estimates of the genetic parameters for 6 time periods for milk yield (MY) after the derivation of covariance functions using Legendre polynomials of 2nd order. In table 9 Legendre polynomials of 3rd order are alternatively used to derive covariance functions.

Table 8: Heritabilities (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) for Milk Yield (MY) after derivation of CF based on Legendre polynomials of 2nd order for lactation stages corresponding to the time periods chosen in the multiple trait estimation

	MY46	MY76	MY106	MY166	MY196	MY256
MY46	**0.37**	0.99	0.94	0.80	0.74	0.70
MY76	0.72	**0.31**	0.98	0.88	0.83	0.80
MY106	0.64	0.71	**0.25**	0.95	0.92	0.89
MY166	0.47	0.59	0.67	**0.22**	0.99	0.98
MY196	0.38	0.52	0.61	0.69	**0.23**	0.99
MY256	0.18	0.28	0.36	0.49	0.56	**0.27**

Table 9: Heritabilities (diagonal), genetic (above diagonal) and phenotypic correlations (below diagonal) for Milk Yield (MY) after derivation of CF based on Legendre polynomials of 3rd order

	MY46	MY76	MY106	MY166	MY196	MY256
MY46	**0.36**	0.88	0.81	0.83	0.74	0.71
MY76	0.61	**0.31**	0.99	0.74	0.54	0.80
MY106	0.47	0.73	**0.25**	0.75	0.54	0.85
MY166	0.44	0.55	0.60	**0.25**	0.96	0.92
MY196	0.43	0.38	0.40	0.65	**0.29**	0.82
MY256	0.42	0.27	0.23	0.47	0.61	**0.20**

4. Discussion

The phenotypic data show very nicely the course of milk, protein and fat yield and contents as well as somatic cell count during the different lactations and prove a good quality of the sampled records. The heritability values estimated for the first lactation data are generally within the range of reported heritabilities for milk performance traits in goats (Bömkes et al.2004a,b, Dolezal et al., 2003, Muller et al., 2002, Analla et al., 1996, Kominakis et al., 2000) and consistent in the course of the lactation except for few outlayers. Comparable analyses of genetic parameters for different time periods within the 1st lactation are not available.

The structure of (co)variances out of the multiple trait analysis raises some question marks. A clear consistent pattern is missing in all three traits. In the case of milk yield the correlations of the fifth time period to the others seem to be implausible compared to the other correlations in the matrix. The same is true for protein yield, where additionally the correlations of time period 2 with 3 and 5 are quite low and hard to interpret from a biological point of view. Also in fat yield, the problematic correlations are those with the time periods 2 and 5. The correlation of zero between time period 2 and 3 is the extreme case of underestimated correlations.

The problem in the estimates are not the values per se but their inconsistent course during the lactation and the not expected low correlations between neighboured time periods. These implausible estimates could mostly be due to the unfavourable data structure of the herds, namely herd-buck confounding for the exclusive use of breeding males within herds, but also insufficient traceable genetic links between breeding societies.

The derivation of covariance functions based on the two step approach seems to be very flexible to smooth the inconsistencies of the parameters from the multiple trait runs. With higher order polynomials the multiple trait estimates can be fitted subjectively better. However, the function becomes more flexible, which causes a shape of genetic parameters (variances and covariances) over lactation which is hard to interpret from a biological point of view.

5. Conclusion

The estimated heritabilities for the 1st lactation are within the plausible ranges and consistent in the course of the lactation except for few outlayers. However, the low genetic correlations between different time periods, especially between neighboured time periods, are not plausible.

The derivation of 2nd order polynomial covariance functions smooth the inconsistencies considerably. Polynomial of higher order show a better fit to the genetic parameters estimated for the different time periods.

Missing genetic links between breeding societies could be a reason for implausible values. Therefore, parameter estimation will be done within those breeding societies with a sufficient data set, i.e. Bavaria and Baden-Wuerttemberg. Soon the data base of Saxony will also be available. In this State recording of test day records has started recently involving numerous large herds. The use of a unique identification system for animals across State borders within Germany, as required by the new EU legislation, will help to improve connectedness over the data.

Finally, it is very important to improve the breeding structure (use of breeding males across herds) in order to get out of the problem caused by herd-buck confounding.

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