



Genetic parameters for dry matter intake, energy balance, residual energy intake, and liability to diseases in German Holstein and Fleckvieh dairy cows

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ABSTRACT

Selection for feed efficiency (FE) is a hot topic in dairy cow breeding. Dry matter intake (DMI) and residual energy intake (REI) are mostly discussed as new selection traits. Selection for lower DMI or REI seems to increase FE if other traits, such as milk yield or health, are not affected negatively. However, genetic relationships with other traits have not been adequately investigated because of the difficulties in recording sufficient feed intake data for genetic evaluations. The aim of this study was to examine the genetic relationships between FE-related traits and liability to diseases throughout lactation. First, heritabilities for all traits are presented. Subsequently, genetic correlations between DMI, energy-corrected milk yield, energy balance (EB), and REI on the one hand and 3 disease categories (mastitis, claw and leg diseases, and all diseases) on the other throughout lactation in German Holstein (GH) dairy cows are illustrated. Production and health data from the projects optiKuh and eMissionCow were used. Data consisted of weekly observations recorded over a 325-wk period in 2,387 GH and over a 300-wk period in 632 Fleckvieh (FV) primiparous and multiparous dairy cows from 13 dairy research farms in Germany. Variance and covariance components were estimated univariately or bivariately with linear random regression models for production data and threshold random regression models for health data. Heritabilities for DMI, EB, and REI were on average 0.17 and 0.15, 0.14 and 0.15, as well as 0.11 and 0.14 in GH and FV, respectively. Heritabilities on the underlying scale for mastitis, claw and leg diseases, and all diseases were on average 0.17 and 0.16, 0.18 and 0.12, as well as 0.15 and 0.11 in GH and FV, respectively. In GH, almost all genetic correlations were negative, especially in early lactation. Within the first 50 d in milk, genetic correlations between DMI and REI on the one hand and

disease categories on the other ranged from -0.25 to -0.14 for mastitis, from -0.31 to -0.13 for claw and leg diseases, and from -0.58 to -0.30 for all diseases. Consequently, selection for lower DMI or REI could lead to a higher liability to diseases, especially in early lactation. A possibility to mitigate these undesirable side effects could be lactation stage-specific selection for FE. For FV, further studies with more data are needed to assess genetic relationships.

Key words: dry matter intake, eMissionCow, feed efficiency, health, optiKuh

INTRODUCTION

Despite numerous publications, scientific suggestions, and even first implementations of feed efficiency (FE) into dairy cow breeding programs by some companies and national breeding organizations, no clear agreement exists on how to optimally breed for the complex trait FE in the future (Brito et al., 2020). Direct selection by considering residual feed intake or residual energy intake (REI) as a single FE trait in the selection index is currently recommended as an appropriate approach. Alternatively, indirect selection by including traits that affect FE in the selection index, especially DMI, is discussed (Kennedy et al., 1993; VandeHaar et al., 2016; Hurley et al., 2017; Houlihan et al., 2021). Berry and Pryce (2014) have already compiled a list of advantages and disadvantages of using residual feed intake or DMI. Furthermore, it is argued that direct selection for residual feed intake or REI is similar to indirect selection for feed intake itself together with energy sink traits, such as milk yield and BW, when the selection index includes correct economic and genetic parameters (Kennedy et al., 1993; Hurley et al., 2017). For more information on efficiency in breeding and production, see Ledinek et al. (2022).

Apart from this discussion, feed intake is generally a key factor for estimating FE as well as residual feed intake or REI (VandeHaar et al., 2016; Negussie et al., 2019). Consequently, the biggest obstacles in breeding for FE are the high costs and difficulties in measur-

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ing cow individual feed intake, which have prevented routine data recording until now (Berry and Crowley, 2013; Seymour et al., 2019; Brito et al., 2020). Actually, energy intake and thus energy efficiency should be favored over feed intake and thus FE (Ledinek et al., 2022), but this requires even more data. Since the introduction of genomic selection in 2001, the estimation of genomic EBV for traits that are difficult to measure became possible by using information from a reference population (Meuwissen et al., 2001; Hayes et al., 2013; de Haas et al., 2014). Therefore, a sufficiently large and preferably population-specific reference population with cow individual feed intake data and associated genotypes is currently the most important prerequisite for breeding for FE (Hayes et al., 2013), whether direct or indirect selection is finally used.

Before a new trait is included into a selection index, a population-specific evaluation of its heritability and genetic correlations with the other traits should be performed (Pryce et al., 2014; Brito et al., 2020). In particular, genetic correlations are critical when selecting for multiple traits, as negative genetic correlations hinder breeding progress (Rauw et al., 1998). Genetic correlations between DMI, residual feed intake, or REI and liability to diseases are a gap in knowledge because a joint analysis of these difficult-to-measure traits is not trivial (Veerkamp, 1998; Tempelman and Lu, 2020). Houlahan et al. (2021) specified genetic correlations between DMI and residual feed intake on the one hand and the case of clinical ketosis and displaced abomasum on the other; they ranged from -0.19 to -0.07 . However, several studies have concluded that DMI is influenced by different genes at different lactation stages, so that DMI should be treated as separate traits depending on lactation stage (Berry et al., 2007; Li et al., 2018; Harder et al., 2020). Hence, consideration of lactation stage is of interest for estimating genetic correlations to determine the effects of selection for higher or lower DMI or REI on dairy cow health.

Selection for lower DMI or REI is generally recommended to improve FE if other traits are not affected negatively (VandeHaar et al., 2016). Nevertheless, a high capacity for DMI is necessary to ensure high energy supply in early lactation and a roughage-based feeding system (Korver, 1988; Spiekens and Ettle, 2020). The energy content of dairy cow rations is limited to maintain rumination. About 30% of DM should be of long roughage to ensure normal rumen function (Korver, 1988). Thus, high DMI is important for a less-severe negative energy balance (EB) in early lactation, which is a prerequisite for healthy cows (Esposito et al., 2014). Accordingly, improved FE and health have conflicting requirements in dairy cows, especially in early

lactation (Tetens et al., 2014). A possibility to mitigate these conflicting requirements might be lactation stage-specific selection for higher DMI in early lactation and lower DMI in mid- and late lactation (Tetens et al., 2014; Harder et al., 2020).

To gain further knowledge about the genetic relationships between FE-related traits and health in the course of lactation, we created a longitudinal data set with production and health data from the projects optiKuh and eMissionCow, which is unique for Germany. The current study presents heritabilities throughout lactation for the traits DMI, EB, REI, and 3 disease categories (mastitis, claw and leg diseases, and all diseases) in German Holstein (GH) and Fleckvieh (FV) dairy cows. Furthermore, genetic correlations between DMI, ECM yield, EB, and REI on the one hand and 3 disease categories on the other throughout lactation in GH dairy cows are illustrated. Additionally, genetic correlations between selected DIM for DMI in both breeds are shown. Special attention was paid to early lactation when the dairy cow has a negative EB.

MATERIALS AND METHODS

Phenotypic Data

This study was based on data from the projects optiKuh and eMissionCow. The research was conducted according to the European guidelines for animal experiments (Directive 2010/63/EU, 2010) and approved by the respective local committees for ethics of animal experiments. All GH and FV dairy cows were housed in freestall barns on a total of 9 GH and 4 FV dairy research farms in Germany. Two of these GH farms participated in only one of both projects. Data were collected between September 2014 and April 2021, primarily during farm-specific feeding trials of different lengths. During the change from the optiKuh to the eMissionCow project, no data were collected from the end of March 2017 to the beginning of July 2017. In the eMissionCow project, additional early-lactation health data were available from 5 GH and 2 FV farms that were recorded outside of their farm-specific feeding trials. Consequently, the data sets contained notably more health data than production data. For the statistical analyses, daily records were combined into weekly averages. These were mostly based on the calendar week but sometimes on a self-defined week, due to experimental designs that included a feeding group change within calendar week. The total GH data set included 101,879 records from 3,901 lactations of 2,387 cows. Numbers of cows within lactation 1, 2, 3, and ≥ 4 were 1,046, 998, 741, and 1,116, respectively. The total FV

Table 1. Descriptive statistics of DMI, ECM yield, BW, energy balance (EB), and residual energy intake (REI) in German Holstein and Fleckvieh dairy cows (lactation wk 1–44)

| Breed | Trait | Unit | No. of observations | Mean | SD |
|-----------------|-----------|--------------------------|---------------------|------|------|
| German Holstein | DMI | kg/d | 76,486 | 22.6 | 4.26 |
| | ECM yield | kg/d | 67,411 | 35.6 | 7.78 |
| | BW | kg/d | 71,881 | 676 | 77.2 |
| | EB | MJ of NE _L /d | 61,544 | 2.74 | 27.0 |
| | REI | MJ of NE _L /d | 58,829 | 0.00 | 17.3 |
| Fleckvieh | DMI | kg/d | 32,879 | 21.4 | 3.76 |
| | ECM yield | kg/d | 30,322 | 31.2 | 7.70 |
| | BW | kg/d | 31,211 | 757 | 75.6 |
| | EB | MJ of NE _L /d | 28,743 | 1.89 | 21.0 |
| | REI | MJ of NE _L /d | 27,630 | 0.00 | 11.4 |

data set included 36,962 records from 1,354 lactations of 632 cows. Numbers of cows within lactation 1, 2, 3, and ≥ 4 were 316, 304, 275, and 459, respectively.

Production Data. Cows were fed ad libitum with partial mixed rations and separate concentrates or TMR. Feed intake was measured via single feeding troughs equipped with a weighing unit and automatic cow identification. Data of ration components, DM, and energy contents (in MJ of NE_L) were recorded according to project guidelines. Net energy of lactation is defined as the energy amount in feed that is available for milk production and body maintenance (Kirchgeßner et al., 2014). Daily milk yield records were based on at least 2 milkings. Proportions of fat, protein, and lactose in the milk were measured once per week. Cow individual BW was recorded automatically after milking using an electronic scale, except in 2 farms that weighed cows once per week. When cows were weighed after milking, daily values were derived by averaging morning and evening BW. The EB was computed as the difference between energy intake and energy requirements. As energy requirements, estimated energy amounts for maintenance, milk production, gestation, and growth in first lactation were considered. Detailed formulas can be taken from Harder et al. (2019). We calculated a phenotype for weekly REI that considered milk energy content, metabolic BW, and BW change as energy sinks in addition to the fixed effects herd-test-week, lactation, and DIM within lactation. Detailed approach to calculation can be found in Becker et al. (2021a). Calendar week-based averages of production traits were analyzed from averaged lactation week 1 to 44. The day of calving was excluded due to incomplete measurements. Thus, this corresponds to averaged DIM 2 to 308. Observations outside the range of ± 4 standard deviations of the mean value were excluded from the analyses. Descriptive statistics of production traits are presented in Table 1. Our statistical analyses included the traits DMI, ECM yield, EB, and REI.

Health Data. Farm staff and veterinarians recorded health data. Data editing according to Becker et al. (2021b) included health data standardization, plausibility checks, aggregation in 8 disease categories, and binary coding of defined disease periods. Disease periods included the first treatment day, calculated average treatment days, and sick days. Disease categories were mastitis (**MAST**), other udder diseases, claw and leg diseases (**CLAW**), metabolic diseases (**METAB**), reproduction disorders, respiratory diseases, digestive diseases, and other diseases. An additional category named all diseases (**ALLDIS**) grouped health data of all mentioned disease categories. First, each daily observation was binary coded with a disease code of 0 for healthy and 1 for diseased. Second, these data were aggregated into weekly averages based on calendar week, with a week receiving a 1 if at least one day that week was coded with 1. Generally, health data from calving to averaged lactation wk 44 were used. This lactation stage is equivalent to averaged DIM 1 to 308. For METAB, the first 11 averaged lactation weeks (DIM 1–77) were included because METAB hardly occurred afterward. Health data were not available for 1 FV farm between calving and the start of feeding trial. Accordingly, METAB in FV included health data from 3 of 4 farms. We analyzed 3 disease categories: MAST, CLAW, and ALLDIS. The disease category METAB was not analyzed due to insufficient data. Table 2 presents an overview of the number of diseased cow weeks as well as cows and lactations with at least 1 diseased week. We calculated the percentage of diseased cows based on their total weekly observations. Relative percentage of diseased cow weeks per lactation week for the analyzed disease categories are shown in Figures 1 and 2.

Genotypic Data

Pedigree information consisted of 4 traced generations. The total pedigree of all GH cows with pheno-

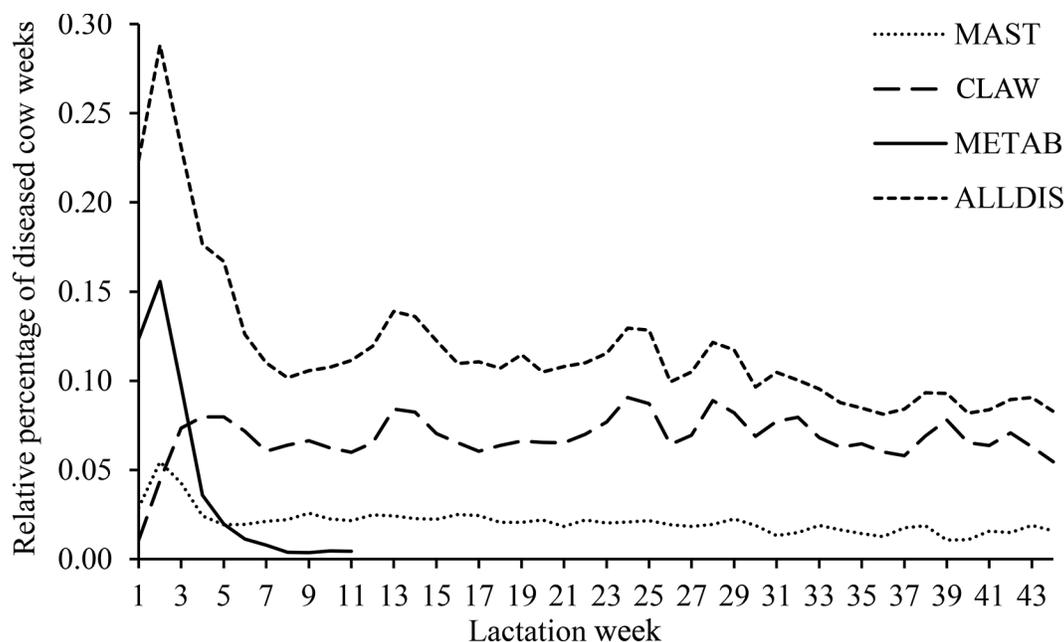


Figure 1. Relative percentage of diseased cow weeks per lactation week for mastitis (MAST), claw and leg diseases (CLAW), metabolic diseases (METAB), and all diseases (ALLDIS) in German Holstein dairy cows.

typic data included 9,820 animals. For FV, the total pedigree included 3,630 animals.

Cows were genotyped with different versions of the Illumina BovineSNP50 BeadChip (Illumina Inc.). For GH, imputed genotypes of 2,194 cows with 45,613 SNP were used. For FV, data of 2 SNP chip versions were available from 561 cows. For this breed, we created a SNP data set including the intersection of both SNP chip versions with 43,375 SNP. To ensure sufficient genotype quality, SNP and samples with a call rate less than 95% were removed. After quality control, the final FV SNP data set contained 533 cows and 41,832 SNP. Subsequently, we calculated a genomic relationship matrix for each breed with the software package Gmatrix

using the default settings (Su and Madsen, 2012). This genomic relationship matrix was later used in DMU to calculate the pedigree-genomic relationship matrix. To control pedigree data, pedigree-based relationship coefficients were calculated using the procedure INBREED in SAS 9.4 and were compared with the genomic relationship coefficients (SAS Institute Inc., 2013).

Statistical Analyses

Genetic parameters were determined within breed by estimating variance and covariance components with the average information restricted maximum likelihood procedure in the DMU package (Madsen and Jensen,

Table 2. Percentage of diseased cow weeks as well as cows and lactations with at least 1 diseased week for 4 disease categories in German Holstein and Fleckvieh dairy cows

| Breed | Disease category ¹ | Lactation stage (wk) | Cow weeks | | Cows (lactations) | |
|-----------------|-------------------------------|----------------------|-----------|--------------|-------------------|--------------|
| | | | Total | Diseased (%) | Total | Diseased (%) |
| German Holstein | MAST | 1–44 | 101,864 | 2.2 | 2,387 (3,900) | 29.5 (20.4) |
| | CLAW | 1–44 | 101,864 | 6.7 | 2,387 (3,900) | 56.4 (45.0) |
| | METAB | 1–11 | 35,655 | 4.4 | 2,329 (3,501) | 22.7 (17.9) |
| | ALLDIS | 1–44 | 101,864 | 12.7 | 2,387 (3,900) | 81.7 (70.6) |
| Fleckvieh | MAST | 1–44 | 36,962 | 1.6 | 632 (1,354) | 24.7 (15.5) |
| | CLAW | 1–44 | 36,962 | 4.5 | 632 (1,354) | 49.4 (36.6) |
| | METAB ² | 1–11 | 9,859 | 2.8 | 484 (985) | 20.3 (11.6) |
| | ALLDIS | 1–44 | 36,962 | 8.1 | 632 (1,354) | 66.5 (58.7) |

¹MAST = mastitis; CLAW = claw and leg diseases; METAB = metabolic diseases; ALLDIS = all diseases.

²Contains data from 3 of 4 farms.

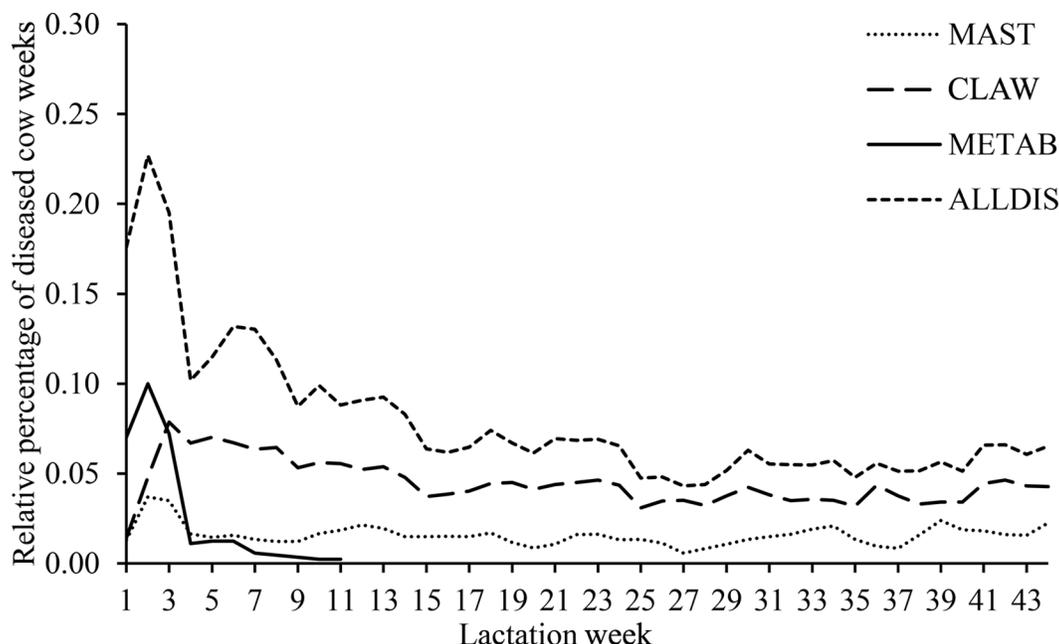


Figure 2. Relative percentage of diseased cow weeks per lactation week for mastitis (MAST), claw and leg diseases (CLAW), metabolic diseases (METAB), and all diseases (ALLDIS) in Fleckvieh dairy cows.

2013). Univariate random regression models and the single-step approach were used to estimate heritabilities and genetic correlations between selected DIM. This approach includes genotyped and non-genotyped animals simultaneously and combines phenotypic, pedigree, and SNP data to estimate most accurate and less biased variance and covariance components (Legarra et al., 2009; Veerkamp et al., 2011; Koivula et al., 2012). To avoid convergence problems and bias, a weight of 0.05 was applied to the pedigree relationship matrix in the calculation of the pedigree-genomic relationship matrix by DMU (Christensen and Lund, 2010; Guarini et al., 2018; Martínez et al., 2020). Daily heritability was defined as $\sigma_a^2 / (\sigma_a^2 + \sigma_p^2 + \sigma_{pl}^2 + \sigma_e^2)$, where σ_a^2 is the additive genetic variance, σ_p^2 is the permanent environmental variance, σ_{pl}^2 is the permanent environmental variance within lactation, and σ_e^2 is the residual variance. Genetic correlations between selected DIM separated by regular intervals of 30 d were estimated for DMI. The linear random regression model for production data and the threshold random regression model for health data are described subsequently. Bivariate random regression models and only pedigree data were used to estimate genetic correlations in GH. Covariances between production traits and disease categories were estimated for all random effects. For the bivariate runs, the models described herein were used, but the random effects in the production data model were sim-

plified as follows: (1) additive genetic effect and permanent environmental effect of the cow regressed with second-degree Legendre polynomial function; (2) no permanent environmental effect within lactation. In the case of the bivariate run for the traits REI and MAST, the permanent environmental effect was considered as a simple effect. For FV, no genetic correlations could be estimated, due to insufficient data.

Production Data Model. First, for each farm, we tested the effect of feeding group using the procedure MIXED and the residual (restricted) maximum likelihood method in SAS 9.4 (SAS Institute Inc., 2013). Therefore, the mixed models included the fixed effects herd-test-week, feeding group, lactation, DIM within lactation according to Ali and Schaeffer (1987), and a random cow effect. In cases of significant group differences, we extended the effect of herd-test-week to a herd-group-test-week. This effect had to contain at least 3 observations; otherwise, the effect class was combined with a neighboring herd-test-week. Second, model fit was evaluated by Akaike information criterion (Burnham and Anderson, 1998) and Bayesian information criterion (Schwarz, 1978) using the maximum likelihood method in SAS 9.4 (SAS Institute Inc., 2013). Subsequently, variance and covariance components for DMI, EB, and REI were estimated using the pedigree-genomic relationship matrix and the following linear random regression model, whereas for REI only the random effects were included:

$$y_{ijklm} = \mu + \text{HTW}_i + \text{LNO}_j + \sum_{n=1}^4 C_{jn} \times \text{as}_{jn} + \sum_{n=1}^4 a_{kn} \\ \times \text{lp}_{kn} + \sum_{n=1}^4 p_{kn} \times \text{lp}_{kn} + p_{kl} + e_{ijklm},$$

where y_{ijklm} is the observation of DMI, EB, or REI; μ is the overall mean; HTW_i is the fixed effect of the i th herd-test-week ($i = 1-2,504$ and $1-1,491$ for DMI in GH and FV; $i = 1-2,209$ and $1-1,370$ for EB in GH and FV); LNO_j is the fixed effect of the j th lactation ($j = 1, 2, 3, \geq 4$ for DMI and EB); C_{jn} is the n th fixed regression coefficient within the j th lactation; as_{jn} is the n th term of the Ali and Schaeffer (1987) function for DIM within the j th lactation with $x_1 = \text{DIM}/308$, $x_2 = (\text{DIM}/308)^2$, $x_3 = \ln(308/\text{DIM})$, and $x_4 = [\ln(308/\text{DIM})]^2$; a_{kn} is the n th random regression coefficient for the additive genetic effect of the k th cow ($k = 1-2,346$ and $1-630$ for DMI in GH and FV; $k = 1-2,308$ and $1-624$ for EB in GH and FV; $k = 1-2,297$ and $1-623$ for REI in GH and FV); lp_{kn} is the n th term of the third-degree Legendre polynomial function for DIM of the k th cow; p_{kn} is the n th random regression coefficient for the permanent environmental effect of the k th cow; p_{kl} is the random permanent environmental effect of the k th cow within the l th lactation ($l = 1-13$ and $1-10$ in GH and FV); and e_{ijklm} is the random residual error.

Health Data Model. Before statistical analyses for health data started, we did an extreme category analysis of all fixed effects (Harville and Mee, 1984). To avoid the extreme category problem, herd-year classes containing a single value (0 or 1) were combined with neighboring classes (Luo et al., 2001). The following threshold random regression model together with the pedigree-genomic relationship matrix was used to estimate variance and covariance components for the disease categories MAST, CLAW, and ALLDIS:

$$E[\pi_{ijkl}] \\ = \Phi \left(\text{HY}_i + \text{LNO}_j + \text{LWK}_k + \sum_{n=1}^3 a_{ln} \times \text{lp}_{ln} + p_l \right),$$

where $E[\pi_{ijkl}]$ is the expected probability for occurrence of the disease category; Φ is the cumulative probability function of standard normal distribution as probit link function; HY_i is the fixed effect of the i th herd-year ($i = 1-48$ and $1-21$ in GH and FV); LNO_j is the fixed effect of the j th lactation ($j = 1, 2, 3, \geq 4$); LWK_k is the fixed effect of the k th lactation week ($k = 1-44$); a_{ln} is the n th random regression coefficient of the additive genetic effect of the l th cow ($l = 1-2,387$ and $1-632$ in GH and FV); lp_{ln} is the n th term of the second-degree

Legendre polynomial function for DIM of the l th cow; and p_l is the random permanent environmental effect of the l th cow.

RESULTS AND DISCUSSION

Disease Frequencies

The trajectories of the relative percentages of diseased cow weeks showed pronounced peaks in the second lactation week for all disease categories, except CLAW. For CLAW, relative percentages of diseased cow weeks were almost constant (Figures 1 and 2). This could be explained by the fact that all claw and leg diseases were grouped in one disease category. Nevertheless, these are typical trajectories of disease frequencies throughout lactation that can also be found in other studies (e.g., Buttchereit et al., 2012; Gernand et al., 2012; Koeck et al., 2012). Relative percentages of diseased cow weeks showed lower values in FV compared with GH, especially for METAB and ALLDIS in early lactation. These differences may be due to the much smaller health data set for FV. Health data for the first 6 lactation weeks were available from only 3 FV farms.

Heritabilities

Production Traits. Heritability for DMI varied between 0.14 and 0.23 in GH and between 0.04 and 0.21 in FV; mean values were 0.17 in GH and 0.15 in FV. For EB in GH, heritability ranged from 0.10 to 0.26 with a mean value of 0.14. In FV, heritability for EB differed between 0.06 and 0.27 with a mean value of 0.15. Heritability for REI varied between 0.09 and 0.21 in GH and between 0.06 and 0.25 in FV; mean values were 0.11 in GH and 0.14 in FV (Figure 3). Heritability for DMI found in the literature has a large range, from 0.04 to 0.58 (Buttchereit et al., 2011; Spurlock et al., 2012; Berry et al., 2014). In recent studies, heritability for DMI has been estimated to be 0.16 or 0.18 (Köck et al., 2018; Heida et al., 2021; López-Paredes et al., 2021). Our estimated heritabilities for EB are in the range of 0.03 to 0.29, which can be found in other studies also using random regressions (Berry et al., 2007; Buttchereit et al., 2011; Spurlock et al., 2012). Studies on the heritability for REI are rare. Hurley et al. (2017) estimated heritabilities ranging from 0.04 to 0.11. Linamo et al. (2015) also published a low heritability for REI of 0.09. In contrast, Mehtiö et al. (2018) estimated a higher heritability of 0.33.

Disease Categories. Heritability on the underlying scale for MAST ranged from 0.04 to 0.47, for CLAW from 0.07 to 0.43, and for ALLDIS from 0.04 to 0.45 in GH and FV. Mean heritabilities for MAST, CLAW,

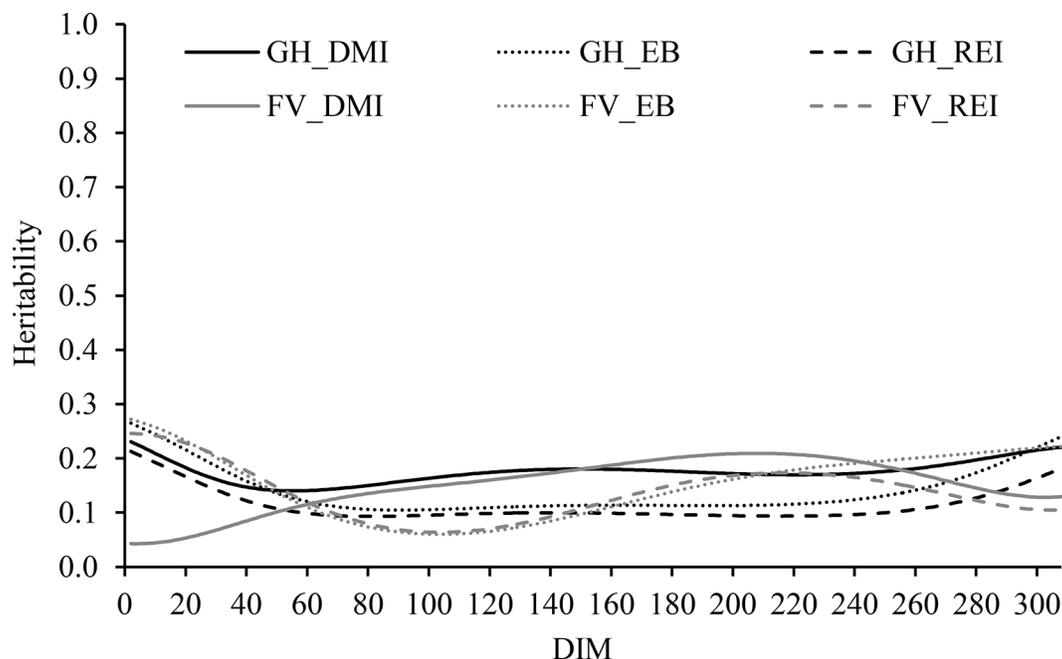


Figure 3. Heritability of DMI, energy balance (EB), and residual energy intake (REI) plotted against DIM in German Holstein (GH; black) and Fleckvieh (FV; gray) dairy cows (DIM 2–308).

and ALLDIS were 0.17 and 0.16, 0.18 and 0.12, as well as 0.15 and 0.11 in GH and FV, respectively. The trajectories of the heritabilities were similar for all disease categories in both breeds (Figure 4). Comparing heritabilities for disease categories of different studies is difficult because, in most cases, the definition of health traits and health data editing differ considerably. In general, heritabilities for health traits are low (e.g., Zwald et al., 2004; Abdelsayed et al., 2017). For example, Buttchereit et al. (2012) estimated a heritability of 0.12 for mastitis and 0.15 for claw and leg diseases in GH dairy cows.

Genetic Relationships Between DMI, ECM Yield, and Disease Categories

Genetic correlations between DMI and ECM yield on the one hand and 3 disease categories (MAST, CLAW, and ALLDIS) on the other in GH are presented in Figure 5. Mostly, the correlations were lowest in early lactation. In the first 50 DIM, genetic correlations between DMI and MAST ranged from -0.25 to -0.16 , between DMI and CLAW from -0.17 to -0.13 , and between DMI and ALLDIS from -0.58 to -0.46 . Genetic correlations between ECM yield and MAST ranged from -0.09 to -0.05 , between ECM yield and CLAW from -0.09 to 0.00 , and between ECM yield and ALLDIS from -0.40 to -0.31 in the first 50 DIM. Thus, genetic correlations between DMI and disease categories

were more negative than genetic correlations between ECM yield and disease categories. To the best of our knowledge, no other study to date has investigated the genetic relationships between DMI and liability to diseases throughout lactation. Søndergaard et al. (2002) estimated a genetic correlation of -0.35 between feed intake capacity and mastitis treatments in the first 50 DIM. Köck et al. (2018) published a negative relationship between DMI and lameness by showing that cows with a high EBV for DMI had lower incidence of lameness than cows with a low EBV for DMI. Undesirable genetic relationships between milk yield and diseases are known from the literature (e.g., Rauw et al., 1998; Berry et al., 2011; Koeck et al., 2012; Pritchard et al., 2013). These cannot be clearly confirmed with our results, as mostly unexpected negative genetic correlations between ECM yield and disease categories were estimated. Nevertheless, we conclude that DMI and ECM yield are genetically mostly negatively correlated with health in GH, especially in early lactation. The strength of correlation depends on disease category.

Genetic Relationships Between EB, REI, and Disease Categories

Genetic correlations between EB and REI on the one hand and 3 disease categories (MAST, CLAW, and ALLDIS) on the other in GH are presented in Figure 6. In the first 50 DIM, genetic correlations between EB and

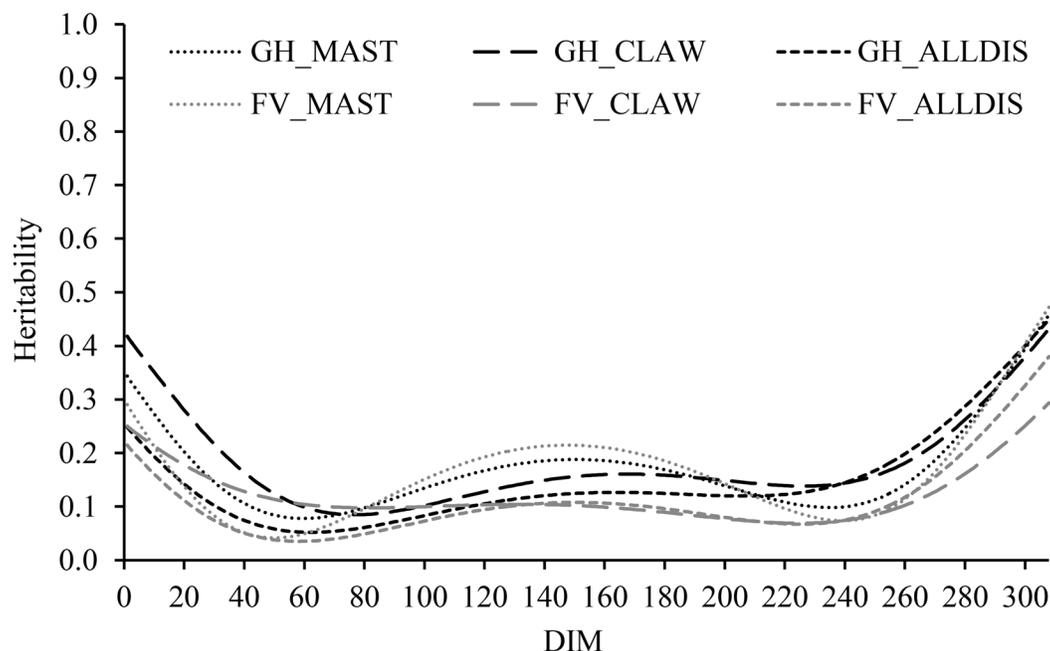


Figure 4. Heritability of mastitis (MAST), claw and leg diseases (CLAW), and all diseases (ALLDIS) plotted against DIM in German Holstein (GH; black) and Fleckvieh (FV; gray) dairy cows (DIM 1–308).

MAST ranged from -0.11 to -0.07 , between EB and CLAW from -0.25 to -0.09 , and between EB and ALLDIS from -0.30 to -0.18 . Genetic correlations between EB and MAST were not strongly negative throughout lactation. Collard et al. (2000) and Pérez-Báez et al. (2019) found no phenotypic relationship between EB and liability to mastitis. In addition, Buttchereit et al. (2010) concluded, based on their breeding value evaluation in GH heifers, that liability to mastitis seems to be unaffected by EB. A possible explanation could be that cows with mastitis decrease DMI and milk yield so that EB becomes smaller (Olson et al., 2011; Pérez-Báez et al., 2019). Collard et al. (2000) found a distinct negative phenotypic relationship between EB and locomotive problems as well as laminitis. Buttchereit et al. (2012) estimated a genetic correlation of -0.23 between EB and claw and leg diseases. Genetic correlations between REI and MAST ranged from -0.25 to -0.14 , between REI and CLAW from -0.31 to -0.17 , and between REI and ALLDIS from -0.41 to -0.30 in the first 50 DIM. If the breeding goal is to select for a lower REI, negative genetic correlations with disease categories are unfavorable. Trajectories of genetic correlations for EB and REI were similar. This can be explained by high correlations between EB and REI (e.g., Seymour et al., 2020; Becker et al., 2021a). Consequently, EB and REI could be considered almost as the same trait, due also to the mathematical similarity of their calculation (Veerkamp, 2002; Savietto et al., 2014). In summary, it

can be concluded that negative genetic correlations also exist between the traits EB and REI on the one hand and health on the other in GH. Here, too, the strength of correlation varies between disease categories.

For FV, we could not estimate the genetic correlations between DMI, ECM yield, EB, and REI on the one hand and disease categories on the other due to insufficient data, especially in early lactation. Li et al. (2018) pointed out that genetic studies on FE and related traits were mainly conducted using data from Holstein cows. Despite the difficulties in recording sufficient data in non-Holstein populations, we recommend a larger data collection for FV to estimate genetic correlations in the future.

Genetic Relationships Depending on Lactation Stage

In GH, genetic correlations between DMI, ECM yield, EB, and REI on the one hand and liability to diseases on the other varied throughout lactation. Studies have shown that DMI should be treated as separate traits depending on lactation stage (Berry et al., 2007; Li et al., 2018; Harder et al., 2020). Table 3 shows the low genetic correlations between early and late lactation in GH and FV. Genetic correlations between lactation stages also differ for EB, residual feed intake, and REI (Hurley et al., 2017; Li et al., 2017; Harder et al., 2020). Martin et al. (2021) and Nehme Marinho et al. (2021) found no phenotypic relationship between DMI

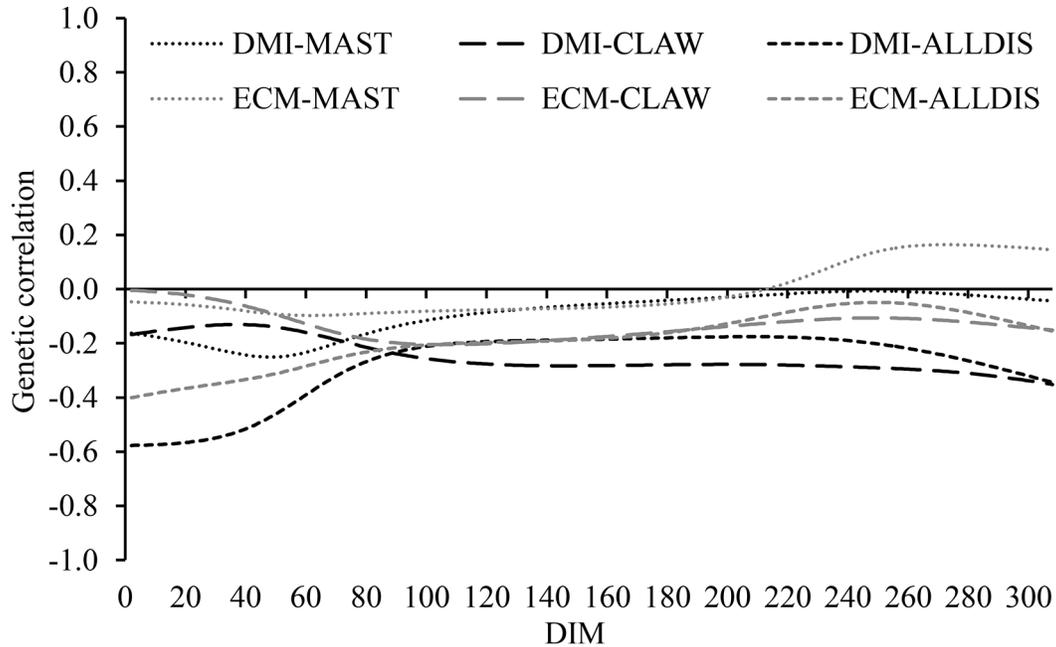


Figure 5. Genetic correlation between DMI (black) as well as ECM yield (gray) and 3 disease categories (MAST = mastitis; CLAW = claw and leg diseases; ALLDIS = all diseases) plotted against DIM in German Holstein dairy cows (DIM 2–308).

and residual feed intake in mid-lactation and health in early lactation. In addition, Seymour et al. (2020) concluded that maximizing FE without affecting health is only possible when EB is close to 0. Therefore, the phenotypic and genetic relationships between DMI,

EB, and REI on the one hand and health on the other might differ between early, mid-, and late lactation, as they are different traits in these lactation stages. Consequently, different genetic correlations throughout lactation should be considered when breeding for FE.

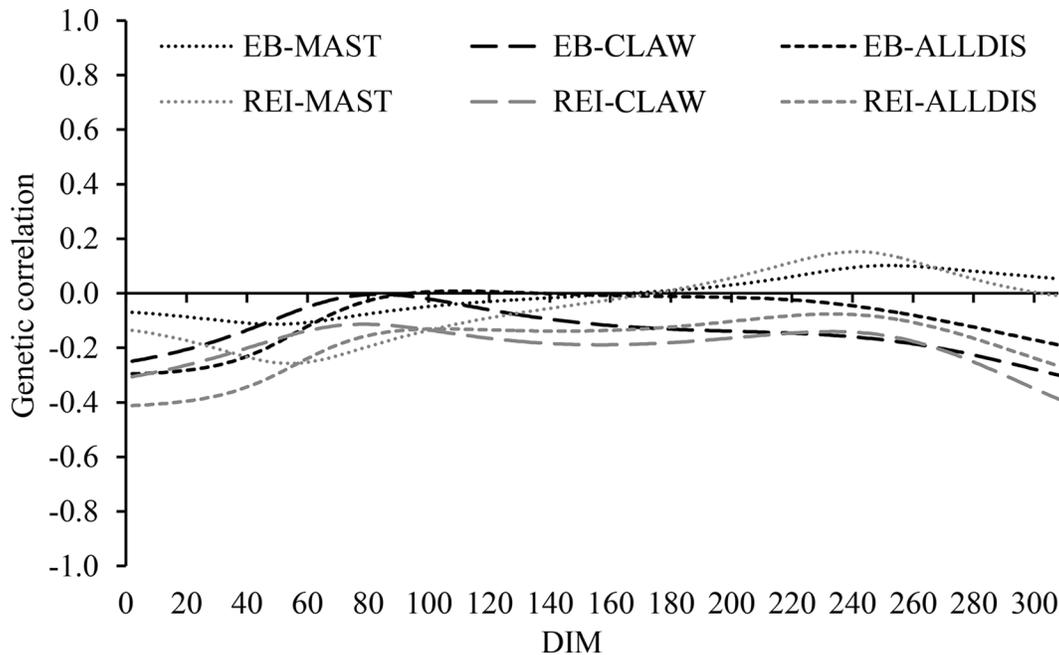


Figure 6. Genetic correlation between energy balance (EB; black) as well as residual energy intake (REI; gray) and 3 disease categories (MAST = mastitis; CLAW = claw and leg diseases, ALLDIS = all diseases) plotted against DIM in German Holstein dairy cows (DIM 2–308).

Table 3. Genetic correlations of selected DIM for DMI in German Holstein (above the diagonal) and Fleckvieh (below the diagonal) dairy cows

| DIM | DIM | | | | | | | | | | |
|-----|-------|------|------|------|------|-------|-------|-------|-------|-------|-------|
| | 5 | 35 | 65 | 95 | 125 | 155 | 185 | 215 | 245 | 275 | 305 |
| 5 | | 0.85 | 0.46 | 0.16 | 0.01 | -0.06 | -0.08 | -0.07 | -0.07 | -0.10 | -0.16 |
| 35 | 0.70 | | 0.86 | 0.64 | 0.50 | 0.41 | 0.35 | 0.32 | 0.30 | 0.30 | 0.28 |
| 65 | 0.46 | 0.95 | | 0.94 | 0.86 | 0.79 | 0.72 | 0.66 | 0.64 | 0.64 | 0.65 |
| 95 | 0.35 | 0.86 | 0.97 | | 0.98 | 0.93 | 0.88 | 0.83 | 0.80 | 0.80 | 0.80 |
| 125 | 0.27 | 0.74 | 0.88 | 0.97 | | 0.99 | 0.95 | 0.91 | 0.88 | 0.88 | 0.86 |
| 155 | 0.21 | 0.57 | 0.74 | 0.87 | 0.97 | | 0.99 | 0.96 | 0.94 | 0.92 | 0.88 |
| 185 | 0.14 | 0.41 | 0.59 | 0.75 | 0.89 | 0.98 | | 0.99 | 0.98 | 0.95 | 0.88 |
| 215 | 0.06 | 0.28 | 0.47 | 0.65 | 0.83 | 0.94 | 0.99 | | 0.99 | 0.97 | 0.89 |
| 245 | -0.05 | 0.21 | 0.41 | 0.61 | 0.79 | 0.92 | 0.98 | 0.99 | | 0.99 | 0.92 |
| 275 | -0.21 | 0.19 | 0.45 | 0.64 | 0.80 | 0.90 | 0.94 | 0.95 | 0.97 | | 0.97 |
| 305 | -0.43 | 0.24 | 0.53 | 0.68 | 0.74 | 0.74 | 0.71 | 0.69 | 0.73 | 0.87 | |

Our results for GH illustrate most negative genetic relationships in early lactation. Houlahan et al. (2021) concluded that selection for FE should occur after peak lactation to avoid the lactation stage with negative EB and thus to have less negative impact on other traits. Consequently, lactation stage-specific selection for higher DMI in early lactation and lower DMI in mid- and late lactation could be a possible strategy to breed for FE (Tetens et al., 2014; Harder et al., 2020). High DMI is incompatible with improved FE. However, our research has shown that cows with less DMI have a higher risk of disease, and diseases lead to poorer animal welfare (Broom and Corke, 2002). Furthermore, diseases can decrease longevity of the cow due to involuntary culling. Short longevity negatively affects farm profitability and sustainability (van Knegsel et al., 2014). Additionally, there are 2 further reasons why breeding for improved FE should be avoided in early lactation to allow high DMI, as follows. (1) Feed costs have strong effects on farm profitability (Hemme et al., 2014). Dairy cow farms are under enormous pressure to reduce production costs due to low milk prices. Energy costs from roughage are usually lower than those from concentrates (Korver, 1988). If more roughage can be fed, the amount of concentrates can be reduced (Veerkamp, 1998; Spiekers and Ettle, 2020). (2) Breeding has to take into account that dairy cow feeding may change in the future (Hayes et al., 2013; Spiekers and Ettle, 2020; Heida et al., 2021). The literature proposed reducing the use of feed suitable for human consumption in livestock production (Schader et al., 2015). Thus, more feed of poor quality, especially with low energy content, could be used in the future (Hayes et al., 2013; Friggens et al., 2017). Consequently, high DMI may be important to ensure adequate energy requirements needed for dairy cows in early lactation. In any case, an adapted feeding strategy to improve FE, such as nutritional grouping, is recommended (Vandehaar et al., 2016; Ledinek et al., 2022).

CONCLUSIONS

This study represents the first evaluation of genetic correlations between DMI and REI on the one hand and dairy cow health on the other, in relation to lactation stage. In GH, negative genetic correlations between these traits were estimated, especially in early lactation. Consequently, future breeding for FE has to consider lactation stage to avoid undesirable side effects on health, regardless of whether selecting for DMI or REI. Restricting selection for higher DMI to early lactation could mitigate the conflictive requirements between improved FE and dairy cow health. For FV, further investigations with a larger data set are needed to estimate genetic correlations.

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