Genetic Parameters for Health Traits using Farmer Recorded Data in the Netherlands and Flanders

J.J. Vosman[1], M.L. van Pelt[1] and G. de Jong[1]
[1] CRV BV Wassenaarweg 20, 6843 NW Arnhem, the Netherlands
Jorien.vosman@crv4all.com

Abstract

Animal health is important in dairy farming, from an economical and animal welfare point of view. In the Netherlands and Flanders breeding values of health traits (udder health, claw health and ketosis) are available, and enables selection for healthier cows. Data is not routinely recorded for all health traits. Farmer recorded data gives the opportunity to develop breeding values for new health traits. The first focus is on reproduction traits and metabolic disorders. The data set for reproduction disorders consisted of ~185,000 observations on ~135,000 cows, and for metabolic disorders ~20,000 observations on ~15,000 cows were available. Genetic parameters were estimated with a linear multi-trait sire model. Five different reproduction disorders were analyzed: retained placenta, endometritis, metritis, cystic ovaries, anoestrum. Incidences of the reproductive disorders ranged from 6 to 11%. Heritabilities for lactation 1 ranged from 0.008 to 0.043, and for lactation 2 and higher heritabilities ranged from 0.011 to 0.020. For metabolic disorders 2 different traits were analyzed: milk fever and clinical ketosis. The incidence for milk fever was 33% and for clinical ketosis the incidence was 14%, both for older cows. The heritability was 0.024 for milk fever and 0.023 for clinical ketosis. Considering the heritability and the genetic standard deviation it is possible to use farmer recorded data to develop breeding values for reproduction and metabolic disorders.

Key words: health traits, farmer recorded data, genetics

Introduction

One of the key points in dairy farm management is animal health. Therefor animal health traits receive more attention over time in animal breeding. The breeding value estimation is based on data that is routinely recorded data. The following breeding values (EBV) for health and functional traits are available: udder health, female fertility, calving traits, gestation length, birth weight, calf survival, hoof health, ketosis and longevity. These EBV enable selection for healthier cows.

Now a days, more animal health record keeping is done in management systems, like the Veemanager system of CRV, than in the past. The farmer recorded data gives the opportunity to develop breeding values for new health traits. The first focus is on the trait groups reproduction disorders and metabolic disorders. The reproduction disorders include the traits retained placenta, endometritis, metritis, cystic ovaries and anoestrum (or inactive ovaries). The metabolic disorders include the traits milk fever (hypocalcaemia) and clinical ketosis.

The aim of this study was the results of the genetic analysis of reproduction and metabolic disorders based on farmer recorded data in the Netherlands and Flanders.

Materials and Methods

Data selection

Farmer recorded data from the Veemanger system of CRV was used to estimate genetic parameters for the reproduction and metabolic disorders. The data included only the treated animals for the specific traits. All herdmates were categorized as healthy for that trait.

The following selection criteria were set: animals had to be 75% Holstein Friesian. Sire, herd, birthdate and calving date had to be known and the animal had to be herdbook registered. Only records from cows between parity 1 and 20 were used, were parities higher than 5 where treated as parity 5. Minimum age at first calving was 640 days. For the parameter estimation extra requirements were set: at least

10 daughters per sire, at least 5% of the animals in the herd should have a diagnosis in one year and at least 1% of the animals in the herd should have a diagnosis for each of the traits per parity per year.

In table 1 the number of observations, number of animals, number of herds and number of sires are given.

Table 1. Number of observations, animals, herds and sires.

Trait	Parity	Anim	Rec	Herds	Sires
Reproduction disorders					
Retained placenta	1	25050	25050	534	1092
	2+	36125	50349	522	1207
Endo metritis	1	21015	21015	427	1032
	2+	28991	41249	409	1172
Metritis	1	15563	15563	304	856
	2+	23720	33327	296	1101
Cystic ovaries	1	20124	20124	403	965
	2+	29760	43174	397	1173
Anoestrum	1	18087	18087	354	1023
	2+	24409	34253	345	1140
Metabolic disorders					
Milk fever	1	1407	1407	37	409
	2	1176	1176	37	397
	3+	1838	2089	37	540
Clinical ketosis	1	5088	5088	116	779
	2	4094	4094	116	808
	3+	6163	7854	116	1080

Statistical models

Genetic parameters were estimated with univariate linear sire models for the different traits. ASREML (Gilmour *et al.*, 2009) was used to estimate variance components. Parameters were estimated according to the following sire-models:

Reproduction disorders
For lactation 1:
$Y1_{ijkmo} = HY_i + YM_j + Age_k + A_m + e_{ijkmo}$

For lactation 2+:
$Y2_{ijlmno} = HY_i + YM_j + Par_l + A_m + PE_n + e_{ijlmno}$

Metabolic disorders
For lactation 1:
$Y1_{ijkmo} = HY_i + YM_j + Age_k + A_m + e_{ijkmo}$

For lactation 2:
$Y2_{ijlmno} = HY_i + YM_j + Par_l + A_m + PE_n + e_{ijlmno}$

For lactation 3+:
$Y3_{ijklmno} = HY_i + YM_j + Age_k + Par_l + A_m + PE_n + e_{ijklmno}$

where:

Y	Observation for reproduction disorder or metabolic disorder on animal m;
HY	herd x year of calving i;
YM	year x month of calving j;
Age	age of heifers at first calving k;
Par	lactation of cows l;
A	additive genetic effect m as sire of cows;
PE	permanent environment effect n;
e	residual.

The effects A, PE and e were random effects, the other effects were fixed effects. Pedigree was traced back 8 generations with the sire and maternal grand sire of the sire of the cow.

Results & Discussion

Incidence

The incidences for reproduction disorders were between 6 and 11 percent, and are shown in figure 1. In general, reproduction disorders occurred more often in older cows, except for anoestrum. For milk fever, a clear difference between heifers and older cows could be observed (figure 2). The incidence for older cows was 30 percent. For clinical ketosis the difference between lactations were smaller, and varied between 8 and 14 percent.

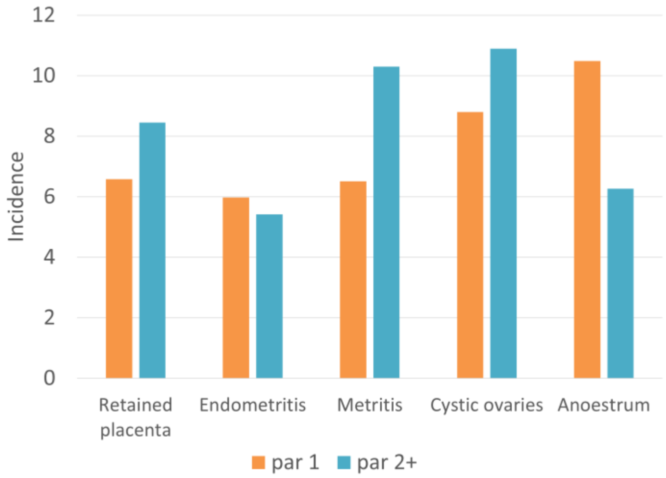

Figure 1. Incidence (%) for the reproduction disorders for parity 1 and 2+.

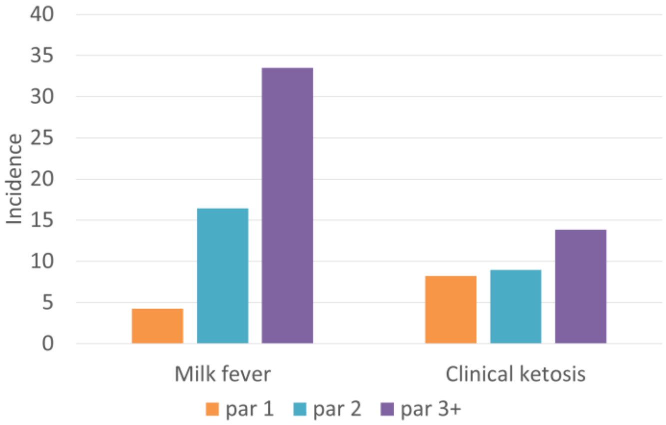

Figure 2. Incidence (%) for the metabolic disorders for parity 1, 2 and 3+.

Table 2. Heritabilities and genetic standard deviation for reproduction disorders, SE in parentheses.

Trait	**parity 1**	**parity 2+**
Heritability		
Retained placenta	0.029 (0.008)	0.020 (0.005)
Endometritis	0.036 (0.005)	0.013 (0.002)
Metritis	0.008 (0.007)	0.011 (0.004)
Cystic ovaries	0.008 (0.005)	0.015 (0.005)
Anoestrum	0.043 (0.011)	0.012 (0.005)
Genetic standard deviation		
Retained placenta	4.17	3.79
Endometritis	6.59	3.35
Metritis	2.15	3.10
Cystic ovaries	2.39	3.69
Anoestrum	6.13	2.62

Table 3. Heritabilities and genetic standard deviation for metabolic disorders, SE in parentheses.

Trait	**parity 1**	**parity 2**	**parity 3+**
Heritability			
Milk fever	0.133 (0.094)	0.079 (0.091)	0.024 (0.033)
Clinical ketosis	0.083 (0.032)	0.035 (0.028)	0.023 (0.013)
Genetic standard deviation			
Milk fever	6.85	9.09	6.48
Clinical ketosis	7.69	5.23	5.00

Genetic analysis

Heritabilities and genetic standard deviations for the reproduction disorders are given in table 2. Heritabilities for reproduction disorders ranged from 0.008 to 0.043. For retained placenta, endometritis and anoestrum heritabilities for heifers were higher than for cows. For metritis and cystic ovaries the heritabilies for older cows were higher than for heifers. The general trend is the higher incidence level, the higher the heritability as expected when analyzing binary traits with a linear model. The low heritabilities are in line with other studies, were heritabilites ranged from 0.005 to 0.03 for reproduction disorders based on farmer recorded data (Zwald *et al.*, 2004; Koeck *et al.*, 2012 and 2014; Parker Gaddis *et al.*, 2017).

Genetic standard deviations ranged from 2.15 to 6.59. Indicating that there is diversity between animals. In general genetic standard deviations were higher in heifers compared to older cows.

Heritabilities and genetic standard deviations for the metabolic disorders are given in table 3. Heritabilities for metabolic disorders were estimated for parity 1, 2, and 3 and higher. The heritabilities ranged from 0.023 to 0.133. The heritabilities for the first parity were 4 to 5 times higher compared to heritabilites of older cows, although the incidence level is lower. Heritabilities for milk fever were higher compared to those for clinical ketosis. It should be noted that standard errors for the metabolic disorders were higher especially for milk fever. Genetic standard deviations were in a range from 5.00 to 9.09. Indicating that there were differences between animals.

Heritabilities for those traits depend strongly on the type of data and method used for analyzing the data. Heritabilities based on farmer recorded binary data were in line with results found in other studies (Parker Gaddis *et al.*, 2017; Koeck *et al.*, 2015; Jamrozik *et al.*, 2016).

Conclusions

Breeding values for health traits based on routinely recorded data are available in the Netherlands. Considering the heritability and the genetic standard deviation it is possible to use farmer recorded data to develop breeding values for reproduction and metabolic disorders. Breeding values could be used for monitoring the metabolic and fertility traits.

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