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Genetic Analysis of Several Economically Important Disease Traits in German Holstein Cows

Dedicated to Professor Dr. Gerhard Seeland on the occasion of his 65th birthday

Abstract

In the present study several disease categories were analysed. Data recording ends after 50, 100, or 300 days in milk. Furthermore, the impact of increasing numbers of daughters per sire (improved genetic structure of the data) was examined and genetic correlations between disease categories were estimated. Diseases were clustered into fertility diseases, udder diseases, metabolic diseases, and claw and leg diseases. In addition, all diseases were analysed simultaneously. Frequencies of the disease categories were moderately high and vary between 7% and 78%. The most frequent disease categories were fertility diseases and udder diseases. Heritabilities for all diseases varied between 0.03 and 0.05, and were 0.02 to 0.05 for fertility diseases, 0.06 to 0.08 for udder diseases, 0.08 to 0.16 for metabolic diseases, and 0.01 to 0.03 for claw and leg diseases, respectively. The genetic correlation between disease categories ranged from – 0.18 to 0.82.

Key Words: disease category, lactation threshold model, heritability, genetic correlation

Zusammenfassung

Titel der Arbeit: **Genetische Analyse verschiedener wirtschaftlich wichtiger Krankheitsmerkmale bei Deutschen Holsteins**

In der vorliegenden Untersuchung wurden verschiedene Erkrankungskategorien analysiert, wobei die Datenerfassung entweder nach den ersten 50, 100 oder 300 Laktationstagen endete. Außerdem wurde der Einfluss einer steigenden Töchterzahl (verbesserte genetische Struktur der Daten) untersucht, und es wurden genetische Korrelationen zwischen den verschiedenen Erkrankungskategorien geschätzt. Die Krankheiten wurden unterteilt in Fruchtbarkeitserkrankungen, Eutererkrankungen, Stoffwechselerkrankungen und Erkrankungen der Klauen und Gliedmaßen. Des weiteren wurden alle Erkrankungen zusammen ausgewertet. Die Erkrankungsfrequenzen schwankten zwischen 7 % und 78 %, wobei die höchsten Frequenzen für Fruchtbarkeitserkrankungen und Eutererkrankungen ermittelt wurden. Die Heritablitäten für alle Erkrankungen lagen zwischen 0,03 und 0,05. Bei den Fruchtbarkeitserkrankungen lagen die Heritabilitäten zwischen 0,02 und 0,05, bei den Eutererkrankungen zwischen 0,06 und 0,08, bei den Stoffwechselerkrankungen zwischen 0,08 und 0,16, und für die Erkrankungen der Klauen und Gliedmassen wurden Heritabilitäten zwischen 0,01 und 0,03 geschätzt. Die genetische Korrelation zwischen den verschiedenen Krankheitskategorien variierte zwischen –0,18 und 0,82.

Schlüsselwörter: Erkrankungskategorie, Laktations-Schwellenwertmodell, Heritabilität, genetische Korrelation

Introduction

Diseases cause considerable economic loss in commercial milk production. Economic losses include prophylactic or clinical treatments, lost milk production, increased days open, and increased culling (KELTON et al., 1998; DISTL, 2001). Furthermore, milk quality is usually reduced and there is an increased disease risk in the future (HERINGSTAD et al., 2000). In addition, health problems led to work loading for the farmers and therefore, the average number of cows, which can be attended by one person, decreases.

The frequencies of different diseases or disease categories per lactation displayed a lot of variation, depending on case definition and data collection. The frequencies of fertility diseases vary widely in different studies. Literature reports of metritis or endometritis frequencies per lactation ranged between 3% and 18% (PÖSÖ and MÄNTYSAARI, 1996; OUWELTJES et al., 1996; GRÖHN and RAJALA-SCHULTZ, 2000). In the analysis of PÖSÖ and MÄNTYSAARI (1996) 10% to 12% of the lactations were affected by ovarian problems, whereas ERIKSSON and WRETLER (1987) reported a lower frequency for cyst ovarian diseases. The frequencies of other fertility problems ranged from 2% to 5% (ERIKSSON and WRETLER, 1987; OUWELTJES et al., 1996; GRÖHN and RAJALA-SCHULTZ, 2000). In addition, mastitis frequency varies over a wide range. GRÖHN and BRUSS (1990) reported a mastitis frequency of 7%, whereas FOURNICHON et al. (2001) reported mastitis frequencies varying between 29% and 51%. HERINGSTAD et al. (1999) observed an increased mastitis frequency per lactation from 1978 to 1994 in Norway.

The heritabilities of different diseases have been estimated in several studies. The most common approach for the estimation of heritabilities has been to consider diseases as "all or none trait" and to apply linear models. The heritabilities of fertility diseases are low, with most values within the interval of 0.01 to 0.05. Heritabilities of metritis were estimated by LYONS et al. (1991), DISTL (1992), OUWELTJES et al. (1996), PÖSÖ and MÄNTYSAARI (1996), and VAN DORP et al. (1998), and estimates for the heritabilities vary between 0.01 and 0.06. Similar heritabilities are estimated for cyst ovarian disease (LYONS et al., 1991; DISTL, 1992; VAN DORP et al., 1998). The heritability of cyst ovarian disease was estimated by HOOIJER et al. (2001) as 0.10. DISTL (1992) estimated heritabilities for retained placenta, metritis, and cystic ovarian. PETERSEN et al. (2002) divided fertility diseases in four disease categories and estimated heritabilities within the interval of 0.08 to 0.14 for the first parity and 0.06 to 0.12 for all parities. As mastitis is the most common udder disease, majority of genetic analyses have involved the study of mastitis data. The heritability of mastitis has been estimated in several studies with most results ranging in the interval of 0.02 to 0.03 (LUND et al. 1994; SANDER NIELSEN et al., 1996; HERINGSTAD et al., 2001a). Higher heritabilities were estimated when threshold models were used (SIMIANER et al., 1991; HERINGSTAD et al., 2001b; HERINGSTAD et al., 2003). The heritabilities of different metabolic diseases cover a wide range in literature reports. For example, LIN et al. (1989), LYONS et al. (1991), URIBE et al. (1995), and VAN DORP et al. (1998) showed heritabilities of milk fever ranging from 0.04 to 0.47. Estimates for heritabilities of ketosis are given by LYONS et al. (1991), SIMIANER et al. (1991), and VAN DORP et al. (1998), and vary between 0.08 and 0.39. Heritabilities of displaced abomasum provided by LYONS et al. (1991), URIBE et al. (1995), and VAN DORP et al. (1998) vary between 0.00 and 0.28. As in the case with other diseases, the heritabilities of claw and leg diseases vary in the literature depending on trait definition. LYONS et al. (1991) differentiate between leg problems, foot problems, and other locomotive problems. The estimated heritabilities of these diseases were 0.09, 0.20, and 0.16, respectively. Estimates for the heritability of lameness are given by BOETTCHER et al. (1998) and VAN DORP et al. (1998) and were 0.10 and 0.26, respectively. Estimates for the heritabilities of all diseases were

given by LYONS et al. (1991) and vary between 0.02 and 0.17, thereby showing similar results to the analysis of SIMIANER et al. (1991).
Genetic correlations between different disease classes were not estimated in most studies. HANSEN et al. (2002) found a genetic correlation of 0.24 between clinical mastitis and other diseases excluding clinical mastitis.
The aim of the present study was to examine several disease categories in German Holsteins. Diseases were clustered into udder diseases, fertility diseases, metabolic diseases, and claw and leg diseases. In addition, analyses were carried out on data sets including all available disease information. The influence of the number of daughters per sire (improved genetic structure of the data) was analysed with data sets where only records from sires with at least 1 (data sets 1.1 – 1.15), 10 (data sets 2.1 – 2.15), 30 (data sets 3.1 – 3.15), or 50 daughters (data sets 4.1 – 4.15) were considered. The frequencies of the disease categories are presented first, followed by the results of the variance component estimation. A further step involves the estimation of genetic correlations between disease categories. Finally, the heritabilities estimated by using lactation threshold models were compared to those estimated by linear lactation models.

Materials and Methods

Data for this study were recorded on three large commercial dairy farms with an overall number of 3200 German Holstein cows, which are involved in a special data-recording scheme (HINRICHS et al., 2006). In this data recording scheme the information, which was stored on farms in computer based management programs should be used for a further improvement of the performance test in dairy cattle. Therefore, farms were visited monthly and security copies (Backups) of the computer based management programs were taken. New information of the last month was checked for plausibility. Questionable new information was discussed with the farm management and the veterinarian and discarded if they cannot be allocated clearly. Furthermore, the same bulls were used for artificial insemination on the three farms. This led to a genetic connection between the farms. Data recording was carried out between February 1998 and December 2002. The considered period of lactation starts with calving date and ends after 50, 100 or 300 days in milk. All medical treatments undertaken by veterinarian or farm staff were recorded and resulted in 75,603 treatments. In a first step diagnoses have been summarised into groups, which were divided into five different disease categories (see Table 1).

Table 1
Disease categories and recorded treatments during the first 50, 100, and 300 days of lactation (Registrierte Behandlungen für die verschiedenen Erkrankungskategorien während der ersten 50, 100 und 300 Laktationstage)

		days in milk		
Disease category		50	100	300
Udder diseases	UD	17,122	23,209	39,943
Fertility diseases	FD	16,203	19,638	24,563
Claw and leg diseases	CD	2138	2916	5085
Metabolic diseases	MD	3410	3615	4131
All diseases	AD	39,954	50,667	75,603

For each disease category several data sets were analysed, where data recording ends after 50, 100, or 300 days of lactation. Furthermore only records from sires with at

least 1, 10, 30 or 50 daughters were considered. The increasing number of daughters per sire was equal to an improved genetic structure of the data. In total 60 data sets were analysed. In the data sets 1.1 to 1.15 all available information was considered. The data sets 2.1 to 2.15 contained only observations from sires with at least 10 daughters, and sires have to have at least 30 or 50 daughters in the data sets 3.1 to 3.15 and 4.1 to 4.15, respectively. Independent of the number of daughters per sire analyses were carried out for all diseases, fertility diseases, udder diseases, metabolic diseases, and claw and leg diseases. Furthermore the data sets were different in the considered period of lactation (50, 100, or 300 days). Observations decrease from 17,183 to 9521, and also the number of animals and sires decrease.

Each observation was allocated a disease code, "1" if a cow showed disease during the observed time period and "0" if not. The significance of fixed environmental effects, lactation and herd calving season, was analysed by using the GENMOD procedure of the SAS package (SAS, 1999). Lactation number four and higher lactations were summarised into one class, whereas lactation one, two, and three were treated as distinct classes. All models include the herd calving season within herd as a multicode. Each year was divided into three calving seasons. Calving time between January and March was summarised to calving season one, as were April to August, and September to December for the other two calving seasons, respectively. All fixed effects were significant ($p < 0.001$) overall models. A threshold liability model (WRIGHT, 1934; DEMPSTER and LERNER, 1950; GIANOLA and FOULLEY, 1983) was used for the estimation of random permanent environmental variance and additive genetic variance. In this study an animal model was applied to all data sets. The following lactation threshold model was used for the estimation of variance components for all data sets:

$$E[\pi_{ijkl}] = \Phi (K_i + L_j + c_1x + c_2x^2 + m_k + t_l),$$

where:

$E[\pi_{ijkl}]$	= expected probability for occurrence of the considered disease	
Φ	= cumulative probability function of the standard normal distribution	
K_i	= fixed effect of the i-th farm calving season	(i = 1,...,45)
L_j	= fixed effect of the j-th lactation	(j = 1,...,4)
c_1x	= linear regression on days in milk	
c_2x^2	= quadratic regression on days in milk	
m_k	= random permanent environmental effect	(k = 1,...,9889)*
t_l	= random effect of the l-th animal	(l = 1,...,15,802)

* The number of random permanent environmental effects decreased from 9889 for data sets 1.1 to 1.15,to 8640, 6595 and 5618 for data sets 2.1 to 2.15, 3.1 to 3.15 and 4.1 to 4.15, respectively.

In the lactation threshold model c_1x and c_2x^2 are the regression on the section x, where x are the days in milk. Therefore animals, which where culled before the end of the considered period (50, 100, or 300 days of lactation) could be retained in the analyses. The posterior distributions of the permanent environmental variance and additive genetic variance for the liability to the different disease classes were determined through the Gibbs sampling algorithm implemented in the LMMG_TH program, a threshold derivate of LMMG (REINSCH, 1996). The LMMG_TH program based on the results presented by SORENSEN et al. (1995). For random effects multivariate normal distribution with zero means and appropriate variance – covariance matrices

were used and improper flat priors for fixed effects. For all models 100,000 cycles were generated and the results from each cycle were retained. The results of the first 10,000 cycles were discarded (burn in plus a safety margin) while the genetic parameters were calculated using the remaining 90,000 cycles by using the MEAN procedure of the SAS package (SAS, 1999). The convergence was determined by visual inspection of plots of realised parameter values against iteration number. Similar convergence detection was used by REINSCH et al. (1999).

Genetic correlations were estimated with a linear multivariate lactation model using the program VCE 4 (GROENEVELD, 1998). The linear lactation model included lactation number and farm calving season as fixed effects. Furthermore, the permanent environmental and the additive genetic effect of the animal and a residual effect were treated as random effects in the linear lactation model. The following linear lactation model was used for the estimation of genetic correlations between the disease categories:

$$y_{ijklm} = \mu + K_i + L_j + c_1x + c_2x^2 + m_k + t_l + e_{ijklm}$$

where:

y_{ijklm} = disease category record
μ = overall mean
K_i = fixed effect of the i-th farm calving season (i = 1,...,45)
L_j = fixed effect of the j-th lactation (j = 1,...,4)
c_1x = linear regression on days in milk
c_2x^2 = quadratic regression on days in milk
m_k = random permanent environmental effect (k = 1,...,9889)*
t_l = random effect of the l-th animal (l = 1,...,15,802)
e_{ijklm} = random residual effect

Table 2
Disease frequencies of different categories of diseases for all data sets (Erkrankungsfrequenzen der verschiedenen Krankheitskategorien für alle Datensätze)

Data set	Daughters at least	AD	FD	UD	MD	CD
Lactation threshold models 50						
1.1 to 1.5	1	61.5	37.9	30.3	10.4	8.1
2.1 to 2.5	10	62.5	39.1	30.9	10.2	7.8
3.1 to 3.5	30	63.7	40.9	32.1	9.7	7.2
4.1 to 4.5	50	64.5	42.4	32.1	9.3	6.9
Lactation threshold models 100						
1.6 to 1.10	1	68.5	44.3	35.6	11.1	10.0
2.6 to 2.10	10	69.2	45.4	35.9	10.8	9.6
3.6 to 3.10	30	70.2	47.2	37.2	10.3	8.9
4.6 to 4.10	50	70.8	48.7	36.9	9.9	8.4
Lactation threshold models 300						
1.11 to 1.15	1	76.9	50.4	46.0	12.6	14.3
2.11 to 2.15	10	77.1	50.8	46.1	12.3	13.4
3.11 to 3.15	30	77.7	52.1	47.3	11.8	12.4
4.11 to 4.15	50	78.0	53.3	47.1	11.4	11.7

AD = all diseases, FD = fertility diseases, UD = udder diseases, MD = metabolic diseases, CD = claw and leg diseases

Results

Frequencies of disease categories

Frequencies of different disease categories for all data sets are shown in Table 2. Fertility diseases were the most frequent disease category, followed by udder diseases.

The third most frequent disease category varied depending on data collection. Metabolic diseases were most prevalent during the first 100 days in milk, whereas claw and leg diseases were the third most frequent disease category when the first 300 days in milk are considered. This suggests that claw and leg diseases are occur during the whole lactation period, whereas metabolic diseases are concentrated at the beginning of lactation (see Table 2).
The frequencies of the disease categories fertility diseases and udder diseases increased with the number of daughters per sire, whereas the frequencies of metabolic diseases and claw and leg diseases decreased with increasing number of daughters per sire.

Variance component estimation
Table 3 summarises the results of the variance component estimation of the analysed diseases categories. Additive genetic variance and permanent environmental variance of all diseases are similar overall in the analysed data sets and, varying between 0.03 and 0.05, and 0.03 and 0.07, respectively.

Table 3
Posterior means of additive genetic variance (σ^2_a) and permanent environmental variance (σ^2_{pe}) of the analysed disease categories depending on days in milk and daughters per sire (different genetic structures of the data) and their corresponding standard errors (SE) (Posteriori Mittelwerte der additiv genetischen Varianz (σ^2_a) und der permanenten Umweltvarianz (σ^2_{pe}) der untersuchten Erkrankungskategorien für die verschiedenen Laktationslängen und die verschiedenen Töchterzahlen je Bulle (unterschiedliche genetische Strukturen der Daten) sowie deren Standardfehler (SE))

		σ^2_a (SE)					σ^2_{pe} (SE)				
DPS	DIM	AD	FD	UD	MD	CD	AD	FD	UD	MD	CD
1	50	0.03 (0.01)	0.06 (0.02)	0.10 (0.02)	0.15 (0.04)	0.02 (0.02)	0.05 (0.02)	0.05 (0.02)	0.11 (0.03)	0.20 (0.06)	0.22 (0.05)
	100	0.05 (0.01)	0.04 (0.01)	0.10 (0.02)	0.13 (0.03)	0.03 (0.02)	0.04 (0.02)	0.06 (0.02)	0.09 (0.03)	0.20 (0.06)	0.24 (0.05)
	300	0.04 (0.01)	0.06 (0.02)	0.08 (0.02)	0.10 (0.03)	0.03 (0.02)	0.03 (0.02)	0.08 (0.03)	0.12 (0.03)	0.19 (0.04)	0.23 (0.04)
10	50	0.03 (0.01)	0.05 (0.02)	0.08 (0.02)	0.18 (0.05)	0.03 (0.02)	0.06 (0.02)	0.05 (0.03)	0.13 (0.03)	0.19 (0.06)	0.23 (0.06)
	100	0.05 (0.02)	0.04 (0.01)	0.08 (0.02)	0.16 (0.04)	0.03 (0.03)	0.03 (0.02)	0.07 (0.03)	0.10 (0.03)	0.18 (0.06)	0.25 (0.06)
	300	0.04 (0.01)	0.03 (0.02)	0.08 (0.02)	0.13 (0.03)	0.03 (0.02)	0.04 (0.02)	0.10 (0.03)	0.12 (0.03)	0.18 (0.05)	0.20 (0.05)
30	50	0.04 (0.02)	0.04 (0.02)	0.09 (0.02)	0.22 (0.06)	0.04 (0.02)	0.07 (0.03)	0.07 (0.03)	0.13 (0.03)	0.21 (0.09)	0.26 (0.08)
	100	0.05 (0.02)	0.04 (0.02)	0.07 (0.02)	0.21 (0.06)	0.03 (0.02)	0.04 (0.03)	0.07 (0.03)	0.09 (0.03)	0.20 (0.08)	0.27 (0.07)
	300	0.05 (0.02)	0.04 (0.01)	0.08 (0.02)	0.14 (0.04)	0.04 (0.02)	0.06 (0.03)	0.09 (0.03)	0.13 (0.04)	0.19 (0.06)	0.23 (0.05)
50	50	0.05 (0.02)	0.03 (0.02)	0.08 (0.03)	0.21 (0.07)	0.03 (0.03)	0.04 (0.03)	0.06 (0.03)	0.11 (0.04)	0.26 (0.10)	0.22 (0.09)
	100	0.05 (0.02)	0.03 (0.02)	0.08 (0.03)	0.22 (0.08)	0.02 (0.02)	0.04 (0.02)	0.08 (0.03)	0.07 (0.03)	0.23 (0.10)	0.28 (0.07)
	300	0.05 (0.02)	0.05 (0.02)	0.08 (0.02)	0.16 (0.05)	0.01 (0.01)	0.04 (0.03)	0.08 (0.04)	0.10 (0.04)	0.14 (0.07)	0.24 (0.06)

DPS = daughters per sire, DIM = days in milk, AD = all diseases, FD = fertility diseases, UD = udder diseases, MD = metabolic diseases, CD = claw and leg diseases

The heritabilities and repeatabilities for the different data sets are shown in Table 4. The estimated heritabilities ranged from 0.01 to 0.16 and between 0.07 and 0.32 for the repeatabilities, respectively.

Table 4
Posteriori means of heritabilities (h^2) and repeatabilities (r) of the analysed disease categories depending on days in milk and daughters per sire (different genetic structures of the data) and their corresponding standard errors (SE) (Posteriori Mittelwerte der Heritabilitäten und Wiederholbarkeiten der untersuchten Erkrankungskategorien für die verschiedenen Laktationslängen und die verschiedenen Töchterzahlen je Bulle (unterschiedliche genetische Strukturen der Daten) sowie deren Standardfehler (SE))

		h^2 (SE)					r (SE)				
DPS	DIM	AD	FD	UD	MD	CD	AD	FD	UD	MD	CD
1	50	0.03 (0.01)	0.05 (0.02)	0.08 (0.02)	0.11 (0.02)	0.02 (0.01)	0.07 (0.02)	0.10 (0.02)	0.17 (0.02)	0.25 (0.03)	0.19 (0.03)
	100	0.05 (0.01)	0.03 (0.01)	0.08 (0.02)	0.10 (0.02)	0.02 (0.02)	0.08 (0.02)	0.09 (0.02)	0.15 (0.02)	0.25 (0.03)	0.21 (0.03)
	300	0.04 (0.01)	0.05 (0.01)	0.07 (0.02)	0.08 (0.02)	0.03 (0.01)	0.07 (0.02)	0.12 (0.02)	0.17 (0.02)	0.22 (0.03)	0.21 (0.03)
10	50	0.03 (0.01)	0.04 (0.01)	0.07 (0.02)	0.13 (0.03)	0.02 (0.02)	0.08 (0.02)	0.08 (0.02)	0.18 (0.02)	0.27 (0.03)	0.21 (0.04)
	100	0.05 (0.02)	0.04 (0.01)	0.07 (0.02)	0.12 (0.03)	0.02 (0.02)	0.07 (0.02)	0.10 (0.02)	0.16 (0.02)	0.25 (0.03)	0.22 (0.04)
	300	0.04 (0.01)	0.03 (0.01)	0.07 (0.02)	0.10 (0.02)	0.02 (0.01)	0.07 (0.02)	0.11 (0.02)	0.17 (0.02)	0.23 (0.03)	0.19 (0.03)
30	50	0.04 (0.02)	0.04 (0.02)	0.07 (0.02)	0.16 (0.04)	0.03 (0.01)	0.10 (0.02)	0.10 (0.02)	0.18 (0.02)	0.30 (0.04)	0.23 (0.05)
	100	0.04 (0.02)	0.04 (0.02)	0.06 (0.02)	0.15 (0.04)	0.02 (0.01)	0.08 (0.02)	0.10 (0.03)	0.14 (0.02)	0.29 (0.04)	0.23 (0.04)
	300	0.05 (0.02)	0.03 (0.01)	0.06 (0.02)	0.11 (0.03)	0.03 (0.01)	0.09 (0.03)	0.12 (0.02)	0.17 (0.02)	0.25 (0.04)	0.21 (0.03)
50	50	0.05 (0.02)	0.02 (0.01)	0.07 (0.03)	0.14 (0.05)	0.02 (0.02)	0.09 (0.03)	0.08 (0.03)	0.16 (0.03)	0.32 (0.05)	0.20 (0.06)
	100	0.04 (0.02)	0.03 (0.01)	0.07 (0.02)	0.15 (0.05)	0.02 (0.02)	0.08 (0.02)	0.10 (0.03)	0.13 (0.03)	0.31 (0.05)	0.23 (0.04)
	300	0.05 (0.02)	0.05 (0.02)	0.07 (0.02)	0.12 (0.04)	0.01 (0.01)	0.08 (0.03)	0.12 (0.03)	0.15 (0.03)	0.23 (0.04)	0.20 (0.04)

DPS = daughters per sire, DIM = days in milk, AD = all diseases, FD = fertility diseases, UD = udder diseases, MD = metabolic diseases, CD = claw and leg diseases

Genetic correlations between disease categories

The genetic correlations between disease categories are shown in Table 5. Table 5 also provides the estimates of heritabilities of disease categories estimated with a linear lactation model. All available disease information and the first 300 days in milk are used for the estimation. The estimates for the heritabilities based on a linear lactation model are low and vary between 0.02 and 0.03 (see Table 5). All estimates of heritabilities are higher if lactation threshold models are used (see Table 4).

Table 5
Genetic correlations between different disease categories (above the diagonal) and heritabilities (on the diagonal) and their corresponding standard errors (SE)(Genetische Korrelationen zwischen den verschiedenen Erkrankungskategorien (oberhalb der Diagonalen) und Heritabilitäten der verschiedenen Erkrankungskategorien (auf der Diagonalen) sowie deren Standardfehler (SE)).

	AD (SE)	FD (SE)	UD (SE)	MD (SE)	CD (SE)
AD	0.02 (0.003)	0.82 (0.059)	0.62 (0.044)	0.18 (0.088)	0.43 (0.103)
FD		0.02 (0.004)	0.17 (0.119)	- 0.02 (0.118)	0.54 (0.161)
UD			0.03 (0.004)	- 0.05 (0.061)	- 0.18 (0.102)
MD				0.03 (0.004)	- 0.18 (0.149)
CD					0.02 (0.004)

AD = all diseases, FD = fertility diseases, UD = udder diseases, MD = metabolic diseases, CD = claw and leg diseases
n = 17,183 lactations, all sires, 300 days in milk

As expected the disease category ‘all diseases’ shows a positive genetic correlation to the other disease categories. Between all diseases and fertility diseases the genetic correlation is 0.82. The genetic correlation between all diseases and udder diseases is also high with an estimate of 0.62. The genetic correlation between all diseases and metabolic diseases is 0.18. For claw and leg diseases this correlation is 0.43, respectively. Another clear correlation exists between the category fertility diseases and claw and leg diseases (0.54). The remaining correlations vary between – 0.18 and 0.26 (see Table 5).

Discussion

Different diagnoses and frequencies of different disease classes and data recording

The aggregation of diagnoses to disease categories was necessary because approximately 350 different diagnoses were observed in this study. A similar set of disease categories were also used by NIELSEN et al. (1999) and COLLARD et al. (2000). Another possible method, adopted by LUND et al. (1994) and HANSEN et al. (2002) is to generate categories by using clinical mastitis and other diseases. Dividing diagnoses into mastitis and other diseases bar mastitis should be used for the analysis of mastitis data only. In this case other diseases include all fertility, metabolic, and claw and leg diseases so these disease categories cannot be analysed separately. The number of daughters per sire (genetic structure of the data) did not generally affect the frequencies of different disease categories. The frequencies across all disease categories of this study are relatively high compared to those observed by NIELSEN et al. (1999), while estimations of COLLARD et al. (2000) are only lower in some disease categories. The varying disease frequencies in the literature are driven by the different data recording schemes, which have been used for the different studies.

The frequencies of fertility diseases vary between 38% and 53% (see Table 2), while NIELSEN et al. (1999) estimated the frequencies of reproductive diseases between 4% and 17%. COLLARD et al. (2000) estimated the frequency of reproductive problems as 16%. NIELSEN et al. (1999) summarised several diagnoses for the disease category reproductive diseases. Differences in frequencies of fertility diseases are affected by trait definition, length of data collection period, and available information. Udder disease frequencies in this study vary between 30% and 47% (see Table 2). These results are again higher than those observed by other studies (NIELSEN et al., 1999; HERINGSTAD et al., 2003). However, some udder disease frequencies are in line with previous studies (COLLARD et al., 2000; FOURNICHON et al., 2001). For udder diseases, trait definition is of less importance, because mastitis is the most frequent udder disease. Frequencies of metabolic diseases vary between 9% and 12%. NIELSEN et al. (1999) reported frequencies for metabolic diseases in the range of 3% to 12%. The frequency of metabolic diseases published by COLLARD et al. (2000) was 19%, which was significantly higher than those analysed in this study (see Table 2). Frequencies of claw and leg diseases in this study vary between 7% and 14%. This is significantly lower than the frequency observed by COLLARD et al. (2000) who provided a lactational incidence of 35%. NIELSEN et al. (1999) reported frequencies from 3% to 7%, which is lower than the incidence in this study. The frequencies of all diseases were relatively high in this study. Estimations vary from 61% to 78% (see Table 2). COLLARD et al. (2000) reported a frequency of 68% for the disease category ‘all diseases’.

It should be noted that diversity of case definition, variations in data recording, and different data sources might result in differences in frequencies. Therefore the comparison of different disease categories from different studies is difficult and could increase with the number of diagnoses summarised to one disease category. Standard evaluation of diagnoses and data recording period are necessary to improve the comparability of different studies.
For the most disease categories data recording could be concentrated on a relatively short phase at the beginning of lactation (e.g. 50 days in milk). For metabolic diseases and udder diseases the first 50 days of lactation are particularly suitable as a data-recording period for genetic analyses because most cases of these diseases occurred during the first 50 days in milk. For claw and leg diseases data recording should be expanded to include the first 300 days in milk. This is due to the fact that claw and leg diseases are distributed over the whole period of lactation. Furthermore, fertility diseases should be divided into the categories 'ovarian problems' and 'non ovarian problems'. Data recording for ovarian problems should be extended to include the first 100 days in milk, whereas the first 50 days in milk could be used for non-ovarian problems.

Variance component estimation
The difference between additive genetic variance and permanent environmental variance for fertility diseases increases with increasing period of data recording (see Table 3). This suggests that fertility diseases during the first 50 days of lactation are more likely to be genetic related than those fertility diseases occurring during the remaining part of lactation. The definition of two categories should lead to an increase in additive genetic variance of fertility diseases. Ovarian issues are treated as one category, while all other fertility diseases are treated as a second group including endometritis and retained placenta. The low additive genetic variance and permanent environment variance resulted in low estimates of the heritability of fertility diseases that ranged between 0.02 and 0.05 (see Table 4). These low heritabilities are in line with the results from LYONS et al. (1991) and NIELSEN et al. (1999).
In our study 95% of all treated udder diseases were mastitis, which made the comparison of heritability estimates for clinical mastitis and udder diseases possible. The estimates of heritabilities for udder diseases (0.06 – 0.08) were in line with those given by HERINGSTAD et al. (2001a, 2003) for clinical mastitis. Most of our estimated heritabilities for udder diseases were higher than the estimates provided by LYONS et al. (1991) and NIELSEN et al. (1999), because these authors used linear models and not the threshold models used in this analysis.
The additive genetic variance, as well as the permanent environmental variance for metabolic diseases was the highest of all disease categories analysed in this study. The additive genetic variance of metabolic diseases ranged from 0.10 to 0.22 and permanent environmental variance of metabolic diseases ranged from 0.14 to 0.26, respectively (see Table 3). In addition, high additive genetic variance also led to higher estimates of heritabilities of metabolic diseases, which vary in this study between 0.08 and 0.16. These estimates are significantly higher than estimates (0.00 – 0.05) provided by NIELSEN et al. (1999). These higher heritabilities are most likely the result of the use of threshold models.
The low additive genetic variance of claw and leg diseases results in low estimates for the heritabilities of claw and leg diseases (0.01 to 0.04). These study results are in line

with heritabilities estimates of NIELSEN et al. (1999) who reported claw and leg disease heritabilities within the range of 0.00 to 0.01. Higher heritabilities for claw and leg diseases where estimated by LYONS et al. (1991), with 0.02 to 0.16. Furthermore repeatabilities for claw and leg diseases observed by LYONS et al. (1991) were not consistent with the repeatabilities (0.19 to 0.23) for claw and leg diseases in this study.
The additive genetic variance for all diseases was fairly constant with values between 0.03 and 0.05, whereas permanent environmental variance for all diseases ranged between 0.03 and 0.07. This led to the low estimates for the heritabilities and repeatabilities of all diseases, which vary between 0.03 and 0.05, and 0.08 to 0.10, respectively. These estimates are low compared to those provided by LYONS et al. (1991), who provided estimates between 0.02 and 0.17 for the heritability, and 0.20 to 0.29 for the repeatability.

Daughters per sire (improved genetic structure of the data)
The number of daughters per sire shows no effect on the frequencies of disease categories, with the exception that fertility and udder diseases slightly increased. This was a result of the special data-recording scheme. This data-recording scheme led to more daughters per sire, i.e. an improved genetic structure of the data in the years 2000 and 2001. Furthermore, in these years the data recording scheme was established and therefore nearly all treatments could be allocate. Due to the fact that fertility and udder diseases are the most important disease categories data recording concentrated first on these two disease categories, followed by metabolic diseases and claw and leg diseases.
The heritabilities of metabolic diseases increases with the number of daughters per sire (improved genetic structure of the data) but the improved genetic structure of the data had no distinct effect on the heritabilities of the remaining disease categories.

Genetic correlations between different disease categories
The positive genetic correlation between disease traits and yield traits is generally accepted and has been estimated in several studies (LYONS et al., 1991; LUND et al., 1994; HERINGSTAD et al., 1999). Only NIELSEN et al. (1999) provided estimates for the genetic correlation between different disease categories, whereas HANSEN et al. (2002) estimated a genetic correlation between mastitis and diseases other than mastitis.
The genetic correlations between the disease category ‘all diseases’ and the remaining disease categories are high because the disease category ‘all diseases’ summarises all available disease information. This leads to high genetic correlation between all diseases and fertility diseases (0.82) and udder diseases (0.62), because these two categories are the most frequent diseases. However, there are still moderate genetic correlations between all diseases and claw and leg diseases (see Table 5).
The genetic correlation between fertility diseases and udder diseases was estimated as 0.17, which was in the line with the genetic correlation (0.19 to 0.47) estimated by NIELSEN et al. (1999). No genetic correlation could be estimated between fertility diseases and metabolic diseases. This is in disagreement with the results provided by NIELSEN et al. (1999), where most estimates of the genetic correlation between fertility diseases and metabolic diseases were positive. Furthermore, the estimated genetic correlation between fertility diseases and claw and leg diseases (0.54) in this study is higher, than that provided by NIELSEN et al. (1999).

The estimate of the genetic correlation between udder diseases and metabolic diseases is low in this study (see Table 4), whereas NIELSEN et al. (1999) provided a moderate positive genetic correlation. NIELSEN et al. (1999) provided a positive genetic correlation between claw and leg diseases, and udder diseases and metabolic diseases, respectively.

Conclusions

Diseases are one of the major problems in commercial milk production and 78% of all lactations in this study were affected by disease problems. The development of recording schemes is therefore necessary. Data recording can be concentrated at the beginning of lactation because most diseases occurred during the first 50 days of lactation. As claw and leg diseases are distributed over the whole period of lactation, data recording should be extended beyond the first 50 days in milk. Fertility diseases should be divided into ovarian problems and non-ovarian problems. The results of our study show that data recording is possible on commercial dairy farms. The creation of diseases categories simplifies genetic analyses because different diagnoses given by different persons do not affect the results of genetic analyses. Considering disease information in commercial breeding schemes would improve the genetic gain of health traits. Furthermore, threshold models should be used for the analysis of disease data sets. The development of test day threshold models is an important area of research, especially for disease categories where repeated cases during lactation are possible.

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