Genetic analysis of mastitis data with different models

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ABSTRACT

The aim of this study was to analyze different mastitis data sets with different statistical models and compare results. Data recording took place on 3 commercial milk farms with an average herd size of 3,200 German Holstein cows. Recording started in February 1998 and was completed in December 2005. During this period, 63,540 treatments for clinical mastitis were recorded. Five different data sets were analyzed and the number of cows varied between 12,972 and 13,618, depending on the data set. Data collection periods contained either the first 50 or the first 300 d of lactation. When the data-recording period ended after 50 d of lactation, data sets were analyzed with a lactation threshold model (LTM), a multiple threshold lactation model (MTLM), and a test-day threshold model (TDTM). In the LTM analysis, mastitis was treated as a binary trait coded as 0 (no mastitis) or 1 (mastitis), whereas in MTLM mastitis, codes were between 0 and 4, depending on the number of estimated days with mastitis. The TDTM treated each day as a single observation coded similarly to that of the LTM. When the data collection period included the first 300 d of lactation, data sets were analyzed with the LTM or MTLM only, because the TDTM was computationally infeasible. Mastitis frequencies in LTM data sets were 25.8 and 39.2%, and 26.9 and 39.2% in MTLM data sets, when data recording ended after 50 and 300 d of lactation, respectively. The mastitis frequency in the TDTM data set was 5.2%. Respective heritability estimates of liability to clinical mastitis were 0.08 and 0.09 using the LTM, and 0.08 and 0.11 using the MTLM. When the TDTM was used, the estimated heritability was 0.15. Rank correlation between breeding values of the different data sets ranged between 0.40 and 0.97. Rank correlation between the LTM and MTLM were higher (0.78 to 0.97) than those between these 2 models and the TDTM (0.40 to 0.59). The MTLM combined

the positive effects of both the LTM, with respect to the size of the data sets, and the TDTM, with respect to the lack of information.

Key words: mastitis, lactation threshold model, multiple threshold lactation model

INTRODUCTION

Mastitis is the most common disease in commercial milk production and it is related to several different cost factors, including medical treatment, milk that has to be discarded due to medical treatment, extra labor, and reduced milk production during the remaining part of lactation. Mastitis also causes lower milk quality (Heringstad et al., 2000).

For decades, mastitis data have been analyzed with different methods. In this respect, previous studies can be divided into 2 different groups: studies that have used linear models and studies that have used threshold models. The main disadvantage of implementing linear models is that a normal distribution of data is assumed, although mastitis is frequently defined as a categorical trait (Heringstad et al., 2000). Therefore, most heritability estimates reported in these studies were low and ranged from 0.02 to 0.03 (Lund et al., 1994; Sander Nielsen et al., 1996; Heringstad et al., 2001a). Higher heritability estimates were reported when threshold models were applied to mastitis data sets, ranging from 0.06 to 0.12 (Heringstad et al., 2001b, 2003a; Hinrichs et al., 2005). Pérez-Cabal et al. (2009) analyzed mastitis data from the Spanish Holstein population. These authors also used the number of mastitis episodes as the definition of the trait; the heritability estimates of the latter varied between 0.09 and 0.10, which was similar to heritability estimates reported by Vazquez et al. (2009). In the last study, authors compared probit modeling strategies and Poisson ordinal thresholds, and heritability estimates were 0.09 and 0.13, respectively.

However, some cows often have more than one case of mastitis during a period, and, therefore, coding the treatment of mastitis as a binary trait does not fully use all of the information provided by the data. Rekaya et al. (1998, 2003) pointed out that alternative model-

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ing of such data is an important area of research, and proposed the development of test-day models for longitudinal binary response for the analysis of mastitis field data. Another question, which has been discussed in the literature, is the time span of data recording (Heringstad et al., 2001b, 2003b; Hinrichs et al., 2005). All of these studies concluded that mastitis data recording should be carried out in early lactation, because these mastitis cases are more related to the genetics of the cow than cases in late lactation, which are more affected by the environment.

The aim of the present study was to analyze different mastitis traits with different models. At first, mastitis was defined as presence or absence of the disease during the first 50 d of lactation. Afterward, presence or absence of mastitis during the first 300 d of lactation was used as the trait definition. Alternatively, mastitis was defined as the number of episodes during the first 50 or 300 d of lactation. Finally, for the first 50 d of lactation each day was treated as a single observation and mastitis was defined as presence or absence of the disease.

MATERIALS AND METHODS

Data recording took place from February 1998 to December 2005 on 3 commercial milk farms with an average herd size of 3,200 German Holstein cows. A pedigree file was constructed by tracing the pedigree of the cows with observations 3 generations back. This resulted in a pedigree file with 22,608 animals. These 3 farms were involved in a project to develop a herd management program based on farm data-recording scheme with special emphasis on health and fertility data. Therefore, the farms were visited monthly by institute staff and security copies (backups) of the computer-based management programs were saved. Every month, new information was checked for plausibility, and questionable information was discussed with the farm management and veterinarians. Records that could not be clearly linked to animals were discarded. During the whole data-recording period 63,540 treatments for mastitis were recorded on the 3 farms. Five different data sets were formed depending on length of data collection period and trait definition.

The first 4 data sets contained only one observation per cow and period of observation. Data set 5 contained one observation for every test day. In data sets 1 and 2, each observation was assigned a mastitis code, 1 if a cow showed mastitis during the observed period and 0 otherwise. In data sets 3 and 4, if a cow did not show mastitis, the observation was coded as 0 (i.e., no mastitis). Otherwise, when a cow was treated for clinical mastitis, the day of treatment and the following 5

Table 1. Mastitis frequency (%) of the different mastitis classes for data sets analyzed with a multiple threshold lactation model¹

Mastitis class	Mastitis days	Mastitis frequency	
		Data set 3 (50-d observations)	Data set 4 (300-d observations)
0	0	73.1	60.8
1	1 to 6	11.5	10.6
2	7 to 12	11.0	14.8
3	13 to 18	2.8	5.9
4	>18	1.7	7.9

¹Mastitis frequency is the percentage of cows with mastitis in mastitis classes 1, 2, 3, and 4. Mastitis class 0 includes cows without mastitis.

d were considered as mastitis days. The 5-d period was chosen because it was the average time in which milk had to be discarded. At the end of the data-recording period all mastitis days were summed up. Depending on total mastitis days, a code ranging from 0 to 4 was assigned to each cow, as shown in Table 1. In data set 5, if there was a recorded treatment, the day of treatment and the following 5 d were coded as 1; all other days were coded as 0.

Data sets 1 and 2 were analyzed with a lactation threshold model (**LTM**), data sets 3 and 4 with a multiple threshold lactation model (**MTLM**), and data set 5 with a test-day threshold model (**TDTM**), as explained later. Table 2 shows the number of observations, the data-recording period, mastitis frequency, and number of cows and sires for the different data sets.

All models of analysis included age at calving and herd-year-season of calving as systematic environmental effects. Age at calving was divided into 8 classes, depending on lactation number: class 1 (20–24 mo), 2 (25–29 mo), and 3 (30–49 mo) for lactation 1, and class 4 (30–39 mo), 5 (40–45 mo), and 6 (46–56 mo) for lactation 2. Lactation 3 corresponded to age-at-calving class 7 (45–75 mo), and lactation 4 and higher were assigned to age-at-calving class 8 (≥ 75 mo). Every year was divided into 3 seasons of calving classes: 1 (January to April), 2 (May and August), and 3 (September to December). This resulted in 72 different herd-year-seasons of calving classes. The TDTM also included the herd week of observation as a systematic environmental effect, with 1,186 classes.

At first, all data sets were checked for extreme categories (i.e., age at calving, herd year season classes, and herd week of observation classes with all responses equal to mastitis or no mastitis). These classes were excluded from the analysis and they were not combined with other classes.

The LTM and MTLM were threshold liability models (Wright, 1934; Dempster and Lerner, 1950; Gianola

Table 2. Length of recording period, model of analysis, mastitis frequency, and number of observations, cows, and sires for 5 data sets¹

Data set	Model ²	Period of data recording (d)	Mastitis frequency (%)	Observations (n)	Cows (n)	Sires (n)
1	LTM	50	25.8	27,519	13,431	933
2	LTM	300	39.2	27,519	13,431	933
3	MTLM	50	26.9	25,285	12,972	920
4	MTLM	300	39.2	27,519	13,431	933
5	TDTM	50	5.2	1,268,507	13,618	949

¹In data sets 1 to 4, mastitis frequency is the percentage of cows with mastitis. In data set 5, mastitis frequency is the percentage of test days on which the cow had mastitis.

²LTM = lactation threshold model, MTLM = multiple threshold lactation model, TDTM = test-day threshold model.

and Foulley, 1983), and were used for the estimation of permanent environmental variance, additive genetic variance, and breeding values.

The following single trait repeatability LTM or MTLM was used for the analysis of data sets 1 to 4, which assumes that mastitis is the same trait in all lactations:

$$\lambda_{ijkl} = K_i + L_j + DIM + (DIM)^2 + m_k + a_l + e_{ijkl} \quad [1]$$

where λ_{ijkl} = unobservable liability to mastitis of the respective observation, K_i = effect of the i th herd year season of calving ($i = 1, \dots, 72$), L_j = effect of the j th age at calving class ($j = 1, \dots, 8$), DIM = linear regression on DIM, $(DIM)^2$ = quadratic regression on DIM, m_k = permanent environmental effect of the cow ($k = 1, \dots, 13,431$), a_l = additive genetic effect of the l th animal ($l = 1, \dots, 22,608$), and e_{ijkl} = residual error.

In the LTM and MTLM, DIM were the days from calving to the end of the sampling period or culling (i.e., cows which were culled before the end of data recording were included in the data sets). It should be noted that in data set 3, the number of permanent environmental effects ranged from 1 to 12,972, due to the extreme category problem.

The following TDTM repeatability model was applied to data set 5:

$$\lambda_{ijklm} = B_i + K_j + A_k + f_{k(\text{days in milk})} + m_l + t_m + e_{ijklmn} \quad [2]$$

where λ_{ijklm} = unobservable liability to mastitis of the respective observation, B_i = effect of the i th herd week of observation ($i = 1, \dots, 1,186$), K_j = effect of the j th herd year season of calving ($j = 1, \dots, 72$), A_k = effect of the k th age at calving ($k = 1, \dots, 8$), $f_{k(\text{days in milk})}$ = lactation curve nested within age of calving class, m_l = permanent environment effect ($l = 1, \dots, 13,431$), t_m =

effect of the m th animal ($m = 1, \dots, 22,608$), and e_{ijklmn} = residual error.

In the TDTM analysis, $f_{k(\text{days in milk})}$ was a fixed effect for the first 7 d of lactation. After the seventh day of lactation, $f_{k(\text{days in milk})}$ was identical to the function used by Ali and Schaeffer (1987).

Posterior distributions of the variance components were estimated with the program LMMG_MTH, a threshold derivative of LMMG software (Norbert Reinsch, Kiel, Germany; Reinsch, 1996), which uses a Bayesian approach for the analysis. An unobservable variable (liability) exists in a threshold model for each observation. Threshold models assume that liability is normally distributed, and that the binary disease variable takes the value 1 when the liability exceeds a fixed threshold. Otherwise, the binary disease variable takes the value 0. In the present study, the liability variables were created by data augmentation, as described by Sorensen et al. (1995). The LMMG_TH program draws random variables from truncated normal distributions. These truncated normal distributions were conditional on the other effects in the model. A detailed description of the Gibbs sampler for threshold models and multiple threshold models was given by Harder et al. (2006).

The Gibbs sampler was run in a single long-chain scheme. For the LTM and MTLM, the sampler ran 1,000,000 iterations and for the TDTM, it ran 100,000 iterations. The result from each round was retained and convergence was determined by visual inspection of trace plots of realized parameter values against iteration number. For the LTM and MTLM, the first 100,000 iterations were discarded as burn-in and for the TDTM, the first 10,000 iterations were discarded as burn-in. The computation time for the LTM and MTLM for 1,000,000 iterations was approximately 24 h, whereas the computation time for 100,000 iterations for the TDTM was 240 h. Furthermore, data sets with more than 2 mastitis levels (data sets 3 and 4) tended to have a longer burn-in period and, therefore, the chains

Figure 1. Trajectory of mastitis incidence during the first 50 d of lactation.

for the LTM and MTLM were extremely long and were used for convergence diagnosis.

To obtain posterior means of breeding values, variance components were fixed, and the other parameters were sampled as described above. Breeding values were multiplied by -1 , so that bulls with daughters with less mastitis received higher breeding values. Breeding values were mainly used for model comparison. Therefore, we calculated Spearman rank correlations between breeding values of the sires in different data sets.

Relative breeding values (RBV) were calculated following the German standard for publication of official breeding values (i.e., mean of 100 and standard deviation of 12), using

$$\text{RBV} = [(\text{breeding value/additive genetic standard deviation}) \times 12] + 100. \tag{3}$$

The reliability of the breeding values (R) was calculated as

$$R = 1 - \left(\frac{PEV_i}{\sigma_a^2} \right), \tag{4}$$

where PEV_i is the predicted error variance of sire i , and σ_a^2 is the posterior mean of the additive genetic variance.

RESULTS

As expected, mastitis frequency increased rapidly during the first days of lactation (i.e., from lactation d 1 to 8), when frequency reached 15.6%. After the eighth day of lactation, mastitis frequency decreased rapidly and almost reached a constant level of approximately 2.5% after 25 d of lactation. Figure 1 shows the trajectory of mastitis during the first 50 d of lactation. Mastitis frequency in the different data sets is given in Table 2, whereas frequencies for the different lactations within data set are shown in Table 3. Table 1 gives an overview of the mastitis frequency by mastitis class in data sets 3 and 4, analyzed with the MTLM.

Results of the variance component estimation are summarized in Table 4. If the available mastitis infor-

Table 3. Number of observations, mean length of lactation, and mastitis frequency for different lactations by data sets¹

Data set	Observations (n)	Mean lactation length, d (SD)	Mastitis frequency (% of observations)
Lactation number 1			
1	10,278	45 (13)	26.9
2 and 4	10,278	219 (113)	35.2
3	9,456	45 (13)	27.9
5	468,263	45 (13)	5.2
Lactation number 2			
1	6,946	47 (11)	22.9
2 and 4	6,946	232 (101)	39.8
3	6,386	47 (11)	24.0
5	331,749	45 (10)	4.5
Lactation number 3			
1	4,805	45 (13)	25.8
2 and 4	4,805	215 (111)	42.8
3	4,405	45 (13)	27.1
5	221,477	45 (13)	5.3
Lactation number >3			
1	5,490	42 (15)	27.4
2 and 4	5,490	191 (119)	42.8
3	5,038	42 (15)	28.6
5	247,018	37 (18)	5.8

¹In data sets 1 to 4, mastitis frequency is the percentage of cows with mastitis. In data set 5, mastitis frequency is the percentage of test-days on which the cow had mastitis.

Table 4. Posterior means (SD) of additive genetic (σ_a^2) and permanent environmental (σ_{pe}^2) variance, heritability (h^2), and repeatability (r), by model of analysis

Data set	Model ¹	σ_a^2	σ_{pe}^2	h^2	r
1	LTM (50)	0.09 (0.02)	0.11 (0.02)	0.08 (0.01)	0.17 (0.01)
2	LTM (300)	0.11 (0.02)	0.11 (0.02)	0.09 (0.01)	0.18 (0.01)
3	MTLM (50)	0.10 (0.02)	0.09 (0.02)	0.08 (0.01)	0.16 (0.01)
4	MTLM (300)	0.13 (0.02)	0.11 (0.02)	0.11 (0.01)	0.20 (0.01)
5	TDTM (50)	0.50 (0.06)	1.82 (0.05)	0.15 (0.02)	0.70 (0.01)

¹LTM = lactation threshold model, MTLM = multiple threshold lactation model, TDTM = test-day threshold model. The number in parentheses refers to length of data-recording period (d).

mation was reduced to mastitis (observation coded as 1) or no mastitis (observation coded as 0), the additive genetic and permanent environmental variance was slightly lower than that estimated from the MTLM when data recording was concentrated on the first 50 d of lactation. However, if the data-recording period was extended to the first 300 d of lactation, use of the MTLM resulted in slightly higher estimates for additive genetic variance, heritability, and repeatability. The estimate for the permanent environmental variance was the same as that in the LTM. As expected, the highest variance component was estimated when the TDTM was used for the analysis, because this model gives daily estimates of variance components.

After variance component estimation, breeding values were estimated for all animals. Sire breeding values are shown in Table 5. The mean of the relative breeding values ranged from 99 to 103, and the difference between the lowest and the highest relative breeding values ranged from 38 to 56, depending on the model and length of data-recording period. Spearman correlation coefficients between breeding values estimated from different models and data-recording periods (Table 6) varied between 0.40 and 0.97. All coefficients were significantly different from zero ($P < 0.0001$). It should be noted that only sires with breeding values with a reliability of at least 0.25 were used for the calculation of rank correlations. The correlation between the LTM and MTLM was higher than the correlation between these 2 models and the TDTM.

Posterior distributions of additive genetic and permanent environmental variances for the LTM and MTLM are shown in Figures 2 and 3. The posterior distributions for the TDTM were similar to the distributions shown in Figures 2 and 3 and, therefore, are not shown here.

DISCUSSION

This paper presents different models for estimation of genetic parameters for the liability to mastitis. Mastitis is one of the biggest problems affecting commercial milk production. Mastitis frequencies from 25.8 to 39.2% were observed in the present study, depending on the data-recording period and trait definition. These frequencies are higher than those reported by Heringstad et al. (1999, 2001b, 2003a) for Norwegian Red, but agree with those given by Fourichon et al. (2001) for Holstein and non-Holstein populations. In the TDTM analysis, mastitis frequency was 5.2%. Hinrichs et al. (2005) used the same TDTM and found a similar mastitis frequency.

Table 3 summarizes mastitis frequencies for different lactation numbers. As expected, in most data sets, mastitis frequency increased with increasing lactation number. However, this was not true for data sets 1 and 3. In these data sets, the frequency of mastitis was higher in lactation 1 than in later lactations. One possible reason for this could be the restriction with respect to the data-recording period (Table 2), because

Table 5. Mean, SD, minimum, maximum, and range of relative sire breeding values by model of analysis

Data set	Model ¹	Mean	SD	Minimum	Maximum	Maximum – Minimum
1	LTM (50)	100	4.4	78	118	40
2	LTM (300)	99	4.8	74	125	51
3	MTLM (50)	100	4.3	79	117	38
4	MTLM (300)	99	5.1	69	125	56
5	TDTM (50)	103	6.8	81	133	52

¹LTM = lactation threshold model, MTLM = multiple threshold lactation model, TDTM = test-day threshold model. The number in parentheses refers to the length of data-recording period (d).

Table 6. Rank correlation between sire evaluations from different data sets and models^{1,2}

Model	LTM (300)	MTLM (50)	MTLM (300)	TDTM (50)
LTM (50)	0.80	0.96	0.78	0.59
LTM (300)		0.79	0.97	0.42
MTLM (50)			0.80	0.59
MTLM (300)				0.40

¹A total of 167 sires were used for the calculation (sires were only used if the breeding value had a reliability of at least 0.25).
²LTM = lactation threshold model, MTLM = multiple threshold lactation model, TDTM = test-day threshold model. The number in parentheses refers to the length of data-recording period (d).

in data sets 2 and 4, mastitis frequency increased with increasing lactation number, and the only difference between these data sets was the data-recording period. Another explanation may be that, during first lactation, mastitis occurs at earlier stages more frequently than during subsequent lactations, where mastitis occurs in later stages of lactation.

Different models were used for the estimation of genetic parameters for the liability to clinical mastitis. In the literature, the traditional approach has been to use linear models (e.g., Lund et al., 1994 and Heringstad et al., 1999) yielding low heritability estimates (0.01 to 0.03). Higher estimates (0.06 to 0.12) were observed when threshold models were used for the analysis of the mastitis data (Heringstad et al., 1997). Heritability estimates of Heringstad et al. (1997) agree with estimates observed in this study using the LTM and MTLM (see Table 4). However, it should be noted that all analyses that define mastitis as a binary trait do not fully use all information in the data because some cows have more cases of mastitis.

One approach to use more information provided by the data is the use of longitudinal threshold models, which was suggested by Rekaya et al. (1998) and Ka-

damideen et al. (2000). However, if these models were to be used, one should be aware of the problem that different observations from the same animal are not uncorrelated. One way to handle this problem was described by Heringstad et al. (2003b). These authors divided lactation into 11 blocks and the heritability was estimated for each block. Most estimates were in the interval between 0.04 and 0.09. Hinrichs et al. (2005) compared the LTM and TDTM, but in the TDTM, each day was used as a single observation. In the present study, the same TDTM was used for the analysis of data set 5 and the estimates were in agreement with those reported by Hinrichs et al. (2005). In the study of the latter authors, the TDTM may have been optimal with respect to utilizing all relevant information. However, if each day was treated as a single observation, the correlation between observations from one animal were higher compared with those using the approach presented by Heringstad et al. (2003b). Furthermore, in the present study, we found that the TDTM was computationally infeasible when the data-recording period covered more than 50 d of lactation.

The MTLM combines the advantages of the TDTM, with respect to information use, and those of the LTM,

Figure 2. Posterior distribution of additive genetic variance for liability to mastitis in different data sets (length of data-recording period in parentheses). MTLM = multiple threshold lactation model, LTM = lactation threshold model.

Figure 3. Posterior distribution of permanent environmental variance for liability to mastitis in different data sets (length of data-recording period in parentheses). MTLM = multiple threshold lactation model, LTM = lactation threshold model.

Figure 4. Posterior distribution of the heritability for liability to mastitis in different data sets (length of data-recording period in parentheses). TDTM = test-day threshold model, MTLM = multiple threshold lactation model, LTM = lactation threshold model.

with respect to computational aspects (e.g., handling of the data sets and computation time). When data recording covered the whole lactation, use of the MTLM resulted in a heritability of 0.11, whereas the LTM gave an estimate of 0.09. When the data-recording period was restricted to the first 50 d of lactation, both models yielded the same heritability estimate. The main advantage of the MTLM is the use of information of repeated cases of mastitis within the same lactation. However, when this information is used, data recording should cover the whole lactation because many repeated cases of mastitis occur after d 50 of lactation. In addition, the MTLM reduces the problem of correlated observations with acceptable loss of information.

Another fact that should be noted is that a lactation curve had to be modeled in longitudinal threshold models. In this study, the lactation curve was modeled as suggested by Ali and Schaeffer (1987). However, alternative functions could be used to model the lactation curve, such as the Wood function (Wood, 1967) or Morant and Ganaskthy curves (Morant and Gnanasakthy, 1989). The effect of these functions on the variance components for mastitis data was studied by Kadamdeen et al. (2000) and the results were very similar for all functions. In addition, Chang et al. (2004) analyzed mastitis data with longitudinal threshold models and concluded that Legendre polynomials were the best function for their data.

Parameters (variance components, heritabilities, and breeding values) were estimated using a Bayesian approach. Posterior distributions of variance components and heritabilities are shown in Figures 2 to 4. All posterior distributions were approximately normal. In addition, posterior distributions of this study have a sharper peak than those in the analysis of Hinrichs et

al. (2005). However, they are comparable to those of Harder et al. (2006) and Heringstad et al. (2003b).

Estimated breeding values (Table 5) suggest that sufficient genetic variation exists for direct selection against clinical mastitis. Rank correlations between breeding values of different models (Table 6) were lower than those observed by Hinrichs et al. (2005). The reason for the lower rank correlation between breeding values was that all sires were included, whereas Hinrichs et al. (2005) used only sires with at least 30 daughters for the calculation. Rank correlations between models increased with increasing reliability of breeding values (e.g., if the reliability of the breeding values were at least 0.25, correlations between the different models were approximately 10% higher than those when all sires were used).

CONCLUSIONS

This study presented different models for the analysis of mastitis data. The use of the MTLM increased the heritability when data recording covered the whole lactation. When data recording was concentrated on early lactation, almost no difference was observed between the MTLM and LTM. As expected, the highest heritability was estimated with the TDTM, but these models are not useful for large data sets. In addition, observations from the same animal were not uncorrelated in the TDTM. Therefore, the use of the MTLM is recommended, as it alleviates the problems due to correlated observations from the same animal. Furthermore, the MTLM used more information provided by the data as compared with the LTM.

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