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RESEARCH ARTICLE

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Genetic variation in surface temperature measured using infra-red thermography and genetic associations with production traits in grazing dairy cattle

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ABSTRACT
Increasing global temperatures and the incidence of extreme weather conditions will result in heat stress becoming a greater issue in production animals. Genetic selection and breeding for heat-tolerant animals have been promoted as a possible mitigation strategy in dairy cattle. The objectives of this study were to obtain in-field skin temperature measurements of the eye, muzzle and udder using infra-red thermography to examine the genetic variation in skin temperature within cows of a dairy herd and to estimate the genetic correlations between skin temperature and production traits. Thermal images and herd test records were obtained for the dairy herd at Massey University's dairy farm 1. Estimates of (co)variances were obtained using the JWAS program with univariate and bivariate animal models. The heritability estimates for the eye, muzzle and udder temperature were low to moderate at 0.20, 0.24 and 0.39, respectively. All genetic correlations between production and temperature traits were positive except for eye temperature with milk yield and protein yield which was negative and weak. These results indicate that it may be possible to select for a greater skin temperature, however, these results need to be validated using a larger sample size.

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Heat stress; dairy cattle; thermotolerance; genetic parameters; heritability

Introduction

Climate change has resulted in rising global temperatures and more frequent extreme weather events. The impact of heat stress on the dairy industry, globally, is becoming a significant animal welfare issue with impacts on health, reproduction, and production (Wankar et al., 2021; Cheruiyot et al. 2022). In pastoral systems, like the New Zealand dairy industry, cattle are exposed to climatic fluctuations and high summer temperatures. They may be required to walk long distances compared to cattle in housed systems. They have a predominantly grazed pasture-based diet, which can generate more heat due to their digestion than concentrated feeds (Bryant et al. 2007).

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Genetic variation in heat tolerance both between and within breeds of cattle has been documented previously (Cheruiyot et al. 2022). Proxies for heat tolerance have been proposed for use in selection due to the complexity of heat stress responses, the multitude of genes involved in conveying heat tolerance and the negative correlation between heat tolerance and production in cattle (Osei-Amponsah et al. 2019; Cartwright et al. 2023).

Australia has developed breeding values for heat tolerance, based on the rate of decline in milk production with increasing temperature-humidity index (THI). Heat-tolerant Holstein-Friesians, selected on their heat-tolerant breeding values, have been observed to exhibit lower rectal and vaginal temperatures, greater skin temperatures, as well as less reduction in milk yield and dry matter intake than their heat-sensitive counterparts (Garner et al. 2016; Jensen et al. 2022). This indicates that skin surface temperature may be a suitable proxy for the selection of increased thermotolerance as cattle with greater skin temperatures may have superior heat dissipation capabilities (Cheruiyot et al. 2022). Infra-red thermography is an ideal method of measuring surface temperatures as it is a non-invasive method that provides accurate measurements and can be conducted whilst the animal is in a pasture (McManus et al. 2016; Giro et al. 2019; Santos Daltro et al. 2017).

The objectives of this study were to examine the genetic variation in surface temperature between members of a single dairy herd using infra-red thermography and to estimate the genetic correlations between surface temperature and production traits. Accurate genetic parameter estimates for infra-red thermography measured surface temperature and its genetic correlations with economically important traits may provide support for large-scale studies developing breeding values for thermotolerance where surface temperature is used as a proxy trait.

Materials and methods

Thermal images were taken of 225 dairy cows (49 Holstein-Friesian (F), 77 New-Zealand Jersey (J), and 99 F × J crossbred) from Massey University's dairy farm 1 in February 2023. Dairy farm 1 operates on a once-a-day milking schedule and spring calving system. Two thermograms were taken for each cow, one covering the eyes and muzzle and one of the hindquarters of the udder, whilst in the paddock during the middle of the day. The study was approved by the Massey University Animal Ethics Committee (protocol #AEC 22/85).

Pedigree and herd test records were extracted from MINDA® (https://www.lic.co.nz/products-and-services/minda/), the database of the Livestock Improvement Corporation (LIC), New Zealand. These records included pedigree information, age, breed composition, calving dates, Breeding Worth (BW), Production Worth (PW), total milk yield (MY), fat (FY), protein (PY), and milk solids (fat plus protein) yield (MSY). From the extracted records the lactation number, energy corrected milk yield (ECMY), days in milk (DIM), median calving date, deviation from herd median calving date and the predicted milk yield on the day of measurement were determined.

Lactation number was divided into four categories with cows in their fourth lactation or higher grouped under lactation number four. The ECMY was calculated using the formula $ECMY(kg) = 0.25MY + 12.2FY + 7.7PY$ as described by Sjaunja et al. (1991). The herd-test records for MY, FY and PY for each cow over the 2022–23 production season were used to model the lactation curves for each cow using random regression with 3rd order Legendre polynomials as described by Lembeye et al. (2016a). Each cow had an average of 8 herd-tests. From these lactation curves the daily predicted milk yield on the day of thermogram measurement was obtained using the corresponding day in milk for each cow.

The climate data specifically hourly ambient temperature and relative humidity were extracted from CliFlo (NIWA 2023) which allows access to New Zealand's National Climate Database. The THI was calculated using the formula $\mathrm{THI} = 1.8\mathrm{T} - (1 - \mathrm{RH})(\mathrm{T} - 14.3) + 32$ where T is the temperature (°C) and RH is the relative humidity (Kibler 1964).

The descriptive statistics (N, mean, standard deviation, minimum and maximum values) for the continuous variables were determined using the MEANS procedure in SAS version 9.4 software (SAS Institute Inc, Cary NC, USA).

Bayesian univariate and bivariate animal models, including the fixed effects of lactation number, breed, their interaction, and as covariates, deviation from median calving date, THI and predicted daily milk yield on the day of thermogram measurement, and the random effects of animal and residual error, were run in Julia version 1.7.3 using the Julia for Whole-genome Analysis Software (JWAS) package to estimate the (co)variance components for the animal additive genetic (σ_a^2) and residual (σ_e^2) variances. Inferences were based on Markov chain Monte Carlo (MCMC) procedures. Marginal posterior distributions of all unknowns were estimated using the Gibbs sampling algorithm. Inference was based on chain lengths of 100 samples, retaining 1 sample every 100 samples.

The heritability (h^2) for the temperature and production traits were calculated using the estimated phenotypic and animal additive genetic variances.

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

$\sigma_p^2 = \sigma_a^2 + \sigma_e^2$

The genetic (r_G) and phenotypic (r_p) correlations were calculated as shown below:

$$r_G = \frac{\sigma_{a1a2}}{\sigma_{a1} \times \sigma_{a2}}$$

and

$$r_P = \frac{\sigma_{p1p2}}{\sigma_{p1} \times \sigma_{p2}}$$

Where σ_{a1a2} is the animal (genotypic) covariance between trait 1 and 2; σ_{p1p2} is the phenotypic covariance between trait 1 and 2; σ_{a1} and σ_{p1} are the genetic and phenotypic standard deviations for trait 1, respectively, and σ_{a2} and σ_{p2} are the genetic and phenotypic standard deviations for trait 2.

Results

Descriptive statistics for the temperature and production traits are presented in Table 1. The 225 cows included in the study ranged from two to ten years of age. The mean eye

Table 1. Descriptive statistics for age, productivity, production, and temperature traits for grazing dairy cows during the 2022–23 production season.

Variable[2]	N	Mean	SD[1]	Min[1]	Max[1]
Age, years	225	4.28	1.99	2.00	10.00
BW, $/5 t DM	185	246.3	79.1	13.0	394.0
PW, $/5 t DM	185	271.4	189.9	−330.0	728.0
Days in milk	225	271.7	22.1	212.0	305.0
MY, kg	225	4,000	898	1,053	6,858
FY, kg	225	216.8	40.3	62.0	336.0
PY, kg	225	169	34.4	46.0	258.0
MSY, kg	225	385.8	72.9	108.0	587.0
ECMY, kg	225	4,946	946	1,374	7,739
PMY, kg	225	8.03	2.12	2.6	13.7
ET, °C	225	37.8	1.16	33.9	43.3
MT, °C	221	37.7	1.51	32.9	42.5
UT, °C	225	38.2	1.19	34.5	41.0

[1] SD = standard deviation, Min = minimum value, Max = Maximum value. [2] BW = Breeding Worth, PW = Production Worth, MY = milk yield, FY = fat yield, PY = protein yield, MSY = milk solids (fat + protein) yield, ECMY = energy corrected milk yield, PMY = predicted milk yield on day of measurement, ET = eye temperature, MT = muzzle temperature, UT = udder temperature.

temperature (ET), muzzle temperature (MT) and udder temperature (UT) were 37.8, 37.7 and 38.2 °C, respectively. The greatest variation, according to the standard deviations, in skin surface temperature was within the muzzle temperature and the least in eye temperature.

The h^2 and variance components with their associated standard deviations (SD) for the production and temperature traits are presented in Table 2. The h^2 estimates for the MY, FY, PY, MSY, ECMY and PMY were 0.40, 0.38, 0.36, 0.33, 0.48 and 0.27, respectively. The h^2 estimates for the ET, MT and UT were 0.20, 0.24 and 0.39, respectively. The magnitude of the heritability estimates was similar for all the traits except for the PMY, ET and MT which were lower.

The estimates for the genetic (r_G) and phenotypic (r_P) correlations between the production and temperature traits are presented in Table 3.

The r_P between MY, FY, PY, MSY and ECMY were all positive ($0.74 \le r_P \le 0.94$). The r_P between the PMY and the other production traits while lower than between MY, FY, PY, MSY and ECMY and they were still positive and high ($0.54 \le r_P \le 0.58$).

Table 2. Variance components and heritabilities (h^2) with associated standard deviations (SD; within brackets) for the production and temperature traits on grazing dairy cows during the 2022–23 production season.

	Variance components[2]			
Trait[1]	σ^2_e	σ^2_a	σ^2_{Total}	h^2
MY, kg	245,913 (34,565)	164,278 (26,056)	410,191 (60,622)	0.40 (0.05)
FY, kg	635.5 (109.6)	394.7 (132.2)	1,030 (241.8)	0.38 (0.11)
PY, kg	447.6 (56.6)	251.8 (67.6)	699.4 (124.3)	0.36 (0.08)
MSY, kg	2,156 (336.4)	1,052 (280.2)	3,208 (616.6)	0.33 (0.08)
ECMY, kg	267,658 (48,412)	248,898 (46,091)	516,556 (94,503)	0.48 (0.08)
PMY, kg	3.01 (0.47)	1.12 (0.33)	4.12 (0.80)	0.27 (0.08)
ET, °C	1.06 (0.15)	0.27 (0.10)	1.33 (0.25)	0.20 (0.08)
MT, °C	1.64 (0.20)	0.51 (0.14)	2.15 (0.34)	0.24 (0.06)
UT, °C	0.69 (0.11)	0.44 (0.07)	1.13 (0.17)	0.39 (0.06)

[1] MY = milk yield, FY = fat yield, PY = protein yield, MSY = milk solids yield (fat + protein), ECMY = energy corrected milk yield, PMY = predicted milk yield on day of measurement, ET = eye temperature, MT = muzzle temperature and UT = udder temperature.

[2] σ^2_a = animal additive genetic variance, σ^2_e = residual error variance, σ^2_{Total} = total variance.

Table 3. Estimates of the genetic (below diagonal) and phenotypic (above diagonal) correlations with their associated standard deviations (SD) for production and temperature traits of grazing dairy cows during the 2022–23 production season.

Trait[1]	MY	FY	PY	MSY	ECMY	PMY	ET	MT	UT
MY		0.74 (0.07)	0.87 (0.07)	0.83 (0.08)	0.86 (0.08)	0.58 (0.06)	0.04 (0.06)	0.03 (0.06)	0.20 (0.06)
FY	0.57 (0.13)		0.81 (0.06)	0.91 (0.09)	0.91 (0.07)	0.54 (0.05)	0.03 (0.06)	0.07 (0.06)	0.22 (0.07)
PY	0.86 (0.11)	0.78 (0.11)		0.91 (0.07)	0.90 (0.07)	0.58 (0.05)	0.03 (0.06)	0.08 (0.06)	0.18 (0.05)
MSY	0.77 (0.10)	0.90 (0.13)	0.87 (0.11)		0.94 (0.07)	0.56 (0.06)	0.05 (0.06)	0.05 (0.07)	0.19 (0.23)
ECMY	0.77 (0.11)	0.88 (0.13)	0.86 (0.09)	0.90 (0.12)		0.57 (0.06)	0.06 (0.07)	0.07 (0.07)	0.23 (0.05)
PMY	0.50 (0.11)	0.42 (0.14)	0.49 (0.09)	0.43 (0.09)	0.39 (0.10)		0.08 (0.06)	0.04 (0.05)	0.17 (0.07)
ET	−0.04 (0.18)	0.25 (0.17)	−0.18 (0.17)	0.10 (0.08)	0.32 (0.21)	0.34 (0.20)		0.71 (0.06)	0.34 (0.06)
MT	0.03 (0.24)	0.31 (0.10)	0.23 (0.10)	0.07 (0.12)	0.02 (0.12)	0.14 (0.20)	0.47 (0.12)		0.33 (0.06)
UT	0.20 (0.12)	0.48 (0.18)	0.15 (0.14)	0.15 (0.08)	0.36 (0.13)	0.27 (0.19)	0.32 (0.19)	0.39 (0.09)	

[1] MY = milk yield, FY = fat yield, PY = protein yield, MSY = milk solids yield (fat + protein), ECMY = energy corrected milk yield, PMY = predicted milk yield on day of measurement, ET = eye temperature, MT = muzzle temperature and UT = udder temperature.

The r_P for ET and MT with the production traits were not different from zero ($0.03 \leq r_P \leq 0.08$). The r_P between ET and MT was positive and high (0.71). The r_P was positive between UT and the production and temperature traits. They were low to moderate ($0.17 \leq r_P \leq 0.23$) between UT and the production traits and moderate between UT and both ET and MT (0.34 and 0.33, respectively).

The genetic correlations between production traits were positive and high ($0.42 \leq r_G \leq 0.90$) except for PMY and ECMY which were positive and moderate (0.39). The genetic correlations between temperature and production traits were positive except between ET and MY and PY which were negative and low. The genetic correlations between ET and FY, MSY, ECMY and PMY were low to moderate ($0.10 \leq r_G \leq 0.34$). They were low to moderate between MT and FY, PY, MSY, and PMY ($0.07 \leq r_G \leq 0.31$). The genetic correlations were close to zero between MT and both MY and ECMY (0.03 and 0.02, respectively). The genetic correlation between ET and MT was moderate(0.47). The genetic correlations between UT and MY, PY, MSY, ECMY, PMY, ET and MT were low to moderate ($0.15 \leq r_G \leq 0.39$) and high between UT and FY (0.48).

Discussion

The MY from the herd at Dairy farm 1 was 4,000 kg with a fat and protein percentage of approximately 5.4% and 4.2% respectively. The calculated ECMY was greater than the MY, this is the result of a high percentage of fat and protein. DairyNZ reported during the 2021–22 season that the average New Zealand dairy cow had a MY of 4,291 L with a fat and protein percentage of 5.03% and 3.94%, respectively (DairyNZ & LIC 2022).

There are many published h^2 values for MY, FY and PY in dairy cattle both in New Zealand and globally. The estimated h^2 values from this study were greater than many of the estimates in the literature published for New Zealand dairy cows with values ranging from 0.12 to 0.35 (Sneddon et al. 2016; Lopez-Villalobos et al. 2018; Jayawardana et al. 2023). The estimated h^2 for MY, FY and PY were similar in magnitude to values published by Lembeye et al. (2016b) for New Zealand dairy cattle and international heritabilities reported for Holsteins by Berry et al. (2003) and Miglior et al. (2007).

There are currently no reported h^2 estimates for skin surface temperature in dairy cattle and no r_G estimates with economically important traits. Potentially the reason for this may be that measurements of skin temperature could be inconsistent and affected by the environmental temperature. However, there have been several studies involving the use of infra-red thermography as a method of measuring body temperature, examining correlations between infra-red measured surface temperatures and rectal temperature, and identification of animals undergoing heat stress (Daltro et al. 2017; Giro et al. 2019; Stumpf et al. 2021). Based on previous studies the best surfaces for measuring body temperature were suggested to be the eye, the lateral side of the udder and the coronary band of the forelimb (Idris et al. 2021; Giro et al. 2019; Stumpf et al. 2021).

Therefore, comparisons between estimates determined in this study with literature values will be with rectal temperature. Reported h^2 estimates in dairy cattle, mostly Holsteins, Holstein crosses and Jerseys, range from 0.06 to 0.31 (Seath and Miller 1947; Dikmen et al. 2012; Luo et al. 2020). h^2 estimates for ET, MT and UT from this study were on the higher end of the heritabilities for rectal temperature in the literature. These h^2 estimates suggest that genetic selection of these traits will be possible.

The genetic correlations between production traits were all positive and ≥0.57, this is consistent with r_G in the literature. The r_G between MY, FY, and PY were greater than the reported values by Sneddon et al. (2016) and Lembeye et al. (2016b) with the exception of MY and PY but were similar to values reported by Miglior et al. (2007) and Lopez-Villalobos et al. (2018).

All r_G among the temperature traits were positive and moderate to strong indicating that there are shared genetic influences (pleiotropy) in the expression of the temperature traits. Therefore, selecting one would result in moderate to strong change in the other traits in the same direction.

All the r_G between temperature and production traits were positive and were weak to moderately strong except for ET with MY and PY, which exhibited weak negative r_G. Additionally, the r_G between MT with both MY and ECMY, were very low, almost negligible. Therefore, it is unlikely that the expression of MT, MY and ECMY have many genes in common that influence their expression. The r_G between ET with FY, ECMY, and PMY; between MT with FY, PY; and between UT and MY, ECMY and PMY were all moderately strong. The r_G between UT and FY was high. Therefore, if there was the selection for increases in the temperature traits there would be changes in the same direction for the other traits where there is a moderate to strong correlation as there is a crossover in the genes affecting the expression of the traits.

Validation of the results of this study is recommended using a much larger data set.

Conclusion

The moderate heritability estimates for eye, muzzle and udder temperatures and the positive r_G between the temperature traits and the production traits indicate that it is possible to select for greater eye, muzzle and udder temperature without compromising production. Udder temperature had the strongest correlation with production traits. The next phase in this research should estimate genetic parameters for the skin temperature traits and their correlations with production traits in a larger study (ideally >1000 animals).

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Disclosure statement

No potential conflict of interest was reported by the authors.

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