

Routine Genetic Evaluation for Direct Health Traits in Austria and Germany

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Abstract

A nation-wide health monitoring system for cattle was started in Austria in 2006 in which diagnoses from veterinarians are recorded. In December 2010, routine genetic evaluations for mastitis, early reproductive disorders, cystic ovaries and milk fever started for Fleckvieh cattle (dual purpose Simmental) as part of the joint Austrian-German genetic evaluation. Heritabilities for the four traits based on a linear AM are 0.020, 0.023, 0.046 and 0.036, respectively. Genetic evaluations are carried out with the program MiX99 using a single trait linear BLUP AM. The fixed effects parity*age, year*month and type of recording*year as well as the random herd*year, random genetic animal and the random permanent environmental effects are included in the model. EBVs are published as relative EBVs with a mean of 100 and 12 points for one genetic SD, where higher values are desirable. EBVs are only published for bulls with a minimum reliability of 30%. Further work will focus on the inclusion of health traits in the total merit index, implementation of sub-indices for fertility and udder health and on other breeds and traits.

Keywords: genetic evaluation, genetic parameters, health traits, fitness, Fleckvieh cattle

1. Introduction

Improved animal health is getting increasingly important worldwide. Health issues may be addressed either directly or indirectly. Indirect measures of health or disease have been included into routine performance tests by many countries. However, to increase efficiency of genetic improvement of health, directly observed measures of health or disease need to be included in recording, evaluation and selection schemes.

In the Scandinavian countries, direct health data have been routinely collected and utilized for years, with recording being based on veterinary medical diagnoses (e.g. Philipsson and Linde, 2003; Heringstad *et al.*, 2007). In the non-Scandinavian countries, experience with direct health data is still limited. In Austria, the project “Health monitoring system in cattle” to establish a nation-wide health monitoring system of diseases started in 2006. The basic concept follows the Scandinavian

approach where registration of health data is carried out in close cooperation with veterinarians.

The objective of this paper was to present background and results of the recently implemented routine genetic evaluations for direct health traits in Fleckvieh cattle (dual purpose Simmental) based on detailed genetic analyses of Koeck (2010) and Koeck *et al.* (2010a,b,c).

2. Material and Methods

2.1 Data

Data from veterinary diagnoses are used for genetic analysis and routine genetic evaluation for direct health traits. Collection of data started in Austria in 2006 as part of the project ‘Health monitoring system in cattle’ for all breeds (Egger-Danner *et al.*, 2007). Recently, similar projects were also started in Germany

but only Austrian data are included in the evaluation so far. In Austria, diagnosis data are either transmitted electronically by the veterinarians or are recorded by the performance recording organizations during routine milk recording.

Precondition for a high reliability of health EBVs is a good data quality. In general it is necessary to differentiate between farms with incomplete diagnosis data and farms with very low incidence rate. Only data from farms fulfilling criteria concerning continuous and complete registration of diagnoses are included in genetic analyses (Egger-Danner *et al.*, 2009). A minimum of one first diagnoses per 10 cows and year (any disease) is required. Diagnosis data are collected for all breeds, but so far data are sufficient for detailed genetic analyses and routine evaluation for Fleckvieh only.

2.2 Traits

At present, four traits or traits groups are used for routine genetic evaluation in Fleckvieh cattle. These are defined as binary traits (0/1 or healthy/diseased) in specific time periods.

Mastitis (MAS):

The observation period for acute and chronic mastitis is 10 d before to 150 d after calving. Culling because of udder health problems

within the observation period is considered as diagnosis.

Early reproductive disorders (EREPRO):

Retained placenta, puerperal diseases and metritis in the period from calving to 30 d after calving are subsumed as early reproductive disorders. Involuntary cullings due to fertility problems are also included.

Cystic ovaries (CYST):

Observation period for cystic ovaries is 30 to 150 d after calving.

Milk fever (MF):

Milk fever diagnoses and cullings due to metabolic diseases for the period of 10 d before and 10 d after calving are considered.

Culled cows were only included, if they had the chance to be under recording until day 100 for MAS and CYST and until day 20 for EREPRO. That means that cows which were culled due to other reasons are only considered as healthy when they were culled after day 100 or 20, respectively.

Data of 5,734 validated farms with 163,377 Fleckvieh cows and 337,292 lactation records were included in the routine evaluation in August 2011. 469,178 animals were included in the pedigree. Frequencies of diagnoses are shown in Table 1.

Table 1. Characteristics of data for routine genetic evaluation in August 2011 (Fleckvieh).

Trait	N	Frequency (%)	Due to culling (%)
Mastitis	291,913	9.5	1.50
Early reproductive disorders	329,073	4.8	0.04
Cystic ovaries	286,721	5.2	
Milk fever	336,138	2.3	0.22

For calculating the genetic parameters, the data set was reduced to records of farms with at least 10 cows and sires with at least 20 daughters. Furthermore data were restricted to data from veterinarians who recorded a minimum of 500 diagnoses over the whole period. Finally, the genetic parameter data set and pedigree consisted of 46,952 and 100,642 records, respectively.

2.3 Model

Koeck (2010) and Koeck *et al.* (2010a,b,c, 2011) compared different statistical models to appropriately analyze (binary) health traits. The analyzed models consisted of univariate logit and probit threshold SM models, univariate and multivariate linear AM and SM and survival analysis. Differences between threshold and linear models in terms of differences between EBVs were rather small but slightly higher between AM and SM. Based on practical considerations the decision was made to go for a linear AM for routine genetic evaluation.

Heritabilities were calculated by means of the software package VCE6 (Groeneveld *et al.*, 2008), routine genetic evaluation is performed using the program MiX99 (Lidauer *et al.*, 2008) based on a univariate linear AM. The following model is used for both analyses:

$$y_{ijklmnopq} = \text{lact}_i * \text{age}_j + y_k * m_l + \text{rec}_m * y_k + h_n * y_k + \text{pe}_o + a_p + e_{ijklmnopq}$$

where $y_{ijklmnopq}$ is the observation for MAS, EREPRO, CYST and MF (0 = healthy, 1 = diseased); $\text{lact}_i * \text{age}_j$ is the fixed effect of parity (1, 2, ..., 5+) by calving age (6 classes for 1st and 2nd parity); $y_k * m_l$ is the fixed effect of calving year and month; $\text{rec}_m * y_k$ is the fixed effect of type of recording (electronic/milk recording) by year; $h_n * y_k$ is the random herd-year effect; pe_o is the random permanent environmental effect; a_p is the random genetic effect of the animal and $e_{ijklmnopq}$ is the random residual effect.

Reliabilities are calculated choosing the approach of Tier and Meyer (2004) using ApaX (Stranden *et al.*, 2001), which is part of the MiX99 package (Lidauer *et al.*, 2008).

3. Results and Discussion

3.1 Genetic parameters

Heritabilities of the univariate runs are shown in Table 2. Heritabilities range from 0.020 to 0.046 on the linear scale. Heritabilities estimated with a threshold model by Koeck *et al.* (2010) were higher on the underlying logistic scale (0.06-0.08), but comparable on the linear scale.

Table 2. Heritabilities (h^2) and standard errors (SE) for health traits of Fleckvieh.

Trait	N	h^2	SE
Mastitis	41,149	0.020	0.005
Early reproductive disorders	45,869	0.023	0.005
Cystic ovaries	40,468	0.046	0.006
Milk fever	46,824	0.036	0.006

3.2 Breeding values and genetic trends

Starting in December 2010, genetic evaluations for health traits are carried out three times a year by ZuchtData as part of the joint genetic evaluation of Austria and Germany. Breeding values for health traits are published as relative EBVs on a rolling base with a mean of 100 and 12 points for one genetic SD, where higher values are desirable. EBVs are only published

for bulls with a minimum reliability of 30%. So far the health traits are not included in the total merit index.

As data recording started just five years ago, little can be said about the genetic trends. However, first results indicate a more or less stable trend (Figure 1). As heritabilities are rather low and diagnosis data are not fully available in all regions, the reliabilities are

particularly low for young bulls. Hence, the number of young bulls (birth year 2006) with

official EBVs (reliability >30%) for health traits is fairly small (Figure 2).

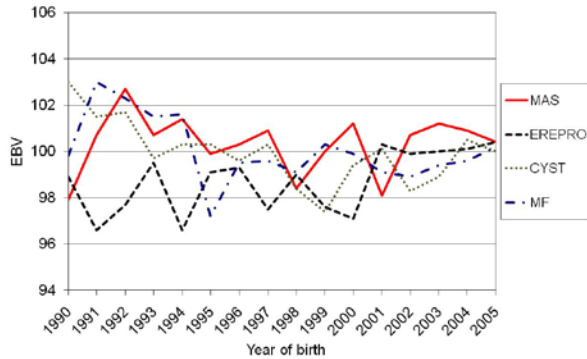


Figure 1. Genetic trends for health traits of Fleckvieh bulls.

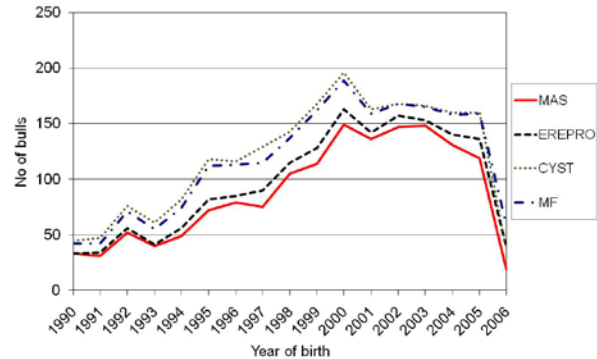


Figure 2. Number of Fleckvieh bulls with official EBV per birth year.

Figure 3 shows the average disease frequencies for the worst and best 20 bulls according to the respective EBV. Although heritabilities are rather low, differences

between the extremes are close to 10% and indicate the possibilities to select on direct health traits.

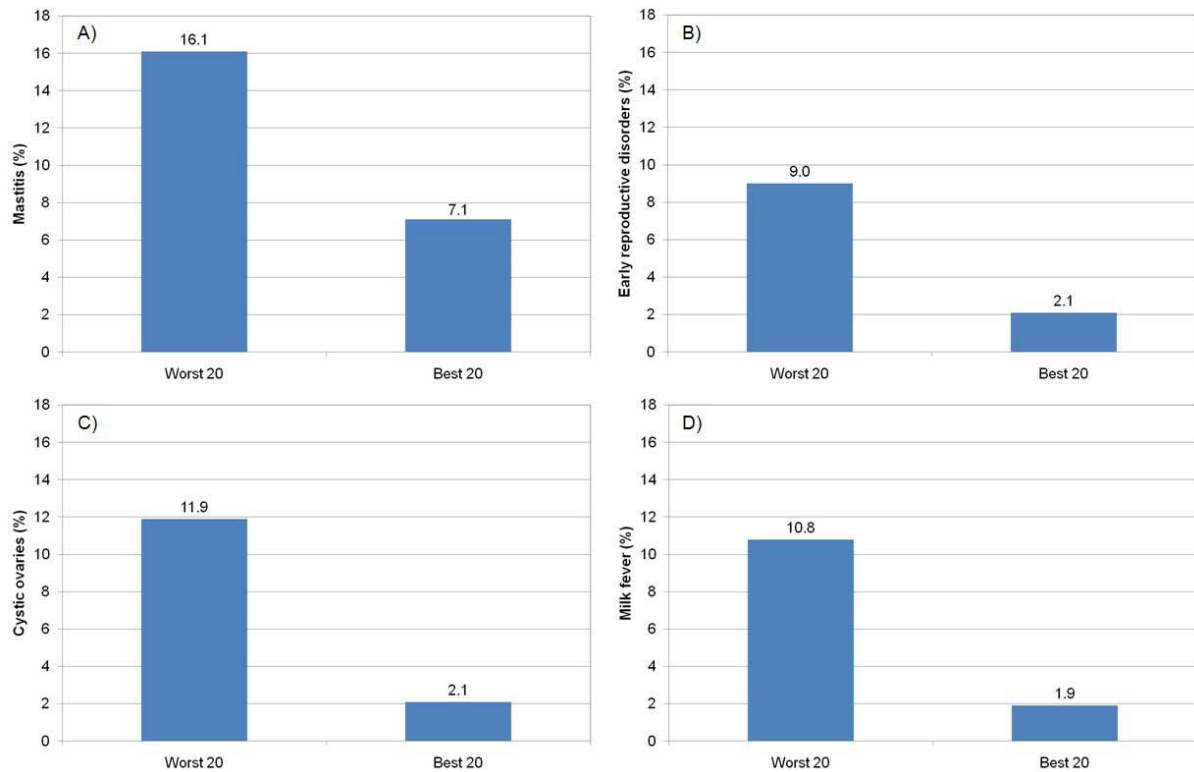


Figure 3. Average frequency of A) mastitis (n=400), B) early reproductive disorders (n=462), C) cystic ovaries (n=919) and D) milk fever (n=802) for worst and best 20 bulls according to respective EBV (reliability >50%, >10 records).

3.3 Relationships with other traits

Table 3 shows EBV correlations between health and other traits. Correlations are mainly slightly negative to milk production but close to 0 to the total merit index. The correlations are positive to most of the functional traits, particularly to longevity. As expected, the EBV correlation of MAS to SCC is relatively high; as estimated by Koeck *et al.* (2010c) the

genetic correlation ranged from 0.64 to 0.77. EBV correlations between the health traits are rather low, except between the two fertility traits EREPRO and CYST. Correlations to conformation traits were mainly close to 0, except for some correlations between MAS and single udder traits. The highest correlation was between MAS and udder depth (0.31) indicating the importance of high udders.

Table 3. Correlations between EBVs for health traits and other official EBVs (Fleckvieh bulls, birth year >1995, reliability >50%).

Trait	MAS	EREPRO	CYST	MF
Total merit index	0.03	0.15	0.00	-0.01
Milk index	-0.22	0.07	-0.10	-0.08
Milk-kg	-0.27	0.05	-0.11	-0.10
Beef index	0.12	0.01	0.03	0.06
Fitness index	0.34	0.18	0.13	0.07
Longevity	0.18	0.21	0.12	0.09
Persistency	0.04	0.10	0.09	0.09
Female fertility	0.18	0.07	0.23	0.02
SCC	0.47	-0.11	0.04	0.06
MAS	1.00	-0.03	0.07	0.13
EREPRO	-0.03	1.00	0.21	0.19
CYST	0.07	0.21	1.00	0.14
MF	0.13	0.19	0.14	1.00

4. Conclusions

In Austrian cattle breeds there is a traditionally high emphasis on fitness and functional traits. Economic weights for functional traits are around 50% within the total merit index for all breeds. However, presently no direct health traits are included. The implementation of routine genetic evaluations for direct health traits can be considered as a milestone to improve health and fitness in the long term.

Next steps will be to include health traits in the total merit index and to introduce sub-indices for fertility and udder health based on economic weights. It is intended to establish a fertility index combining the female fertility traits (non-return-rate, interval from calving to first insemination, interval from first to last insemination) with EREPRO and CYST. An udder health index including somatic cell score, MAS and some udder conformation traits should also be constructed. Focus of

further research is on other breeds (particularly Brown Swiss) and possible other traits like claw disorders.

Heritabilities are low but in the range of other functional traits. To get high reliabilities it is necessary to have a more or less complete data recording and a higher number of daughters. It will be necessary to get a larger number of bulls with high reliabilities, because so far no genomic evaluation is feasible for direct health traits.

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