

Usability of bacteriological milk samples for genetic improvement of udder health in Austrian cattle

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For the estimation of routine mastitis breeding values the state of infection is currently not considered. Through the integration of results of bacteriological milk samples into the central Austrian cattle database, developed in a pilot study, the first standardised data set including milk culture results was available. Therefore the objectives of this study were to derive traits from this data source for potential use in breeding for improved mastitis resistance and to investigate genetic associations to udder health traits routinely recorded in Austrian Fleckvieh. Traits were defined as binary, apart from SCS where measures were available continuously. Multivariate analysis using a linear animal model was applied for estimating heritabilities and genetic correlations. Three traits based on culture results were defined: presence of first occurrence of infection by (1) Gram-positive (GRAM+), (2) Gram-negative bacteria (GRAM-) and (3) presence of any bacteriological infection (BACI). Diagnoses of acute (AcM) and chronic mastitis (ChM) as well as culling due to udder health problems (CULL) were considered as direct udder health traits. SCS₃₀₅ was defined as lactation mean somatic cell score considering test-day records. The heritabilities for BACI, GRAM+ and GRAM- were 0.01. For AcM, ChM and CULL, heritabilities were 0.04, 0.03 and 0.02, respectively. As expected, the highest heritability was estimated for SCS ($h^2=0.19$). Genetic correlations between BACI and GRAM+ towards mastitis and SCS traits were positive and high (0.6 to 0.9). The genetic relationship of GRAM+ seemed to be particularly high with traits that are indicators for persistent, poorly healing udder diseases (ChM, CULL). Genetic correlation between GRAM+ and GRAM- was close to zero, indicating differences in genetic control. Using pathogen data as additional direct information may enable more efficient breeding for improved mastitis resistance.

Genetic analyses of cow-specific diet digestibility based on spectral analysis of faecal samples

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The objective of this study was to estimate genetic parameters of dry matter digestibility (DMD) and indigestible neutral detergent fibre (iNDF) concentration in faeces (iNDF_{fc}). Faeces and feed samples were collected from three research farms in Finland and one research farm in Norway during 2012 to 2016. Faecal samples were collected during different stages of lactation and spot samples from three to five consecutive days were combined to one composite sample. The iNDF contents in faeces and feed samples were predicted by near-infrared reflectance spectroscopy (NIRS) and predictions were used to calculate $DMD = 1 - (iNDF_{feed} / iNDF_{fc})$. The final data consisted of 819 DMD and iNDF_{fc} observations from 311 cows. Variance components were estimated by REML method using the DMU software package. A repeatability animal model was fitted including fixed effects of herd, breed (Nordic Red, Holstein), parity (primiparous, multiparous), lactation stage (3 classes) and year × season (8 classes), and random effects of permanent environment, animal genetic effect and random residual. The pedigree was pruned to 8 generations and had a total of 6,567 animals. The heritability estimate for DMD was 0.15 whereas it was only 0.01 for iNDF_{fc}. Several reasons may have contributed to the low heritability estimate for iNDF_{fc}. The data used in this study was collected from different farms, over time there were changes in the sampling protocols, genetic ties between some herds were weak and accuracy of NIRS predictions differed across herds. Modelling of this data shall be improved to better evaluate whether iNDF_{fc} could be a potential indicator for DMD. Nevertheless, the estimate of heritability for DMD indicates that there is genetic variation among cows in the ability to digest feed.