Inferring genetic parameters for prenatal heat stress effects on calf diseases and cow productivity

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Abstract

The aim of this study was to infer genetic and genomic effects of heat stress (HS) during late gestation of dams on disease occurrences and productivity of ~20,000 genotyped calves and cows, respectively, from an across-generation perspective. The climatic descriptor was the temperature-humidity index (THI) during the last week of pregnancy. For diseases, climatic sensitivity was studied via random regression coefficients nested within maternal genetic effects on prenatal THI alterations. For production traits, a genomic interaction model with THI ≥ 60 indicating prenatal HS, was applied. Maternal heritablities for pneumonia increased from 0.03 to 0.10 with increasing THI from 60 to 74, but was largest for diarrhea at THI 60 (0.07). Genotype by HS interaction variances for production traits explained maximal 3.79% of the total variances. The novel modelling strategies enabled the assessment of maternal climatic sensitivity and the estimation of variances caused by HS.

Introduction

As a heat sensitive breed, Holstein cattle showed variations in phenotypic performances and breeding values under heat stress (HS) conditions. For example, protein yield significantly decreased at THI 68 (Gernand et al., 2019). Genetically, random regression models were applied to infer genetic (co)variance components along a continuous climatic descriptor, i.e., the temperature-humidity index (THI; Bohlouli et al., 2019). Such modelling approach was also used to detect possible genotype x environment interactions (GxE; Bohlouli et al., 2019). Most of the genetic studies focused on immediate responses to HS, i.e., considering THI at the measuring day, or the average THI shortly before the measuring day. Phenotypically, HS during late gestation in dams, termed as prenatal HS, significantly impaired growth, immune competence and functional traits in offspring (Tao and Dahl, 2013). Monteiro et al. (2016) studied long-term effects prenatal HS on female fertility and performance traits recorded in offspring and identified most detrimental impact of HS from the last 6 weeks of gestation. Genetically, Halli et al. (2021) and Kipp et al. (2021) identified alterations of genetic variances for primary traits and GxE in young dual-purpose cattle and in first lactating dairy cows in response to prenatal THI.

In this regard, the aim of this study was to apply alternative modelling strategies and additionally considering genomic data to infer the effects of prenatal HS on genetic parameters for calf diseases and for test-day and lactation production traits in German Holstein cattle. Solutions for genetic effects were used in ongoing genome wide association studies (GWAS). Suggestively associated SNPs from GWAS were considered in gene annotations.

Materials & Methods

Calf diseases and cow production traits were recorded in 53 large-scale co-operator herds located in two federal states located from the north-eastern part of Germany.

Dataset for calf diseases. The calf diseases pneumonia (PNEU) and diarrhea (DIAR) were diagnosed by veterinarians or herd producers based on the official hierarchical health diagnosis

key from the International Committee for Animal Recording (Stock et al., 2013). For PNEU, we focused on the period from 0 to 180 d after birth for female calves. DIAR mostly occurs in a short period after birth (0 to 30 days of age). Hence, both sexes were considered for DIAR. For each of the calf diseases, at least one entry within the respective period implied a score = 1 (diseased calve); otherwise, a score = 0 (healthy calve) was assigned. The pedigree file included 338,158 animals. Among them, 19,247 Holstein cattle were genotyped with the *Illumina BovineSNP50 v2 BeadChip* or the *Illumina Bovine Eurogenomics 10K low-density chip*. The number of genotyped calves with phenotypes was 12,728 for PNEU and 10,170 for DIAR. After quality control, 41,135 SNPs were considered for ongoing analyses.

Dataset for cow production traits. Test-day records from the first official test-day after calving (5 to 35 days in milk) included milk yield (TMY), fat percentage (TFP), fat yield (TFY), protein percentage (TPP), protein yield (TPY) and somatic cell score (TSCS). First lactation records were considered for milk yield (LMY), fat percentage (LFP), fat yield (LFY), protein percentage (LPP) and protein yield (LPY). The lactation lengths for lactation records varied from 275 to 305 days in milk. In total, 41,139 SNPs from 14,188 genotyped cows were used for the ongoing genomic analyses. All genotyped cows had milk production records.

Meteorological data. Pairwise distances (in km) were calculated between weather stations and cowherds. According to the minimal distances, we allocated 33 weather stations to the 53 herds. Hourly THI were calculated considering hourly temperature (T) and relative humidity (RH) as follows (NRC, 1971):

$$\mathrm{THI} = [1.8 \times \mathrm{T} + 32] - [0.55 - 0.0055 \times \mathrm{RH}] \times [1.8 \times \mathrm{T} - 26].$$

Afterwards, we calculated the prenatal THI for the week before birth (0-7 d) by averaging hourly THI. For calf diseases, all THI values < 60 were set to 60 to eliminate the impact of possible cold load. The average THI for the week before calving was scaled using -1+2((THI-60)/(74-60)), where 60 = minimum THI value and 74 = maximum THI value. The scaled THI were used in the analyses for calf diseases. For cow production traits, a dummy variable with values of either 0 (THI < 60) or 1 (THI ≥ 60) was used to indicate prenatal HS. We focused on different strategies to consider THI, because data structures and applied models were not the same for the two trait categories.

Statistical models. For calf diseases, an animal model with maternal effects considering prenatal THI in the week before birth, was applied. The statistical in matrix notation was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Qd} + \mathbf{Wm} + \mathbf{Sp_m} + \mathbf{e} \quad (1)$$

where $\mathbf{y}$ = vector of records for PNEU or DIAR; $\mathbf{b}$ = vector of fixed effects including herd, birth year, birth month, gestation length classes, lactation-calving-age classes for dams, sex-birth type and regressions on scaled THI nested within birth year; $\mathbf{d}$ = vector of direct additive-genetic effects; $\mathbf{m}$ = vector of maternal genetic effects for random intercepts and slopes on scaled THI; $\mathbf{p_m}$ = vector of maternal permanent environmental effects for random intercepts and slopes on scaled THI ; $\mathbf{e}$ = vector of random residual effects.

For cow production traits, a genomic interaction model (Yao et al., 2017) considering interactions between genotype and prenatal HS was defined:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zg} + \mathbf{Wg_{hs}} + \mathbf{e} \quad (2)$$

where $\mathbf{y}$ = vector of observations for test-day or lactation records; $\mathbf{b}$ = vector of fixed effects including herd, calving year, calving month, age at first calving classes, lactation-calving-age classes for dams, classes for days in milk (for the test-day traits), lactation length classes (for lactation traits) and a dummy variable indicating the presence of HS during the week before calving; $\mathbf{g}$ = vector of additive genomic effects; $\mathbf{g_{hs}}$ = vector of genotype by HS interaction effects for cows with prenatal HS; $\mathbf{e}$ = vector of random residuals. The variances of $\mathbf{g}$ and $\mathbf{g_{hs}}$

were defined as common genomic and interaction variance, respectively. The common genomic variance consistently existed for all cows regardless of prenatal HS. The interaction variance represented the variance due to prenatal HS. Proportions of the common genomic and the interaction variance in relation to the phenotypic variance were defined as common heritability (h_c^2) and interaction heritability (h_i^2), respectively. Additionally, a genomic animal model without interaction effects was applied to identify changes of the heritabilities due to genotype by HS interactions. Gibbs sampling and AIREML algorithms as implemented in the software packages THRGIBBS1f90 and AIREMLf90 (Misztal et al., 2002) were used to estimate variance components for calf diseases and cow production traits, respectively.

Results

Direct heritabilities for PNEU were quite stable with 0.10 at THI 60 to 0.08 at THI 74. For DIAR, the direct heritabilities ranged from 0.16 to 0.17. Maternal heritabilities for PNEU increased from 0.03 to 0.10 along the THI gradient. Oppositely, the maternal heritability for DIAR was slightly larger at THI 60 (0.07) than under prenatal HS conditions. The genetic correlations between maternal effects at THI 60 with the remaining THI values for both calf diseases decreased with increasing THI distances (Figure 1). The smallest correlations of 0.42 for DIAR and 0.26 for PNEU were estimated between the most distant prenatal THI values.

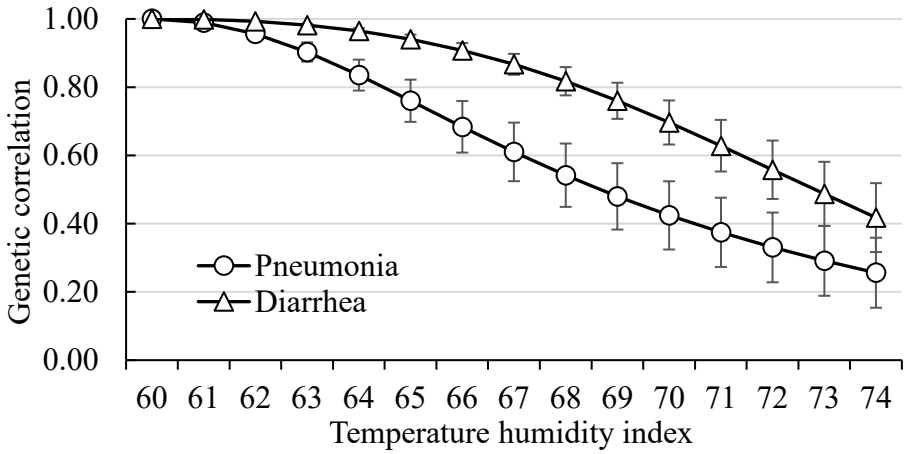

Figure 1. Posterior means for genetic correlations with respective posterior standard deviations between maternal effects at THI 60 and at the remaining THI.

From model 2, h_c^2 were 0.13 for TMY, 0.19 for TFP, 0.15 for TFY, 0.24 for TPP, 0.10 for TPY, and 0.08 for TSCS (Figure 2). For lactation milk production traits, h_c^2 were 0.37 for LMY, 0.72 for LFP, 0.35 for LFY, 0.70 for LPP, and 0.28 for LPY. In general, common genomic heritabilities for milk production traits were identical to genomic heritabilities estimated from the alternative model without GxE interaction effects (results not shown). Among all traits, TPP displayed the largest heritability due to genotype by HS interactions (3.79%). For TFP, TFY, TPY, TSCS, LFP, and LPY, h_i^2 were < 1%.

Discussion

Increases in direct heritabilities for cow diseases (Kipp et al., 2021) and milk yield (Bohlouli et al., 2019) along prenatal and prompt THI, respectively, indicate pronounced genetic differentiation in challenging environments. Compared to cow traits, genetic effects of calf diseases comprise direct and maternal genetic effects. Consequently, we focused on the effects of prenatal THI on maternal genetic effects. For PNEU, larger maternal genetic variations were identified in dams exposed to extreme prenatal HS. Oppositely, DIAR displayed larger maternal genetic variances under comfort conditions. Hence, responses of maternal genetic effects on

prenatal THI alterations are trait-specific. Genetic correlations smaller than 0.80 for calf diseases recorded at THI 60 with corresponding diseases at THI 74 suggest obvious time-lagged GxE for maternal genetic effects. Time-lagged GxE for direct genetic effects due to HS in late pregnancy were reported by Kipp et al. (2021) for primary and functional traits in lactating cows. For cow production traits, the ranking of sires according to estimated breeding values under comfort and prenatal HS conditions was almost the same. In analogy, identical heritabilities were estimated for production traits from the model with or without genotype by HS interactions. Additionally, for all traits, the interaction variances only explained small proportions of the total phenotypic variances (up to 3.79%). Similarly, Kipp et al. (2021) confirmed the absence of time-lagged GxE for milk production traits, using a random regression sire model. In contrast, ratios of environment-specific genomic variances to overall variances for feed efficiency traits (Yao et al., 2017) were larger than h_i^2 from this study. Consequently, the effect of prenatal HS during late pregnancy is smaller than the prompt herd effect due to geographical impact across latitudes. Nevertheless, effects of HS on direct and maternal genetic (co)variance components of traits in offspring are first indications for epigenetic mechanisms, suggestion ongoing molecular genetic studies in this regard.

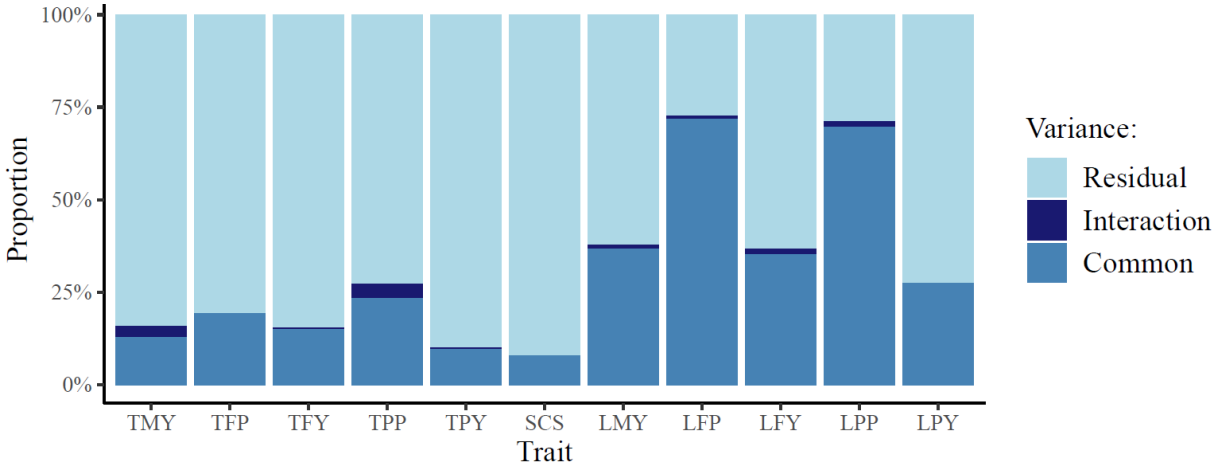

Figure 2. Proportions of common genomic, interaction and residual variances in relation to the total variance for test-day and lactation production traits.

References

Bohlouli, M., Alijani, S., Naderi, S., Yin, T., and König, S. (2019). J. Dairy Sci. 102(1):488–502.

Gernand, E., König, S., and Kipp, C. (2019). J. Dairy Sci. 102(7):6660–6671.

Halli, K., Brügemann, K., Bohlouli, M., Yin, T., and König, S. (2021). J. Anim. Sci. 99(5).

Kipp, C., Brügemann, K., Yin, T., Halli, K., and König, S. (2021). J. Dairy Sci. 104(9):10029–10039.

Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T., et al. (2002). Proc. of the 7th WCGALP, Montpellier, France.

Monteiro, A.P.A., Tao, S., Thompson, I.M.T., and Dahl, G.E. (2016). J. Dairy Sci. 99(10):8443–8450.

NRC (1971). A guide to environmental research on animals. National Academy Science, Washington, D.C., United States.

Stock, K.F., Cole, J., Pryce, J., Gengler, N., Bradley, A., et al. (2013). ICAR Tech. Ser. 17:75–81.

Tao, S., and Dahl, G.E. (2013). J. Dairy Sci. 96(7):4079–4093.

Yao, C., de los Campos, G., VandeHaar, M.J., Spurlock, D.M., Armentano, L.E., et al. (2017). J. Dairy Sci. 100(3):2007–2016.