Investigations on the relationship of dry matter intake and energy balance to health in German dairy cattle using conventional and genomic breeding values

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Abstract

The implementation of genomic selection has enabled selection for difficult-to-measure traits, like dry matter intake (DMI) or energy balance (EB). To improve health traits like metabolic stability, a less pronounced energy deficit postpartum is considered to be a key challenge. On the other hand, feed efficiency is gaining economic importance possibly leading to conflicts in the design of breeding goals.

Although several significant phenotypic associations between health and EB traits were reported in the literature, little is known about their genetic relationship as datasets containing the necessary information are still scarce and usually small.

For first lactating Holstein cows of the Karkendamm research herd it could be shown that animals belonging to the best 20 % of the herd with regard to classically estimated breeding values for EB represented the only group with positive average breeding values for metabolic stability.

Karkendamm data from 336 cows have recently also been used within the project “optiKuh”. The aim of this project was to build a German reference population for the traits DMI and EB. The total data set contained DMI records from 1,341 cows and EB records from 1,322 cows, respectively. 1,163 cows were also genotyped. Applying a random regression model and using the Single Step method, genomic breeding values for DMI and EB were estimated. In April, vit (Verden) published for the first time genomic breeding values for direct health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) and this opens up the possibility to investigate the relationship of DMI and EB to health using genomic breeding values. A subset of 269 Karkendamm cows had genomic breeding values for both, EB traits and health traits. On average, the cows in the optiKuh reference population exhibited a negative EB during the first 75 days. Thus, health breeding values were correlated with both, the average lactation day 1 to 75 breeding values for DMI and EB (hereinafter referred to as “BV1-75”) and the average lactation day 1 to 350 breeding values for DMI and EB. Correlations were all positive and generally stronger if the BV1-75 were considered. The closest relationship was found between the BV1-75 for EB and RZhealth ($r=0.41$, $P < 0.0001$). RZmetabol was most closely correlated with BV1-75 for DMI ($r=0.35$, $P < 0.0001$ vs. $r=0.27$ ($P <0.0001$) with BV1-75 for EB), indicating that selection for decreased DMI might have detrimental effects on metabolic stability. This is especially relevant if DMI can be considered in the breeding goal, but genomic evaluation for health traits is not (yet) possible. International collaboration (e.g. within the framework of the global Dry Matter Initiative II) is necessary to further enhance our knowledge on the associations between DMI, EB, and health traits.

Keywords: energy balance, dry matter intake, health

Introduction

The application of genomic selection has opened up the possibility to select for difficult-to-measure traits, like DMI or EB. However, selection for these traits has to be seen in the context of conflictive requirements regarding animal health and efficiency (Tetens *et al*., 2014). To improve health traits (e.g. metabolic stability), a less pronounced energy deficit postpartum is supposed to be an important challenge. On the other hand, feed efficiency is gaining importance due to economic and ecologic reasons. Although several significant phenotypic associations between health and EB traits were reported in the literature (e.g. Collard *et al*., 2000), little is known about their genetic relationship as datasets containing the necessary information are still scarce and limited in size. With exception of the Nordic countries, which have been recording health traits for many years, large-scale recording of health traits is limited to auxiliary traits or recording of direct health traits has only recently been implemented (Boichard and Brochard, 2012). The impact of selection for improved feed efficiency should be carefully considered to avoid potential negative consequences (Spurlock *et al*., 2012; Veerkamp *et al*., 2013), especially in countries where DMI can be considered in the breeding goal, but genomic evaluation for health traits is not yet possible. In this study, the relationship of DMI and EB to health in German dairy cattle was examined using both, conventional and genomic breeding values. The results give a first indication on whether undesirable genetic associations exist that should be considered and further studied.

Material and methods

Three different datasets provided the basis for the investigations. A summary of the datasets and used methods is given below.

Analyses based on conventional breeding values

1,589 Holstein Friesian primiparous cows were studied during their first 180 days in milk at the dairy research farm Karkendamm of the Institute of Animal Breeding and Husbandry, Kiel University, Germany. Within the observation period a bull dam performance test was run and all Karkendamm bull dam candidates had to complete a test period under commercial conditions until day 180 in milk. Non-qualified cows left the herd afterwards. Therefore, only records from the first 180 days in milk were used.

Disease data were recorded between 2000 und 2010. All medical treatments by veterinarians or farm staff were recorded and allocated to disease classes. Three disease categories were analysed: mastitis, claw and leg diseases, and metabolic disorders. Disease codes were generated in an analogous manner for all three categories. Each observation day was allocated a code, “1” if the cow showed a disease and “0” otherwise. For mastitis, the day of the treatment and the following five days in milk were coded with “1”. An 8-day disease period was considered for claw and leg diseases and metabolic disorders. Breeding values were estimated applying a threshold model.

Individual DMI, milk yield and live weight per day were recorded for day 11 to 180 in milk between 2006 and 2009. EB was calculated as the difference between energy intake and estimated energy requirements for milk output and maintenance. The results provided the basis for the estimation of EB breeding values for 526 cows using a random regression model.

Data and models were described in detail by Buttchereit *et al.* (2010).

On average, cows exhibited a negative EB during the first 42 days in milk, therefore, daily relative breeding values for EB from day 11 to 42 were averaged, grouped and related to relative breeding values for the three health traits.

Analyses based on genomic breeding values

Recently, data from the German project “optiKuh” have been successfully used to estimate sufficiently accurate genomic breeding values for DMI and EB. These breeding values were correlated to the newly available official genomic breeding values for health estimated by vit (Verden, Germany). The Pearson correlations between breeding values, albeit not as informative as genetic correlations, provide new insights into the genetic relationship among EB, DMI, and several health traits.

Breeding value estimation for DMI and EB

Karkendamm data from 336 cows were used within the project “optiKuh”. The aim of this project was to build a German reference population for the traits DMI and EB. Data were recorded from 2014 to 2017 on eight German research farms (Braunschweig, Dummerstorf, Futterkamp, Hohenheim, Iden, Karkendamm, Neumühle, and Riswick). Feed intake data recording was standardized across farms. EB was estimated using phenotypic information on milk yield, milk ingredients, live weight, gestation stage, and feed intake. The total data set contained average weekly DMI records from 1,341 cows and average weekly EB records from 1,322 cows, respectively. 1,163 cows were also genotyped. Applying a random regression model and using the Single Step method, genomic breeding values for DMI and EB were estimated. The optiKuh dataset and the effects considered in the random regression model were described in detail by Harder *et al.* (accepted).

Breeding value estimation for direct health traits

In this year, vit (Verden) has introduced genomic breeding values for direct health traits. The data basis (n=676,508 cows and 1,490,285 lactations) came from animal health recording in herds (veterinarians, farmers, claw trimmers). The definition of the health traits was based on the German version of the ICAR Health Key. For the evaluation, 13 health traits were considered which can be assigned to four complexes: udder health, claw health, reproduction, and metabolic stability. The respective number of disease events within lactation was evaluated for all traits. An animal without any recorded information for a trait was defined as a healthy animal for this trait, provided that it was present in herd at least 75% of the trait specific time span without having a diagnosis. The time span for most traits included the entire lactation (day of calving to day 305 in milk). For mastitis, data from 10 days before calving were taken into account.

For traits predominantly occurring at the beginning of lactation, only records until day 50 in milk (retained placenta, (endo)metritis) or day 100 in milk (left-displaced abomasum, milk fever) were considered. For ovary cycle disorders, the risk period was defined as lactation day 51 to 305. Cows with health data collected in multiple lactations were considered as repeated observations. For "udder health", "reproduction" and "metabolic stability" breeding values were estimated within the respective trait complex using a multi trait animal model including repeated measures. Only for claw health traits the breeding values were estimated based on a single trait model including repeated measures. Comprehensive information on the genetic parameters, the statistical model and additional information traits (culling reason information of all cows under milk recording born from 1995 onward) can be found in the description of the genetic evaluation published at the vit-Homepage (VIT, 2019).

Considering the 336 Karkendamm cows with genomic breeding values for DMI and EB, a subset of 269 cows also had genomic breeding values for health traits and was used for further analyses.

Results and discussion

The relationship of DMI and EB to health was studied using conventional and genomic breeding values. These breeding values were estimated using distinct datasets. The analyses based on conventional breeding values were performed using only data from the pre-genomic era. For the analyses based on genomic breeding values, the data basis was more up-to-date and comprehensive, especially for the health traits. Therefore, we have placed greater emphasis on the results from the analyses based on genomic breeding values.

Analyses based on conventional breeding values

Figure 1 shows the average breeding values for claw and leg health, udder health and metabolic health plotted against breeding value classes for EB depending on the average breeding values from day 11 to 42. Primiparous cows with very low EB breeding values also had the worst average breeding values for claw and leg health. Udder health seems to be unaffected by EB, which is, however, not in line with the results from the analyses based on genomic breeding values. Most noticeable, the group of primiparous cows with the best EB breeding values was the only group with positive average breeding values for metabolic health.

Analyses based on genomic breeding values

On average, the cows in the optiKuh reference population exhibited a negative EB during the first 75 days, which was 33 days longer in comparison to the energy deficit period observed in primiparous Karkendamm cows recorded earlier (2006 to 2009 (dataset used for conventional breeding value estimation) vs. 2014 to 2017 (optiKuh dataset used for genomic breeding value estimation)). The duration of the negative EB found for the optiKuh reference population is in line with the results of Coffey *et al.* (2002) who reported that cows in lactation 1 to 3 returned to positive EB between day 72 and day 95 in milk. Moreover, studying primiparous cows of the Karkendamm herd, von Leesen *et al.* (2014) have already shown that the duration of the energy deficit postpartum has increased over time (42 days (Buttchereit *et al.*, 2010; data recording from 2006 to 2009) vs. 55 days (von Leesen *et al.*, 2014; data recording from 2006 to 2012)). Accordingly, the longer duration of the energy deficit period was considered

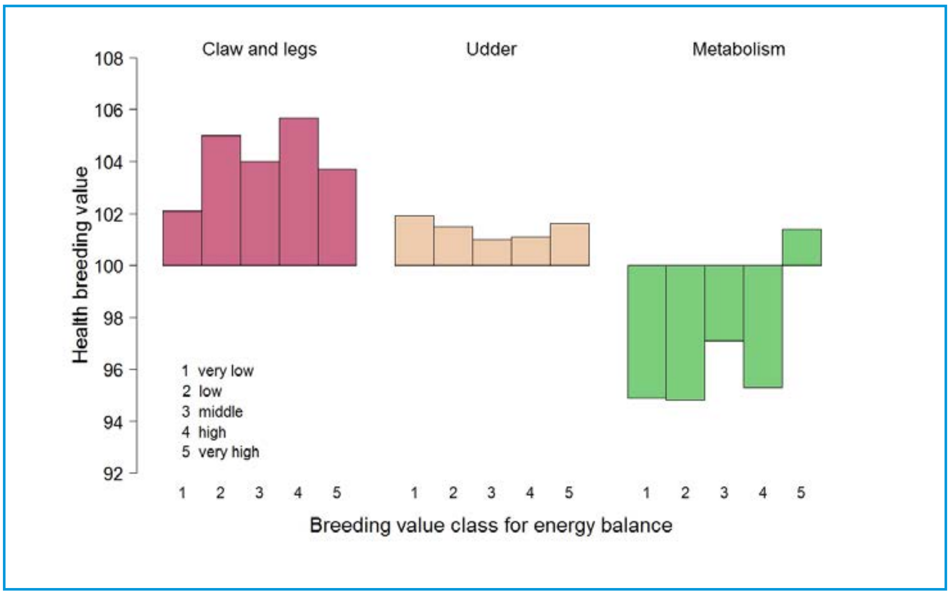

Figure 1. Average relative breeding values for health traits plotted against breeding value classes for energy balance (EB). All breeding values were derived from conventional breeding value estimation using threshold and random regression models, respectively, on data from cows recorded within the first 180 days in milk; on average, cows exhibited a negative EB during the first 42 days in milk, therefore, daily relative breeding values for EB from day 11 to 42 were averaged and used for grouping. Figure adapted from Figure 2 in Buttchereit et al., 2010 (n=526 Holstein Friesian cows).

for all analyses described below. Health breeding values were correlated with both, the average lactation day 1 to 75 breeding values for DMI and EB (hereinafter referred to as “BV1-75”) and the average lactation day 1 to 350 breeding values for DMI and EB. Correlations were all positive and generally stronger if the BV1-75 were considered (see Table 1), meaning that cows with a higher feed intake, especially in early lactation, are less prone to health problems. The most pronounced relationship was found between the BV1-75 for EB and RZhealth ($r=0.41$, $P < 0.0001$). RZmetabol was most closely correlated with BV1-75 for DMI ($r=0.35$, $P < 0.0001$ vs. $r=0.27$ ($P <0.0001$) with BV1-75 for EB), indicating that selection for decreased DMI might have detrimental effects on metabolic stability. This was in line with the findings from the analyses based on conventional breeding values, also suggesting that selection for a higher feed intake in the beginning of lactation would have favourable effects on metabolic health. Correlations with non-health traits including the total merit index are also given in Table 1. The results indicate that a selection for a less pronounced energy deficit postpartum would have no negative side-effects.

Analogous to the analyses based on conventional breeding values, the daily genomic breeding values for DMI and EB from day 1 to 75 were averaged, grouped (3 vs. 5 classes due to the smaller dataset) and related to the genomic breeding values for health traits (see Figure 2 and 3). The use of the genomic breeding values resulted in a clearer picture which is most probably due to the better data basis and more reliable breeding value estimation for the health traits. The findings indicate that a higher feed intake is beneficial with regard to all health traits. However, selection against severe energy deficits would be even more helpful in this context as the group differences were generally more pronounced.

Table 1. Pearson correlations between official genomic enhanced breeding values (gEBV) estimated by vit (Verden) and genomic breeding values for dry matter intake (DMI) and energy balance (EB) from the optiKuh-project (n = 269 Holstein Friesian cows).

Official gEBV for ...	**Average lactation day 1 to 350 genomic breeding value for ...**		**Average lactation day 1 to 75 genomic breeding value for ...**	
	DMI	**EB**	**DMI**	**EB**
Mastitis resistance	0.13	0.26	0.22	0.32
Claw health	0.26	0.30	0.30	0.32
Resistance to reproductive disorders	0.12	0.18	0.27	0.32
Resistance to metabolic disorders	0.27	0.20	0.35	0.27
Total health	0.23	0.32	0.34	0.41
Production	0.54	0.10	0.50	n.s.
Longevity	0.23	0.29	0.33	0.41
Reproduction	n.s.	n.s.	n.s.	0.14
Conformation	0.16	0.15	0.15	0.16
Total merit index	0.57	0.24	0.56	0.24

n.s. = not significant (p-value ? 0.05).

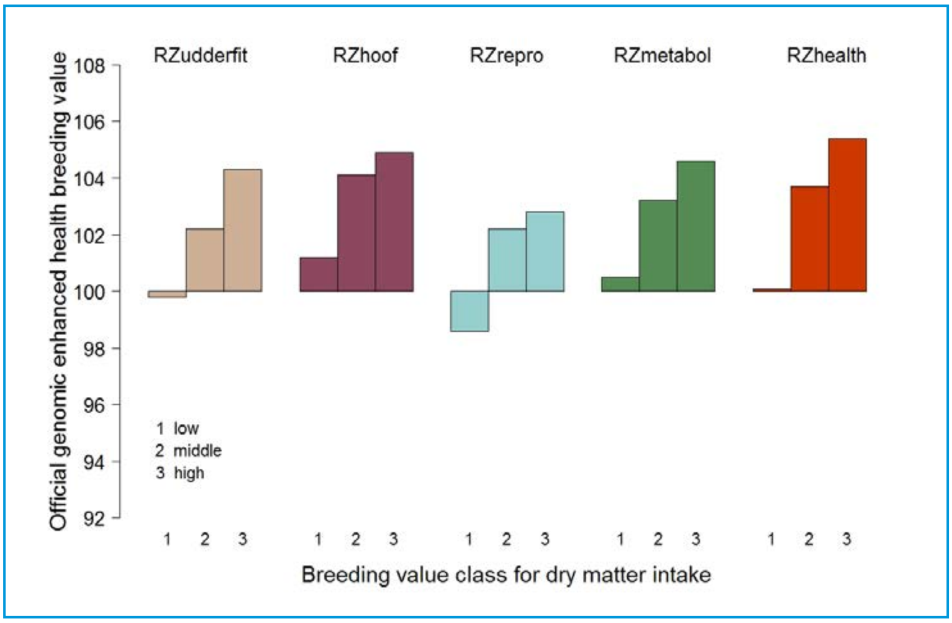

Figure 2. Official genomic enhanced breeding values for health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) plotted against breeding value classes for dry matter intake (DMI). The DMI breeding values were derived from a genomic breeding value estimation using a random regression model and the Single Step method; on average, cows exhibited a negative energy balance during the first 75 days in milk, therefore, genomic breeding values for DMI from day 1 to 75 were averaged and used for grouping (n=269 Holstein Friesian cows).

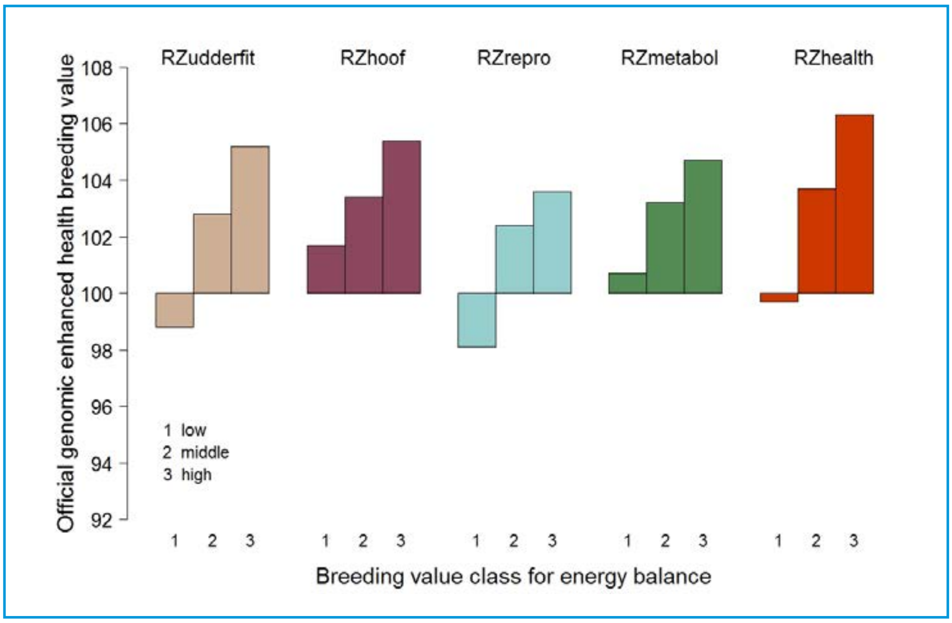

Figure 3. Official genomic enhanced breeding values for health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) plotted against breeding value classes for energy balance (EB). The EB breeding values were derived from a genomic breeding value estimation using a random regression model and the Single Step method; on average, cows exhibited a negative EB during the first 75 days in milk, therefore, genomic breeding values for EB from day 1 to 75 were averaged and used for grouping (n=269 Holstein Friesian cows).

Conclusions

The results suggest that, with regard to health traits, selecting for higher feed intake or a less severe energy deficit in early lactation would be beneficial. This complicates the current efforts to improve feed efficiency. International collaboration (e.g. within the framework of the global Dry Matter Initiative II) can help to further enhance our knowledge on the genetic relationships between DMI, EB, and health traits, thereby enabling the design of balanced breeding goals aiming to avoid unwanted correlated responses, which is especially relevant for countries without a genomic evaluation for health traits.

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