Statistical Indicators
E-44
Breeding value metabolic disorders

▪ Introduction

Animal health remains an important topic within herd management in the dairy industry. More and more farmers record health issues in their management systems. Some of these health issues are metabolic disorders. Metabolic disorders cause high treatment costs and a reduction in milk yield. The farmer recorded data that is becoming available via management systems gives the opportunity to develop breeding values to select against metabolic disorders.

▪ Traits and breeding goal

In the breeding value estimation of metabolic disorders, two disorders are analysed: milk fever (MFE) and clinical ketosis (CKE).

Metabolic disorders are different for heifers than for cows, therefore in the breeding value estimation a distinction is made between parity 1 (heifers), parity 2 (young cows) and parity 3+ (older cows). Because MFE almost never occurs in the first two lactations, only the breeding value for parity 3+ is published. For CKE the breeding values of parity 1, 2 and 3+ are combined into an overall breeding

▪ Data

Observations
Data about metabolic disorders becomes available as farmer recorded observations in an animal health system. The traits are analysed based on a 0/100 score. Only the treated animals for the specific disorder are in the dataset, they are categorized as sick (score 100). All herd mates at that specific moment were categorised as healthy for that disorder (score 0).

Selection data for the breeding value estimation
Data is used in the breeding value estimation when they meet the following requirements:
1. A cow must be herd book registered (S) and the sire of the cow must be known;
2. Treatment and diagnoses before January 1st, 2006 are not included;
3. If treatment and diagnosis are executed or observed before the first known calving date, the data is not included;
4. If various diagnoses are recorded per metabolic disorder per cow-herd-year combination, then only one diagnoses per metabolic disorder is included;
5. A minimum of 3% of the animals present on the farm in one year have a diagnosis;
6. Diagnoses within 20 days of a previous diagnosis are excluded;
7. Age at calving is a minimum of 640 days;

▪ Statistical model

The breeding values for metabolic disorders are estimated with an animal model, following the BLUP technique (Best Linear Unbiased Prediction). All traits are analysed with the same model, with little differences for parity 1, 2 and 3+. For parity 3+ more than one observation is possible, due to more lactations, therefore a permanent environmental effect is included.

Different statistical models are used for the various parities:

$$Y1_{ijkmno} = BJ_i + YM_j + AGE\_C_k + HET_m + REC_n + A_o + Error_{ijkmno}$$
$$Y1_{ijmno} = BJ_i + YM_j + HET_m + REC_n + A_o + Error_{ijmno}$$
$$Y3_{ijlmnop} = HYi + YM_j + PAR_l + HET_m + REC_n + A_o + PERM_p + Error_{ijlmnop}$$

in which:

$Y1_{ijkmno}$: Observation for metabolic disorder on heifer o, with herd-year i and in year-month j, age at calving k, with heterosis effect m and recombination effect n;

$Y2_{ijmno}$: Observation for metabolic disorder on young cow o, with herd-year i and in year-month j, with heterosis effect m and recombination effect n;

$Y3_{ijlmnop}$: Observation for metabolic disorder on older cow o, with herd-year i and in year-month j, in parity l, with heterosis effect m and recombination effect n;

HYi : Herd-year i;
YM_j : Year-month j;
AGE_C_k : Age at calving for heifers k;
PAR_l : Parity for cows l;
HET_m : Heterosis class m;
REC_n : Recombination class n;
A_o : Additive genetic effect (or breeding value) of animal o;
$PERM_p$: Permanent environment effect on animal p;
$Error_{ijkmno}$: Errorterm of Y1, which is not explained by the model;
$Error_{ijmno}$: Errorterm of Y2, which is not explained by the model.
$Error_{ijlmnop}$: Errorterm of Y3, which is not explained by the model.

The effects A, PERM and Error are random effects, the remaining effects are fixed effects.

▪ Parameters

In total, in the breeding value estimation for metabolic disorders, 5 traits are analysed: MFE in parity 2 and 3+ and CKE in parity 1, 2 and 3+. The disorders are analysed as correlated traits. The heritability, repeatability, and genetic standard deviation are shown in Table 1. The heritability is a measure of the fraction explained by genetics. Results are based on univariate analyses for parameter estimation in ASReml. The repeatability is a measure for how much one observation corresponds to a subsequent observation on the same animal. Genetic correlations between metabolic disorders per parity are shown in Table 2, these are based on a bivariate analysis in ASReml.

Table 1. Heritability (h^2), repeatability, and genetic standard deviation for metabolic disorders in parity 1, 2 and 3+

Trait	h^2	repeatability	genetic standard deviation
MFE par 2	0.052		8.41
MFE par 3+	0.035	0.08	7.00
CKE par 1	0.089		7.13
CKE par 2	0.036		6.87
CKE par 3+	0.033	0.05	6.27

Table 2. Genetic correlations (below diagonal) between metabolic disorders

	MFE par 2	MFE par 3+	CKE par 1	CKE par 2	CKE par 3+
MFE par 2					
MFE par 3+	0.81				
CKE par 1	0.40	0.08			
CKE par 2	0.52	0.50	0.54		
CKE par 3+	0.30	0.25	0.26	0.81	

▪ Index – metabolic disorders

The breeding values intended for publication are MFE in parity 3+, and overall breeding value for CKE and an index breeding value for metabolic disorders based on MFE, CKE and subclinical ketosis (SCK). For the breeding value estimation of SCK, see E-chapter 34). The overall breeding value for CKE is calculated from the breeding values for parity 1, parity 2 and parity 3 and higher (3+):

$$BV_i = 0.41 \times BV_{i1} + 0.33 \times BV_{i2} + 0.26 \times BV_{i3+}$$

in which:
BV_i : Overall breeding value for CKE

The derivation of the factors (0.41, 0.33 and 0.26) are described in E-chapter 7. The weighing factors for the first three lactations from the testday model are used.

The heritability for the overall trait for CKE is 0.096. The genetic standard deviation is 6.44.

The average prevalence, relative damage, genetic standard deviation and the relative weight per metabolic disorder is indicated in Table 3. The average costs are based on an estimate of economic values. This is an estimate, because economic costs per metabolic disorders differs a lot in literature. The costs for MFE are about double the costs of CKE. Based on research from Guard(2008), this is $334 and $145 respectively. Based on Yildiz (2018), this is $257 and $109. The costs of subclinical ketosis are about half of the costs of clinical ketosis. Therefore for the index calculation the relative damage is 4:2:1. The relative weight is the proportion of the breeding value that is used in the index. This is based on the relative damage and genetic standard deviation of the trait, as well as correlations between the traits.

Table 3: Average prevalence, relative damage, genetic standard deviation and relative weight per metabolic disorder

Trait	Prevalence	Relative damage	Genetic standard deviation	Relative weight
MFE	18%	4	7.00	0.78
CKE	8%	2	6.44	0.36
SCK	10%	1	3.00	0.08

The index metabolic disorders is derived according to the formula:

$$BV_{met.rel} = 100 + 0.78 \times (BV_{mfe} - 100) + 0.36 \times (BV_{cke} - 100) + 0.08 \times (BV_{sck} - 100)$$

This relative breeding value or index, just like the breeding values for the underlying metabolic disorders, has an average of 100 and a standard deviation of 4.
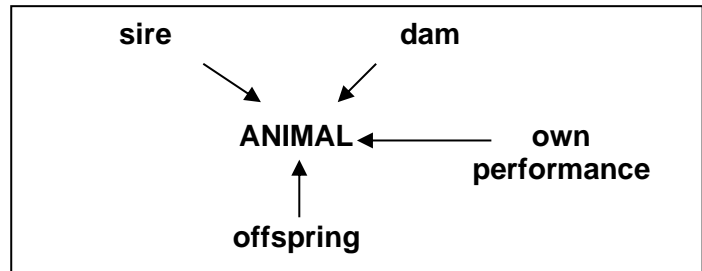
▪ Reliability

Breeding values are estimations of genetic potential. The word 'estimation' indicates that there is a certain inaccuracy in a breeding value. The reliability of a breeding value indicates the amount of difference that can exist between the estimated breeding value and the true genetic value.

The reliability is dependent on the amount of information available from an animal. There are three information sources:
1. own performance
2. offspring
3. parents

Information about metabolic disorders of (half) sisters, grandparents, etc. is included via the parents; information about granddaughters etc. are included via the offspring.

▪ Base

See chapter 'Bases for breeding values and base differences'.

▪ Publication

Presentation
The breeding values for the metabolic disorders are presented with an average of 100 and a standard deviation of 4. With this it is important to keep in mind that figures above 100 are desirable. An index for metabolic disorders of more than 100 indicates that metabolic disorders will occur *less* frequently in the daughter group.

Publication requirements
See chapter 'Publication rules sires'.

▪ Literature

Guard, C. (2008, October). The costs of common diseases of dairy cattle. In *Proceedings* (pp. 695-700).
Yildiz, A. S. (2018). Effects of some diseases observed at postpartum period of cows in dairy farms: Economic perspective. *Indian Journal of Animal Sciences*, *88*(6), 645-650.