J. Dairy Sci. 97:1–16
http://dx.doi.org/10.3168/jds.2014-8023

Modeling heat stress effect on Holstein cows under hot and dry conditions: Selection tools

M. J. Carabaño,[*1] **K. Bachagha,**[*] **M. Ramón,**[†] **and C. Díaz**[*]
[*]Departamento de Mejora Genética Animal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Madrid 28040, Spain
[†]Centro Regional de Selección y Reproducción Animal, 13300 Valdepeñas, Spain

ABSTRACT

Data from milk recording of Holstein-Friesian cows together with weather information from 2 regions in Southern Spain were used to define the models that can better describe heat stress response for production traits and somatic cell score (SCS). Two sets of analyses were performed, one aimed at defining the population phenotypic response and the other at studying the genetic components. The first involved 2,514,762 test-day records from up to 5 lactations of 128,112 cows. Two models, one fitting a comfort threshold for temperature and a slope of decay after the threshold, and the other a cubic Legendre polynomial (LP) model were tested. Average (T_{AVE}) and maximum daily temperatures were alternatively considered as covariates. The LP model using T_{AVE} as covariate showed the best goodness of fit for all traits. Estimated rates of decay from this model for production at 25 and 34°C were 36 and 170, 3.8 and 3.0, and 3.9 and 8.2 g/d per degree Celsius for milk, fat, and protein yield, respectively. In the second set of analyses, a sample of 280,958 test-day records from first lactations of 29,114 cows was used. Random regression models including quadratic or cubic LP regressions (TEM_) on T_{AVE} or a fixed threshold and an unknown slope (DUMMY), including or not cubic regressions on days in milk (DIM3_), were tested. For milk and SCS, the best models were the DIM3_ models. In contrast, for fat and protein yield, the best model was TEM3. The DIM3DUMMY models showed similar performance to DIM3TEM3. The estimated genetic correlations between the same trait under cold and hot temperatures (ρ) indicated the existence of a large genotype by environment interaction for fat ($\rho = 0.53$ for model TEM3) and protein yield (ρ around 0.6 for DIM3TEM3) and for SCS ($\rho = 0.64$ for model DIM3TEM3), and a small genotype by environment interaction for milk (ρ over 0.8). The eigendecomposition of the additive genetic covariance matrix from model TEM3 showed the existence of a dominant component, a constant term that is not affected by temperature, representing from 64% of the variation for SCS to 91% of the variation for milk. The second component, showing a flat pattern at intermediate temperatures and increasing or decreasing slopes for the extremes, gathered 15, 11, and 24% of the variation for fat and protein yield and SCS, respectively. This component could be further evaluated as a selection criterion for heat tolerance independently of the production level.

Key words: Holstein cattle, heat stress, genetic selection

INTRODUCTION

The climate of a large proportion of the Iberian Peninsula is classified as temperate with dry and hot summers, or as hot steppe. More than half of the Peninsula surface presents monthly average maximum daily temperatures in July and August well over 30°C (AEMET, 2011). Climate change is expected to worsen the temperature situation over the next decades. Segnalini et al. (2013) predicted that, by 2050, large areas of the center, south, and northeast of the Iberian Peninsula will reach, according to the predicted values of temperature-humidity indices (**THI**), discomfort ($72 \leq \text{THI} < 75$) and alert conditions ($75 \leq \text{THI} < 79$) for livestock in the summer months. These conditions will also affect most of the Mediterranean basin and might extend to more northern latitudes. A significant proportion of the dairy cattle farms in Spain (around 20%) is located in these areas. Similar hot and dry climate conditions affect or will affect other large areas of the planet and their milk production industry. Selection of animals tolerant to heat stress without altering their potential for milk production might be needed to support the dairy cattle industry under hot weather conditions.

Several studies have previously dealt with the determination of the effect of heat stress on milk production and the estimation of genetic components of heat stress resistance. Misztal (1999) proposed a model fitting a comfort zone, with no effect of temperature on produc-

---

Received February 6, 2014.
Accepted August 14, 2014.
[1]Corresponding author: mjc@inia.es

tion, followed by a linear decay in production, providing 2 parameters: the thermotolerance threshold and the subsequent slope of decay for each animal in the most complex model (Sánchez et al. 2009b). Bernabucci et al. (2014) followed a similar approach through the use of a dummy covariable and fixing a comfort threshold equal for all animals a priori. This type of model is attractive because of the direct biological interpretation of the parameters obtained for each animal. However, it relies on strong assumptions, such as that production decays abruptly after the threshold, that the decay is then linear, and, in the simplest versions, that a common known or unknown comfort threshold exists for all animals. In the most parameterized model, where individual threshold and slopes are fitted, slow mixing and convergence rates have been observed (Sánchez et al., 2009a). Moreover, the parameters representing the overall level of production (intercept) and the tolerance to heat stress (slope) are genetically antagonistic (Ravagnolo and Misztal, 2000; Sánchez et al., 2009a; Bernabucci et al., 2014), which indicates that selection for the tolerance parameter is likely to result in a decrease in the production level and vice versa. Alternatively, Brügemann et al. (2011) have used random regressions to fit both the effects of DIM and THI on production traits. Random regression parameters lack biological interpretation, but these models are attractive for 2 reasons. First, they have large flexibility to fit smoother patterns of decay and, second, they allow the use of eigendecomposition of the additive genetic covariance matrix to find selection criteria (as in Kirkpatrick et al., 1990). Such selection criteria are not correlated among themselves and could help in the improvement of tolerance to heat stress with no effect on production level. For test-day models used for selection on production, one of these eigenfunctions has been associated with the persistency of lactations. This eigenfunction has been also advocated as a selection criterion for this trait to avoid the problems of the antagonistic relationship between production level and other persistency measures (see, for example, Togashi and Lin, 2006). Both approaches, which we have named the splines (**SP**) model of Misztal (1999) and the random regression reaction norm model based on Legendre polynomials (**LP**), have not been formally compared until now.

This study aimed at defining the models that can best predict the population response and the individual genetic components of heat tolerance, using data from Spanish Holstein-Friesian farms under hot and dry conditions. Possibilities of selection for heat tolerance independent from production level are also explored.

MATERIALS AND METHODS

Production and SCC data as well as pedigree information were provided by the Confederation of the Spanish Friesian Associations (CONAFE; Madrid, Spain). Weather records were provided by the meteorological state agency [Agencia Estatal de Meteorología (AEMET), Madrid, Spain]. The production and SCC database consisted of test-day records from the first 5 lactations of Spanish Holstein cows calving between 2002 and 2012 in Castile la Mancha and Andalusia. These regions were chosen because they are the areas of highest summer temperatures in Spain.

For SCC, SCS were obtained using the following expression (Ali and Shook, 1980):

$$\mathrm{SCS} = \log_2(\mathrm{SCC}/100) + 3.$$

After filtering for abnormal records of production, SCC and environmental indicators, the final data set comprised information on test-day milk, fat, and protein yields and SCS records of 2,514,762 test-day records from 128,112 cows in 568 herds from 2002 to 2012, inclusive.

Concerning the weather stations, records from 718 stations in both regions (Castile la Mancha and Andalusia) were provided by AEMET. Not all weather stations collect humidity data. Therefore, the average distance between weather stations from which THI could be calculated and farms was larger than for stations providing only temperatures. For temperature, the average distance was 7.24 km, with a maximum of 29.65 km and a standard deviation of 5.0, whereas the average distance for stations where THI could be obtained was 13.29 km, with a maximum of 29.98 km and a standard deviation of 7.90 km. Temperature-humidity indices were highly correlated with temperatures and showed an almost identical pattern of change as did temperatures alone along the year (data not shown). Thus, due to the high similarity between temperature and THI and the fact that stations with humidity records were at a greater distance from herds than stations with only temperature records, daily average ($\mathbf{T_{AVE}}$) and maximum ($\mathbf{T_{MAX}}$) temperatures were used in the subsequent analyses to avoid lack accuracy in the estimates of responses to different heat loads.

Two sets of analyses were performed. The first one dealt with the estimation of the response to increasing heat loads for production traits and SCS at the population level. The second set of analyses aimed at modeling the individual genetic components of response to heat in this population.