Genetic line comparisons and genetic parameters for endoparasite infections and test-day milk production traits

Katharina May,*† Kerstin Brügemann,* Tong Yin,* Carsten Scheper,* Christina Strube,† and Sven König*¹

*Institute of Animal Breeding and Genetics, Justus-Liebig-University of Gießen, 35390 Gießen, Germany

†Institute for Parasitology, Centre for Infection Medicine, University of Veterinary Medicine Hannover, 30559 Hannover, Germany

ABSTRACT

Keeping dairy cows in grassland systems relies on detailed analyses of genetic resistance against endoparasite infections, including between- and within-breed genetic evaluations. The objectives of this study were (1) to compare different Black and White dairy cattle selection lines for endoparasite infections and (2) the estimation of genetic (co)variance components for endoparasite and test-day milk production traits within the Black and White cattle population. A total of 2,006 fecal samples were taken during 2 farm visits in summer and autumn 2015 from 1,166 cows kept in 17 small- and medium-scale organic and conventional German grassland farms. Fecal egg counts were determined for gastrointestinal nematodes (FEC-GIN) and flukes (FEC-FLU), and fecal larvae counts for the bovine lungworm *Dictyocaulus viviparus* (FLC-DV). The lowest values for gastrointestinal nematode infections were identified for genetic lines adopted to pasture-based production systems, especially selection lines from New Zealand. Heritabilities were low for FEC-GIN ($0.05\text{--}0.06 \pm 0.04$) and FLC-DV (0.05 ± 0.04), but moderate for FEC-FLU (0.33 ± 0.06). Almost identical heritabilities were estimated for different endoparasite trait transformations (log-transformation, square root). The genetic correlation between FEC-GIN and FLC-DV was 1.00 ± 0.60 , slightly negative between FEC-GIN and FEC-FLU (-0.10 ± 0.27), and close to zero between FLC-DV and FEC-FLU (0.03 ± 0.30). Random regression test-day models on a continuous time scale [days in milk (DIM)] were applied to estimate genetic relationships between endoparasite and longitudinal test-day production traits. Genetic correlations were negative between FEC-GIN and milk yield (MY) until DIM 85, and between FEC-FLU and MY until DIM 215. Genetic correlations between FLC-DV and MY were negative throughout lactation, indicating

improved disease resistance for high-productivity cows. Genetic relationships between FEC-GIN and FEC-FLU with milk protein content were negative for all DIM. Apart from the very early and very late lactation stage, genetic correlations between FEC-GIN and milk fat content were negative, whereas they were positive for FEC-FLU. Genetic correlations between FEC-GIN and somatic cell score were positive, indicating similar genetic mechanisms for susceptibility to udder and endoparasite infections. The moderate heritabilities for FEC-FLU suggest inclusion of FEC-FLU into overall organic dairy cattle breeding goals to achieve long-term selection response for disease resistance.

Key words: endoparasite trait, test-day production trait, genetic parameter, random regression model

INTRODUCTION

Endoparasite infections lead to measurable milk production losses in dairy cows, have a detrimental effect on product quality, and cause economic losses in affected herds (Charlier et al., 2005; Holzhauer et al., 2011). Gastrointestinal nematodes (GIN), as well as the bovine lungworm (*Dictyocaulus viviparus*), negatively affected growth and health of first-season grazing calves (Ploeger and Kloosterman, 1993; Schnieder et al., 1993). In addition, a significant detrimental effect on productivity of older cattle was observed (Charlier et al., 2009). Schunn et al. (2013) reported seroprevalence rates up to 31.2% for German cattle herds for *D. viviparus*. Infections with the liver fluke *Fasciola hepatica* in adult cattle were mainly subclinical (Kaplan, 2001); nevertheless, substantial economic loss due to reduced milk production has been reported even for subclinical infections (Knubben-Schweizer et al., 2010). For *F. hepatica*, Kuerpick et al. (2013) observed seroprevalence rates up to 38.4% in different German federal states.

In recent years, the percentage of German consumers demanding milk from cows kept in pasture-based production systems is increasing (BÖLW, 2016). As a consequence, and due to other aspects such as high indoor feeding costs and fluctuations of conventional

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¹Corresponding author: sven.koenig@agrar.uni-giessen.de

milk payment systems, milk from organic or pasture-based production systems is considered as an attractive economic alternative. However, German Holstein cows (**GHC**), in particular, have been selected for modern and large-scale indoor systems for decades, raising questions of possible genotype $\times$ environment interactions and their adaptation capability to harsh environments (König et al., 2005a). In this regard, in grassland systems dairy cows are exposed to higher infection pressure with endoparasites. A challenge for the farm management in organic farming systems is that medical anthelmintic treatments for adult cattle are strongly restricted. Moreover, an increasing resistance of sheep and cattle nematodes against anthelmintics has been observed (Bisset, 1994; Moll et al., 2000; McMahon et al., 2013).

Application of breeding instruments and targeted selection of cattle or of cattle breeds with enhanced resistance against specific pathogens (i.e., gastrointestinal nematodes) was suggested by Morris et al. (1997). Several studies identified phenotypic variations of host resistances among cattle breeds from non-European countries for gastrointestinal nematode infections (Suarez et al., 1990, 1995; Peña et al., 2000; Oliveira et al., 2009); however, those study designs mostly addressed comparisons between *Bos indicus* and *Bos taurus* purebreds or crossbreds under (sub)tropical conditions. Within cattle breeds, endoparasite resistance was compared among specific sire lines (Seifert, 1977; Kloosterman et al., 1978; Barlow and Piper, 1985). Within-breed selection implies availability of genetic parameters for endoparasite resistance, and ongoing genetic evaluations. Heritability estimates in cattle for different gastrointestinal nematode species were low to moderate (reviewed in Table 1), in a range from 0.04 to 0.36 (Barlow and Piper, 1985; Burrow, 2001). For the susceptibility to liver fluke, McClure et al. (2014) reported a heritability of 0.15 for dairy cattle in Ireland. Moreover, infections and reinfections with the bovine lungworm are of economic importance in dairy cattle

herds (Holzhauer et al., 2011; Dank et al., 2015), but not addressed in quantitative-genetic studies.

Genetic correlations between gastrointestinal nematode resistances or fecal egg counts with production parameters (e.g., growth, weight gain) in sheep and beef cattle populations were estimated in various previous studies (Bisset et al., 1992; Gray, 1997; Bouix et al., 1998; Eady et al., 1998; Bishop et al., 2004; Silva et al., 2012). Including milk production traits, genetic correlations were -0.21 between milk yield and fecal nematode egg count, and -0.17 between fat plus protein yield and fecal nematode egg count for Saanen goats in New Zealand (**NZL**; Morris et al., 1997). In contrast, with a focus on gastrointestinal worm egg counts in crossbred ewes, Afolayan et al. (2009) found a slightly positive but unfavorable genetic correlation (0.08) with milk yield and a moderate genetic relationship (0.42) with protein percentage.

To our knowledge, a substantial gap exists addressing (1) genetic associations between endoparasite infections with production traits in dairy and dual-purpose cattle populations and (2) selection strategies for improved endoparasite resistances. Selection and breeding of appropriate genetic lines within the Black and White dairy and dual-purpose cattle population being best adapted to grazing systems might be one possible breeding strategy. During recent decades, breeding organizations in NZL strongly focused on such alternative breeding strategies (i.e., breeding cattle lines for grazing systems by including alternative functional traits into overall breeding goals; Miglior et al., 2005). In terms of economic efficiency, productivity per hectare of grassland and reproduction performance, Holstein Friesian (**HF**) cows from NZL were superior over other cattle breeds or lines in pasture-based production systems in Ireland and Switzerland (McCarthy et al., 2007; Piccand et al., 2013).

The objectives of the present study were 2-fold. First, we used a selection line comparison for endoparasite infections including different Black and White selection

Table 1. Heritability estimates from literature for fecal egg counts of gastrointestinal nematodes (GIN) in cattle

Reference	Country	Breed	h^2
Barlow and Piper, 1985	Australia	Hereford	0.04–0.29
Burrow, 2001	Australia	Australian Belmont Red	0.36
Coppieters et al., 2009	The Netherlands	Dutch Holstein Friesian	0.07–0.21
Gasbarre et al., 1990	United States	Angus	0.08–0.27
Kloosterman et al., 1992	Germany	Dutch Holstein Friesian (pure), Dutch Friesian $\times$ British Friesian, Dutch Friesian $\times$ American Friesian	0.14–0.78
Leighton et al., 1989	United States	Angus	0.29
Mackinnon et al., 1991	Australia	Zebu-cross	0.12–0.25
Morris et al., 2003	New Zealand	Angus	0.32
Morris and Amyes, 2012	New Zealand	Angus and Hereford	0.11–0.28
Passafaro et al., 2015	Brazil	Nellore	0.06–0.33
Zinsstag et al., 2000	Africa	West African N'Dama	0.18

lines based on an established cross-classified research design. Second, we estimated genetic (co)variance components for endoparasite infections and productivity in the Black and White cattle population including all selection lines simultaneously via the full genetic relationship matrix.

MATERIALS AND METHODS

Research Design

A pasture genetics project was established in pasture-based production systems in northwest Germany in 2007 to compare the effect of different sire origins on productivity and functional traits. The present study was incorporated in the framework of the pasture genetics project and considered 17 farms (13 organic, 4 conventional) with a strong focus on milking cow grazing (>8 h/d). The grassland farms were located in 4 federal states in northwest Germany. Herd sizes ranged from 19 to 215 milking cows, with an average of 72 cows per farm. Requirements for herd selection were (1) no treatments with anthelmintics in the sampling year and (2) access to pasture before June 1. In addition, all farms agreed to use a specific, but randomized mating scheme; that is, the insemination of defined proportions of GHC with Holstein sires from NZL, and with German Holstein (GH) pasture sires from Germany. Those GH pasture sires, which are suited to grazing conditions, represented bulls of German origin with outstanding breeding values for the traits being important in NZL (i.e., small body size, high fat percentage, low SCS, high nonreturn rate, short interval from calving to first insemination). A third genetic line in all herds included female offspring from matings of GHC with GH HF bulls representing the conventional selection strategy for indoor systems, with a strong focus on breeding values for milk yield (GH milk sires). For matings, farmers were encouraged to use GH milk sires with at least 1 breeding value standard deviation above the population mean (~500 kg for milk yield). Milk yield breeding values for GH milk sires ranged from 146 to 1,841 kg, and from -485 to 1,076 kg for GH pasture sires (database for national genetic evaluations from August 2016). Hence, the following 3 genetic lines were

established and included in the present study: GHC × NZL sires (HF-NZL; 72 cows), GHC × GH milk sires (HF-GHm; 639 cows), and GHC × GH pasture sires (HF-GHp; 70 cows). A fourth genetic line included local Black and White dual-purpose cows of the Deutsche Schwarzbunte Niederungsrind (DSN; 363 cows), the founder of the current German Holstein population. All 4 lines were genetically related among each other, with the lowest relationship coefficient of 0.6% between DSN and HF-GHm. The research design was cross-classified (several genetic lines per herd). A remaining set of 22 herd contemporaries was assigned to the category mixed breed (MIX), including GH × Jersey and Angler F₁ crossbreds, and F₁ crossbreds between GH with dual-purpose Fleckvieh.

Data

Test-Day Production Traits. Test-day data for all 1,166 cows included repeated measurements for the production traits milk yield (MY), protein percentage (Pro%), fat percentage (Fat%), fat-to-protein ratio (FPR), and SCC. Somatic cell counts were log-transformed into SCS = log₂ (SCC/100.000) + 3 (Ali and Shook, 1980). Lactation number ranged from 1 to 11 with a mean of 2.7; 26.1% of all records were from the first lactation, 27.2% from the second lactation, 17.3% from the third lactation, 12.2% from the fourth lactation, and 17.2% from later lactations. Cows with less than 5 test-day records were excluded from the analysis. Descriptive statistics for the test-day production traits are given in Table 2.

Endoparasite Traits. In total, 2,006 fecal samples were collected during 2 farm visits (June–July 2015 and September–October 2015) from the 1,166 dairy cows, including repeated measurements for 840 cows. Fecal larvae counts for the bovine lungworm *D. viviparus* (FLC-DV) were detected with the Baermann technique (Baermann, 1917) using 40 g of feces per cow. Fecal egg counts per gram of feces for GIN (FEC-GIN) were determined by a modified McMaster technique, according to Thienpont et al. (1979), with a sensitivity of 25 eggs/g of feces (EPG). Sedimentation technique with 10 g of feces per cow was used to detect eggs of flukes. The liver fluke *F. hepatica* and the rumen

Table 2. Descriptive statistics for test-day production traits

Trait	Number of test-day records	Mean	SD	Minimum	Maximum
Milk yield (kg)	10,132	22.06	6.97	2.20	57.20
Protein content (%)	10,125	3.37	0.38	2.38	6.32
Fat content (%)	10,125	4.30	0.72	1.75	9.09
Fat-to-protein ratio	10,125	1.28	0.19	0.40	3.29
SCS	10,115	3.02	1.64	0.01	10.01

Table 3. Total number of fecal samples and prevalence rates [number (no.) and % of positive samples (%)] for *Dictyocaulus viviparus*, gastrointestinal nematodes (GIN), and flukes in summer, autumn, and in both sampling periods (summer + autumn)

Item	<i>D. viviparus</i>			GIN			Flukes		
	Prevalence			Prevalence			Prevalence		
	Total	No.	%	Total	No.	%	Total	No.	%
Summer ¹	960	7	0.7	961	320	33.3	963	97	10.1
Autumn ²	1,028	35	3.4	1,036	242	23.4	1,043	96	9.2
Summer + autumn	1,988	42	2.1	1,997	562	28.1	2,006	193	9.6

¹Time span between June 29 and July 31.²Time span between September 1 and October 5.

fluke *Paramphistomum* spp./*Calicophoron* spp. were detected, and the sum of counts from both species was defined as the trait fecal egg count for flukes (**FEC-FLU**). The maximal value was 46 for FLC-DV, 225 for FEC-GIN, and 89 for FEC-FLU. Prevalence rates for all 3 endoparasite traits for the different sampling periods are given in Table 3. For GIN and flukes higher prevalence rates were found during the summer month, but for *D. viviparus* prevalences were larger in autumn.

To achieve a Gaussian-like distribution of traits, endoparasite larvae and egg counts (FLC-DV, FEC-GIN, and FEC-FLU) were log-transformed with $\log_E(\text{untransformed endoparasite trait} + 100)$ (**LogFLC-DV**, **LogFEC-GIN**, and **LogFEC-FLU**, respectively), and square roots of untransformed endoparasite traits were computed (**SqrtFLC-DV**, **SqrtFEC-GIN**, and **SqrtFEC-FLU**, respectively). However, all trait definitions did not follow a Gaussian distribution (based on the results from the Shapiro-wilk test). Furthermore, endoparasite traits were defined as binary data for *D. viviparus* (**BinFLC-DV**), for gastrointestinal nematodes (**BinFEC-GIN**), and for flukes (**BinFEC-FLU**). The threshold for a cow to be

defined as infected was 25 EPG for FEC-GIN, 1 egg/10 g of feces for FEC-FLU, and 1 larva/40 g of feces for FLC-DV. Infected cows received a score of 1; otherwise a score of 0 was assigned. Descriptive statistics for all endoparasite trait definitions are given in Table 4.

Statistical Models

Genetic Line Comparisons. Analyses of variance and estimation of least squares means (**LSM**) were carried out using the statistical software SAS version 9.4 (SAS Institute; Cary, NC). For the endoparasite traits FLC-DV, FEC-GIN, and FEC-FLU, the following linear mixed model (model 1; PROC MIXED) was applied:

$$y_{ijklmn} = \mu + \text{Farm}_i + \text{Lstage}_j + \text{Parity}_k + \text{GL}_l(\text{sp}_m) + \text{Cow}_n + e_{ijklmn}, \quad [1]$$

where y_{ijklmn} = observations for FLC-DV, FEC-GIN, and FEC-FLU; μ = overall mean effect; Farm_i = fixed effect of the i th farm (1, ..., 17); Lstage_j = fixed ef-

Table 4. Descriptive statistics for endoparasite traits

Endoparasite trait ¹	No. of observations	No. of cows	Mean	SD	Minimum	Maximum
FLC-DV	1,988	1,163	0.17	2.14	0	46.0
LogFLC-DV	1,988	1,163	4.61	0.02	4.61	6.78
SqrtFLC-DV	1,988	1,163	1.72	0.41	0	4.98
BinFLC-DV	1,988	1,163	0.02		0	1.00
FEC-GIN	1,997	1,166	11.35	22.57	0	225.0
LogFEC-GIN	1,997	1,166	4.70	0.17	4.61	15.0
SqrtFEC-GIN	1,997	1,166	0.05	2.90	0	5.78
BinFEC-GIN	1,997	1,166	0.28		0	1.00
FEC-FLU	2,006	1,166	0.63	3.70	0	89.0
LogFEC-FLU	2,006	1,166	4.61	0.03	4.61	9.43
SqrtFEC-FLU	2,006	1,166	0.21	0.76	0	5.24
BinFEC-FLU	2,006	1,166	0.10		0	1.00

¹FLC-DV = fecal larvae count for *Dictyocaulus viviparus*; FEC-GIN = fecal egg count for gastrointestinal nematodes; FEC-FLU = fecal egg count for flukes; LogFLC and LogFEC = log-transformed endoparasite fecal larvae and egg counts; SqrtFLC and SqrtFEC = square rooted endoparasite fecal larvae and egg counts; BinFLC and BinFEC = infection status (positive or negative) for the 3 endoparasites.

fect of the j th lactation stage according to Huth (1995; ≤ 14 , 14–77, 78–140, 141–231, and ≥ 232 DIM); Parity_k = fixed effect of the k th parity number (1, 2, 3, 4, and >4); $\text{GL}_l(\text{sp}_m)$ = fixed effect of the l th genetic line (HF-NZL, HF-GHm, HF-GHp, DSN, and MIX) crossed with the m th sampling period sp (1, 2); Cow_n = random effect of the n th cow accounting for the 2 repeated measurements per cow; and e_{ijklmn} = random residual effect.

Analyses of variance for the binary endoparasite traits (BinFLC-DV, BinFEC-GIN, and BinFEC-FLU) were conducted by applying generalized linear mixed models (model 2) with a logit link function, as implemented in the GLIMMIX procedure of SAS version 9.4:

$$\text{logit}(\pi_{rstuvw}) = \log[\pi_{rstuvw}/(1 - \pi_{rstuvw})] = \varphi + \text{Farm}_r + \text{Lstage}_s + \text{Parity}_t + \text{GL}_u(\text{sp}_v) + \text{Cow}_w, \quad [2]$$

where π_{rstuvw} was the probability for a cow to be positive for endoparasite infections; φ was the overall mean effect; Farm_r , Lstage_s , Parity_t , and GL_u crossed with the sampling period sp_v were fixed effects as defined in model [1]; and Cow_w was the random cow effect accounting for the 2 repeated measurements.

Estimation of Genetic Parameters. Estimations of genetic (co)variance components for endoparasite and test-day production traits were conducted by applying the software package DMU (Madsen and Jensen, 2013) and using the AI-REML algorithm for animal models. For quantitative genetic analyses, all 4 Black and White selection lines (i.e., HF-NZL, HF-GHm, HF-GHp, and DSN) were considered simultaneously via the full additive genetic relationship matrix. Due to the different selection line strategies, consideration of genetic group effects or modeling of phantom parent groups might be a further alternative. Nevertheless, the same grand sires were identified in the 3 HF lines. In consequence, the cows from the different Black and White selection lines are also not separated in official national genetic evaluations.

Standard errors for heritabilities were calculated by using R (version 3.3.0, R Core Team, 2013), and applying a Taylor series expansion as reported by Fischer et al. (2004). Standard errors for genetic correlations were calculated as suggested by Lynch and Walsh (1998). Standard errors of phenotypic correlations between endoparasite traits were approximated considering the variances of (co)variance estimates for genetic, permanent environmental, and residual effects, and applying the delta-method as implemented in the R package msm (Jackson, 2016).

For genetic analyses of repeated measured endoparasite traits (FLC-DV, LogFLC-DV, SqrtFLC-DV,

FEC-GIN, LogFEC-GIN, SqrtFEC-GIN, FEC-FLU, LogFEC-FLU, and SqrtFEC-FLU), the following repeatability model (**RM**; model 3) was defined:

$$y_{ijklmn} = \mu + \text{Farm}_i + \text{Lstage}_j + \text{Parity}_k + \text{sp}_l + \text{AG}_m + \text{pe}_n + e_{ijklmn}, \quad [3]$$

where y_{ijklmn} = observations for FLC-DV, FEC-GIN, and FEC-FLU; μ = overall mean effect; Farm_i = fixed effect of the i th farm (1, ..., 17); Lstage_j = fixed effect of the j th lactation stage according to Huth (1995; <14 , 14–77, 78–140, 141–231, and ≥ 232 DIM); Parity_k = fixed effect of the k th parity number (1, 2, 3, 4, and >4); sp_l = fixed effect of the l th sampling period (1, 2); AG_m = random additive genetic effect of the m th animal in the pedigree data set; pe_n = random effect for the permanent environment of the n th cow accounting for the 2 repeated measurements per cow; and e_{ijklmn} = random residual effect.

A random regression test-day model (**RRTDM**) with DIM as time covariate was applied to estimate genetic parameters for the test-day production traits (MY, Pro%, Fat%, FPR, and SCS) in the course of lactation. The RRTDM (model 4) followed the notation by Bohmanova et al. (2008), and was defined as

$$y_{ijklmnop} = \text{HTD}_i + \text{Parity}_j + \text{TS}_k + \text{YS}_l + \sum_{n=1}^q \alpha_n \mathbf{z}_n(s) + \sum_{n=1}^q \beta_{mn} \mathbf{z}_n(s) + \sum_{n=1}^q \gamma_{mn} \mathbf{z}_n(s) + e_{ijklmnop}, \quad [4]$$

where $y_{ijklmnop}$ = p th test-day record of the m th cow for MY, Pro%, Fat%, FPR, and SCS; HTD_i = fixed effect of the i th herd-test-date; Parity_j = fixed effect of j th parity number (1, 2, 3, 4, and >4); TS_k = fixed effect of k th time span between each test-day record and the endoparasite sampling date (≤ -200 , > -200 ; and ≤ -100 , > -100 ; and ≤ 0 , > 0 ; and ≤ 100 , > 100); YS_l = fixed effect of l th year-season of last calving (spring, summer, autumn, and winter within each year); q = the number of covariates (Legendre polynomials of order 2, implying $q = 3$); α_n = n th fixed regression coefficient by DIM; β_{mn} = n th random regression coefficient for the additive genetic effect of cow m by DIM; γ_{mn} = n th random regression coefficient for the permanent environmental effect of cow m by DIM; $\mathbf{z}(s)$ = vector of covariates of size q (modeled with Legendre polynomials of order 2) describing the shape of the lactation curve of fixed and random regressions evaluated at s DIM; and $e_{ijklmnop}$ = random residual effect. Model [3] was applied to estimate genetic correlations among endoparasite traits

in bivariate runs. For the bivariate runs, the following trait combinations (2 traits at a time) were considered. First, the combinations of the untransformed endoparasite traits (FLC-DV, FEC-GIN, and FEC-FLU); second, the combination of log-transformed endoparasite traits (LogFLC-DV, LogFEC-GIN, and LogFEC-FLU); and, third, the combination of square rooted endoparasite traits (SqrtFLC-DV, SqrtFEC-GIN, and SqrtFEC-FLU).

Genetic correlations between endoparasite traits and test-day traits were inferred by applying models [3] (for the endoparasite traits FLC-DV, FEC-GIN, and FEC-FLU) and [4] (for the longitudinal test-day traits MY, Pro%, Fat%, FPR, and SCS).

The (co)variance structure for random effects in bivariate RM [3] was

$$\text{var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{pe}_1 \\ \mathbf{pe}_2 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{g}_{11}\mathbf{A} & \mathbf{g}_{12}\mathbf{A} & 0 & 0 & 0 & 0 \\ \mathbf{g}_{12}\mathbf{A} & \mathbf{g}_{22}\mathbf{A} & 0 & 0 & 0 & 0 \\ 0 & 0 & \mathbf{pe}_{11}\mathbf{I}_{\text{pe}} & \mathbf{pe}_{12}\mathbf{I}_{\text{pe}} & 0 & 0 \\ 0 & 0 & \mathbf{pe}_{12}\mathbf{I}_{\text{pe}} & \mathbf{pe}_{22}\mathbf{I}_{\text{pe}} & 0 & 0 \\ 0 & 0 & 0 & 0 & \mathbf{r}_{11}\mathbf{I}_{\text{n}} & \mathbf{r}_{12}\mathbf{I}_{\text{n}} \\ 0 & 0 & 0 & 0 & \mathbf{r}_{12}\mathbf{I}_{\text{n}} & \mathbf{r}_{22}\mathbf{I}_{\text{n}} \end{bmatrix},$$

where $\mathbf{a}_1$ and $\mathbf{a}_2$ were vectors for additive-genetic effects for both traits, $\mathbf{pe}_1$ and $\mathbf{pe}_2$ were vectors for permanent environmental effects for both traits, $\mathbf{e}_1$ and $\mathbf{e}_2$ were vectors for residual effects for both traits; $\mathbf{g}_{11}$, $\mathbf{g}_{12}$, and $\mathbf{g}_{22}$ = additive genetic (co)variances for endoparasite traits; $\mathbf{A}$ was an additive genetic relationship matrix; $\mathbf{pe}_{11}$, $\mathbf{pe}_{12}$ and $\mathbf{pe}_{22}$ = permanent environmental (co)variances for endoparasite traits; $\mathbf{r}_{11}$, $\mathbf{r}_{12}$, and $\mathbf{r}_{22}$ = residual (co)variances for endoparasite traits; $\mathbf{I}_{\text{pe}}$ and $\mathbf{I}_{\text{n}}$ were identity matrices for pe cows and n observations, respectively.

The (co)variance structure for random effects in bivariate models including the RM for endoparasite traits (3) and the RRTDM (4) for test-day production traits was

$$\text{var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{pe}_1 \\ \mathbf{pe}_2 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{G}_{11} \otimes \mathbf{A} & \mathbf{G}_{12} \otimes \mathbf{A} & 0 & 0 & 0 & 0 \\ \mathbf{G}_{21} \otimes \mathbf{A} & \mathbf{G}_{22} \otimes \mathbf{A} & 0 & 0 & 0 & 0 \\ 0 & 0 & \mathbf{PE}_{11} \otimes \mathbf{I}_{\text{pe}} & \mathbf{PE}_{12} \otimes \mathbf{I}_{\text{pe}} & 0 & 0 \\ 0 & 0 & \mathbf{PE}_{21} \otimes \mathbf{I}_{\text{pe}} & \mathbf{PE}_{22} \otimes \mathbf{I}_{\text{pe}} & 0 & 0 \\ 0 & 0 & 0 & 0 & \mathbf{R}_{11}\mathbf{I}_{\text{n}} & \mathbf{R}_{12}\mathbf{I}_{\text{n}} \\ 0 & 0 & 0 & 0 & \mathbf{R}_{21}\mathbf{I}_{\text{n}} & \mathbf{R}_{22}\mathbf{I}_{\text{n}} \end{bmatrix},$$

where $\mathbf{G}_{11} = 3 \times 3$ (co)variance matrix of random regression coefficients for the additive genetic effects for test-day traits; $\mathbf{A}$ was an additive genetic relationship matrix; $\mathbf{G}_{12}$, $\mathbf{G}_{21}$ = additive genetic covariance matrix between endoparasite and test-day traits; $\mathbf{G}_{22}$

= additive genetic variance for endoparasite traits; $\mathbf{PE}_{11} = 3 \times 3$ (co)variance matrix of random regression coefficients for permanent environmental effects for test-day traits; $\mathbf{PE}_{12}$, $\mathbf{PE}_{21}$ = covariance matrix for permanent environmental effects between test-day and endoparasite traits; $\mathbf{PE}_{22}$ = variance for permanent environmental effects for endoparasite traits; $\mathbf{R}_{11}$ = residual variances for test-day traits; $\mathbf{R}_{12}$, $\mathbf{R}_{21}$ = residual covariances between endoparasite and test-day traits; and $\mathbf{R}_{22}$ = residual variances for endoparasite traits; $\mathbf{I}_{\text{pe}}$ and $\mathbf{I}_{\text{n}}$ were identity matrices for pe cows and n observations, respectively.

RESULTS

Genetic Line Comparisons

Results for the test of significance for fixed effects (sum of squares type III) as included in model [1] are given in Table 5. The genetic line effect significantly influenced FLC-DV ($P < 0.05$) and FEC-GIN ($P < 0.0001$), but was not significant ($P > 0.05$) for FEC-FLU. For FLC-DV in autumn, LSM were significantly higher for DSN compared with HF-GHm (differences of LSM = 0.54; $P \leq 0.05$). In summer, LSM for FLC-DV in HF-NZL and HF-GHp were quite similar [i.e., differences of LSM (0.01) were not significant ($P > 0.05$)]. For the contrast of both grassland lines with HF-GHm, differences of LSM were 0.04 for HF-GHm–HF-NZL, and 0.05 for HF-GHm–HF-GHp ($P > 0.05$). The same trends of genetic line comparisons for FLC-DV were observed in autumn.

Least squares means for FEC-GIN within genetic lines (1) in summer and autumn are shown in Figure 1. Line comparisons in summer were in agreement with results from autumn. For FEC-GIN, LSM decreased from the first (June–July) to the second (September–October) sampling period. Lowest values for FEC-GIN were identified for pasture lines HF-NZL and HF-GHp. For HF-NZL, the LSM for FEC-GIN was 5.0 EPG in summer and 11.4 EPG in autumn. In the first sampling period, FEC-GIN with 18.0 EPG was largest in

Table 5. Significance (P -value) of fixed effects on endoparasite traits

Fixed effect	Endoparasite trait ¹		
	FLC-DV	FEC-GIN	FEC-FLU
Genetic line	0.0057	0.0001	0.1221
Farm	0.5240	0.0001	0.0001
Parity	0.0001	0.0001	0.0287
Lactation stage	0.0012	0.0001	0.2117

¹FLC-DV = fecal larvae count for *Dictyocaulus viviparus*; FEC-GIN = fecal egg count for gastrointestinal nematodes; FEC-FLU = fecal egg count for flukes.

Figure 1. Least squares means [model (1)] with corresponding SE for gastrointestinal nematode egg counts (FEC-GIN) within genetic lines for different sampling periods (summer and autumn 2015). Different letters (a,b) within sampling periods indicate significant differences ($P < 0.05$). HF-NZL = German Holstein cow (GHC) $\times$ New Zealand (NZL) sires; HF-GHm = GHC $\times$ German Holstein milk sires; HF-GHp = GHC $\times$ German Holstein pasture sires; DSN = Black and White dual-purpose cows (Deutsche Schwarzbuntes Niederungsgrind); mixed = crossbreds between German Holstein $\times$ beef cattle, Jersey, or Angler.

DSN cows, followed by MIX (17.6 EPG) and HF-GHm (16.2 EPG). Interestingly, similar FEC-GIN levels were identified for DSN cows and high-yielding Holsteins (HF-GHm). A significant difference ($P \leq 0.05$) in autumn was observed when comparing FEC-GIN from HF-GHm and HF-NZL, with larger values for HF-GHm (differences of LSM = 6.60).

The highest GIN egg excretion was identified in first-parity cows in the early lactation stage (Figure 2). Least squares means for FEC-GIN were significantly higher for cows in parity 1 compared with cows in parity 3 ($P \leq 0.05$) and 4 ($P < 0.0001$). Cows in lactation stage 1 (<14 DIM) showed a significantly higher LSM for FEC-GIN compared with cows in lactation stage 2 ($P \leq 0.001$; 14–77 DIM), 3 ($P \leq 0.05$; 78–140 DIM), 4 ($P < 0.0001$; 141–231 DIM), and 5 ($P < 0.0001$; ≥ 232 DIM).

With regard to the binary endoparasite trait definitions [model 2], line comparisons for BinFEC-GIN were in agreement with the results from model [1] for the untransformed trait FEC-GIN. The lowest probability for a GIN infection in summer was identified for the pasture genetic lines HF-NZL (27.3%) and HF-GHp (25.4%).

The DSN cattle showed the highest infection rate for GIN (42.2%), whereas prevalences were slightly lower for HF-GHm (32.3%) and MIX (30.4%). Differences for infection rates in different lines in the summer period were not significant ($P > 0.05$). In autumn, prevalences for a GIN infection were significantly lower ($P \leq 0.05$) in the HF-NZL line (10.4%) compared with HF-GHm (24.4%) and DSN (26.2%). Also, for the binary trait definition, infection probability for GIN decreased with increasing parity number. In agreement with results from the linear mixed model [1], highest GIN infection rates (35.9 and 24.8%, respectively) were observed in the first (<14 DIM) and in the third (78–140 DIM) lactation stage, whereas infection rates (19.9%) were lowest in the last lactation stage (≥ 232 DIM).

Genetic Parameters for Endoparasite Traits

Heritabilities. Heritability estimates from the bivariate models including all endoparasite trait definitions [i.e., for untransformed (FLC-DV, FEC-GIN, FEC-FLU), log-transformed (LogFLC-DV, LogFEC-GIN, LogFEC-FLU), and square-rooted data (Sqrt-

Figure 2. (A) Least squares means [model (1)] with corresponding SE for gastrointestinal nematode egg counts (FEC-GIN) for different parities. (B) Least squares means [model (1)] with corresponding SE for FEC-GIN for different lactation stages. Different letters (a–c) indicate significant differences ($P < 0.05$). Parity numbers 1 to 5 represent parities 1, 2, 3, 4, and >4 , respectively; lactation stage was classified as 1: ≤ 14 DIM, 2: 14–77 DIM, 3: 78–140 DIM, 4: 141–231 DIM, and 5: ≥ 232 DIM.

FLC-DV, SqrtFEC-GIN, SqrtFEC-FLU)] were quite stable with small standard errors (Table 6). Heritabilities from bivariate models with 2 endoparasite traits were almost identical with estimates from the RRTDM, including 1 endoparasite and 1 test-day production trait (not shown). The FEC-FLU was more heritable (0.33 ± 0.06) than FEC-GIN ($0.05\text{--}0.06 \pm 0.04$) and FLC-DV (0.05 ± 0.04 ; Table 6). Heritabilities from log-transformed (LogFEC-FLU) and square-rooted data (SqrtFEC-FLU) were even slightly higher (0.39 ± 0.06

and 0.40 ± 0.07 , respectively) than from the raw FEC-FLU data. For FLC-DV and FEC-GIN, heritabilities from log and square root transformations confirmed the low estimates from the original untransformed data. For the evaluation of endoparasite trait definitions, we compared Akaike information criteria from univariate RM [model 3] for the 3 endoparasite traits; Akaike information criterion values were always smallest for the untransformed data. Hence, the original untransformed endoparasite data set was used to infer genetic associations between endoparasite and milk production traits.

Genetic and Phenotypic Correlations Among Endoparasite Traits. The genetic correlation between FEC-GIN and FLC-DV was exactly 1.00, but close to zero between FEC-GIN and FEC-FLU (-0.10) and close to zero between FLC-DV and FEC-FLU (0.03 ; Table 6). Standard errors for genetic correlations were quite high, but consistent genetic correlations were found when using log-transformed data in bivariate models. For SqrtFLC-DV and SqrtFEC-GIN, genetic correlations were slightly smaller than for untransformed or log-transformed data. Transformation of data had no effect on phenotypic correlations among endoparasite traits, which were close to zero in a range from -0.05 to 0.07 (± 0.02).

Genetic Correlations Between Endoparasite and Milk Production Traits. Daily heritabilities from the RRTDM for all production traits across the whole lactation (MY = $0.35\text{--}0.45$; Pro% = $0.05\text{--}0.51$; Fat% = $0.33\text{--}0.65$; FPR = $0.28\text{--}0.51$; SCS = $0.14\text{--}0.22$) were in a reasonable range. Variations of additive genetic variances and heritabilities by DIM indicate that different genes are switched on and off during lactation. Negative genetic correlations between MY and FLC-DV were observed during the whole lactation period (Figure 3). Genetic correlations between MY and FEC-FLU were negative until 215 DIM and changed to positive values in the later lactation stage at 220 DIM (Figure 3). Genetic correlations between MY and FEC-GIN were positive throughout, from 90 DIM to the end of lactation, with the largest correlation of 0.25 at 220 DIM (Figure 3). Both FEC-GIN and FEC-FLU were negatively correlated with Pro% through the whole lactation period (Figure 4), whereas genetic correlations for Pro% and FLC-DV were slightly negative between 40 and 220 DIM. A negative genetic correlation was also observed between Fat% and FEC-GIN from 25 to 295 DIM (Figure 5). In contrast, Fat% was positively correlated with FEC-FLU apart from the last lactation stage (Figure 5). The Fat% was positively correlated with FLC-DV during the whole lactation (but close to zero between 135 to 185 DIM), with the highest genetic correlation of 0.58 at 365 DIM (Figure 5). Genetic correlation curves between FPR and endoparasite traits

Table 6. Heritabilities¹ (bold on diagonal), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for the untransformed (FLC-DV, FEC-GIN, FEC-FLU), log-transformed (LogFLC and LogFEC) and square rooted (SqrtFLC and SqrtFEC) endoparasite traits *Dictyocaulus viviparus*, gastrointestinal nematodes (GIN), and flukes

Endoparasite trait ²	FLC-DV	FEC-GIN	FEC-FLU	LogFLC-DV	LogFEC-GIN	LogFEC-FLU	SqrtFLC-DV	SqrtFEC-GIN	SqrtFEC-FLU
FLC-DV	0.05 ± 0.04	1.00 ± 0.60	0.03 ± 0.30	—	—	—	—	—	—
FEC-GIN	0.06 ± 0.02	0.05–0.06 ± 0.04	–0.10 ± 0.27	—	—	—	—	—	—
FEC-FLU	–0.05 ± 0.02	0.07 ± 0.02	0.33 ± 0.06	—	—	—	—	—	—
LogFLC-DV	—	—	—	—	0.99 ± 0.68	0.03 ± 0.28	—	—	—
LogFEC-GIN	—	—	—	0.05 ± 0.04	0.04–0.05 ± 0.04	–0.11 ± 0.30	—	—	—
LogFEC-FLU	—	—	—	–0.05 ± 0.02	0.07 ± 0.02	0.39–0.40 ± 0.06	—	—	—
SqrtFLC-DV	—	—	—	—	—	—	0.08 ± 0.04	0.97 ± 0.78	0.01 ± 0.23
SqrtFEC-GIN	—	—	—	—	—	—	0.06 ± 0.02	0.03 ± 0.04	–0.07 ± 0.39
SqrtFEC-FLU	—	—	—	—	—	—	–0.05 ± 0.02	0.07 ± 0.02	0.40 ± 0.07

¹Estimates from the different bivariate runs (only 1 value for the heritability = identical heritabilities from all bivariate runs, otherwise the range of heritabilities from the bivariate runs is given). Values after ± are the SE of estimates.

²FLC-DV = fecal larvae count for *D. viviparus*; FEC-GIN = fecal egg count for gastrointestinal nematodes; FEC-FLU = fecal egg count for flukes; LogFLC and LogFEC = log-transformed endoparasite larvae and egg counts; SqrtFLC and SqrtFEC = square rooted endoparasite fecal larvae and egg counts.

Figure 3. Daily genetic correlations with corresponding SE (gray areas) between the endoparasite traits fecal egg count for gastrointestinal nematodes (FEC-GIN), fecal larvae count for *Dictyocaulus viviparus* (FLC-DV), and fecal egg count for flukes (FEC-FLU) with test-day milk yield (MY).

(Figure 6) were quite similar compared with corresponding estimates for Fat% endoparasite trait associations. Moderate genetic correlations throughout lactation in the range from 0.35 to 0.48 were identified between SCS and FEC-GIN (Figure 7). For the middle lactation period, genetic correlations were negative between SCS with FLC-DV, and negative throughout between SCS with FEC-FLU. Generally, the highest and lowest genetic correlations were found at the beginning and

Figure 4. Daily genetic correlations with corresponding SE (gray areas) between the endoparasite traits fecal egg count for gastrointestinal nematodes (FEC-GIN), fecal larvae count for *Dictyocaulus viviparus* (FLC-DV), and fecal egg count for flukes (FEC-FLU) with test-day protein percentage (Pro%).

Figure 5. Daily genetic correlations with corresponding SE (gray areas) between the endoparasite traits fecal egg count for gastrointestinal nematodes (FEC-GIN), fecal larvae count for *Dictyocaulus viviparus* (FLC-DV), and fecal egg count for flukes (FEC-FLU) with test-day fat percentage (Fat%).

the end of lactation period; however, standard errors were also largest at the extreme ends of the time scale.

DISCUSSION

Genetic Line Comparisons

Only a few studies addressed endoparasite infection comparisons between genetic lines or among cattle sub-

populations. Barlow and Piper (1985) observed significant intrabreed sire effects for endoparasite infections in Hereford, Simmental, Friesian, and Brahman cattle. For Dutch Friesian calves, Kloosterman et al. (1978) identified variation among sires regarding resistance to GIN. In the present study, the lowest susceptibility for GIN was identified for the HF-NZL line, reflecting the New Zealand breeding goal with a focus on adaptation to grazing systems (McCarthy et al., 2007). The HF-NZL line was more resistant against GIN compared with the HF-GHm line, which has been bred and selected for indoor production systems over decades. In this regard, König et al. (2005a) identified genotype by environment interactions for production and functional traits when stratifying the HF-data set according to the production system characteristics indoor in east Germany versus grassland in west Germany. For novel functional traits (e.g., hock lesion score, BCS, lameness score, hygiene score), Brügemann et al. (2015) confirmed the superiority of HF-NZL over German Holstein selection lines. Knaus (2016) studied energy deficiency during lactation and identified an optimal BCS and energy balance in HF-NZL dairy cows, especially when comparing to high-yielding HF cows in grassland systems.

Collard et al. (2000) defined metabolic stress as response to a negative energy balance and as response to a quick mobilization of body fat depots in high-yielding dairy cows. Especially in the first third of lactation, metabolic stress caused metabolic disorders, but also increased susceptibility to other disease categories (claw disorders, fertility disorders, clinical mastitis;

Figure 6. Daily genetic correlations with corresponding SE (gray areas) between the endoparasite traits fecal egg count for gastrointestinal nematodes (FEC-GIN), fecal larvae count for *Dictyocaulus viviparus* (FLC-DV), and fecal egg count for flukes (FEC-FLU) with fat-to-protein ratio (FPR).

Figure 7. Daily genetic correlations with corresponding SE (gray areas) between the endoparasite traits fecal egg count for gastrointestinal nematodes (FEC-GIN), fecal larvae count for *Dictyocaulus viviparus* (FLC-DV), and fecal egg count for flukes (FEC-FLU) with SCS.

Collard et al., 2000; Fleischer et al., 2001). In this context, König et al. (2005b) stated that “health problems appear to occur in clusters”; that is, a cow in a negative energy balance with increased SCS was also susceptible for claw disease infections. Hence, adaptive breeding for grassland systems with a focus on an optimal BCS might contribute to lower GIN prevalence rates, as observed in the HF-NZL line.

However, grazing systems in New Zealand differ from those in Germany, suggesting the implementation of specific selection lines being adapted to German grazing conditions. A first compromise in this regard was the creation of the HF-GHp line, based on German Holsteins with alternative breeding goals (i.e., strong weight on such breeding traits being important in NZL). In the present study and with regard to GIN infections, the HF-GHp line was competitive with HF-NZL.

Quite similar and highest LSM for FEC-GIN were identified for DSN and high-yielding Holstein cows (HF-GHm). A lower susceptibility with lower GIN egg excretion was expected for DSN, as DSN cattle have a long breeding history in the German grassland region of East Frisia, located at the coast of the federal state of Lower Saxony (Mügge et al., 1999). Utilizing a cross-classified research design with DSN and HF cows in the same herd, Al-Kanaan (2016) studied mechanisms of disease susceptibility in harsh environments. Al-Kanaan (2016) focused on physiological traits and found out that DSN cows were more susceptible to heat stress challenges compared with high-yielding HF. As a justification, the author described principles of selection theory as described by Via and Lande (1985); for example, reduced heat stress response might be due to lower phenotypic and genetic variations in intensively selected HF cows. A further explanation for higher prevalence rates in DSN cows addressed genetic analogy. In a comprehensive pedigree analysis, Jaeger et al. (2016) identified influential DSN sires not only from the East Frisia grassland region, but also from large-scale indoor herds in Berlin-Brandenburg, Germany. Artificial insemination DSN sires from the breeding organization of Berlin-Brandenburg were genetically closer related to the current DSN milking cow population compared with sires from western Germany grassland regions.

In the grassland outdoor production system, HF-GHm cows (selected for indoor systems) acquired immunity against GIN infections because they had access to pasture during the heifer stage. Nevertheless, due to the pronounced selection strategy effect, infection rates were lower for HF-GHp. Generally, the immunity effect was proven in the present study. Our findings for highest GIN egg counts in primiparous cows are in agreement with results by Gasbarre et al. (2001), who

identified a better immune response to GIN infections in later lactations. In contrast, other studies observed no effect of parity number on fecal egg counts for GIN (Agneessens et al., 2000; Borgsteede et al., 2000; Perri et al., 2011). Regarding the lactation stage, Perri et al. (2011) found highest FEC-GIN values around the time of calving and during the early lactation stage due to a lower immunity status as a result of metabolic stress.

In general, prevalence rates for GIN were higher for MIXED compared with purebred HF-NZL or HF-GHp cows. Because of the utilization of 100% of heterosis effects in F₁ crossbred cows, especially for low-heritability functional traits, lower prevalence rates were expected (Sørensen et al., 2008). Our finding corroborate with those by Suarez et al. (1995) in Argentina, who observed that purebred Angus cattle were more resistant against GIN than crossed Angus. In contrast, other authors reported a stronger endoparasite resistance in crossbred cattle compared with purebreds (O’Kelly, 1980; Peña et al., 2000; Oliveira et al., 2009).

Heritabilities and Genetic and Phenotypic Correlations for Endoparasite Traits

Regarding the most common endoparasite trait definitions, fecal egg counts were used to estimate genetic parameters for endoparasite resistance in ruminants (Barlow and Piper, 1985; Bryan and Kerr, 1989; Oliveira et al., 2009). In adult cattle, mostly zero-inflated data sets were databases for quantitative genetic studies because egg counts decrease with the host’s aging due to acquired immunity. To cope with this statistical problem, and to achieve a Gaussian-like data distribution, previous studies applied logarithmic transformations of endoparasite fecal egg counts (Bisset et al., 1992; Zinsstag et al., 2000; Coppieters et al., 2009). Square root transformations for nematode egg counts were used by Bisset et al. (1992) and Woolaston et al. (1991). Heritability estimates for original and transformed data for different endoparasite species differed by approximately ± 0.13 (Bisset et al., 1992), reflecting larger heritability estimate variations for different trait definitions than in the present study. Our heritability estimates for LogFEC-GIN and FEC-GIN (0.04–0.06) were in agreement with those by Coppieters et al. (2009) for log-transformed fecal egg counts (0.07–0.21) in Dutch Holstein-Friesian cows. In the present study, heritabilities for LogFLC-DV and FLC-DV (0.05) and for LogFEC-GIN and FEC-GIN (0.04–0.06) were small and very similar, reflecting that both endoparasites (*D. viviparus* and GIN) represent the same order, Strongylida. Low heritabilities for FEC-GIN and FLC-DV were due to a large environmental influence (i.e., large re-

sidual variances for both traits). An even broader range of heritabilities of untransformed and transformed GIN fecal egg counts with low to moderate heritabilities in a range from 0.04 to 0.36, as estimated in previous studies, is given in Table 1. Heritability estimate variations within same populations were due to research design configurations [e.g., artificial versus natural infections (Mugambi et al., 2005; Amarante et al., 2009), time and repetition of fecal sampling (Zinsstag et al., 2000), and animal age (Kornaš et al., 2015; Passafaro et al., 2015)]. In contrast to our study, most previous studies estimated genetic parameters for GIN in calves or heifers (Kloosterman et al., 1978; Gasbarre et al., 1990), or in beef cattle populations (Morris and Amyes, 2012). Genetic statistical modeling for lactating cows differed from those for calves or beef cattle because parity and lactation stage has to be taken into account (Coppie et al., 2009; Perri et al., 2011).

Due to the larger additive-genetic and the lower residual component (not shown), the heritability for FEC-FLU was substantially larger (0.33) compared with FEC-GIN (0.05–0.06) and FLC-DV (0.05). For dairy and beef cattle in Ireland grassland systems, McClure et al. (2014) used a binary trait definition and estimated a lower heritability of 0.15 for the presence of liver flukes (*F. hepatica*). Twomey et al. (2016) reported a smaller heritability, in the range from 0.01 and 0.09, for the binary traits liver damage caused by *F. hepatica* and antibody response to *F. hepatica* in Irish dairy and beef cattle. Threshold models for categorical endoparasite traits with 2 or more classes were also applied by Passafaro et al. (2015). Passafaro et al. (2015) compared heritabilities for endoparasite traits from both linear and threshold models, but differences in heritability estimates from both models were not significant.

The pronounced positive genetic relationship (1.00) between FEC-GIN and FLC-DV simplifies selection strategies. Selection on improved resistance against GIN implies associated infection resistance against *D. viviparus* and vice versa. This phenomenon was emphasized in previous studies in sheep (Woolaston and Eady, 1995; Gray, 1997), where a higher resistance to *Haemonchus contortus* was accompanied with lower egg counts for other GIN species. In the present study, the phenotypic correlation between FLC-DV and FEC-GIN was also positive but close to zero. Accordingly, Morris et al. (2003) compared genetic and phenotypic correlations for different GIN species by using log-transformed fecal egg counts and endoparasite antibody traits in 2 calf-crops of Angus cattle. They identified large genetic correlations among all endoparasite traits, whereas phenotypic correlations between fecal egg counts and endoparasite antibody traits were substantially lower.

Genetic Correlations Between Endoparasite Traits with Milk Production Traits

According to the genetic correlation estimates from the present study, breeding for increasing milk yield at the beginning of lactation will decrease genetic susceptibility to endoparasite infections (*D. viviparus*, GIN, and *F. hepatica*). Conversely, susceptibility to endoparasite infections at the genetic scale is associated with a lower milk production level. Explanations for strong genetic correlations between endoparasite infections and milk productivity could be due to pleiotropic effects or due to linkage, suggesting ongoing genomic analyses based on dense high-throughput SNP marker data. Our results for quantitative genetic relationships are in contrast to most of the previous studies conducted at phenotypic scales (Barger, 1993; Sordillo et al., 2009; Perri et al., 2011), where energy deficiency combined with metabolic diseases during the onset of lactation impaired the immune system, making high-yielding cows more susceptible to GIN infections. The genetic correlation close to zero between MY and the endoparasite trait FEC-FLU indicates that breeding and selection on resistance to *F. hepatica* improves disease resistance without reducing productivity in grazing herds. Apart from the late lactation stage, genetic correlations between Fat% and FEC-FLU were positive. For FLC-DV, a positive genetic correlation with Fat% was found during the whole lactation. A possible explanation addresses the naturally genetically antagonistic relationship between Fat% and MY (Collard et al., 2000; Yin et al., 2012).

The shape of genetic correlation curves with FLC-DV, FEC-GIN, and FEC-FLU were similar for Fat% and FPR. A high FPR early in lactation, especially due to high Fat%, indicates energy deficiency and metabolic stress (Buttchereit et al., 2011). As outlined at the phenotypic scale, cows in a pronounced negative energy balance mobilize their body fat depots too quickly, contributing to disease susceptibility at the beginning of lactation (Lassen et al., 2003); this was shown in the present study for *D. viviparus* and flukes via genetic relationships with FPR.

Protein content was genetically negatively correlated with FEC-GIN and FEC-FLU during the whole lactation. Genetic correlations between Pro% and FLC-DV were close to zero. This outcome is in contrast to Afolayan et al. (2009), who found a positive genetic correlation (0.42) between Pro% and worm egg counts in ewes, reflecting different genetic mechanisms in different species (Barillet, 2007; Bishop and Morris, 2007) or effect of selection (Veerkamp et al., 2003; Haenlein, 2007). Another explanation for different findings addresses

statistical modeling of longitudinal data; Afolayan et al. (2009) used cubic splines, but we used Legendre polynomials for the modeling of the lactation curve.

Positive genetic correlations between FEC-GIN and SCS are in agreement with estimates in dairy sheep (Sechi et al., 2009), indicating that the same cows are genetically susceptible for both udder and endoparasite infections. A physiological explanation for this relationship might be that infections with GIN increased gastrointestinal permeability (McKellar, 1993), resulting in a migration of other pathogens in the bloodstream and in the udder. So far, such pathogenic mechanisms have not been identified for *D. viviparus* and *F. hepatica*. For FEC-FLU (genetic negative correlation with SCS), we hypothesized that an increase of somatic cells in the milk was due to the host immune response. Our hypothesis was based on findings by Molina-Hernández et al. (2015), who found that an infection with *F. hepatica* depressed initiation of an immune response, probably resulting in a lower SCS.

In the present study, daily genetic correlations from the RRTDM between FEC-GIN and FLC-DV with test-day production traits were more extreme at the beginning and at the end of lactation. In comparison for FEC-FLU, the shape of the genetic correlation curves was more consistent during lactation, and corresponding standard errors were smaller. Our finding of inflated genetic correlations for the low heritability traits FEC-GIN and FLC-DV at the extreme ends of the continuous scale correspond with accuracies of random regression results for functional energy efficiency or fertility traits (Ravagnolo and Misztal, 2002; Buttchereit et al., 2011).

CONCLUSIONS

In conclusion, infections with the endoparasites *D. viviparus* and GIN differed in Black and White cattle selection lines. Lowest and similar infection rates for GIN were identified for the HF-NZL and the HF-GHp line, reflecting better adaptation of grassland selection lines to grassland systems. The transformation of endoparasite data had no effect on genetic parameters estimates (i.e., genetic parameters were almost identical for the original data, log-transformations, and square rooted data). The moderate heritability estimate of 0.33 for FEC-FLU indicates substantial genetic variation for *F. hepatica* in selected lines of Black and White cattle, which can be used for breeding on disease resistance in overall dairy cattle breeding goals. Negative genetic correlations (desired in terms of breeding) between the most important production traits, MY and Pro%, with endoparasite traits allow genetic progress in both trait categories simultaneously.

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