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 since 2012 (GMON) and used in an across-country evaluation of breeding values for the breeds Fleckvieh (dual purpose Simmental) and German Braun Swiss. Four different diseases or disorders are evaluated in 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 are 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 organisation 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 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 analysed 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