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Phenotypic, genetic, and single nucleotide polymorphism marker associations between calf diseases and subsequent performance and disease occurrences of first-lactation German Holstein cows

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ABSTRACT

A total of 31,396 females born from 2010 to 2013 in 43 large-scale Holstein-Friesian herds were phenotyped for calf and cow disease traits using a veterinarian diagnosis key. Calf diseases were general disease status (cGDS), calf diarrhea (cDIA), and calf respiratory disease (cRD) recorded from birth to 2 mo of age. Incidences were 0.48 for cGDS, 0.28 for cRD, and 0.21 for cDIA. Cow disease trait recording focused on the early period directly after calving in first parity, including the interval from 10 d before calving to 200 d in lactation. For cows, at least one entry for the respective disease implied a score = 1 (sick); otherwise, score = 0 (healthy). Corresponding cow diseases were first-lactation general disease status (flGDS), first-lactation diarrhea (flDIA), and first-lactation respiratory disease (flRD). Additional cow disease categories included mastitis (flMAST), claw disorders (flCLAW), female fertility disorders (flFF), and metabolic disorders (flMET). A further cow trait category considered first-lactation test-day production traits from official test-days 1 and 2 after calving. The genotype data set included 41,256 single nucleotide polymorphisms (SNP) from 9,388 females with phenotypes. Linear and generalized linear mixed models with a logit link-function were applied to Gaussian and categorical cow traits, respectively, considering the calf disease as a fixed effect. Most of the calf diseases were not significantly associated with the occurrence of any cow disease. By trend, increasing risks for the occurrence of cow diseases were observed for healthy calves, indicating mechanisms of disease resistance with aging. Also by trend, occurrence of calf diseases was associated with decreasing milk, protein, and fat yields. Univariate linear and threshold animal models were used to estimate heritabilities and breeding values (EBV) for all calf and cow traits. Heritabilities for cGDS and cRD were 0.06 and 0.07 for cDIA. Genetic correlations among all traits were estimated using linear-linear animal models in a series of bivariate runs. The genetic correlation between cDIA and cRD was 0.29. Apart from the genetic correlation between flRD with cGDS (−0.38), EBV correlations and genetic correlations between calf diseases with all cow traits were close to zero. Genome-wide association studies were applied to estimate SNP effects for cRD and cDIA, and for the corresponding traits observed in cows (flRD and flDIA). Different significant SNP markers contributed to cDIA and flDIA, or to cRD and flRD. The average correlation coefficient between cRD and flRD considering SNP effects from all chromosomes was 0.01, and between cDIA and flDIA was −0.04. In conclusion, calf diseases are not appropriate early predictors for cow traits during the early lactation stage in parity 1.
Key words: calf and cow disease, genetic parameter, genetic and genomic associations

INTRODUCTION

As reviewed by Egger-Danner et al. (2015), a variety of recent quantitative genetic studies have focused on the estimation of genetic (co)variance components for cow health traits, with a focus on mastitis, claw disorders, metabolism, and female fertility. Especially in the phase of a natural negative energy balance during the first third of lactation, disease incidences were quite large (Gernand et al., 2012). For most of the disease traits recorded during the early lactation period, low heritabilities and antagonistic genetic relationships with productivity were identified. Nevertheless, in deterministic predictions (König et al., 2005), a sustainable selection response for cow health after calving was only generated through direct selection strategies instead of using health indicators; for example, functional conformation traits.

In the era of genomic selection, large cow training sets combining phenotypes with high-throughput genomic SNP marker data allow implementation of selection strategies for novel functional traits (Buch et al., 2012). A second major advantage of genomic selection is the

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substantial reduction of generation intervals (Schaeffer, 2006). In such a perspective, traits measured early in life (e.g., calf traits) may be valuable early predictors for subsequent health or cow productivity.

The most important disease problems observed in calves in the past decades in North America (Curtis et al., 1988) and central Europe (Perez et al., 1990) include respiratory infections and different kinds of diarrhea. Despite optimization of farm management, including calf feeding strategies and improvements of calf husbandry systems, both disease categories still have high incidence rates. The importance of both diseases was shown based on a random herd sampling in the Norwegian Red population (Gulliksen et al., 2009a,b), based on a farmer survey in Austria (Klein-Jöbstl et al., 2015), and when referring to official calf mortality statistics in the United States and Asia (Cho and Yoon, 2014). Especially in the Holstein breed (e.g., Becher et al., 2004), moderate to high incidences were identified for respiratory infections and diarrhea.

Presence of diarrhea or respiratory diseases in calves affects the performance and productivity of the animal later in life. In most cases, occurrence of a calf disease increases the probability of heifer health disorders (e.g., Sivula et al., 1996). Warnick et al. (1994) indicated that calf respiratory disease was phenotypically associated with an increased occurrence of dystocia at first calving. Rossini (2004) studied phenotypic associations between calf respiratory and digestive diseases with age at first calving and first-lactation production traits. Nonsignificant effects were identified for 305-d milk and fat yields, but protein yield moderately decreased by 0.05 kg/d. Also, age at first calving was higher for calves with multiple occurrences of respiratory disease. In contrast, Mousa et al. (2015) identified negative correlations between calf scours and age at first calving. Bünger et al. (1979) reported reduced DM feed intake in lactating dairy cows due to infections during the calfhood stage. Reduced feed intake causes negative energy balance with associated health problems (e.g., Collard et al., 2000). In a similar context, Beam et al. (2015) focused on calf growth rates and starter feed intake, and identified positive associations with performance traits and BW in mature cows.

Phenotypic relationships revealed that calf diseases mostly appeared in clusters. This means that, for example, a calf being susceptible to digestive infections also showed symptoms for a respiratory disease. Rossini (2004) reported that occurrence of calfhood digestive disease was associated with a 2-fold increase in the probability of occurrence of calf respiratory disease. Lundborg et al. (2003) confirmed the positive relationships between calf diarrhea and calf respiratory disease. In a study conducted in New York State (Henderson et al., 2011), the residual correlation between calf respiratory and bloat disease was positive and that between respiratory and umbilical disease slightly negative.

So far, only a few studies have estimated quantitative genetic parameters for diseases in calves of dairy or dual-purpose breeds. In the study by Henderson et al. (2011), heritabilities for bloat, respiratory, and umbilical diseases were 0.040, 0.095, and 0.139, respectively. Fuerst-Waltl et al. (2010) estimated genetic parameters for diseases in Austrian dual-purpose Fleckvieh heifer calves: heritability was 0.027 for liability to diarrhea and 0.039 for liability to respiratory diseases. Based on the Norwegian health data recording system and using records from 250,212 Norwegian Red calves, the heritability for respiratory disease on the underlying liability scale was 0.05 (Heringstad et al., 2008). Given the low heritability combined with a low incidence rate (only 0.7% of the calves had a veterinary treatment for respiratory disease within the first 180 d of age), Heringstad et al. (2008) saw limited possibilities for genetic improvement. Nevertheless, the same authors pointed to the accurate genetic predictions of sires for respiratory disease resistance. With regard to genetic associations among calf traits, genetic correlations differed substantially from phenotypic correlations. For example, in the study by Henderson et al. (2011), the phenotypic correlation between calf bloat disease with respiratory disease was close to zero, but the genetic correlation between the same traits was quite high (0.62).

Given a data set of genotyped females, application of genome-wide association studies (**GWAS**) allows detection of important SNP markers contributing to the phenotypic health trait expression. Pimentel et al. (2011) suggested utilization of specific SNP to improve simultaneously selection response for antagonistically related production and fertility traits. Until now, GWAS have focused on cow health; that is, addressing classical health disorders (e.g., van der Spek et al., 2015), specific diseases with low incidences (displaced abomasum, Biffani et al., 2014), infectious diseases (e.g., Bermingham et al., 2014), or immune responses (Thompson-Crispi et al., 2014). To our knowledge and with regard to GWAS in calves, the size of SNP marker effects was only estimated for calf birth weight (Cole et al., 2014).

The objective of the present study was to infer relationships between calf diseases and cow production and health traits from the early lactation period in first parity on the phenotypic, quantitative genetic, and genomic scales. The objective implies for (1) the application of linear and generalized linear mixed model analyses for cow traits considering the calf disease as a fixed effect, (2) the estimation of genetic correlations