GENOTYPE BY IN FARM TEMPERATURE INTERACTION ON DOE REPRODUCTIVE PERFORMANCE AND LENGTH OF PRODUCTIVE LIFE

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ABSTRACT

The aim of this study was to assess the magnitude of the interaction between in farm temperature and additive genetic effects for prolificacy, weaning weight and longevity. Data came from Caldes line, which has been selected for post-weaning growth since 1983. A total of 18,491, 16,868 and 6,743 records for total born (TB), number of weaned kits (NW) and average weaning weight (avg-WW), and longevity (Long) were considered. For TB, NW and avg-WW different Bayesian Hierarchical models were employed while Long was studied using a semiparametric Bayesian proportional hazard model. The estimated magnitude of the interaction between additive genetic effects and temperature descriptors was nearly null for TB and Long, while for NW and avg-WW it shown a relevant magnitude. For these two traits the most likely form for this interaction was that in which genetic variation exist for both the temperature onset in which the animals experiment a linear change in their performances and for the change itself. Checking the estimated values of the heritabilities for the two definitions of heat stress for NW and avg-WW it can be concluded that the variation on the onset of heat stress is that showing the stronger genetic determination, but between each other a positive and high genetic correlation exist (around 0.74); however it must be noted that the genetic correlation between both definitions of heat stress and the performance of the trait is negative, around -0.7. Thus, although there is room for selective breeding to increase tolerance to heat stress on avg-WW, restrictions should be imposed to avoid average performances of the traits being reduced.

Key words: Genetic parameters, heat stress, prolificacy, weaning weight, longevity.

INTRODUCTION

Recently animal´s tolerance to heat has received attention in several species (Zumbach *et al.,* 2008; Sánchez *et al.,* 2009). The effects of heat on animals could be measured basically in two ways: i) indirectly through the usage of physiological markers of stress, which could be difficult to record and might not be perfectly correlated with the performances of the animals (Bernabucci *et al.,* 2010; Yousef, 1985); and ii) directly, by checking the effects on animal's performance when the animals are subject to high temperature (Ravagnolo *et al.,* 2000). This second approach have been the most widely used when the objective was precisely to prevent the negative effects of heat on animal´s performances. The objective in selection programs would be raise animals' tolerance to any value of temperature, i.e. they should be able to keep their performance irrespectively the environmental temperature. To identify those outstanding animals regarding this feature the breeder need to have records of each animal, or close relatives, under different environments, characterized by different temperatures. Then the evaluation model must allow fitting the animal´s breeding values as a temperature dependent factor, *i.e.* fitting the interaction between breeding value and temperature, which is a particular case of genotype by environment interaction.

Applied studies on selection for genetic tolerance to heat or on selection for production traits in the presence of heat have usually consider some temperature or index combining temperature and humidity to regress on the genetic effects. In the field of GxE interaction fitting these models are

named reaction norm models (Kirkpatrick and Heckman, 1989), as for each animal a function (norm) is defined, describing how it will performs under the different values of the environment, in this case the norm is indexed by different temperature values. The statistical tools for fitting such features are models where coefficients of the norm are nested to the individuals under study; in these models, for identification purposes, informative priors are assumed for these coefficients. A wide variety of functions has been proposed, either linear or non linear.

The final objective of this study was to assess whether the effect of high temperature on prolificacy, average weaning weight and longevity interacts with the genes involved in the control of these traits. A number of models to account for the interaction between genotype and temperature would be proposed and they would be compared in terms of goodness of fit.

MATERIALS AND METHODS

Animals and data

The animals belonged to the Caldes line which is selected for daily gain during the fattening period. They were bred and reared at the IRTA experimental farm in Caldes de Montbui (Barcelona, Spain). This farm has an insulated roof, walls and cooling ventilation systems to avoid animals' exposure to extreme temperatures; however, because of the not total isolation of the buildings, the indoor temperature records partially reflected the seasonality of the outdoor temperature.

Males and females began their reproductive life at 5 mo and 4.5 mo of age, respectively, and they were bred under a photoperiod of 16 h light per day. Females were served on a semi-intensive rhythm basis, leading to 42 d between subsequent parturitions. Data were collected from November 1983 to October 2008. Natural mating was used for reproduction until June 2003, after that, artificial insemination with hormonal treatment to induce female ovulation and receptivity was used until the end of the study. At parity, the number of kits born alive and stillborn in each litter was recorded. During the whole lactation period, the number of died kits and the date when it occurred in each litter were also recorded. At weaning (32 days of age), litters were weighed.

The analyzed traits were total number of kits born (TB); number of kits alive at weaning (NW); average weaning weight of the litter (avg-WW); and Length of Productive Life (Long). There were a total of 18,491 records from 5,929 does for TB and 16,868 records from 5,353 does for NW and avg-WW; regarding longevity a total of 6,743 records were considered out of which 33.6% were right censored.

Models

In order to assess the magnitude of the interaction between genes and temperature for prolificacy and average litter weight at weaning a Bayesian hierarchical model, with different prior assumptions, was employed. Each record was assumed to follow this conditional distribution.

$$p\left(y_{ij}\middle|\boldsymbol{\beta},\mathbf{a}_i,\sigma_e^2\right) \propto N\left(\mathbf{x}_{ij}\boldsymbol{\beta} + a_{i1} + \max\left\{\left(T_{ij} - a_{i3}\right),0\right\}a_{i2},\sigma_e^2\right)$$

Assuming conditional independence the join conditional distribution of all the records was:

$$p\left(\mathbf{y}\middle|\boldsymbol{\beta},\mathbf{a},\sigma_e^2\right) = \prod_{\nabla ij} p\left(y_{ij}\middle|\boldsymbol{\beta},\mathbf{a}_i,\sigma_e^2\right)$$

In a second hierarchical stage priors distribution where assigned to $\boldsymbol{\beta}$, $\mathbf{a}$ and σ_e^2. For both $\boldsymbol{\beta}$ and σ_e^2 bounded uniform priors were assumed, while four different assumptions were adopted for $\mathbf{a}$ all of them under the same basic form:

$$p\left(\mathbf{a}\middle|\boldsymbol{\alpha},\mathbf{u},\mathbf{P}_0\right) \propto N\left(\mathbf{X}\boldsymbol{\alpha} + \mathbf{Z}\mathbf{u},\mathbf{I} \otimes \mathbf{P}_0\right) \qquad [1]$$

Under a first assumption (**RTr**) $p\left(\mathbf{a}\middle|\boldsymbol{\alpha},\mathbf{u},\mathbf{P}_0\right)$ was assumed to be a normal distribution. A linear change in the animal's performance could be expected only when temperature descriptors reach a certain animal-specific threshold, being possible to observe individual variation both for the threshold

itself and for the degree of change in performance beyond it. $\mathbf{a}$ was a vector formed by the concatenation of the vectors: $\mathbf{a}_1$ (containing individual intercepts or performance in absence of heat) $\mathbf{a}_2$ (individual slopes) and $\mathbf{a}_3$ (individual thresholds). $\boldsymbol{\alpha}$ is a vector of length three, including the mean of each unobserved random variables $\mathbf{a}_1$, $\mathbf{a}_2$ and $\mathbf{a}_3$ for each individual; both $\boldsymbol{\alpha}$ and $\mathbf{P}_0$ were assumed to follow bounded uniform distributions; $\mathbf{u}$ was assumed to follow a normal distribution:

$$p(\mathbf{u}) = N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}_0)$$

Being A the additive genetic relationship matrix and $\mathbf{G}_0$ was the additive genetic variance-covariance matrix. Finally the assumed prior distribution for $\mathbf{G}_0$ was bounded uniform.

In the first hierarchical level the vector of systematic effects $\boldsymbol{\beta}$ included the effect of Management Group (defined by the mating date for TB and by parturition date for NW and Avg-WW) and Phisilogical Status (This factor include the combination between the parturition order and whether the animal was lactating when became pregnant for the case of TB; for ND and avg-WW it included the combination between parturition order and whether the female was pregnant during that particular lactation).

In a second prior assumption (**FTr**) all a_{i3} were assumed to be equal to a constant value previously estimated using the model for fitting overall performances (Sánchez et al., 2009). Under this assumption individual variation was only assumed to exist for the slope beyond the threshold. Thus $\mathbf{a}$ was a vector formed by the concatenation of $\mathbf{a}_1$ and $\mathbf{a}_2$ i.e. intercepts and the slopes; being $p(\mathbf{a}|\boldsymbol{\alpha}, \mathbf{u}, \mathbf{P}_0)$ a normal distribution. Thus $\boldsymbol{\alpha}$ was a vector of length 2 and $\mathbf{P}_0$ is a square matrix of dimension two. The elements of $\boldsymbol{\alpha}$ and $\mathbf{P}_0$ were assumed to follow a uniform bounded distribution. With regard to $\mathbf{u}$ the same assumption as for RTr was adopted, but with the appropriate changes in the dimensions, thus $\mathbf{G}_0$ is now a square matrix of dimension two.

In a third prior assumption (**LIN**) all a_{i3} were assumed to be equal to 1, which is a value lower than any recorded temperature descriptor. Thus, all records would be subject to a linear change no matter the temperature value under which it was produced. In this case the same assumptions as under FTr were adopted for $p(\mathbf{a}|\boldsymbol{\alpha}, \mathbf{u}, \mathbf{P}_0)$ and for the lowest levels of hierarchy.

A fourth prior assumption was considered (**NULL**), in this case all the a_{i2} elements were constrained to be zero (no slope) while a_{i3} were assumed constant and equal to 1. Thus, no interaction between genes and temperature descriptors was considered. $p(\mathbf{a}|\boldsymbol{\alpha}, \mathbf{u}, \mathbf{P}_0)$ was considered to be a normal distribution but now $\mathbf{a}$ only include the individual intercepts, $\mathbf{a}_1$. Under this prior assumption $\boldsymbol{\alpha}$, $\mathbf{P}_0$ and $\mathbf{G}_0$ are scalars, representing the mean of the individual intercepts and the permanent and additive genetic variances. All these elements were assumed to follow a bounded uniform distribution.

For the analysis of longevity the following semi-parametric piecewise constant hazard model was used, following Sánchez *et al.* (2006).

$$h_m\left(d \middle| YS_i(d), EF_j(d), TC_k(d), OPP_l(d), a_{1,m}, T(d), a_{2,m}\right) =$$
$$h_0(d) \times \exp\left\{YS_i(d) + PS_j(d) + BA_k(d) + OPP_l(d) + a_{1,m} + T(d)a_{2,m}\right\},$$

Where the hazard at day d for the animal m was explained by a baseline hazard $h_0(d)$, which was assumed to be a piecewise constant function, with step changes on the death dates; YS, PS, BA and OPP were the time-dependent effects of the Year Season class, of the Physiological Status of the doe, of the number of kits Born Alive in each parturition, and of the ordinal of positive pregnancy test,

respectively. Also it was considered the additive genetic effect, a_1, as well as the effect of an individual regression on weekly average mean temperature ($T(d)$) a_2. These two factors were assumed to be independent and both of them were assumed normally distributed with variance-covariance matrix proportional to the additive genetic relationship matrix.

To assess model performances for prolificacy and average weaning weight, goodness-of-fit combined weight by model complexity was considered. For this purpose DIC was used as criteria.

RESULTS AND DISCUSSION

Table 1 shows goodness of fit (DIC) for the different models and traits. For NW and avg-WW the preferable hypothesis is that under the model RTr, while for TB a linear relationship between gene effects and temperature is preferable. These forms of the relationship between genes and temperature are in agreement with the estimated pattern of the temperature effect of the different traits, observed by Piles *et al.* (2012) (not published yet), *i.e.* fairly linear for TB; with a drop at late temperatures for NW and a clear threshold response with the onset around 20 ℃ for avg-WW.

Table 1: Goodness-of-fit (DIC) for the different models and traits.

	NULL	LIN	FTr	RTr
TB	89841	89822	89826	89833
NW	76621	76588	76609	76244
avg-WW	61465	61395	61439	61121

For that model selected by DIC the estimates of the ratios between additive variances to the total variance in the second hierarchical are presented in table 2. In the same table are presented the estimates of the effective heritabilities (Yazdi *et al.,* 2002) for both intercept and slope for the longevity trait.

Table 2: Heritabilities estimates for the different trait under the DIC selected model.

Parameter	TB	NW	avg-WW	Longevity
h^2_1	0.18(0.08)	0.07(0.03)	0.08(0.02)	0.43(0.03)
h^2_2	0.00(0.00)	0.02(0.01)	0.01(0.01)	0.00(0.00)
h^2_3		0.09(0.06)	0.06(0.03)	

By checking the estimates of heritability it can be see that for TB the magnitude of the GxE interaction is low, as h^2_2 is null. For NW the magnitude of h^2_3 is medium but this estimate was very imprecise. Thus, results must be interpreted with caution despite DIC favors RTr model. avg-WW is the trait that can be said to be the most strongly subset to gene effects by temperature interaction, being more important this interaction at the level of the individual onset of heat effects than at the level of drops in avg-WW beyond this threshold. For avg-WW the estimated genetic correlation between intercepts and both, slopes and threshold were unfavorable but imprecise: -0.60(0.27) and -0.63(0.42), respectively. For the case of NW a negative value was estimated between intercept and slope, -0.53(0.34), being the estimate between intercept and individual thresholds close to zero: -0.04(0.47). For this trait both estimates show a large error. Regarding the genetic correlation between slopes and threshold for awg-WW and NW positive and high value were estimated, 0.74(0.16) and 0.78(0.19), indicating that by selecting for one of them the other will be modified on the desired direction.

For longevity, similarly to TB, the magnitude of the interaction between genes and temperature does not seem to be important. In this case DIC was not computed but the effective heritability for the slope was nearly null. The results for this trait have to be considered with caution because the model for the analysis assumes intercepts and slopes to be independent which is an important constraint. In fact

when a regular animal model was fitted, excluding the individual regressions on temperature, the effective heritability drops to 0.38(0.03).

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