Genetic analysis of reproductive disorders and their relationship to fertility and milk yield in Austrian Fleckvieh dual-purpose cows

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ABSTRACT

The objective of this study was to estimate genetic parameters for various reproductive disorders based on veterinary diagnoses for Austrian Fleckvieh (Simmental) dual-purpose cattle. The health traits analyzed included retained placenta, puerperal diseases, metritis, silent heat and anestrus, and cystic ovaries. Three composite traits were also evaluated: early reproductive disorders, late reproductive disorders, and all reproductive disorders. Heritabilities were estimated with logit threshold sire, linear sire, and linear animal models. The threshold model estimates for heritability ranged from 0.01 to 0.14, whereas the linear model estimates were lower, ranging from 0.005 to 0.04. Rank correlations among random effects of sires from linear and threshold sire models were high (>0.99), whereas correlations between any sire model (linear, threshold) and the linear animal model were lower (0.88–0.92). Genetic correlations among reproductive disorders, fertility traits, and milk yield were estimated with bivariate linear animal models. Fertility traits included interval from calving to first insemination, nonreturn rate at 56 d, and interval between first and last insemination. Milk yield was calculated as the mean from test-day 1 and test-day 2 after calving. 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. Genetic correlations between reproductive disorders and fertility traits were favorable, whereas antagonistic relationships were observed between milk yield in early lactation and reproductive disorders. Pearson correlations between estimated breeding values for reproductive disorders and other routinely evaluated traits were computed, which revealed noticeable favorable relationships to longevity, calving ease maternal, and stillbirth maternal.

The results showed that data from the Austrian health monitoring project can be used for genetic selection against reproductive disorders in Fleckvieh cattle.

Key words: reproductive disorder, fertility, linear model, threshold model

INTRODUCTION

Functional traits such as fertility and health traits are becoming increasingly important in selection decisions worldwide because of economic reasons as well as animal welfare concerns and consumer demands for healthy and naturally produced products.

In most dairy cattle populations, the primary selection objective during the past several decades was milk production, whereas fertility and health traits received less attention (Miglior et al., 2005). As a consequence, genetic trends in fertility are negative because of an unfavorable correlated selection response (VanRaden et al., 2004; Liu et al., 2008). A slight decrease in fertility was also observed in Austrian dual-purpose breeds such as Fleckvieh (dual-purpose Simmental; Fuerst and Gredler, 2009). In contrast, genetic fertility trends are constant or even positive for the different Nordic Red breeds, arising from a simultaneous and consequent selection of bulls for production and fertility for more than 30 yr (Fogh et al., 2003; Philipsson and Lindhé, 2003; Andersen-Ranberg et al., 2005).

In Austria, genetic evaluations for fertility based on nonreturn rate at 90 d were carried out from 1995 to 2008; since 2002, genetic evaluations for all traits have been performed jointly with Germany for Fleckvieh cattle (Fuerst and Egger-Danner, 2002). However, female fertility has many components and cannot simply be explained by 1 trait only. Female fertility is represented by different abilities: the ability to show heat or maturity, the ability to conceive and to carry on to term, the ability to resist disorders, and the ability to recycle. Hence, in 2008 a new fertility index was introduced (Fuerst and Gredler, 2009) based on the results of Gredler (2008). Several traits are combined in this index: interval from calving to first insemination

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(CFI), nonreturn rate at 56 d (NR56), and interval from first to last insemination (FLI). The trait CFI describes mainly the ability of a cow to come into estrus and show heat, and NR56 and FLI are measures of the ability of a heifer or cow to conceive after insemination. The latter traits also include losses because of embryonic death. Because the physiological status of heifers is quite different from that of cows, the traits NR56 and FLI 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 cattle because no recording system of diseases existed until recently. A project to establish a nationwide 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 to provide support for herd management and to obtain breeding values for health traits. Health traits are, so far, routinely evaluated only in the Scandinavian countries (Interbull, 2009), where disease recording programs have been carried out on a large scale for more than 30 yr. The routine Scandinavian genetic evaluation of disease traits is based on linear models, which assume normal distribution of the data. Because diseases are treated as binary traits in genetic evaluation, nonlinear threshold models would be, at least theoretically, more appropriate for variance component and breeding value estimation (Gianola and Foulley, 1983).

Based on data from the Austrian health monitoring project, besides mastitis, reproductive disorders are the most frequent disease category in Fleckvieh cattle. Therefore, the objectives of this study were 1) to estimate heritabilities with threshold and linear models for various reproductive disorders; 2) to compare sire rankings for reproductive disorders from genetic evaluations with threshold and linear models; 3) to investigate relationships between reproductive disorders, fertility traits, and milk yield in early lactation (MY); and 4) to assess correlations between reproductive disorders and other traits that are routinely evaluated.

MATERIALS AND METHODS

Data

Health Monitoring. In Austria, under legal obligation, veterinary diagnoses and treatments have to be documented. These documents must be kept for 5 yr by the veterinarians as well as the farmers. However, up until now these data have been neither collected nor stored in a database. Since July 2006, diagnosis data from veterinarians have been recorded in Austria within

the framework of the project called “Health monitoring in cattle” (Egger-Danner et al., 2007). For this purpose, a standardized diagnosis key is used that consists of 10 disease groups (diseases of calves; diseases of the digestive tract; metabolic diseases; infertility and disorders associated with parturition; udder diseases; diseases of the claw and other diseases of the legs; diseases of the respiratory tract; cardiovascular diseases, diseases of the blood and urinary tract; diseases of the central nervous system, skin and infectious diseases; and other diseases) covering 65 different disease codes. The diagnosis data from veterinarians are collected monthly by the milk recording technicians or are sent electronically to the database by the veterinarians. The data are stored within the Austrian central cattle database (Rinderdatenverbund). Recording of health data on farms is currently voluntary.

Data Validation and Editing. A basic prerequisite for an efficient use of health data is a correct data validation. Several measures were applied to ensure adequate reporting within individual herds. Before recording the data in the database, routine plausibility checks were carried out. To distinguish farms with low frequencies of diseases from those with incomplete documentation and recording, at least 1 diagnosis per 10 cows, year, and farm must have been reported. Additionally, continuous recording and reporting by the veterinarians and farmers was a precondition. Furthermore, only data from veterinarians who recorded at least 500 diagnoses during the whole period were considered in this analysis to rule out inconsistent data collection. About 25% of the farms had to be excluded by data editing, assuming unreliable documentation and recording.

At present, about 70% of all cows participating in the Austrian milk recording scheme belong to the Fleckvieh breed (ZAR, 2009), so the analyses were carried out for this breed only. Records of 33,362 Fleckvieh cows with a maximum non-Fleckvieh gene proportion of 25%, calving between January 1, 2007 and November 30, 2008, were used in this study. Only cows from first to fifth lactation with an age at first calving between 19 and 43 mo were included. Records of animals with a calving interval <300 d or >800 d were excluded.

Traits. Reproductive disorders with an incidence far below 1% were not considered in the analyses; these were uterine prolapse (0.10%), abortion (0.19%), injuries incidental to parturition (0.21%), and difficult calving (0.34%). The latter proportion is low because only veterinary-assisted calvings are included, whereas calving ease scores are reported by farmers (Fürst and Fürst-Waltl, 2006). Thus, the following disease traits were analyzed: retained placenta (RP), puerperal diseases (PUERP), metritis (MET), silent heat and anestrus (ESTRUS), and cystic ovaries (CYST).

Table 1. Stage of lactation, measured as days after calving, for first incidence (%) of retained placenta (RP), puerperal diseases (PUERP), metritis (MET), silent heat and anestrus (ESTRUS), and cystic ovaries (CYST) based on cows that completed 300 d after calving

Days from calving	RP (n = 1,038)	PUERP (n = 549)	MET (n = 1,024)	ESTRUS (n = 1,889)	CYST (n = 2,455)
0–7	94.2	83.8	10.2	0.4	0.2
8–14	1.6	4.4	9.0	0.6	0.4
15–30	0.5	4.6	24.6	3.6	4.4
31–60	0.8	1.6	23.8	20.9	25.7
61–90	0.1	2.6	11.8	30.0	28.0
91–120	0.0	0.6	7.2	18.9	18.2
121–150	0.1	0.7	5.1	10.2	9.0
151–180	0.3	0.0	2.4	7.2	6.5
181–210	0.3	0.0	2.5	4.6	3.8
211–240	0.2	0.6	1.5	2.0	2.0
241–270	0.7	0.6	1.4	1.1	1.1
271–300	1.2	0.5	0.5	0.5	0.7

Table 1 shows the distribution of first occurrence of each reproductive disorder according to days after calving. The majority of cases of RP and PUERP occurred within 7 d after calving, whereas treatments of MET were reported mainly during the first 30 d after calving and the breeding period. As expected, most cases of ESTRUS and CYST were treated during the breeding period. Thus, veterinary diagnoses were considered from calving to 7 d after calving for RP, from calving to 30 d after calving for PUERP, and from calving to 150 d after calving for MET, ESTRUS, and CYST. For MET, ESTRUS, and CYST, 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 ESTRUS, CYST, and MET after 150 d were not taken into account to avoid bias caused by culling of cows.

Besides the individual traits, 3 composite traits were also evaluated. Because of the rather low incidences for most diseases, composite traits are more suitable for genetic evaluation than single traits. A more general disease definition leads to higher incidences and possibly to more accurate estimated breeding values. The following composite traits were evaluated. All reproductive disorders that occurred within 150 d after calving were joined into 1 category, reproductive disorders (**REPRO**). The trait early reproductive disorders (**EREPRO**) included all reproductive disorders that were treated within 30 d after calving, whereas the trait late reproductive disorders (**LREPRO**) included all reproductive diseases occurring between 31 and 150 d after calving. The trait EREPRO consisted mainly of diseases that were associated with calving (RP, PUERP, puerperal MET), whereas the trait LREPRO was dominated by hormonal and late infectious diseases (CYST, ESTRUS, 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 1 veterinary treatment within a defined time interval.

The fertility traits NR56, CFI, and FLI were calculated from calving and insemination data. Insemination records were used only from cows with CFI values in the range of 20 to 300 d. The interval between calving to last insemination had to be between 20 and 500 d. Records with FLI values longer than 300 d were deleted, as were records with a gestation length shorter than 270 d or longer than 310 d (breed average: 290 d $\pm$ 3 SD). The calculation of NR56 was based on first inseminations and the record was discarded when several inseminations had occurred within a 5-d period (double insemination). If the cow was culled within 56 d after first insemination, the record was excluded. The trait NR56 was scored as 0 if the cow had a second insemination within 56 d after the first insemination and 1 otherwise. The fertility trait FLI was considered only if a subsequent calving was present.

In Austria, milk yield is recorded on a monthly basis. For MY in early lactation, the average of test-days 1 and 2 after calving was calculated and used for genetic analyses.

All data sets were further restricted separately to include only cows from herd-year-season (for reproductive disorders) or herd-year (for fertility traits and MY) classes with at least 3 records. Seasons were January to March, April to June, July to September, and October to December. Additionally, sires were required to have at least 20 daughters. A summary of the analyzed data is given in Table 2.

Pedigree File. 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. The animal pedigree file was generated by tracing the pedigrees of cows with data 5 generations back. The resulting pedigree file included the relationship of 183,525 animals.

Table 2. Description of analyzed reproductive disorder, fertility, and production traits

Trait	Description	Days from calving	Records, n	Mean
Reproductive disorder				
RP, %	Retained placenta	0–7	22,355	2.6
PUERP, %	Puerperal diseases	0–30	20,986	2.5
MET, ¹ %	Metritis	0–150	13,958	3.8
ESTRUS, ¹ %	Silent heat and anestrus	0–150	13,958	6.3
CYST, ¹ %	Cystic ovaries	0–150	13,958	9.6
EREPRO, %	Early reproductive disorders	0–30	20,986	7.2
LREPRO, %	Late reproductive disorders	31–150	14,958	14.3
REPRO, %	Reproductive disorders	0–150	15,616	19.2
Fertility trait				
CFI, d	Interval from calving to first insemination		24,725	69.7
NR56, %	Nonreturn rate at 56 d		20,578	66.4
FLI, d	Interval from first to last insemination		11,262	23.4
Production trait				
MY, ² kg	Milk yield, early lactation		22,649	28.5

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

²Average of test-day 1 and 2 after calving.

Statistical Models

Univariate Threshold Model. The reproductive disorders RP, PUERP, MET, ESTRUS, CYST, EREPRO, LREPRO, and REPRO were analyzed using a threshold model (Wright, 1934; Gianola, 1982; Gianola and Foulley, 1983) that accounted for the binary (0, 1) nature of the data. The software package ASREML (Gilmour et al., 2006), the working algorithm of which is based on generalized linear mixed models, was used for threshold model analyses. Generalized linear mixed models are based on finding a relationship (link function) between the expected value of a random variable and a linear function of explanatory variables (Tempelman, 1998; Kachman, 2000). Variance components were estimated by applying the binomial distribution with a logit link function. In matrix notation, the threshold model was as follows:

$$\lambda = \mathbf{X}\beta + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_s\mathbf{s} + \mathbf{W}\mathbf{p} + \mathbf{e},$$

where λ is a vector of unobserved liabilities to RP, PUERP, MET, ESTRUS, CYST, EREPRO, LREPRO, and REPRO; β is a vector of systematic effects, including fixed effect of parity; $\mathbf{h}$ is a vector of random herd-year-season of calving effects; $\mathbf{s}$ is a vector of sire effects; $\mathbf{p}$ is a vector of permanent environmental effects of the cow; $\mathbf{e}$ is a vector of residuals; and $\mathbf{X}$, $\mathbf{Z}_h$, $\mathbf{Z}_s$, and $\mathbf{W}$ are the corresponding incidence matrices.

Because the average herd size in Austria is quite small (~16 cows per herd; ZAR, 2009), herd-year-season effects were treated as random to minimize loss of information. Additionally, the well-known extreme category problems (i.e., all observations in individual subclasses are either 0 or 1) of the threshold model that occur especially in traits with low incidences are allevi-

ated by using random effects (Sorenson and Gianola, 2002). The threshold model analyses were based on a sire model because the generalized linear mixed model methodology for binary threshold traits is not reliable under an animal model (Gilmour et al., 2006).

Heritabilities were calculated using the variance of the logit link function. This requires a correction of the residual variance by the factor $\pi^2/3$. Thus, heritability was calculated as follows:

$$h^2 = \frac{4\sigma_s^2}{\sigma_s^2 + \sigma_h^2 + \sigma_p^2 + \frac{\pi^2}{3}}.$$

Univariate Linear Model. For comparison, reproductive disorders (RP, PUERP, MET, ESTRUS, CYST, EREPRO, LREPRO, and REPRO) were analyzed with linear sire and linear animal models. To obtain REML estimates of the variance components, the VCE6 package was used (Groeneveld et al., 2008). The fixed and random effects for these traits were as described above.

Bivariate Linear Model. Genetic correlations were calculated with bivariate linear animal models. Genetic correlations were calculated 1) between single traits (RP, PUERP, MET, ESTRUS, and CYST), and 2) between composite traits (EREPRO, LREPRO, REPRO), fertility (NR56, CFI, FLI), and MY in early lactation. Linear animal models were applied because the number of observations was low and animal models use information from all known relationships. Besides, genetic correlations are reported to be correct for binary traits using linear models (Heringstad et al., 2005; Negussie et al., 2008). The model used for reproductive disorders was as given above. For NR56, CFI, FLI, and MY, the following model was applied:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_a\mathbf{a} + \mathbf{W}\mathbf{p} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of observations for NR56, CFI, FLI, and MY; $\boldsymbol{\beta}$ is a vector of systematic effects, including fixed effects of age at calving–parity interaction for all traits, year-month of insemination for NR56, and year-month of calving for CFI, FLI, and MY; $\mathbf{h}$ is a vector of random herd-year of insemination effects for NR56 and herd-year of calving effects for CFI, FLI, and MY; $\mathbf{a}$ is a vector of animal effects; $\mathbf{p}$ is a vector of permanent environmental effects of the cow; $\mathbf{e}$ is a vector of residuals; and $\mathbf{X}$, $\mathbf{Z}_h$, $\mathbf{Z}_a$, and $\mathbf{W}$ are the corresponding incidence matrices.

Calving age classes were formed for each of the first 2 parities. Age at first calving had 14 classes in which <25 mo was the first class, ≥ 37 mo was the last class, and other classes were single months. Age at second calving was grouped into 15 classes in which <37 mo was the first class, ≥ 50 mo was the last class, and other classes were single months. For older cows, age-parity classes were parity 3, 4, and 5.

Service sire was not considered in the model for NR56. In Austrian dual-purpose Fleckvieh cattle, Gredler (2008) found that service sires accounted for only a very small fraction (0.2–0.4%) of the phenotypic variation.

Genetic Evaluations

Breeding values for the composite traits EREPRO, LREPRO, and REPRO based on linear animal models were estimated by using the software package PEST (Groeneveld, 2006). The resulting genetic solutions were reversed in sign. Thus, higher breeding values indicate genetically favorable sires with fewer diseased daughters. In accordance to the Austrian routine breeding value estimation, EBV were standardized to relative breeding values with a mean of 100 and a genetic standard deviation of 12 points. Pearson correlations between breeding values of sires with at least 50 daughters for EREPRO, LREPRO, and REPRO with other traits that are routinely evaluated were computed.

RESULTS AND DISCUSSION

Descriptive Statistics

Phenotypic values for the analyzed traits are shown in Table 2. The incidences of RP, PUERP, MET, ESTRUS, CYST, EREPRO, LREPRO, and REPRO within the defined time periods were 2.6, 2.5, 3.8, 6.3, 9.6, 7.2, 14.3, and 19.2%, respectively, across the first 5 lactations of Austrian Fleckvieh cows. The average for NR56 was 66.4%. Mean values for CFI and FLI

were 69.7 and 23.4 d, respectively. Because the mean value for FLI was lower than in earlier studies (Gredler, 2008), the results involving FLI should be interpreted with caution. The average milk yield from test-days 1 and 2 after calving was 28.5 kg.

Heritabilities

Estimates of heritability from logit threshold model analyses are given in Table 3. Heritabilities were 0.06, 0.14, 0.06, 0.01, and 0.08 for RP, PUERP, MET, ESTRUS, and CYST, respectively. For the composite traits EREPRO, LREPRO, and REPRO, heritabilities of 0.08, 0.05, and 0.05, respectively, were estimated. The heritability estimates of composite traits were slightly lower than the estimates of single traits. There is a loss of information about genetic variation when single traits are pooled into composite traits. However, standard errors were lower for composite than for single traits. The results are generally in agreement with other studies, despite slightly different trait definitions and models. Wassmuth et al. (2000) found heritability estimates of RP transformed to the underlying liability scale of 0.03, 0.09, and 0.10 for Danish Jersey, Danish Holstein, and Danish Red, respectively. Other estimates of heritability of RP from threshold models range from 0.06 to 0.09 (Heringstad, 2009a; Heringstad et al., 2009b). For PUERP, no heritability estimates were available in the literature. Pösö and Mäntysaari (1996) found heritability estimates transformed to the liability scale ranging from 0.02 to 0.05 for ovulatory disorders and 0.04 to 0.05 for metritis. Zwald et al. (2004a) obtained heritabilities of 0.07 and 0.05 for MET and CYST, respectively, from threshold model analyses that included all available lactation records. Considering only first-lactation cows, they found slightly higher heritabilities. In first-lactation Norwegian Red cattle, Heringstad (2009a) reported heritabilities of 0.03 and 0.07 for MET and CYST, respectively. For ESTRUS, Heringstad (2009a) obtained a heritability of 0.06, which is higher than our estimate.

As expected, the heritability estimates from the linear model analyses were lower and ranged from 0.005 to 0.04 (Table 3). However, the results from linear and logit threshold models cannot be compared directly because the estimates are on a different scale. The estimates of logit threshold models are expressed on the underlying logistic scale, whereas the estimates of linear models are on the observable scale. Overall, the heritability estimates from the linear model analyses were in the range of previous studies (Pösö and Mäntysaari, 1996; Van Dorp et al., 1998; Wassmuth et al., 2000; Dechow et al., 2004).

Table 3. Estimated heritabilities for retained placenta (RP), puerperal diseases (PUERP), metritis (MET), silent heat and anestrus (ESTRUS), cystic ovaries (CYST), early reproductive disorders (EREPRO), late reproductive disorders (LREPRO), and reproductive disorders (REPRO) based on logit threshold sire models (TSM), linear sire models (LSM), and linear animal models (LAM)¹

Trait	TSM	LSM	LAM
Single trait			
RP	0.060 (0.037)	0.006 (0.004)	0.007 (0.004)
PUERP	0.143 (0.054)	0.017 (0.006)	0.019 (0.005)
MET	0.062 (0.036)	0.012 (0.006)	0.009 (0.004)
ESTRUS	0.012 (0.015)	0.005 (0.004)	0.006 (0.004)
CYST	0.077 (0.027)	0.031 (0.010)	0.040 (0.009)
Composite trait			
EREPRO	0.079 (0.025)	0.021 (0.007)	0.023 (0.006)
LREPRO	0.048 (0.018)	0.026 (0.009)	0.035 (0.009)
REPRO	0.050 (0.016)	0.031 (0.009)	0.039 (0.010)

¹Standard errors for the estimates are shown in parentheses.

Threshold and Linear Models

An important question is to what extent the ranking of sires for various reproductive disorders agrees across models. For this purpose, rank correlations between random effects of sires with progeny in the data set from logit threshold sire, linear sire, and linear animal models were compared (Table 4). The correlations between random effects of sires obtained with linear sire and threshold sire models were >0.99, whereas correlations between any sire model (linear, threshold) and the animal model were lower ($r = 0.88$ – 0.92) for all traits. The effects associated with applying an animal model instead of a sire model were more important than the differences resulting from the different methodology (linear or threshold model). The study from Boettcher et al. (1999) showed that the EBV of sires from linear sire and threshold sire models were highly correlated ($r = 0.98$), whereas the correlations between animal models and linear sire or threshold sire models were 0.87 and 0.86, respectively. Furthermore, Vazquez et al. (2009) carried out a cross validation to assess the predictive ability of logit sire and linear sire models for mastitis. The correlations between the expected values

of logit and linear models were 0.998, which suggest equal overall predictive performance for both models.

Genetic Correlations Between Reproductive Disorders

Genetic correlations between single traits (RP, PUERP, MET, ESTRUS, and CYST) are shown in Table 5. The traits RP, PUERP, and MET in early lactation (puerperal metritis) are considered to be related. It is well known that RP increases the risk of uterine infections after calving (LeBlanc, 2008). However, the obtained genetic correlation of 1 between RP, PUERP, and MET was surprising. This may imply that veterinarians partly did not distinguish precisely between these codes. Other studies have reported much lower correlations among these traits. Lin et al. (1989) found a genetic correlation of 0.24 between RP and MET in first-lactation cows, whereas in the study of Van Dorp et al. (1998) the estimates of genetic correlations between RP and MET were positive but close to 0. Using field data of more than 500,000 first-lactation Norwegian Red cows, Heringstad (2009a) estimated a

Table 4. Rank correlations between random effects of sires with progeny in the data set for retained placenta (RP), puerperal diseases (PUERP), metritis (MET), silent heat and anestrus (ESTRUS), cystic ovaries (CYST), early reproductive disorders (EREPRO), late reproductive disorders (LREPRO), and reproductive disorders (REPRO) based on logit threshold sire models (TSM), linear sire models (LSM), and linear animal models (LAM)

Trait	Sires, n	TSM-LSM	TSM-LAM	LSM-LAM
Single trait				
RP	253	0.999	0.882	0.880
PUERP	240	0.994	0.884	0.891
MET	173	0.996	0.913	0.914
ESTRUS	173	0.993	0.876	0.887
CYST	173	0.995	0.905	0.914
Composite trait				
EREPRO	240	0.998	0.921	0.922
LREPRO	182	0.996	0.889	0.899
REPRO	186	0.995	0.920	0.923

Table 5. Estimated parameters for retained placenta (RP), puerperal diseases (PUERP), metritis (MET), silent heat and anestrus (ESTRUS), and cystic ovaries (CYST) based on linear animal models¹

Trait	RP	PUERP	MET	ESTRUS	CYST
RP	0.007 (0.003)	1.000 (<0.001)	1.000 (<0.001)	0.388 (0.084)	-0.014 (0.180)
PUERP		0.019 (0.005)	1.000 (0.001)	0.466 (0.139)	0.676 (0.114)
MET			0.010 (0.005)	0.054 (0.443)	0.217 (0.235)
ESTRUS				0.006 (0.004)	0.849 (0.280)
CYST					0.041 (0.010)

¹Heritabilities are on the diagonal and genetic correlations are above the diagonal. Standard errors for the estimates are shown in parentheses.

genetic correlation of 0.64 between MET within 300 d after calving and RP.

Low to moderate genetic correlations were found between ESTRUS and RP, PUERP, and MET, whereas a strong positive correlation of 0.85 was found between ESTRUS and CYST. As reviewed by Garverick (1997) and Vanholder et al. (2006), the clinical signs that accompany ovarian cysts are variable, but many cows with cysts are recognized to be anestrus. Heringstad (2009a) reported that all genetic correlations in Norwegian Red cows involving ESTRUS (RP, MET, CYST) were low and that none of the genetic correlations could be considered to be different from 0.

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

In the current study, a strong positive genetic correlation of 0.68 was estimated between CYST and PUERP. Genetic correlations involving PUERP were, however, not available in the literature.

Genetic correlations among the composite traits EREPRO, LREPRO, and REPRO are presented in Table 6. A moderately positive genetic correlation of 0.57 was found between EREPRO and LREPRO. This was expected because genetic correlations between individual reproductive disorders that appear in early

lactation and those in late lactation were low to moderate (Table 5). The differentiation between EREPRO and LREPRO is also reasonable; based on the results of our study, the traits that occur mainly around calving (RP, PUERP, MET) were highly correlated and CYST and ESTRUS also seem to share the same genetic background to a great extent. However, between the hormonal diseases (CYST, ESTRUS) and MET, an inflammation of the uterus, a low genetic correlation was found. Thus, for genetic evaluation, reproductive 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 in 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 EREPRO and LREPRO in the first 3 lactations for Danish Holstein and Red Danish cattle.

Genetic Correlations with Fertility and Milk Yield

Genetic correlations between EREPRO, LREPRO, REPRO, fertility (NR56, CFI, FLI), and MY in early lactation are given in Table 6. Estimates of genetic correlations between disease and fertility traits were all favorable. Low to moderate genetic correlations were found between CFI and the different disease traits. Genetic correlations between NR56 and EREPRO, LREPRO, and REPRO were in the range from -0.40 to -0.87. Even higher favorable correlations were

Table 6. Estimated parameters for early reproductive disorders (EREPRO), late reproductive disorders (LREPRO), reproductive disorders (REPRO), interval from calving to first insemination (CFI), nonreturn rate at 56 d (NR56), interval from first to last insemination (FLI), and milk yield (MY) based on linear animal models¹

Trait	EREPRO	LREPRO	REPRO	CFI	NR56	FLI	MY
EREPRO	0.023 (0.006)	0.574 (0.141)	0.781 (0.080)	0.112 (0.039)	-0.396 (0.264)	0.846 (0.104)	0.309 (0.108)
LREPRO		0.037 (0.009)	0.959 (0.020)	0.525 (0.127)	-0.865 (0.134)	0.826 (0.099)	0.209 (0.078)
REPRO			0.041 (0.009)	0.488 (0.070)	-0.774 (0.230)	0.972 (0.119)	0.267 (0.115)
CFI				0.034 (0.007)	-0.234 (0.231)	0.520 (0.176)	0.340 (0.102)
NR56					0.008 (0.004)	-0.930 (0.132)	-0.587 (0.130)
FLI						0.014 (0.006)	0.441 (0.192)
MY							0.190 (0.013)

¹Heritabilities are on the diagonal and genetic correlations are above the diagonal. Standard errors for the estimates are shown in parentheses.

Table 7. Pearson correlations between EBV of sires with at least 50 daughters for early reproductive disorders (EREPRO), late reproductive disorders (LREPRO), and reproductive disorders (REPRO) based on linear animal models and EBV for other traits routinely evaluated

Item	EREPRO (109 sires)	LREPRO (92 sires)	REPRO (94 sires)
Milk, kg	−0.05	−0.15	−0.07
Fat, %	0.04	0.13	0.08
Fat, kg	−0.02	−0.05	−0.01
Protein, %	0.05	0.07	0.03
Protein, kg	−0.02	−0.14	−0.07
Longevity	0.27**	0.13	0.27**
Persistence	0.11	0.02	0.11
Nonreturn rate at 56 d (heifers)	−0.10	0.00	−0.07
Nonreturn rate at 56 d (cows)	−0.03	0.04	−0.03
Interval from calving to first insemination	0.21*	0.30**	0.34**
Interval from first to last insemination (heifers)	0.00	0.16	0.11
Interval from first to last insemination (cows)	0.23*	0.29**	0.32**
Calving ease direct	−0.15	−0.06	−0.01
Calving ease maternal	0.37***	0.21*	0.28**
Stillbirth direct	−0.02	0.02	0.14
Stillbirth maternal	0.22*	0.10	0.21*

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

obtained between FLI and reproductive disorders. The literature lacks studies of genetic relationships of reproductive disorders with fertility traits. Pösö and Mäntysaari (1996) found genetic correlations of 0.80 and 0.37, the latter, however, not being significantly different from zero, between days open and ovulatory disorders and MET, respectively. Schnitzenlehner et al. (1998) reported a genetic correlation of 0.54 between RP and days open. Low genetic correlations of 0.24 and 0.11 between RP and CFI and between RP and NR56, respectively, were obtained by Heringstad et al. (2009b). However, the estimates from the latter study were not significantly different from zero.

Genetic correlations between MY in early lactation and EREPRO, LREPRO, and REPRO were in the range of 0.21 to 0.31, suggesting that selection for higher milk yield would increase susceptibility to reproductive disorders. Pösö and Mäntysaari (1996) found higher unfavorable genetic associations of 0.42 and 0.68 between 305-d MY and ovulatory disorders and MET, respectively. Hooijer et al. (2001) reported a genetic correlation of 0.34 between 305-d MY and CYST. Genetic correlations among fertility (NR56, CFI, and FLI) and MY in early lactation were generally in agreement with previous estimates in Austrian Fleckvieh cattle (Gredler, 2008).

Correlations of Breeding Values with Production and Fitness Traits

Pearson correlations between breeding values of sires with at least 50 daughters for EREPRO (109 sires), LREPRO (92 sires), and REPRO (94 sires) based on linear animal models with official breeding values for

production and fitness traits are shown in Table 7. Correlations between breeding values are always an underestimation of genetic correlations unless accuracies of EBV are close to 1. Thus, these results should be interpreted only as general indications. Again, it should be noted that higher breeding values indicate genetically favorable sires with fewer diseased daughters.

Low, but nonsignificant, antagonistic relationships were observed between milk production and all reproductive disease traits. Positive correlations were found with longevity, suggesting that selection for disease resistance would improve longevity as well, which is in agreement with the study of Zwald et al. (2004b).

Because the physiological status of heifers is quite different from that of cows, it was not unexpected that heifer fertility traits showed low positive or even negative correlations to disease resistance traits in cows. Larger positive correlations were calculated when fertility traits of cows were considered. As soon as an adequate number of diagnoses are available for heifers, these should also be included in further analyses. Further, positive correlations were found between reproductive disorders and calving ease maternal and stillbirth maternal, indicating that cows with easier and normal calving have fewer reproductive problems. A low positive, albeit nonsignificant, genetic relationship between retained placenta and calving difficulties has been shown earlier by Schnitzenlehner et al. (1998). Other genetic studies dealing with these traits were not available in the literature.

CONCLUSIONS

The results showed that the data from the Austrian health monitoring project can be used for genetic evalu-

ation of reproductive disorders. Generally, heritability estimates of reproductive disorders are low regardless of the applied methodology (threshold or linear). Although linear models ignore the binary nature of disease traits, high rank correlations among random effects of sires obtained with linear and threshold models were calculated. Linear models have been found to be robust against deviations of the assumptions of normal distribution. All genetic correlations between reproductive disorders and fertility traits in Austrian Fleckvieh cattle were favorable. Thus, selection against reproductive disorders will result in improvement of fertility. As a correlated selection response, this would lead to higher NR56 and shorter CFI and FLI. Breeding mainly for higher MY in early lactation would lead to increased susceptibility to reproductive disorders.

This study was based on a relatively small data set, so the genetic parameters could not be estimated precisely. Therefore, it is important to reestimate these parameters as soon as a larger data set is available and to include reproductive disorders and fertility traits of heifers. Moreover, the genetic relationships between calving ease, stillbirth, and reproductive disorders should be investigated in further studies.

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