

Development of a Genetic Evaluation for Fertility Disorders in Austrian Fleckvieh cows

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Abstract

A project to establish a nation-wide health monitoring system for cattle was started in Austria in 2006 in which diagnoses from veterinarians are recorded. Based on these data, fertility disorders are the most frequent disease category in Fleckvieh cows. Thus, the aim of this study was to explore the genetic background of fertility disorders in Fleckvieh cows. Heritabilities for fertility disorders were low and ranged from 0.01 to 0.14 on the underlying logistic scale, whereas on the observable scale heritabilities were between 0.006 and 0.041. Estimated genetic correlations were 1 among metritis, retained placenta and puerperal diseases and 0.85 between silent heat/anestrus and cystic ovaries. Low to moderate correlations (-0.01 to 0.68) were obtained among the other disorders. Correlations between estimated breeding values for fertility disorders and other routinely evaluated traits were computed, which revealed noticeable favorable relationships to longevity, interval from calving to first insemination, interval from first to last insemination (cows) and maternal calving ease and stillbirth. The results showed that data from the Austrian health monitoring project can be used for genetic evaluation of fertility disorders in Fleckvieh cows.

Introduction

Fertility and health traits are becoming increasingly important in selection decisions. In Austria genetic evaluations for fertility are carried out since 1995, since 2002 genetic evaluations are performed jointly with Germany for Fleckvieh cattle (Fuerst and Egger-Danner, 2002). Genetic evaluations for fertility are based on an index, in which several traits are combined: interval from calving to first insemination, non-return rate at 56 days and interval from first to last insemination. The traits non-return rate at 56 days and interval from first to last insemination are analyzed separately for heifers and cows. The fertility index is included in the total merit index with a relative weight of 6.8 % for Fleckvieh cattle (Fuerst and Gredler, 2009).

At present, no direct health traits are included in the total merit index of Austrian Fleckvieh (dual purpose Simmental) cattle, because there was no recording system of diseases until recently. A project to establish a nation-wide health monitoring system for cattle was started in Austria in 2006 in which diagnoses from veterinarians are recorded

(Egger-Danner *et al.*, 2007). The main project aims are the provision of support for herd management and to obtain breeding values for health traits.

Based on data from the Austrian health monitoring project, fertility disorders is the most frequent disease category in Fleckvieh cows besides mastitis. Therefore the objectives of this study were: 1) to estimate heritabilities for fertility disorders; 2) to investigate genetic correlations between fertility disorders; and 3) to assess correlations between fertility disorders and production and fitness traits that are routinely evaluated.

Materials and Methods

Data

Diagnoses data from the Austrian project “Health monitoring in cattle” (Egger-Danner *et al.*, 2007) were used for genetic analysis of fertility disorders. To ensure that all cows were from herds with reliable health recording, only farms with at least one recorded diagnosis (any disease) per 10 cows and year were considered.

Furthermore, only data from veterinarians who recorded at least 500 diagnoses distributed over the whole period were included.

Records of 33,362 Austrian Fleckvieh cows calving between January 1, 2007 and November 30, 2008 were available for this study. Cows from first to fifth lactation with an age at first calving between 19 and 43 months were considered. Animals with a calving interval shorter than 300 d or longer than 800 d were excluded.

All data sets were further restricted separately (for each fertility disorder) to cows from herd-year-season classes with at least 3 cows in the data set and sires with a minimum of 20 daughters. Seasons were: January-March, April-June, July-September and October-December.

An animal pedigree file was generated by tracing the pedigrees of cows with data 5 generations back. The resulting pedigree file contained the relationship of 63,238 animals. Additionally, a sire pedigree file was generated by tracing the pedigrees of sires and maternal grandsires 5 generations back. A total of 4,878 sires were included in this pedigree file.

Definition of Traits

The following fertility disorders were analyzed: retained placenta (RP), puerperal diseases (PD), metritis (MET), silent heat and anestrus (SH) and cystic ovaries (CO).

Veterinary treatments were considered from calving to 7 d after calving for RP, from calving to 30 d after calving for PD and from calving to 150 d after calving for MET, SH and CO. For MET, SH and CO an additional constraint was introduced. Only cows that completed at least two-thirds of the opportunity period (100 d) were included in the analyses. This should ensure that each cow has a sufficient chance to express the trait. Cases of SH, CO and MET after 150 d were not taken into account to avoid bias due to culling of cows. Because of the rather low incidences for most diseases, composite traits are more suitable for genetic evaluation than single traits. Thus, the following composite traits were evaluated. All reproductive disorders that occurred within 30 d after calving were joined into one category early fertility disorders (EF), whereas in the trait late fertility disorders (LF) all fertility disorders occurring between 31 and 150 d after calving were considered. EF consists mainly of diseases that are associated with calving (RP, PD, puerperal MET), whereas the trait LF is dominated by hormonal and late infectious diseases (CO, SH, MET in late lactation). Absence or presence of each of the reproductive disorders was coded as 0 or 1 based on whether or not the cow had at least one veterinary treatment within a defined time interval. Summary statistics of the analyzed fertility disorders are given in Table 1. The mean frequencies of RP, PD, MET, SH, CO, EF and LF were 2.6, 2.5, 3.8, 6.3, 9.6, 7.2 and 14.3 %, respectively, across the first five lactations.

Table 1. Description of analyzed fertility disorders.

Trait		Days from calving	Records, no.	Mean
Single traits				
RP, %	Retained placenta	0 to 7 d	22,355	2.6
PD, %	Puerperal diseases	0 to 30 d	20,986	2.5
MET ¹ , %	Metritis	0 to 150 d	13,958	3.8
SH ¹ , %	Silent heat and anestrus	0 to 150 d	13,958	6.3
CO ¹ , %	Cystic ovaries	0 to 150 d	13,958	9.6
Composite traits				
EF, %	Early fertility disorders	0 to 30 d	20,986	7.2
LF, %	Late fertility disorders	31 to 150 d	14,958	14.3

¹Information of cows that completed at least two-thirds of the opportunity period (100 d) was considered in the data.

Statistical Model

Heritabilities and genetic correlations between fertility disorders were calculated with bivariate linear animal models. Effects included in the model were as follows:

$$y_{ijklm} = L_i + hys_j + a_k + pe_l + e_{ijklm}$$

where y_{ijklm} is the observation for RP, PD, MET, SH, CO, EF and LF (0 = healthy, 1 = diseased); L_i is the fixed effect of parity ($i = 1, 2, \dots, 5$); hys_j is the random effect for herd-year-season of calving ($j = 1, 2, \dots, 4874$); a_k is the random genetic effect for animal ($k = 1, 2, \dots, 63238$); pe_l is the random permanent environmental effect of the cow ($l = 1, 2, \dots, 17523$); and e_{ijklm} is the random residual effect.

(Co-)variance components were estimated with REML using the VCE6 package (Groeneveld *et al.*, 2008).

Additionally, fertility disorders were analyzed with a univariate logit threshold sire model. The fixed and random effects were as described above. The software package ASREML (Gilmour *et al.*, 2006) was used for threshold model analyses.

A more detailed description of data and statistical methods is given by Koeck *et al.* (2010).

Results and Discussion

Genetic parameters

Heritabilities and genetic correlations between single traits are shown in Table 2. Heritability estimates on the underlying logistic scale ranged from 0.01 to 0.14, whereas on the observable scale heritabilities were between 0.006 and 0.041. Estimated genetic correlations between RP, PD and MET were 1. This may imply that veterinarians partly did not distinguish precisely between these codes. Other studies have reported much lower correlations among these traits. In first lactation Norwegian Red cows, Heringstad (2009) found a genetic correlation of 0.64

between RP and MET within 300 d after calving.

Low to moderate genetic correlations were obtained between SH and RP, PD and MET, whereas between SH and CO a strong positive correlation of 0.85 was estimated. In contrast, Heringstad (2009) reported that all genetic correlations in Norwegian Red cows involving SH (RP, MET, CO) were low and not different from 0.

There was no significant genetic correlation between CO and RP and MET, which is in agreement with previous studies of Van Dorp *et al.* (1998) and Zwald *et al.* (2004). In the study of Heringstad (2009), genetic correlations between CO and MET were not different from zero, whereas between CO and RP a negative correlation of -0.26 was found.

A strong positive genetic correlation of 0.68 was estimated between CO and PD. Genetic correlations involving PD were, however, not available in the literature.

Estimated genetic parameters for composite traits are presented in Table 3. The heritability estimates from the logit threshold model analyses were 0.079 and 0.048 for EF and LF, respectively, whereas heritability estimates on the observable scale were lower (0.023 and 0.037 for EF and LF, respectively). A moderately positive genetic correlation of 0.57 was found between EF and LF. This was expected, as genetic correlations between individual fertility disorders that appear in early lactation and those in late lactation were low to moderate (see Table 2). The differentiation between EF and LF is also reasonable as based on the results of our study the traits that occur mainly around calving (RP, PD, MET) were highly correlated and also CO and SH seem to share the same genetic background to a great extent. However, between the hormonal diseases (CO, SH) and MET, an inflammation of the uterus, a low genetic correlation was found. Thus, for genetic evaluation, fertility disorders should be regarded as different traits at least in early and later stages of lactation as it has been developed for the joint genetic evaluation of Denmark, Sweden and Finland (Johansson *et al.*, 2008). Johansson *et al.* (2008) reported

even lower genetic correlations ranging from 0.25 to 0.40 between EF and LF in the first 3

lactations for Danish Holstein and Red Danish cattle.

Table 2. Heritabilities, genetic correlations and their standard errors for retained placenta (RP), puerperal diseases (PD), metritis (MET), silent heat and anestrus (SH) and cystic ovaries (CO).

	Heritabilities		Genetic correlations			
	threshold	linear	PD	MET	SH	CO
RP	0.060 _{0.037}	0.007 _{0.003}	1.000 _{<0.001}	1.000 _{<0.001}	0.388 _{0.084}	-0.014 _{0.180}
PD	0.143 _{0.054}	0.019 _{0.005}		1.000 _{0.001}	0.466 _{0.139}	0.676 _{0.114}
MET	0.062 _{0.036}	0.010 _{0.005}			0.054 _{0.443}	0.217 _{0.235}
SH	0.012 _{0.015}	0.006 _{0.004}				0.849 _{0.280}
CO	0.077 _{0.027}	0.041 _{0.010}				

Table 3. Heritabilities, genetic correlation and their standard errors for early fertility disorders (EF) and late fertility disorders (LF).

	Heritabilities		Genetic correlation
	threshold	linear	LF
EF	0.079 _{0.025}	0.023 _{0.006}	0.574 _{0.141}
LF	0.048 _{0.018}	0.037 _{0.009}	

Correlations of Breeding Values with Production and Fitness Traits

Correlations of breeding values of sires with at least 50 daughters for EF (109 sires) and LF (92 sires) with official breeding values for production and fitness traits are shown in Table 4. Please note, that the resulting genetic solutions were reversed in sign. Thus higher breeding values indicate genetically favorable sires with fewer diseased daughters. Positive correlations were found with longevity,

suggesting that selection against fertility disorders would improve longevity. Heifer fertility traits showed low positive or even negative correlations to fertility disorders in cows. Larger positive correlations were calculated when fertility traits of cows were considered. Further, positive correlations were found between fertility disorders and calving ease maternal and stillbirth maternal.

Results are described in more detail by Koeck *et al.* (2010).

Table 4. Correlations between estimated breeding values of sires with at least 50 daughters for early fertility disorders (EF) and late fertility disorders (LF) and EBVs for other traits routinely evaluated.

	EF (109 sires)	LF (92 sires)
Milk kg	-0.05	-0.15
Fat %	0.04	0.13
Fat kg	-0.02	-0.05
Protein %	0.05	0.07
Protein kg	-0.02	-0.14
Longevity	0.27**	0.13
Persistency	0.11	0.02
Non-return rate at 56 days-heifers	-0.10	0.00
Non-return rate at 56 days-cows	-0.03	0.04
Interval from calving to first insemination	0.21*	0.30**
Interval from first to last insemination-heifers	0.00	0.16
Interval from first to last insemination-cows	0.23*	0.29**
Calving ease direct	-0.15	-0.06
Calving ease maternal	0.37***	0.21*
Stillbirth direct	-0.02	0.02
Stillbirth maternal	0.22*	0.10

*P < 0.05; **P < 0.01; ***P < 0.001.

Outlook

For the routine genetic evaluation it is planned to use the traits

- early reproductive disorders (retained placenta, puerperal diseases and metritis) in the period from calving to 30 d after calving, and
- cystic ovaries in the period from 30 to 150 d after calving.

Further it is intended to use a threshold animal model for routine genetic evaluation of health traits.

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