Genetic analyses of ketosis and a newly developed risk indicator in Fleckvieh, Braunvieh and German Holstein

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Abstract

Data related with health traits of cattle can be used to improve and to optimize the management of dairy herds in a short term. Using these data in a breeding context will improve the health status in herds and in the whole population in the long term. In Baden-Württemberg data for direct heath traits were collected in a health monitoring project since 2012 (GMON) and used in an across-country evaluation of breeding values for the breeds Fleckvieh (dual purpose Simmental) and Braunvieh (German Braun Swiss). Four different diseases or disorders are evaluated at the moment. But due to the data collecting scheme only the more severe cases are usually recorded and used in the breeding value evaluation. The frequency of recorded cases for metabolic disorders is generally very low. This and the binary character of the traits lead to very low estimates for the heritabilities. Therefore the utilization of other data sources which also can detect subclinical cases especially for metabolic disorders would be very interesting. In 2015 a model for the prediction of ketosis risk has been developed at the German milk recording organization LKV BW. The model is based on routinely registered ketosis diagnoses by veterinarians. Data from 396 farms with a total of 112.545 milk samples linked to healthy cows and 194 samples linked to ketosis were available for model calibration and validation. The samples were collected on Fleckvieh, Braunvieh and German Holstein cows during the first 120 days in milk. Ketosis risk probability was modelled by using a Lasso regularized generalized logistic regression model on a combination of standard milk recording parameters and milk components calculated from standardized milk mid infrared spectra (MIR). The final model showed robust prediction results and has been applied since October 2015 on the LKV BW dairy population in order to provide the farmer with ketosis risk indicators in the early lactation stage. Genetic analyses for ketosis and one of the ketosis risk indicators (KetoMIR-index) were conducted. Via the GMON project direct observed cases of ketosis were analyzed as a binary trait, while the KetoMIR-index has quantitative characteristics. Next to these two traits data from the standard milk recording scheme are used to estimate genetic correlations between the ketosis traits and the performance traits in the three breeds. Heritabilities for the KetoMIR-index are considerable higher than for ketosis itself. It looks promising that the estimators for the heritabilities and the genetic correlations might be used in the routine breeding value evaluation in order to lower the impact of a metabolic disorder like ketosis.

Keywords: Ketosis, risk indicator, heritabilities, genetic correlations

Introduction

Ketosis is a metabolic disorder in ruminants. Indigestion, decreasing food consumption as well as very high milk fat percentages and a rapid decrease in total milk yield are some symptoms of this disorder. As a result, infection risk and the susceptibility for other diseases increase. Also, fertility declines. Ketosis is boosted by various factors: for example, this can be feeding mistakes but also genetic factors. Different authors showed low heritabilities for metabolic diseases or problems (Stock *et al.*, 2014). Vosman *et al.* (2015) found heritabilities for ketosis within a range of 0.13 to 0.18, depending on stage of lactation. Their analysis was based on 1.23 million cows in the Netherlands. They used a combination of a sire- with a multi-trait-model. In field studies, subclinical ketosis is seldom detected. As a result, data on subclinical ketosis are mostly not available as phenotype information. Therefore it is difficult to analyse the genetic background of ketosis risk. Based on the mid-infrared spectral analysis of milk samples within the routine milk performance testing a risk indicator for ketosis (KetoMIR-index) was developed (Grelet *et al.*, 2016). The risk indicator was originally intended to be a herd management tool but the study at hand analysed if KetoMIR-index could also be used for breeding purposes.

Materials and methods

Ketosis risk in dairy cows is highest if the energy supply from the fodder does not match the high energy needs after birth. The resulting energy deficit leads to a mobilization of body fat and finally to an increase in free fatty acids (FFAs) in the blood. Some of these fatty acids are rebuilt to ketone-bodies (acetoacetic acid, hydroxibutyric acid, and acetone) through metabolic processes. An increased number of ketone-bodies finally cause ketosis. Two progressive forms of ketosis are defined, subclinical and clinical ketosis. Clinical ketosis can be clearly seen by definite expression of ketosis symptoms. Animals with subclinical ketosis do not show clear symptoms. Therefore, it is difficult to detect them. The frequency of clinical ketosis within early lactating cows is 3-5%, the frequency of subclinical ketosis 20-30% (LKV Baden-Wuerttemberg 2016). The biggest losses in dairy production are caused by subclinical ketosis.

The KetoMIR-index was derived by combining direct recorded health data from the health monitoring system (GMON) with the routinely assessed MIR-spectra of test-day milk samples (Grelet *et al.*, 2016). Cases of acute ketosis from the health monitoring data were used as calibration basis for the calculation of KetoMIR-index. Besides the usual milk ingredients other information like the amount of ketone-bodies are part of the KetoMIR-index. Additionally, breed effect and calving number were used as factors when standardizing the KetoMIR-equation. The final index results in continuous values between 0 and 1. Figure 1 shows a hypothetical probability distribution of the KetoMIR-index and the classification in three hazard classes ("healthy", low and high ketosis risk).
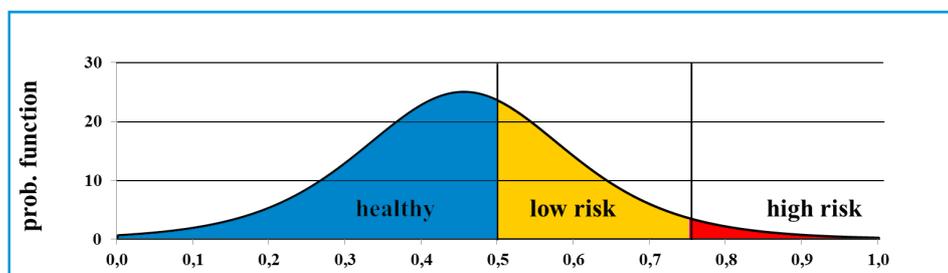

Figure 1. Probability function of KetoMIR-index and ketosis hazard classes.

The equation derived from health monitoring and milk testing data was used retroactively for interpreting the test day samples from the last years. The genetic analysis was carried out for the main dairy cattle breeds in Baden-Wuerttemberg, Fleckvieh (FV), German Holstein (DH) and Braunvieh (BV). In a first step, performance and pedigree data files were compiled. For FV 37.846 lactation were analysed, for DH 31.425 lactations and for BV 15.771 lactations. For each lactation, the first three test-day milk samples were used for analysis. Prerequisite was that somatic cell score and KetoMIR-index were available for these test-day milk samples additionally to the milk ingredients. Also, the direct ketosis-diagnoses from the GMON data were assigned as 0/1-trait to the corresponding lactations. Variance components were estimated with the software program VCE 6.0 (Groeneveld *et al.*, 2010). A within breed repeatability model was used. The model compiled the factors herd-year-season, lactation number, days in milk, permanent environmental effect and additive animal effect. The results of the first three milk samples were analyzed either as single traits or as mean of the three samples (variant "I"). The KetoMIR-index was analyzed as continuous trait (variant "I") and as categorical hazard classes (variant "C3"). Furthermore, the hazard classes were merged into binary traits in two different ways. Once the class "healthy" was compared with the group "at risk" (compiling low and high risk class) (variant "B050") and once again the compiled class "healthy and low risk" was compared with the group "high risk" (variant "B075").

The overall question is to check if the KetoMIR-index could be used as auxiliary trait in a breeding program. Within the current study it is analyzed if the KetoMIR-index or the hazard classes are heritable and how the KetoMIR-index is genetically related to ketosis.

Results and discussion

Table 1 shows the heritabilites of the KetoMIR-index and the categorical and binary analyzed hazard classes for the three different breeds. There are similar trends for all breeds. The heritabilities for the KetoMIR-index are considerable higher than for the hazard classes (categorical and binary). Looking at the variant "I", heritability ranges between 0.22 and 0.24 for the first test-day milk sample and increase with increasing test day. The increase is higher for the dairy breeds DH and BV than for the dual purpose FV. The results for the test day mean reflect these similarities resp. differences. The standard errors for the estimated heritabilities range between 0.01 and 0.05. All heritabilities estimated for the hazard classes (categorical and binary) are very low. Assigning continuous data to classes leads to a loss of information. Therefore, using the continuous index trait seems to be the most promising approach.

Table 1. Heritabilities for the KetoMIR-index, categorical and binary classes.

TD	FV				DH				BV			
	I	C3	B050	B075	I	C3	B050	B075	I	C3	B050	B075
1	**0.22**	0.09	0.09	0.02	**0.23**	0.11	0.09	0.02	**0.24**	0.13	0.12	0.04
2	**0.22**	0.04	0.05	0.01	**0.28**	0.08	0.09	0.01	**0.28**	0.12	0.12	0.02
3	**0.30**	0.04	0.05	0.01	**0.34**	0.11	0.11	0.01	**0.39**	0.13	0.13	0.01
Ø	**0.30**	0.08	0.08	0.01	**0.33**	0.11	0.10	0.00	**0.34**	0.15	0.14	0.03

FV = Fleckvieh; DH = German Holstein; BV = Braunvieh; TD = test day; I = KetoMIR-index; C3 = hazard classes; B050 = comparing hazard class health with classes at risk; B075 = comparing hazard classes healthy and low risk with high risk class.

Table 2 shows the genetic correlations between KetoMIR-index and the observed ketosis diagnoses. Correlations for FV are not shown because due to the far less ketosis diagnoses in FV than in DH and BV the equation system converged but the estimate for all correlations was equal to 1.00.

The highest genetic correlations to the acute ketosis-diagnoses were estimated for the KetoMIR-index values of the first test day. This relation is consistent with the temporal occurrence of ketosis within early lactation and shortly after calving.

Table 2. Genetic correlations between ketosis (clinical) and the KetoMIR-index and categorical classes.

TD	DH		BV	
1	0.44	(0.20)	0.75	(0.29)
2	0.05	(0.18)	0.38	(0.22)
3	0.05	(0.18)	0.07	(0.27)
Ø	0.32	(0.17)	0.24	(0.29)

TD = test day; FV = Fleckvieh; DH = German Holstein; BV = Braunvieh.

Conclusions

With relatively high heritabilities combined with low to medium genetic correlations the KetoMIR-index could be an additional tool in breeding to reduce the susceptibility of dairy cows to ketosis in the long term.

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