Genetic Correlations among Health Traits in Different Lactations

Ulrik Sander Nielsen[1], Gert Aamand Pedersen [1], Jørn Pedersen [1]and Just Jensen [2]
[1] The Danish Agricultural Advisory Centre, Udkaersvej 15, Skejby, DK-8200 Aarhus N, Denmark
[2]The Danish Institute of Agricultural Sciences, Research Centre Foulum, P.O. Box 39, DK-8830 Tjele, Denmark

1. Introduction

Diseases reduce animal welfare and result in economic losses for the farmer in the form of extra veterinary treatments and labour, decreasing milk production, discarded milk and involuntary early culling. A reduction in the frequency of diseases by selection is desirable from a general ethical point of view, it might increase consumer acceptance and it is of course of economic importance. If an improvement of the disease resistance is included in dairy cattle breeding programs, it is necessary to obtain reliable estimates of heritabilities, genetic and phenotypic correlations for the disease and milk production traits.

The objectives of this project were:

- to estimate the genetic parameters for four categories of disease traits
- to estimate the genetic relationships between udder diseases and somatic cell count
- to estimate the genetic relationships between disease and milk production
- to estimate the genetic relationships between disease incidence in different lactations

Previous studies of the genetic parameters of diseases have shown that most diseases have low heritabilities and are generally unfavourably correlated to milk production traits. The published results have mostly been from analysis of small data sets, the definition of the disease traits have been varying and consequently the results have been variable:

- *Udder diseases:* The heritabilities of the udder diseases (or mastitis) have been reported to be 0.01 - 0.04 when analysed on the observable scale (Syväjärvi et al., 1986; Madsen et al., 1987; Emanuelson et al., 1988; Weller et al., 1992; Koenen et al., 1994; Groen et al., 1994; Pösö & Mäntysaari, 1995).
  In threshold models the estimates have been 0.07 - 0.12 (Simianer et al., 1991; Emanuelson et al., 1993; Uribe et al., 1995). Unfavourable genetic correlations with milk production in the range of 0.15 - 0.50 have been reported (Syväjärvi et al., 1986; Madsen et al., 1987; Simianer et al., 1991; Groen et al., 1994; Pösö & Mäntysaari, 1995).
- *Somatic cell count:* The heritabilities of somatic cell count have been 0.05 - 0.15. (Monardes & Hayes, 1985; Emanuelson et al., 1988; Banos & Shook, 1990; Schutz et al., 1990; Welper & Freeman, 1992; Rogers et al., 1995; Pösö & Mäntysaari, 1995). The genetic correlation between udder diseases (mastitis) and somatic cell count has been around 0.5 - 0.7 (Madsen et al., 1987; Emanuelson et al., 1988; Pösö & Mäntysaari, 1995).
- *Reproductive diseases*: The diseases analysed have been retained placenta, metritis, ovarian cysts or the total number of reproductive diseases. The heritabilities have been in the range of 0.02 - 0.08 (Lyons et al., 1991; Koenen et al., 1994; Uribe et al., 1995).
- *Digestive diseases:* The disease traits that have been analysed are ketosis, milk fever, displaced abomasum or the total number of digestive disorders and the heritabilities have been in the range of 0.00 - 0.17 (Philipson et al., 1980; Emanuelson, 1988; Lyons et al., 1991; Mäntysari et al., 1991; Simianer et al., 1991; Uribe et al., 1995).
- *Feet & leg diseases:* The heritabilities of feet and leg diseases have been reported to be 0.01 - 0.08 (Philipson et al., 1980; Lyons et al., 1991; Groen et al., 1994).

2. Material and methods

2.1. The data

Data from the Danish health recording system were analysed separately for Red Danish cattle (RD), Danish Friesian (DF) and Danish Jerseys (DJ). Only cows initiating a lactation in the period 1990-1994 were included in the analysis. In order to obtain an acceptable number of disease records from second and later lactations data was accepted even if there was no first lactations included. This might introduce some bias due to selection but probably the bias would be small.

The data were edited as described in the following and Table 1 shows the number of records and the average results of the data used in the analyses:

- The definition of a disease trait was the number of treatments reported by veterinarians or farmers in the period)10 to 305 days from calving. All cows initiating a lactation were included. The time of culling was ignored. The maximum number of treatments included per category of disease was three. Repeated treatments within 2 days of the first treatment were not counted.

Table 1. Averages results and number of observations used in the analyses.

	Number of observations			Average results		
	RD	DF	DJ	RD	DF	DJ
Protein yield, 1st lact. (kg)	57,237	160,195	30,767	209	211	176
Somatic cell count, 1st lact. ($\log_e$)	43,364	125,097	23,655	11.05	11.18	11.05
Somatic cell count, 2nd lact. ($\log_e$)	21,827	112,077	26,470	11.63	11.65	11.37
Somatic cell count, 3rd lact. ($\log_e$)	10,581	61,627	16,547	11.97	11.87	11.65
Udder diseases, 1st lact.	58,259	163,361	31,559	0.41	0.38	0.44
Udder diseases, 2nd lact.	41,465	191,557	43,756	0.42	0.38	0.33
Udder diseases, 3rd lact.	23,666	115,844	29,052	0.51	0.46	0.37
Reproductive d., 1st lact.	58,259	163,361	31,559	0.14	0.12	0.05
Reproductive d., 2nd lact.	41,465	191,557	43,756	0.15	0.14	0.07
Reproductive d., 3rd lact.	23,666	115,844	29,052	0.17	0.16	0.07
Digestive diseases, 1st lact.	58,259	163,361	31,559	0.12	0.12	0.10
Digestive diseases, 2nd lact.	41,465	191,557	43,756	0.15	0.12	0.10
Digestive diseases, 3rd lact.	23,666	115,844	29,052	0.26	0.20	0.19
Feet and legs, 1st lact.	58,259	163,361	31,559	0.08	0.08	0.05
Feet and legs, 2nd lact.	41,465	191,557	43,756	0.05	0.05	0.03
Feet and legs, 3nd lact.	23,666	115,844	29,052	0.06	0.06	0.03

- Only first lactations from herds with more than 12 first lactation records per year were included. For second and later lactation this requirement was reduced to 3 second lactations per herd-year. Due to these editing rules the number of second lactations included was higher than the number of first lactations (Table 1). There is no explanation for the difference other than the editing was made in two steps and there was no time for reruning the editing of the first lactation data.
- Somatic cell count was the average of natural logarithm of test day somatic cell count in the period)10 to 180 days from calving. It was required that the cows were not culled before 180 days from calving.
- The yield record used in the analyses was 305 days protein yield including extended records. Only cows with disease records were included. Additionally, yield records on cows culled within the first 45 days of the lactation were deleted. This explains why the number of observations on protein yield is lower than the number of disease observations (Table 1).

2.2. Disease categories

The treatments were summarized for all diseases in the four main categories: udder diseases, reproductive diseases, digestive diseases and feet and leg diseases. The maximum of 3 treatments per disease applied to the category of disease and not to a specific disease. The four categories included the following diseases:

- *Udder diseases* include summer mastitis, teat dermatitis, teat amputation, teat surgery, teat tramp, mastitis, acute mastitis, necrotzing mastitis, subclinical mastitis, dry period mastitis, mastitis due to teat tramp and other udder diseases.
- *Reproductive diseases* include abortion, endometritis, uterine prolapse, uterine torsion, endometritis treatment, follicular cysts, retained placenta, caesarian section, vaginitis and other reproductive diseases.
- *Digestive diseases* include diarrhoea, traumatic reticuloperitonitis, ludigestion, hypomagnesemia, ketosis, milk fever, abomasal displacement, abomasal indigestion, rumen acidosis, enteritis, bloat and other digestive and metabolic diseases.
- *Feet and leg diseases* include heel erosion, interdigital dermatitis, claw trimming by veterinarian, interdigital necrobacillosis, interdigital skin hyperplasia, laminitis, arthritis, sole ulcer, pressure injuries, tenosynovitis of hoofs and other leg diseases.

2.3. Estimation

Diseases in different lactations were regarded as different traits. With three lactations included the number of disease traits analysed was 12. Additionally, somatic cell counts in three lactations and first lactation protein yield were included in the analyses such that the total number of traits was 16. (Co)variance components were estimated using a bi- or tri-variate REML method (Madsen et al. 1994) with a linear sire model. The DMU-program developed by Jensen & Madsen (1994) was used. All data were analysed on the observed scales, i.e. no transformations were applied and there was no accounting for the non-continuous type of distributions.

The following linear sire model was applied for all traits:

Effect		Type of effect
Y =	herd*year	fixed
+	year*month	fixed
+	calving age	fixed (only first lactation)
+	additive breed effects	covariable
+	heterosis effects	covariable
+	sire	random
+	residual	random

The (co)variance component for RD and DJ for the three lactations within udder diseases, reproductive, digestive and feet&leg diseases were estimated in trivariate analyses whereas all the remaining parameters were estimated in bivariate analysis. The choice between bi- or trivariate analyses was determined by the computer resources available.

The variances of the (co)variance components were estimated from the average of the observed and the expected information matrices. The standard errors of the population parameters were then calculated using Taylor series approximations. The DMU-program (Jensen & Madsen, 1994) includes a routine for these calculations.

3. Results and discussion

The Tables 2 - 6 show the estimates of the genetic parameters obtained. The genetic parameters were not estimated for all possible combinations of the traits and therefore there are empty cells in the tables. Table 2 shows the estimated genetic parameters of udder diseases, somatic cell count and protein yield. The Tables 3, 4 and 5 show the estimates of the genetic parameters of digestive, reproductive, feet&leg diseases and protein yield.

3.1. Udder diseases, somatic cell count and protein yield

The heritabilities of udder diseases were 0.05 - 0.06 in RD, 0.04 in DF and a little lower in DJ (0.02 - 0.04). The heritabilities of somatic cell counts were 0.09 - 0.15, DF showing the most constant results (0.13 - 0.15).There was no evidence of differences in the heritabilities between the lactations for udder diseases and somatic cell counts.

With the exception of udder diseases in 1st lactation in DJ, there were very high genetic correlations for the same disease in subsequent lactations. For udder diseases the estimates were above 0.95 and for somatic cell counts above 0.92. The genetic correlations between udder diseases and somatic cell counts in the same lactation were 0.5 - 0.6 in DF, 0.4 - 0.5 in DJ and 0.4 - 0.7 in RD.

The results for RD and DF are very similar to the results stated in the literature cited previously when similar model were used. An exception was that the heritability of udder diseases was quite high, considering the definition of udder diseases and that the analysis was made on the observed scale. The high genetic correlations between lactations indicate that udder diseases and somatic cell counts are nearly the same trait in all lactations and for estimating of breeding values a repeatability model would be a useful alternative.

For DJ in 1st lactation the estimates of the genetic correlations of udder diseases were very different from the estimates for the other breeds and lactations. The genetic correlation to udder diseases in subsequent lactation was lower (0.76) than in the other two breeds and especially remarkable was the correlation to somatic cell count. The estimate of this correlation was close to 0. The consequence is that the somatic cell count can not be used as an indicator trait for udder diseases in DJ. The reason might be that the frequencies of the specific udder diseases were different from the frequencies in later lactations. The distribution mastistis treatments within first lactation was also different from the other breeds and lactations. In 1st lactation in DJ the major part of the treatments was registered just after calving whereas the distribution was more uniform in later lactations and in the other two breeds. This indicates that mastitis in 1st lactation in DJ has other causes than in the other breeds.

The unfavourable genetic correlations between yield and udder diseases were 0.24 in RD, 0.34 in DF and 0.55 in DJ (1st lactation estimates).

3.2. Reproductive, digestive, feet & leg diseases and protein yield

The results of the three other categories of diseases are shown in the Tables 3, 4 and 5. The heritabilities of the reproductive diseases were 0.02 in RD and DF and 0.00 - 0.01 in DJ. For the digestive diseases the estimates were 0.02 in DF, 0.003 - 0.02 in DJ and 0.01 - 0.04 in RD. For RD and DJ there might be a tendency towards increasing heritability with lactation number. For feet and leg diseases the heritabilities were very low in all breeds, between 0.005 and 0.01.

In DJ the standard error of the estimates of the genetic correlations was high and the estimates varied very much. For DF the estimates of the genetic correlations between 2nd and 3rd lactation were above 0.90 but lower between 1st and 2nd lactation. The results were more variable in RD and DJ than in DF but the same tendencies were observed.

An interesting result was a high genetic correlation between digestive diseases and feet&leg diseases (0.85 - 0.95 in 1st lactation, 0.6 - 0.8 in later lactations). This might be due to the fact that the most common diseases in feet, laminitis, are caused by digestive problems.

The genetic correlations between reproductive, digestive and feet&leg diseases and yield were generally unfavourable in the range of 0.15 - 0.25.

The estimates of heritability of the reproductive, digestive, and feet&leg diseases obtained in these analyses were a little lower than reported in the literature cited previously. It might be due to the broad definition of diseases used in the present study. Most of the previous studies have been on specific diseases such as ketosis, milk fever or metritis and on data from environments where these diseases have high frequencies.

3.3. Udder diseases and the other disease categories

Table 6 shows the genetic and phenotypic correlations between udder diseases and the other disease categories. For reproductive and digestive diseases there was a general tendency in RD that the correlations were negative or close to zero in 1st lactation. In 2nd and 3rd the correlation were increasingly positive. In DF and DJ the correlations were generally positive, in most cases in the range of 0.00 - 0.30. The positive genetic correlations indicate that the udder diseases are followed by problems with other categories of diseases.

3.4. Somatic cell count and the other disease categories

There were low genetic correlations between SCC and the three disease categories excluding mastitis. The first lactation results of the reproductive, digestive and feet&leg diseases were 0.02, 0.02 and)0.02 in DF, and 0.05, 0.11 and 0.1 in RD. In DJ the standard errors were very high (none of these results are shown in tables).

3.5. Protein yield

The estimates of heritability of protein yield were 0.20 - 0.24. This was lower than previous estimates on Danish data using sire models (0.25 - 0.30). The reason was probably that the model was not designed especially for milk production data and therefore the residual variance was higher than usual.

3.6. Effects of heterosis

The estimates of the fixed effects (herd*year, year*month of calving and age at 1st calving) reflect local Danish conditions and are not of general interest. The breed effects depend very much on the timing and type of imports made to the original Danish breeds and do not reflect general breed differences. The estimates of heterosis are shown in Table 7. Since the analyses were conducted within populations, only the heterosis between subpopulations was estimated. Most of the estimates of heterosis were not statistically significant but all the estimates were negative (favourable direction).

Table 2. Genetic parameters of udder diseases, somatic cell count in first, second and third lactation and first lactation protein yield. Genetic correlations below diagonal. Phenotypic correlations above diagonal and heritabilities on diagonal; the subscripts are the standard errors of the estimates; S.d. = phenotypic standard deviation; the estimates in the shadowed areas are from trivariate analyses and the others from bivariate analyses.

	P1	M1	M2	M3	SCC1	SCC2	SCC3	S.d
				Red Danish (RD)				
Protein yield, 1st lact. (P1)	**.23$_{.01}$**	-.05		.10	-.10			30.0
Mastitis, 1st lactation (M1)	.24$_{.07}$	**.06$_{.01}$**	.10	.06	.23	.14	.11	0.76
Mastitis, 2nd lactation (M2)		.96$_{.03}$	**.05$_{.01}$**	.11	.06	.23	.14	0.71
Mastitis, 3rd lactation (M3)	.42$_{.13}$	.92$_{.05}$	1.0$_{.03}$	**.05$_{.01}$**	.05	.08	.22	0.76
Som. cell count, 1st lact. (SCC1)	.04$_{.06}$	.65$_{.06}$	.57$_{.09}$	.59$_{.12}$	**.14$_{.01}$**	.36	.23	0.89
Som. cell count, 2nd lact. (SCC2)		.63$_{.08}$	.43$_{.10}$	.50$_{.13}$	.92$_{.03}$	**.10$_{.01}$**	.41	0.95
Som. cell count, 3rd lact. (SCC3)		.61$_{.10}$	.68$_{.09}$	.71$_{.10}$	.80$_{.06}$	.94$_{.04}$	**.15$_{.02}$**	0.95
				Danish Friesian (DF)				
Protein yield, 1st lact. (P1)	**.24$_{.01}$**	-.02		.08	-.06			28.3
Mastitis, 1st lactation (M1)	.34$_{.05}$	**.04$_{.01}$**	.11	.07	.20	.12	.10	0.71
Mastitis, 2nd lactation (M2)		.95$_{.01}$	**.04$_{.01}$**	.13	.08	.22	.13	0.67
Mastitis, 3rd lactation (M3)	.30$_{.07}$	.86$_{.04}$	.98$_{.01}$	**.04$_{.01}$**	.06	.10	.23	0.72
Som. cell count, 1st lact. (SCC1)	.15$_{.04}$	.57$_{.04}$	.47$_{.05}$	.38$_{.07}$	**.14$_{.01}$**	.34	.25	0.79
Som. cell count, 2nd lact. (SCC2)		.51$_{.05}$	.54$_{.04}$	.41$_{.06}$	.92$_{.02}$	**.15$_{.01}$**	.41	0.91
Som. cell count, 3rd lact. (SCC3)		.52$_{.07}$	.52$_{.06}$	.54$_{.06}$	.84$_{.03}$	.97$_{.01}$	**.13$_{.01}$**	0.93
				Danish Jerseys (DJ)				
Protein yield, 1st lact. (P1)	**.19$_{.02}$**	-.05		.06	-.14			24.9
Mastitis, 1st lactation (M1)	.55$_{.11}$	**.04$_{.01}$**	.07	.04	.17	.12	.13	0.75
Mastitis, 2nd lactation (M2)		.76$_{.09}$	**.03$_{.01}$**	.11	.06	.20	.12	0.61
Mastitis, 3rd lactation (M3)	.39$_{.16}$	.65$_{.15}$	.99$_{.10}$	**.02$_{.01}$**	.07	.10	.20	0.65
Som. cell count, 1st lact. (SCC1)	.01$_{.10}$	.00$_{.14}$	.20$_{.16}$	.35$_{.19}$	**.12$_{.02}$**	.39	.29	0.88
Som. cell count, 2nd lact. (SCC2)		-.08$_{.15}$	.40$_{.12}$	.43$_{.15}$	.94$_{.03}$	**.10$_{.01}$**	.46	1.03
Som. cell count, 3rd lact. (SCC3)		-.10$_{.18}$	.43$_{.13}$	.47$_{.14}$	.87$_{.05}$	1.0$_{.01}$	**.15$_{.02}$**	1.07

Table 3. Red Danish. Genetic parameters of reproduction diseases, digestive diseases and feet&leg diseases in first, second and third lactation and first lactation protein yield.
Genetic correlations below diagonal. Phenotypic correlations above diagonal and heritabilities on diagonal; the subscripts are the standard errors of the estimates; the estimates in the shadowed areas are from trivariate analyses and the others from bivariate analyses.

	P1	R1	R2	R3	D1	D2	D3	L1	L2	L3
Protein, 1st lact. (P1)	**.23**$_{.01}$	.01		.04	-.03		.08	-.02		.03
Reproductive, 1st (R1)	.23$_{.10}$	**.02**$_{.004}$	.14	.07	.02			.01		
Reproductive, 2nd.(R2)		.68$_{.10}$	**.02**$_{.004}$	.16		.05			.01	
Reproductive, 3rd (R3)	.19$_{.16}$	.45$_{.10}$	.96$_{.08}$	**.02**$_{.005}$			.05			.02
Digestive, 1st lact. (D1)	.25$_{.13}$	.18$_{.17}$			**.01**$_{.002}$	.05	.03	.81		
Digestive, 2nd lact. (D2)			.33$_{.14}$		.62$_{.12}$	**.02**$_{.004}$	.08		.59	
Digestive, 3rd lact. (D3)	.05$_{.12}$			.43$_{.16}$	.43$_{.17}$	.78$_{.10}$	**.04**$_{.008}$			.51
Feet&leg, 1st lact.(L1)	.21$_{.14}$	.02$_{.18}$			.89$_{.05}$			**.01**$_{.003}$	.06	.07
Feet&leg, 2nd lact.(L2)			-.06$_{.20}$			.54$_{.13}$		.96$_{.08}$	**.01**$_{.003}$	.03
Feet&leg, 3rd lact.(L3)	.31$_{.22}$			.49$_{.28}$			.64$_{.20}$	.58$_{.29}$	.68$_{.29}$	**.00**$_{.003}$
Phen. std. dev.	30.0	0.38	0.39	0.40	0.41	0.41	0.53	0.33	0.24	0.27

Table 4. Danish Friesian. Genetic parameters of reproduction diseases, digestive diseases and feet&leg diseases in first, second and third lactation and first lactation protein yield.
Genetic correlations below diagonal. Phenotypic correlations above diagonal and heritabilities on diagonal; the subscripts are the standard errors of the estimates; the estimates in the shadowed areas are from trivariate analyses and the others from bivariate analyses.

	P1	R1	R2	R3	D1	D2	D3	L1	L2	L3
Protein, 1st lact. (P1)	**.24**$_{.01}$	.01		.03	-.05		.04	-.03		.02
Reproductive, 1st (R1)	.23$_{.07}$	**.02**$_{.002}$	.14	.04	.03			.01		
Reproductive, 2nd.(R2)		.64$_{.08}$	**.01**$_{.002}$	.13		.02			.01	
Reproductive, 3rd (R3)	.28$_{.09}$	.64$_{.09}$	.95$_{.03}$	**.02**$_{.003}$			.03			.01
Digestive, 1st lact. (D1)	.16$_{.07}$	.60$_{.09}$			**.01**$_{.002}$	.05	.03	.79		
Digestive, 2nd lact (D2)			.33$_{.10}$		.78$_{.06}$	**.02**$_{.002}$	.06		.64	
Digestive, 3rd lact. (D3)	.09$_{.09}$			.28$_{.11}$	.77$_{.08}$	.93$_{.03}$	**.02**$_{.003}$			.56
Feet&leg, 1st lect.(L1)	.02$_{.09}$	.56$_{.10}$			.93$_{.02}$			**.01**$_{.002}$	.04	.03
Feet&leg, 2nd lact.(L2)			.34$_{.11}$			.83$_{.04}$		.86$_{.06}$	**.01**$_{.002}$	.05
Feet&leg, 3rd lact.(L3)	.30$_{.11}$			.14$_{.15}$			.43$_{.11}$	.94$_{.06}$	1.0$_{.05}$	**.01**$_{.002}$
Phen. std. dev.	28.3	0.36	0.37	0.39	0.40	0.37	0.47	0.32	0.24	0.27

Table 5. Danish Jerseys. Genetic parameters of reproduction diseases, digestive diseases and feet&leg diseases in first, second and third lactation and first lactation protein yield.
Genetic correlations below diagonal. Phenotypic correlations above diagonal and heritabilities on diagonal; the subscripts are the standard errors of the estimates; the estimates in the shadowed areas are from trivariate analyses and the other from bivariate analyses.

	P1	R1	R2	R3	D1	D2	D3	L1	L2	L3
Protein, 1st lact. (P1)	**.19**$_{.02}$	.02		.02	-.02		.06	-.01		.02
Reprod., 1st (R1)	.70$_{.36}$	**.002**$_{.001}$	.19	-.01	.03					
Reprod., 2nd (R2)		-.56$_{.49}$	**.01**$_{.002}$	.15						
Reprod., 3rd (R3)	-.35$_{.24}$	-.94$_{.59}$	.81$_{.15}$	**.01**$_{.004}$						
Digest., 1st (D1)	.16$_{.21}$				**.003**$_{.001}$	.05	.05			
Digest., 2nd (D2)					.90$_{.18}$	**.02**$_{.004}$	.07			
Digest., 3rd (D3)	-.22$_{.15}$				.90$_{.20}$	.94$_{.06}$	**.02**$_{.005}$			
Feet&leg, 1st (L1)	-.92$_{3.04}$							**.001**$_{002}$	.06	.03
Feet&leg, 2nd (L2)								.98$_{.83}$	**.01**$_{002}$	.07
Feet&leg, 3rd (L3)	-.21$_{.21}$							.78$_{.81}$	.69$_{.21}$	**.01**$_{003}$
Phen. std. dev.	24.9	0.24	0.27	0.28	0.34	0.33	0.44	0.24	0.17	0.19

Table 6. Genetic and phenotypic correlations between udder diseases (M1-M3) on one side and reproductive (R1-R3), digestive(D1-D3), feet&leg(L1-L3) diseases on the other.
The subscripts are the standard errors of the estimates.

	Red Danish		Danish Friesian		Danish Jerseys	
	r_g	r_p	r_g	r_p	r_g	r_p
Reproductive, 1st (M1-R1)	.05$_{.12}$	.00	.32$_{.08}$	.01	.90$_{6.6}$	.00
Reproductive, 2nd(M2-R2)	.36$_{.13}$	-.01	.18$_{.08}$	-.01	.65$_{.18}$	-.02
Reproductive, 3rd (M3-R3)	.70$_{.15}$	-.02	.01$_{.10}$	-.01	.13$_{.29}$	.00
Digestive, 1st (M1-D1)	-.16$_{.15}$	.00	.25$_{.09}$	.00	-.15$_{.26}$	.01
Digestive, 2nd (M2-D2)	.33$_{.12}$	.01	.21$_{.08}$	.00	.37$_{.15}$	.02
Digestive, 3rd (M3-D3)	.59$_{.13}$	.02	.29$_{.09}$	-.01	.20$_{.19}$	.01
Feet&leg, 1st (M1-L1)	-.20$_{.16}$	.01	.28$_{.10}$	.00	-.96$_{1.56}$	.02
Feet&leg, 2nd (M2-L2)	.19$_{.17}$	.00	.26$_{.09}$	-.01	.34$_{.19}$	.01
Feet&leg, 3rd (M3-L3)	-.12$_{.27}$	.00	.28$_{.11}$	-.01	.53$_{.23}$	.00

Table 7. Estimates of heterosis in 1st lactation.

	ORD x ABS	ORD x RHF	ABS x RHF	ODF x AHF	ODJ x NZJ	ODJ x USJ	NZJ x USJ
Udder diseases, 1st	).05$_{.06}$	).05$_{.06}$	).21$_{.26}$	).05$_{.03}$	).54$_{.30}$	).06$_{.11}$	).37$_{.35}$
Reproductive, 1st	).01$_{.03}$	).05$_{.14}$	).14$_{.08}$	).01$_{.02}$			
Digestive, 1st lact.	).01$_{.03}$	).29$_{.15}$	).22$_{.14}$	).03$_{.02}$			

ORD = Original Red Danish, ABS = American Brown Swiss, RHF = Red Holstein Friesian
ODF = Original Danish Friesian, AHF = American Holstein Friesian
ODJ = Original Danish Jerseys, NZJ = New Zealand Jerseys, USJ = US Jerseys

4. Conclusion

- The results for the breeds Red Danish and Danish Friesian were similar. The number of observations available for the estimation of genetic parameter were lowest in Red Danish and the standard errors of the estimates were quite high and consequently the results varied more for Red Danish than for Danish Friesian. The results of Danish Jerseys were different from those obtained in the other two breeds. This might be due to differences in the frequencies of the diseases. But some of the results also indicate that the genetic relationship between the traits differ in Danish Jerseys.
- The estimates of the heritability of udder diseases were 0.05-0.06 and the genetic correlations between lactations were high. The heritabilities of the somatic cell counts were 0.12-15 and the genetic correlations between udder diseases and somatic cell counts were 0.5-0.6.
- The estimates of the heritability of reproductive disease were 1-2%.
- The estimates of the heritability of digestive diseases were 1-2%.
- The estimates of the heritability of feet and leg diseases were 1% or below. The genetic correlations between lactations were very high.
- The genetic parameters of udder diseases in 1st lactation for Danish Jerseys behaved differently from the parameters of the other breeds and the other lactations in Danish Jerseys. It will be necessary to analyse this problem in more detail if somatic cell counts should be used for prediction of breeding values for udder diseases.
- The estimates of heterosis were generally non-significant but the estimates were all in the favourable direction, indicating a favourable effect of heterosis on the frequency of diseases.
- The results of this analyses have shown that there is a genetic variation in the frequency of diseases which can be utilized in breeding programs.

References

Banos, G. and Shook, G.E. 1990. Genotype by environment interaction and genetic correlations among parities for somatic cell count and milk yield. *J. Dairy Sci. 73,* 2563-2573.

Emanuelsen, U. 1988. Recording of production diseases in cattle and possibilities for genetic improvements: A review. *Livest. Prod. Sci. 20,* 89-106.

Emanuelson, U., Danell, B. and Philipson, J. 1988. Genetic parameters for clinical mastitis, somatic cell counts and milk production estimated by multiple-trait restricted maximum likelihood. *J. Dairy Sci. 71,* 467-476.

Emanuelsen, U., Oltenacu, P.A. and Gröhn, Y.T. 1993. Nonlinear mixed model analyses of five production disorders of dairy cattle. *J. Dairy Sci. 76,* 2765-2772.

Groen, A.F., Hellinga, I. and Oldenbroek, J.K. 1994. Genetic correlations of clinical mastitis and feet and legs problems with milk yield and type traits in Dutch Black and White cattle. *Netherlands J. Agric. Sci. 42-4,* 371-378.

Applied to Livestock Production, August 7-12, 1994, Guelph, Canada, Vol 22, 45-46.

Jensen, J. and Madsen, P. 1994. DMU: A package for the analysis of multivariate mixed models. *Proc. of the 5th World Congress on Genetics*

Koenen, E., Berglund, B., Philipson, J. and Groen,

A. 1994. Genetic parameters of fertility disorders and mastitis in the Swedish Friesian breed. *Acta Agric. Scand., Sect. Anim. Sci. 44,* 202-207.

Lyons, D.T., Freemann, A.E. and Kuck, A.L.. 1991. Genetics of health traits in Holstein cattle. *J. Dairy Sci. 74,* 1092-1100.

Madsen, P., Nielsen, S.M., Rasmussen, M.D., Klastrup, O., Jensen, N.E., Jensen, P.T., Madsen, P.S., Larsen, B. and Hyldgaard-Jensen, J. 1987. Investigations on genetic resistance to bovine mastitis (In Danish). 621. Report from the National Institute of Aminal Science. Landhusholdningsselskabets Forlag, København, 227pp.

Madsen, P., Jensen, J. and Thompson, R. 1994. Estimation of (co)variance components by REML in multivariate mixed linear models using average observed and expected information. *Proc. of the 5th World Congress on Genetics Applied to Livestock Production,* August 7-12, 1994, Guelph, Canada, Vol 22, 19-22.

Monardes, H.G. and Hayes, J.F. 1985. Genetic and phenotypic relationships between lactation cell counts and milk yield and composition of Holstein cows. J. Dairy Sci. 68:, 1250-1256.

Mäntysaari, E.A., Gröhn, Y.T. and Quass, R.L. 1991. Clinical Ketosis: Phenotypic and genetic correlations between occurences and with milk yield. *J. Dairy Sci. 74,* 3985-3993.

Philipson, J., Thafvelin, B. and Hedebro-Velander, I. 1980. Genetic studies on disease recordings in first lactation cows of Swedish dairy breeds. *Acta Agric. Scand. 30,* 327-335.

Pösö, J. and Mäntysaari, E.A. 1995. Genetic relationship between udder health and milk yield in Finnish Ayrshire. *46th Ann. Meet. of EAAP,* Prague, Czech Republic, 4-7 September 1995.

Rogers, G.W., Hargrove, G.L. and Cooper, J.B. 1995. Correlations among somatic cell scores of milk within and across lactations and linear type traits of Jerseys. *J. Dairy Sci. 78,* 914-920.

Schutz, M.M., Hansen, L.B., Steuernagel, G.R., Reneau, J.K. and Kuck, A.L. 1990. Genetic parameters for somatic cells, protein and fat in milk of Holsteins. *J. Dairy Sci. 73,* 493-502.

Simianer, H., Solbu, H. and Schaeffer, L.R. 1991. Estimated genetic correlations between disease and yield traits in dairy cattle. *J. Dairy Sci. 74,* 4358-4365.

Shook, G.E. 1989. Selection for disease resistance. *J. Dairy Sci. 72,* 1349-1362.

Syväjärvi, J., Saloniemi, H. and Gröhn, Y. 1986. An epidemiological and genetic study on registered diseases in Finnish Ayrshire cattle. *Acta Vet. Scand. 27,* 223-234.

Uribe, H.A., Kennedy, B.W., Martin, S.W. and Kelton, D.F. 1995. Genetic parameters for common health disorders of Holstein cows. *J. Dairy Sci. 78,* 421-430.

Weller, J.I., Saran, A. and Zeliger, Y. 1992. Genetic and environmental relationships among somatic cell count, bacterial infection, and clinical mastitis. *J. Dairy Sci. 75,* 2532-2540.

Welper, R.D. and Freeman, A. E. 1992. Genetic parameters for yield traits of Holsteins including lactose and somatic cell score. *J. Dairy Sci. 75,* 1342-1348.