

Genetic Control Of Prolificacy And Weaning Production Traits In Rabbits Shows Interaction With In Farm Temperature

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Introduction

Temperatures out of the limits of the animal's thermoneutrality adversely influence reproduction and reduce resistance to diseases and animal welfare. Rabbits are very sensitive to high temperatures since they have few functional sweat glands, limiting thus their ability in eliminating excess body heat, when the environmental temperature is high (Marai et al., 2002). Usually the existence of extreme temperatures inside the farm is avoided through the insulation and the use of cooling and ventilation systems. A complementary approach could be to raise animals' tolerance to heat; this strategy may be particularly interesting in some regions or developing countries where access to technology is difficult, or in situations of high cost of energy. This can be achieved by using animals from breeds or crossbreeds that are tolerant to heat, but this strategy is difficult to implement if high efficiency of production is also required. An alternative is genetic improvement for heat tolerance but there is a complete lack of information concerning within population genetic variability for this trait. The objective of this research was to assess whether the observed additive genetic variation for prolificacy and weight at weaning traits depends on some descriptor of temperature, which would indicate the existence of genetic variation for heat tolerance.

Material and methods

Animals. Data from the Caldes line (Piles et al., 2005) were used, this line is selected for growth rate since 1984 and it is housed in an experimental farm placed in Caldes de Montbui (Barcelona), Spain. Data relates to the period between its founding and October 2008. The analyzed traits were prolificacy traits: total number of kids born (**TB**), number of kids born alive (**BA**), number of kids alive at weaning (**NW**); and litter weight (**litW**) and individual average weight at weaning (**avWW**). There were a total of 18,491 records for TB and BA from 5,929 females, and 16,868 records from 5,353 females for NW, litW and avWW. Pedigree files had all the information about animals' relationships from the origin of the line, including 7,082 and 6,497 individuals for the analysis of prolificacy and weight traits, respectively. More details on the breeding and management of this line can be found in Piles et al., 2005.

Temperature measurements. Temperature was daily recorded with a maximum-minimum thermometer since 1995 until 2005, then the farm was provided with automatic temperature recorders. Temperature records before this period and in the days when they were not recorded were predicted using second degree polynomial regression equations using as

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predictors the temperatures outside of the farm, which were obtained from a public weather station situated in the same experimental center as the farm. The coefficients of determination of the equations for predicting minimum, mean and maximum daily temperatures were higher than 0.90. From these data, several descriptors of temperature at different sensitive days or periods of the female reproductive cycle were obtained and the association between them and the studied traits was estimated in a set of preliminary analyses. After them it was decided to use for the analysis in this study the maximum temperature at the mating day and at the parturition day since they showed the strongest linear relationships with the considered traits, although the magnitude of these associations were low.

Statistical models. Three types of Bayesian models were employed in this study. A regular animal repeatability linear model (**M0**) which was considered to represent the null hypothesis, i.e. additive genetic and permanent environmental variances do not show dependence on the temperature. In this model the considered systematic effects were: i) the physiological status of the female at mating (3 levels: nulliparous, lactating multiparous and non lactating multiparous) and ii) the day in which AI or Parturition (depending of the trait under study) took place; which defines groups of females under the same management and environmental conditions.

The previous model was extended to include a linear regression effect on the recorded temperature; this regression was nested both within the additive genetic and the permanent environmental effects (**M1**). Within a frequentist framework, this model is usually called repeatability random regression model. The same set of systematic effects was considered. Both for **M0** and **M1** standard prior assumptions were adopted (Sorensen and Gianola, 2002). Finally two hierarchical models were employed to assess other than linear dependence of the additive genetic and permanent variances on the temperature; in these models it was assumed constant variances up to a certain value of temperature, beyond which this variance was allowed to be different. This was achieved by fitting a linear change in the additive genetic and permanent environmental effects beyond such a threshold temperature. In one of these models a unique threshold value was assumed for all the animals (**M2**), being this threshold a random variable in the other model (**M3**). Details on these models can be found in Sanchez et al. (2009). In addition to these hierarchical models, the hierarchical counterpart of model **M1** was fitted, by constraining the unique threshold to the minimum temperature in the data set (**M1-h**).

Models were compared using DIC (Spiegelhalter et al., 2002) and the MCMC process to generate marginal posterior samples comprised 500K rounds with a burning period of 50K. Afterward 1 in each 50 samples were retained and therefore statistic from marginal posterior distributions were computed with a total of 9000 samples.

Results and discussion

For the five studied traits and for the two considered temperature descriptors model **M1** was always preferable (based on DIC results, the lower the best) over model **M0**. This indicates that the hypothesis of a linear dependence of the additive genetic and permanent environmental effects on these temperatures is more likely than constant values of these effects for the whole range of recorded temperatures.

Regarding the hierarchical models, that assuming a random onset of heat stress (M3) was never better, in terms of DIC, than that assuming a constant onset of heat stress (M2). However, when the last model (M2) was compared with the hierarchical counterpart of model M1 (M1-h) either no differences or differences clearly favoring the model assuming an entirely linear relationship were observed. The only exception to this rule was observed for ND when temperature at AI was considered, for this case the model assuming that the onset of heat stress starts at 24.12 degrees was favored (DIC 33 units lower) over M1-h. Also for all the traits better DIC results were obtained when temperatures at AI day were consider as regression variable than when it was used the temperature at parturition day (Table1). These results indicate that maximum temperature of the AI day was the one that more strongly interacts with the genetic variability of the considered traits. This is true even for traits like avWW and LitW, which could be said to have two components, one related to the weight gain during weaning and the other related with prolificacy.

Table 1: DIC by traits, models and temperature descriptors

	TB	BA	NW	LitW	avWW
Max. temperature at AI day					
M0	89841.35	93752.78	76648.18	60588.33	61393.91
M1	89821.96	93720.73	76583.58	60441.98	61209.68
M1_h	55837.56	59738.66	45583.00	29522.98	30396.07
M2	55848.79	59735.28	45550.44	29523.44	30578.48
M3	60926.92	60984.21	45599.94	34472.31	30147.66
Max. temperature at Parturition day					
M0	89841.35	93752.78	76648.18	60588.33	61393.91
M1	89836.21	93733.69	76575.85	60480.52	61279.34
M1_h	55849.98	59749.13	45575.50	29563.85	30470.84
M2	55849.79	59751.17	45602.85	29603.51	30538.25
M3	55642.31	61983.27	45676.25	32556.92	32011.25

Figure 2 shows, according to M1-h, the pattern of change of heritabilities as functions of maximum temperature at the mating day. Fairly linear changes for these parameters were observed, being litW and NW the traits showing the greatest changes in heritability, around 0.12, from 13 °C to 30 °C. For TB and BA the magnitude of the change was 0.07 and 0.09, respectively. avWW was the trait with a genetic control less related to temperature since the heritability only changes from 0.16 to 0.21.

This is the first assessment of the interaction between genes and farm temperature in rabbit. We conclude that a complete linear relationship between the temperature and both permanent environmental and genetic effects is preferable over a constant value for these effects within the considered temperature range. In other species other relationships have been assessed, for example M3 has been shown to be applicable for fitting heat stress in dairy cattle (Sánchez et al., 2009), and frequentist versions of M2 have been considered to be appropriate for fitting the changes in the genetic control of growth in pigs as functions of indexes combining temperature and humidity (Zumbach et al., 2008).

In our case the sizes of the data sets were relatively small, if we consider the information required for properly estimating the parameters involved in complex models, like M2 and M3. In addition to the actual biology of the relationship between temperature and genetic

variability this could be also a reason why we have not observed an appropriate behavior of those more parametrized models.

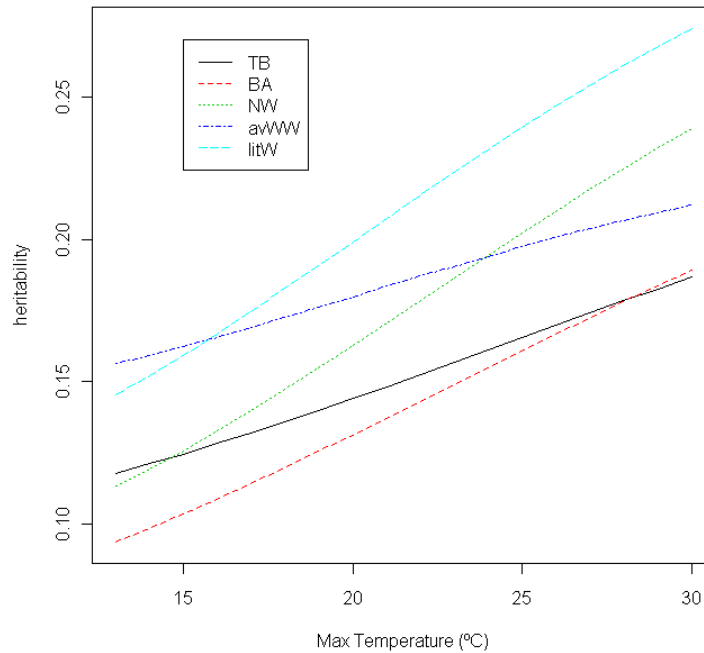


Figure 2: Heritabilities as function of Max. Temperature of the mating day

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