Genetic parameters for body temperature under hot and humid conditions in an Angus–Brahman multibreed population

R.G. Mateescu[1], S. Dikmen[2], P.J. Hansen[1], M.A. Elzo[1]

[1] *University of Florida, Department of Animal Sciences, Gainesville, FL 32608, USA*
raluca@ufl.edu (Corresponding Author)
[2] *Uludag University, Department of Animal Science, Bursa 16059, Turkey*

Summary

Climatic stress is a major limiting factor of production efficiency in beef cattle in tropical and subtropical environments. This stress is expected to increase due to climate change. More than half of the cattle in the world are maintained in hot and humid environments, including about 40% of beef cows in the US. Substantial differences in thermal tolerance exist among breeds and among animals within breeds indicative of opportunities for selective improvement. First step in the process of revealing the genetic architecture of traits defining thermal tolerance using *Bos indicus* influenced cattle is to estimate the genetic parameters. Vaginal temperature was measured at 5-min intervals for 5 days in 286 cows over two years (2015 and 2017) from the multibreed herd (ranging from 100% Angus to 100% Brahman) of the University of Florida. Ambient environmental conditions were monitored using HOBO data loggers, which continuously record temperature, humidity, solar radiation, black globe temperatures, and wind speed which were used to calculate a temperature humidity index (THI). There was a breed effect on body temperature with Angus and 3/4 Angus cows had a vaginal temperature higher 39°C even during lower heat stress conditions while Brahman cattle were the only ones able to maintain a lower vaginal temperature throughout the 24h-day during high heat stress conditions. Heritabilities for all different vaginal temperature measures were low or medium and ranged from 0.11 to 0.27. The lowest heritability estimate is for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively).

Keywords: genetic parameters, body temperature, beef cattle

Introduction

Heat stress is a principal factor limiting production of animal protein and negatively affecting health and welfare of cattle in subtropical and tropical regions. Detrimental effects on livestock productivity associated with heat stress are expected to intensify dramatically and expand into currently temperate zones upon the realization of predicted climate change (IPCC, 2007). Most animal-producing areas in the US are predicted to experience extreme summer conditions (Luber and McGeehin, 2008) and by 2100, average temperatures in the US are projected to increase 2° to 6°C, depending on the emissions scenario and climate model applied (USGCRP, 2009). The number of days with maximum temperatures above 32°C (90°F) is also expected to increase. The SE and SW areas of the US currently average 60 such days per year but are projected to experience at least 150 such days a year by the end of the century.

Development of effective strategies to improve the ability to cope with heat stress is imperative to enhance productivity of the US livestock industry and secure global food supplies.

Substantial differences in thermal tolerance exist among breeds and among animals within breeds indicative of opportunities for selective improvement. For example, *Bos indicus* cattle exhibit increased resistance to many environmental stressors relative to *Bos taurus,* but tend to have slower growth, lower fertility and poor meat quality as they have not been as intensively selected for these traits as specialized *Bos taurus* breeds. Use of genomic tools to produce an animal with superior ability for both thermal adaptation and production represents an energy-efficient sustainable approach to meet the challenge of global climate change.

Quantitative measures of the thermal environment and the animal's responses to heat stress are needed to assess thermal tolerance. Commonly used measures of the thermal environment are temperature, humidity, solar radiation, and wind, while coat characteristics, body temperature, skin temperature, respiratory rate and sweating rate describe thermal environment from an animal perspective. Riley et al. (2012) reported heritabilities of 0.19 and 0.27 for rectal temperature and coat score in a Brahman x Angus crossbred population, and a genetic correlation of 0.24 between these traits. Dikmen et al. (2012) reported heritability of 0.17 for rectal temperature in dairy cattle. Both studies were conducted during hot and humid summers in Florida. These heritabilities demonstrate genetic variation and supports the hypothesis that selection for improved thermal tolerance is possible if animals with genetically superior core body temperature regulation when exposed to environmental thermal stress can be identified. Selection for improved thermal tolerance using classical approaches is not feasible due to cost and difficulty of collecting appropriate phenotypes on large numbers of animals. To determine an animal's response to heat stress (and therefore to assess its thermal tolerance), high frequency measurements of relevant traits are required, hence the importance of fine-scale high-throughput phenotyping.

Development and use of population specific genomic tools in selection and management to improve thermal adaptation in concert with all other economically important traits represents an energy-efficient strategy to meet the challenges of global climate change and improve sustainability and profitability of beef industry in Florida and other hot and humid regions of the US. The objectives of this research were to characterize the genetic parameters of body temperature phenotypes in crossbred cattle ranging from 100% Angus to 100% Brahman.

Material and methods

Resource Population and Phenotypes.
This study utilized 286 cows over two years (2015 and 2017) from the multibreed herd of the University of Florida. Cattle in the multibreed herd were assigned to six breed groups according to the following breed composition ranges: 100% Angus = (1.0 to 0.80) Angus (0.0 to 0.20) Brahman; 75% Angus = (0.79 to 0.60) Angus (0.21 to 0.40) Brahman; Brangus = (0.625) Angus (0.375) Brahman; 50% Angus = (0.59 to 0.40) Angus (0.41 to 0.60) Brahman, 25% Angus = (0.39 to 0.20) Angus (0.61 to 0.80) Brahman; and 100% Brahman: (0.19 to 0.0) Angus (0.81 to 1.00) Brahman.

Vaginal temperature was measured at 5-min intervals for 5 days with an iButton temperature measuring device (iButton data loggers, type DS1922L, temperature range -40°C to 85°C, accuracy +/- 0.5°C, 11-bit for 0.0625°C resolution, Embedded Data Systems). Each iButton was calibrated before the study started and pre-programmed to record body temperature at 5 min intervals on a 24-h cycle. Ambient environmental conditions were monitored using HOBO data loggers, which continuously record temperature, humidity, solar radiation, black globe temperatures, and wind speed. The temperature humidity index was calculated as: THI =

$(1.8 \times T + 32) - [(0.55 – 0.0055 \times RH) \times (1.8 \times T – 26)]$, where T = air temperature (°C) and RH = relative humidity (%) (Dikmen et al., 2008).

Statistical Analysis.

Body temperature
The effect of breed group (breed composition) on body temperature was estimated using the PROC GLM procedure of SAS using a fixed effects model which breed group (100% Angus, 75% Angus, 50% Angus, 25% Angus, 100% Brahman, Brangus), age (2, 3, ≥4 years) and evaluation year (2015 or 2017) as fixed effects. Least squares means were separated using the PDIFF option of GLM in SAS.

The initial dataset consisted of vaginal temperature measured every 15 minutes for 3 days. A two-consecutive day window (24 hours) was identified with data for all cows in each replicate. The hourly average vaginal temperature was calculated for each cow over the 24-hour window. A repeated measures analysis of the effect of replicates (3), and breed group (6) on vaginal temperature was performed using PROC MIXED procedure of SAS, with covariance structure described by autoregressive order one model AR(1). The model used was:

$Y = X\beta + e$

Where $X\beta$ models the fixed effects of replicate (3), breed group (6) and hour (24) and e models the random variation. With AR(1) model the covariance matrix R of e is block diagonal specified by the SUBJECT = cow(replicate*breed group) option in the REPEATED statement of PROC MIXED procedure.

The heat stress level was evaluated for each replicate using the THI. Replicates were classified as low heat stress, medium heat stress and high heat stress. A separate analysis to for each replicate was performed to untangle the sources of replicate by breed group interaction.

Genetic Parameters
Based on the minimum and maximum THI in all replicates across both years, a THI interval between 74 and 74.5 was defined as "Low THI", between 84 and 84.5 as a "High THI" and between 77 and 77.5 as an "average THI". Vaginal temperature for each cow for these three THI categories was calculated as the average vaginal temperature of all the 5-min measurements when the cow was exposed to that respective THI. Subsequently, the difference in vaginal temperature when cow was exposed to high and low THI periods was calculated within each cow.

For each body temperature trait, restricted maximum likelihood procedures were used to estimate genetic and residual variances as well as heritability, based on an univariate animal models fitted to the data using WOMBAT (Meyer, 2007; http://didgeridoo.une.edu.au/km/wombat.php).

In matrix notation, the basic model equation was:

$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}u + \mathbf{e}$

Where the design matrices $\mathbf{X}$ and $\mathbf{Z}$ relate phenotypic observations in the vector $\mathbf{y}$ to fixed ($\boldsymbol{\beta}$) and random (u) effects, respectively. The vector e contains random residual effects specific to each animal. The vectors u and e were assumed to be normally distributed with $\mathbf{0}$ means and variances $\mathbf{A}\sigma^2_a$ and $\mathbf{I}\sigma^2_e$, respectively, where $\mathbf{I}$ is an identity matrix of order equal to the number of animals with observations, $\mathbf{A}$ is the additive relationship matrix, σ^2_a is the additive genetic variance, and σ^2_e is the residual variance.

Contemporary groups were defined based on age when the body temperature was measured (2, 3, ≥4 years), breed group (100% Angus, 75% Angus, 50% Angus, 25% Angus, 100% Brahman, Brangus), and year when the body temperature was measured (2015, 2017) for a total of 30 groups. Contemporary groups were fit as fixed effects in all analyses.

A pedigree file with 602 individuals including identification of all animal, sire, and dam trios was used to define relationships among animals in the data set.

Results and discussion

Breed effect on body temperature
Least square means for vaginal temperature under high low and average THI, and the difference in vaginal temperature between high and low THI for each of the 6 breed groups are presented in **Table 1**.

The hourly vaginal temperature under high heat stress (high intensity and long duration THI), medium heat stress (lower intensity and long duration) or low heat stress (lower intensity and short duration) showed a significant breed effect for each heat stress level. **Figure 1** shows the pattern of hourly variation in vaginal temperature for Angus, 3/4Angus x 1/4Brahman (3/4A, 1/4B), Brangus, 1/2Angus x 1/2Brahman (1/2A, 1/2B), 1/4Angus x 3/4Brahman (1/4A, 3/4B) and Brahman cows under low heat stress (left panel) and high heat stress conditions (right panel). Angus and 3/4 Angus cows had a vaginal temperature higher 39°C even during lower heat stress conditions while Brahman cattle were the only ones able to maintain a lower vaginal temperature throughout the 24h-day during high heat stress conditions.

Genetic Parameters
Heritability estimates for body temperature under high, low and average heat stress (THI) as well as the difference between high and low, are presented in **Table 2**. Heritabilities for all different vaginal temperature measures were low and ranged from 0.11 to 0.27. The lowest heritability estimate is for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively). All values of heritability are close to values on rectal temperature reported by Riley et al. (2012) in a Brahman x Angus crossbred population (0.19) and rectal temperature in dairy cattle reported by Dikmen et al. (2012) in Florida (0.17).

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Table 1. Least square means and SE for difference in vaginal temperature between the high and low THI (Temp Diff Hi-Low) , vaginal temperature under high THI (Temp High), vaginal temperature under low THI (Temp Low), and vaginal temperature under average THI (Temp Mean) for 6 different breed groups.

Breed Group	N	Temp Diff Hi-Low	Temp High	Temp Low	Temp Average
100% Angus - 0% Brahman	51	0.32 (0.04)	39 (0.04)	38.68 (0.04)	38.65 (0.04)
75% Angus - 25% Brahman	35	0.39 (0.05)	39.1 (0.05)	38.7 (0.05)	38.71 (0.04)
Brangus	37	0.41 (0.05)	39.01 (0.05)	38.59 (0.05)	38.63 (0.04)
50% Angus - 50% Brahman	41	0.41 (0.05)	39.11 (0.05)	38.69 (0.05)	38.63 (0.05)
25% Angus - 75% Brahman	34	0.35 (0.06)	39.14 (0.06)	38.79 (0.04)	38.66 (0.05)
0% Angus - 100% Brahman	88	0.04 (0.05)	38.84 (0.04)	38.81 (0.05)	38.5 (0.04)

Table 2. Genetic (σ^2_a) and residual (σ^2_e) variance and heritability (h^2) estimates for difference in vaginal temperature between the high and low THI (Temp Diff Hi-Low) , vaginal temperature under high THI (Temp High), vaginal temperature under low THI (Temp Low), and vaginal temperature under average THI (Temp Mean)

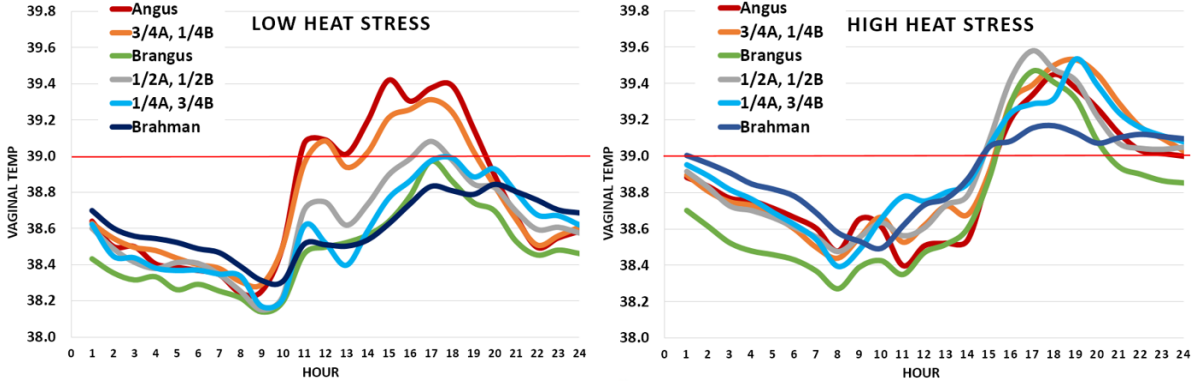| Trait	σ^2_a	σ^2_e	h^2
Temp Diff Hi-Low	0.17	0.45	0.27
Temp High	0.07	0.56	0.11
Temp Low	0.14	0.42	0.25
Temp Average	0.09	0.35	0.20

Figure 1. Daily variation in vaginal temperature in UF cows of different breed composition presented as average temperature over a 5-day period for each breed group during low heat stress (low intensity and short duration THI throughout the day) or high heat stress conditions (high intensity and long duration THI).