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Characterisation of Goats' Response to Heat Stress: Tools to Improve Heat Tolerance

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Abstract

This chapter aims to review present knowledge about the effects of heat stress on goats, summarising what is known about its measurement, its impact on the performances of the animals, mainly milk traits, the physiological and genetic bases of the animals' response and the improvement of resilience through selection. A short historic review of the climatic indexes used to measure heat stress, with special emphasis on the temperature humidity indexes, and the main consequences on milk yield and composition are followed by a description of the results of experiments carried out to study the physiological and metabolic consequences of heat stress. The results of the quantitative analyses of the genetic bases of heat stress using norm of reaction models and of the application of omic techniques, particularly transcriptomic and genomic, to understand the complexity of the genetic background of animal's reaction to thermal stress, constitute the next points. The chapter ends treating the possible ways and difficulties of applying selection to increase resilience to heat stress.

Keywords: heat stress, physiological response, genetic analysis, selection for resilience

1. Introduction

The extraordinary results obtained through artificial selection in all domestic animals had some undesirable side effects, such as low reproductive efficiency, increased susceptibility to diseases and higher sensitivity to sudden environmental changes [1]. In particular, artificial selection to increase milk yield has been proved to reduce heat tolerance in dairy cattle [2, 3] and dairy sheep [4]. Heat stress (HS) has also been proved to be one of the main causes of economic losses

[5, 6]. Temperature increase and rainfall reduction are expected during the next decades in many areas of the world and, particularly, in the Mediterranean region, where the largest part of goats in Europe are raised [7]; therefore, knowledge of the physiological and genetic bases of the response to the consequences of climate change is needed to reduce its impact. The study of physiological indicators and the quantification of the genetic variation of the response to HS, as well as the genomic and other –omic analyses to find candidate genes involved in this response and the changes in gene expression so induced, allow for the identification of animals with a positive response to HS and the design of methods to select them.

Research works described in this chapter aimed to ascertain the effects of HS on milk traits and to study the physiological and genetic bases of these effects in order to allow for the inclusion of resilience to HS as a new goal in the selection programmes of three Spanish breeds of goats.

2. Climatic indexes and characterisation of the effect of heat stress on milk and reproduction traits in goats

In order to know the effects of HS on production, a measurement of the climate effect on the animal comfort is needed. The first index, specifically developed for animals, to measure the stress produced by some climatic conditions was the Iberian heat tolerance test (HTC) [8], which was used to assess the heat tolerance of cattle by measuring how much rectal temperature exceeds the normal value of 101.0°F (38.33°C). Heat tolerance was determined by the value of HTC, so the higher the HTC the more heat tolerant the animal is perceived to be. This index was followed by other indices such as the coefficient of adaptability [9], the biochemical index of heat tolerance [10], the discomfort index [11] or the milk production decline index [12].

Johnson et al. [13] showed for the first time the relation of temperature and relative humidity with comfort and dairy performance in cattle, which is the base of the combination of temperature and relative humidity in an index, called temperature humidity index (THI). Some adaptations of the previously described indexes had followed (e.g. Bianca [14] adapted the HTC index to express rectal temperature in °C), Kibler [15] being the first to use an index with the current THI philosophy for livestock. The index was later refined on a number of studies. Berry et al. [12], for example, incorporated dry and wet bulb temperatures to the index. Since then, the THI (in its various formulations) has been widely used to assess the response of animals to heat stress.

Heat balance is a complex phenomenon affected by numerous climatic factors (e.g. ambient temperature, relative humidity, wind speed, radiant heat and other factors such as altitude), animal factors (e.g. age, genotype, hair coat characteristics, degree of acclimatisation, health status, physical activity, level of performance, reproductive state, etc.) and management factors (e.g. housing, provision of shade, fans and others). However, in its usual formulation, the THI index only reflects the influence of the temperature and humidity to which the animal is subjected, without considering other important effects such as thermal radiation (solar and long-wave), wind speed or the duration of the exposure to these conditions. The reliability of using THI to predict animal responses to thermal stress has been examined in Refs. [3, 16–18], showing all of them some limitations of the index, the major one being that it does not account

for solar load or wind speed [19], parameters of great impact on animal physiology, especially in grazing species. In addition, it does not take into account the breed, the genotype or other animal differences (e.g. age, level of production). Gaughan et al. [20] concluded that the THI may not adequately describe the effect of hot climatic conditions on livestock (and much less on the effects of cold conditions). Furthermore, with the exception of the case of cattle, most THIs have not been specifically designed for their own species (and much less for a specific breed exploited in certain geographic and climatic conditions). Thus, in the case of the goat species, the scarce number of studies carried out so far has used THI formulations developed for beef and dairy cattle, with the exception of the works carried out by our research group [21–24] in which a modification of the THI developed for sheep exploited under Mediterranean environmental conditions by Finocchiaro et al. [4] was used. Only very recently the feasibility and the validity of a heat stress score specifically developed for intensive dairy goat farms has been tested [25].

It is generally recognised that goats are more tolerant to HS than sheep, and both are superior to this respect than cows, due to the morphological and physiological differences between these species related to heat dissipation [26]. However, it is also well known that high temperatures and relative humidity values affect productivity of small ruminants [27, 28]. As opposed to the case of dairy cattle, few woks have dealt with the effects of HS on milk yield and composition in goats. In several studies lately carried out to quantify these effects on native breeds of goats, Murciano-Granadina and Payoya [21], Florida [22], Malagueña [29], raised mostly in the South of Spain, it has been observed that the animals are exposed to stressing climatic conditions, due to high temperatures, during 45–55% of the year (**Figure 1**), generating losses of 1.9 and 3.1% of annual fat plus protein yields in Murciano-Granadina and Payoya goats, respectively (**Figure 2**). Sano et al. [30] found milk yield losses of 3–13% in dairy Saanen goats exposed to moderate or severe HS for 4 days (THI, 81 or 89), respectively. Brown et al. [31] reported that
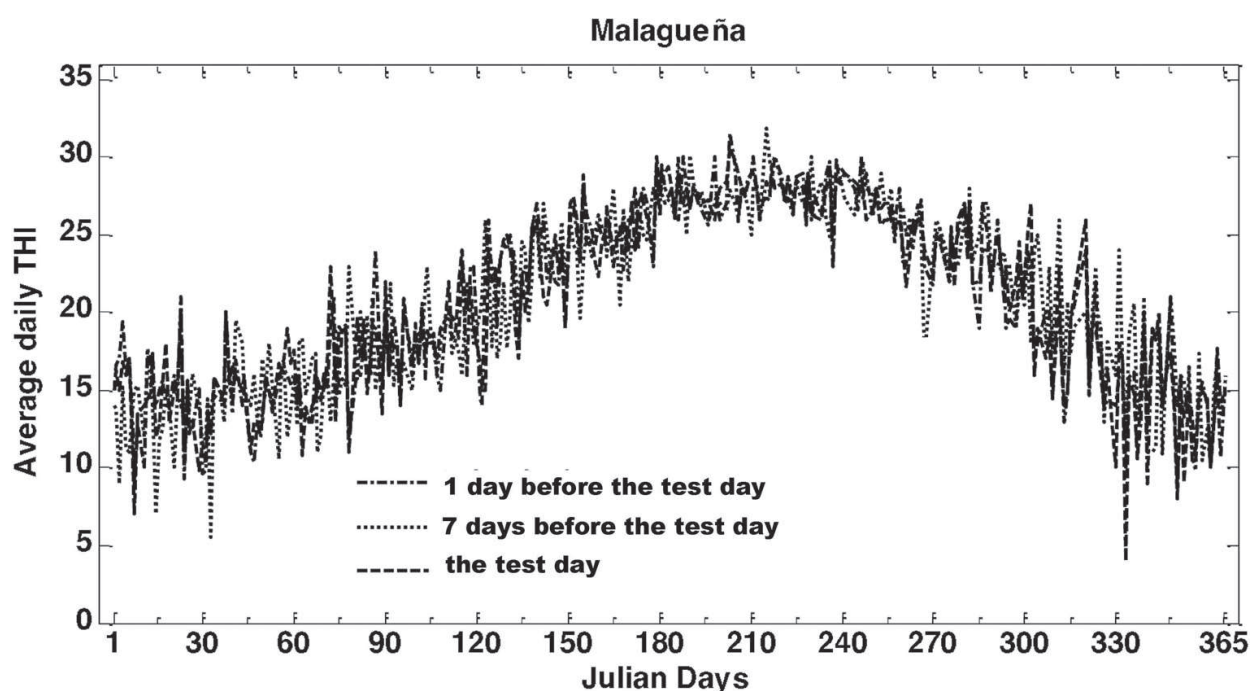

Figure 1. Evolution through the year of THI values in the South of Spain (from Ref. [22]).
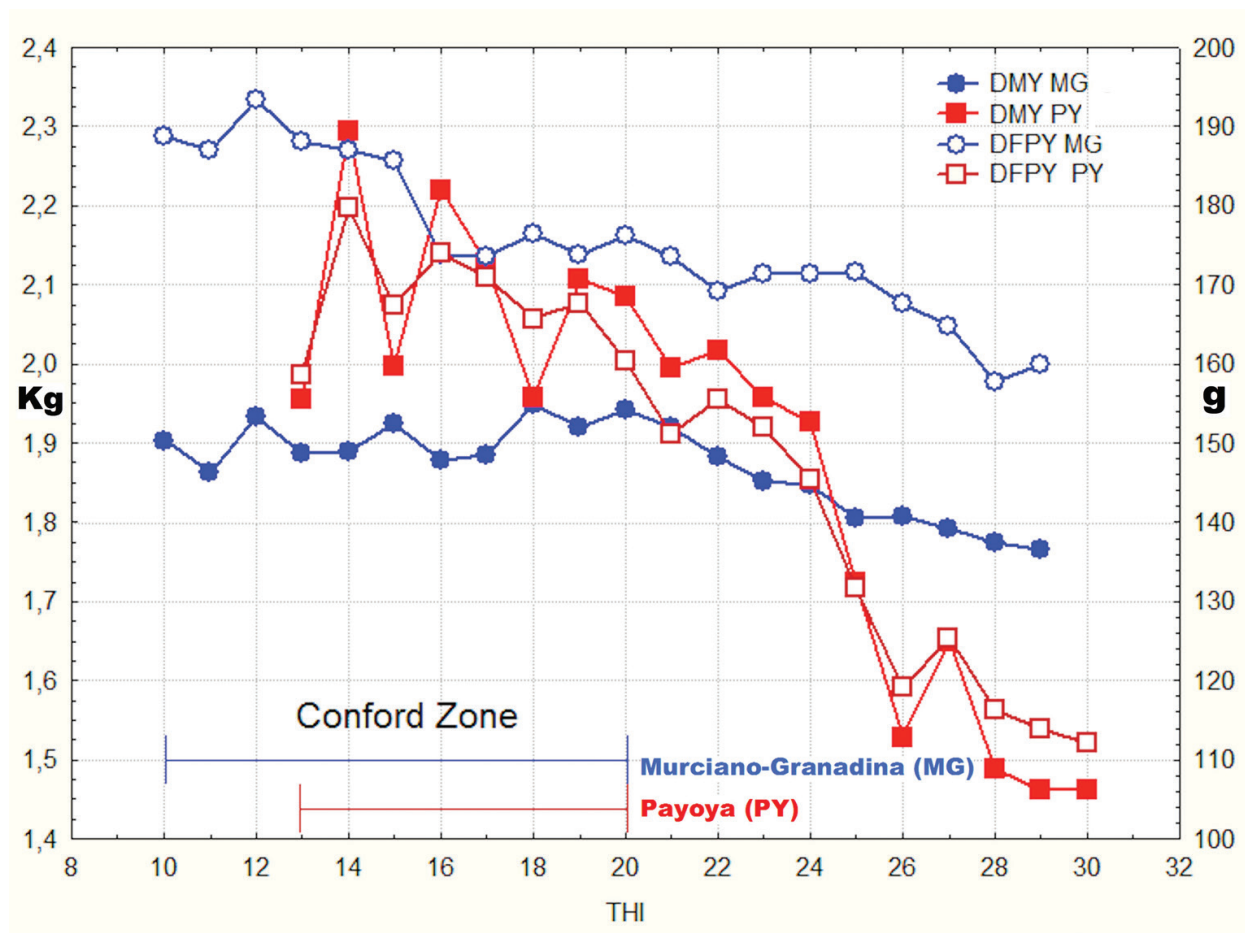
Figure 2. Graph of daily kg of milk yield (DMY) and g of fat plus protein yield (DFPY) as a function of THI for Murciano-Granadina (MG) and Payoya (PY) goats (from Ref. [29]).

the exposure of dairy goats to moderate HS conditions (THI = 79) decreased milk yield in Alpine but not in Nubian goats. Differences in the genetic potential for adaptive traits and also for production might explain these differences.

3. Physiological and metabolic response to heat stress under controlled conditions

Animals respond to HS reducing feed intake to decrease metabolic heat production and launching heat dissipation mechanisms like increased perspiration and respiratory rate. The combined effect of lower dry matter intake (DMI) and higher energy expenses to maintain body temperature may provoke a negative energy balance and a deficit of nutrients with negative effects on production and reproduction, as well as on the animal health status. In dairy cattle, only 40% of the reduction of milk yield has been proved to be due to a lower feed intake [32, 33]. Heat stress is accompanied by metabolic changes that are also responsible for the decrease in production. In dairy goats maintained in climatic chambers to generate a

HS situation (THI = 77–85), results shown in Refs. [34, 35] indicate that although a substantial reduction in DMI (22–35%) coupled with an increased rectal temperature (+0.58 °C) and respiration rate (+48 breaths/min) were observed, reduction in milk yield was relatively low (3–10%) with reduced contents of fat, protein and lactose. As in cattle, the reduced intake was not accompanied by increasing levels of non-esterified fatty acids (NEFAs), which is typical in feed-restricted animals under thermal neutral conditions. In cattle, this seems to respond to a shift in the energy metabolism from using fat to using glucose as main fuel under HS [32, 36]. In dairy goats, the lack of fat mobilisation was not accompanied by decreased glucose levels and increased levels of insulin as it is in cattle [34, 35]. These authors launched several hypotheses to explain this different behaviour in goats, one of them being that the pancreas of HS goats is less sensitive, which could be a way to maintain normal glucose levels in blood. Overall, the effect of heat stress on goats seems milder than in highly producing dairy cattle and the metabolic consequences may be attenuated with respect to those in cattle.

The effect of HS on reproduction takes place through a reduction of oestrus duration and intensity [37, 38], malfunction of the axis hypothalamus-pituitary-ovary and low quality of the oocyte [39], anomalous spermatogenesis [40] and a bad embryo development [39, 41, 42]. Among the effects of HS on the health status is a higher risk of mastitis [43], but it is not clear that this is due to a direct action of the stress on the animal immune system or to higher rates of proliferation and survival of pathogens [26].

According to Silanikove [28], rectal temperature is the best physiological indicator of HS. Heritabilities between 0.12 and 0.22 were estimated for rectal temperature by Prayaga and Henshall [44] in Australian beef cattle and an estimate of 0.17 was obtained by Dikmen et al. [45] in dairy cattle. These heritabilities permit to expect a positive response to decrease rectal temperature under HS conditions, as it was proven by Burrow and Prayaga [46] in a selection experiment also carried out in Australian beef cattle. However, rectal temperature is not an easy trait to be routinely registered in a large population; therefore, most of the quantitative genetic analyses of the response to HS have used bioclimatic indexes reflecting the level of thermal comfort of the animal. One of the most used is the formerly described temperature humidity index (THI) combining dry bulb temperature and relative humidity, proposed by Kelly and Bond [47].

4. Quantitative genetic analyses of individual reaction norm

The current approach to the quantitative genetic analysis of the response of milk traits to HS uses frequently random regression models based on the concept of norm of reaction: the different phenotypic expressions of a gene in different environments [48]. The magnitude of the change in the value of a given trait from one environmental condition to another measures the plasticity of an individual for a given trait and it is also a measure of the genotype by environment interaction. According to their norm of reaction, animals can be classified as stable or robust for a certain trait if the value of that trait remains constant through the range of values of the environmental variable and unstable or plastic if the value of the trait changes.

These models include two types of quantitative variables: the test-day values of milk traits (yield, contents of fat, protein or any other milk component) registered periodically to each animal in each farm and the values of a certain climatic variable (most frequently THI) registered in meteorological stations located the closest the possible to the farm. Misztal [49] and Ravagnolo et al. [50] were the first to apply this methodology for the estimation of the genetic components of the response to HS in dairy cattle. The model proposed by Misztal presented the test-day milk yield as a function of the THI with an independent term or intercept, standing for general genetic component of the trait, and a random coefficient or slope, representing the specific response of daily milk yield to a unit increase in the THI, which can be considered a measure of the susceptibility to HS. This model has been later modified including an individual threshold value of the climatic index considered, below which the animal is in a comfort state with no effects of HS. This threshold is different for each animal [51, 52].

Quantitative genetic analyses of the response of milk traits to HS in small ruminants are scarce, as opposed to those in dairy cattle. The first study carried out in small ruminants presented the results of a study on dairy sheep in the Mediterranean region [4], showing similar results to those observed in dairy cattle. The first application to the study of the effects of HS on milk traits in goats was performed in the region of Andalusia, in South Spain, in a native dairy breed (Payoya) raised under semi-extensive conditions [53]. A modified version of Finocciaro's THI and the selection criterion of the breeding programme of the breed (protein plus fat yield) were used as climatic variable and as quantitative trait, respectively. Genetic variation for the response to the increasing values of THI was found, with some animals showing a stable genetic response through the range of values of THI and others showing a significant reduction of their breeding value for the trait under HS conditions.

Later studies went deeper into the analysis of the response of milk traits to HS in other native Spanish breeds: Murciano-Granadina, Malagueña, Florida and Payoya (**Table 1**). A real comfort zone under a given THI value cannot be observed, but a smooth increase of the level of production up to 20–30 units of THI and a negative slope afterwards as a consequence of HS was found. The estimated average loss of fat plus protein yield as an effect of HS ranged between 1.9 and 3.1% [21]. It is easy to understand the importance of the economic loss in a region in which the animals might be under HS condition an average of 140 days per year. Menéndez-Buxadera et al. [21, 29] described the change of the components of the genetic variation, the heritability (h^2) and the estimated breeding values (EBVs) throughout the scale of values of the THI.

	Murciano-Granadina	Malagueña	Florida	Payoya
Years	2000 – 2006	2006 – 2012	2006 – 2012	2002 – 2007
No. of milk records	63,640	160,067	129,450	81,625
No. of animals in pedigree	6037	14,089	12,268	9917
No. of herds	20	17	20	18
Average daily milk yield (kg)	2.06 ± 0.93	2.01 ± 0.96	2.30 ± 1.10	1.89 ± 0.83
Average daily fat + protein yield (g)	176.4 ± 80.48	191.60 ± 82.13	189.20 ± 83.2	161.6 ± 71.0

Table 1. General statistics of the data used in the heat stress studies of native Spanish breeds of goats (from Refs. [22, 29]).

The general form used in these works for the estimation of the variance components is a random regression model including the combination of herd and date of recording of the trait, the combination of age and parity number, the number of kids born, and a fixed function of the covariables of the THI trajectory (modelled with a Legendre polynomial) as fixed effects, and the additive genetic function of the animal with milk records and their parents without data, the permanent environmental function of the animal with milk records through the THI trajectory (modelled with Legendre polynomials) and the residual (with homogeneous variance) as random effects. With the variance components estimated in these analyses, it was possible to compute the heritability (h_i^2), genetic correlations ($r_{a_{ij}}$) for each trait and for all points (i and j) of the trajectory of the THI values and the EBV for any animal with milk records or without milk records if it is in the pedigree.

The main results obtained are similar in the four studied breeds and they can be summarised as follows:

1. In general, the genetic variances for the intercepts (defining the overall genetic value for the trait that does not change with the heat load) of the functions of responses of milk traits to THI were much higher than those of their slopes (specific HS tolerance). The genetic covariances between intercepts and slopes were negative, indicating that high-yielding animals are less tolerant to HS. The covariances between the intercepts and the slopes for the permanent environmental effects were also negative.

2. Heritability estimates varied through the scale of values of THI, as can be seen in **Figure 3**. The pattern is very similar in all four breeds; therefore, only the estimates of h^2 in Murciano-Granadina and Payoya goats are presented in **Table 2**.

3. Genetic correlations between adjacent points in the THI scale are high (over 0.90), whereas these values are low between distant THI points, reaching values below 0.80 which is the threshold value proposed by Robertson [54] as indicative of a significant genotype by environment interaction (G×E). This implies that the genetic potential for production under hot and cold conditions is ruled by at least partially different genetic backgrounds. The ratio between the variances of the slopes and the intercepts indicates the magnitude of this interaction. **Figure 4** presents the values of genetic correlations (r_g) throughout the THI trajectory in Malagueña and Payoya breeds. Permanent environmental correlations (r_p) between pairs of points in the THI scale showed a similar pattern to those of r_g. The pattern of these correlations is an indicator of the persistence of the expression of the performance of the animal through the THI conditions. Differences between the four studied breeds were observed to this respect, PY being the breed with a better ability to adapt to stress conditions. This breed is raised under a semi-extensive production system and its average milk yield is lower than that of the other breeds which are raised under more intensive conditions.

4. The EBVs are not constant throughout the range of values of THI, as can be seen in **Figure 5**, which represents the evolution through the scale of values of THI of EBVs of the 100 animals of Murciano-Granadina breed with the highest EBVs at THI = 31 (a value corresponding to HS conditions) and the 100 animals with the lowest EBVs at the same THI. Three types of responses to THI were observed: non-tolerant animals, with their EBV decreasing as THI increases; robust, with EBV independent of THI and tolerant, with EBV increasing as THI increases.
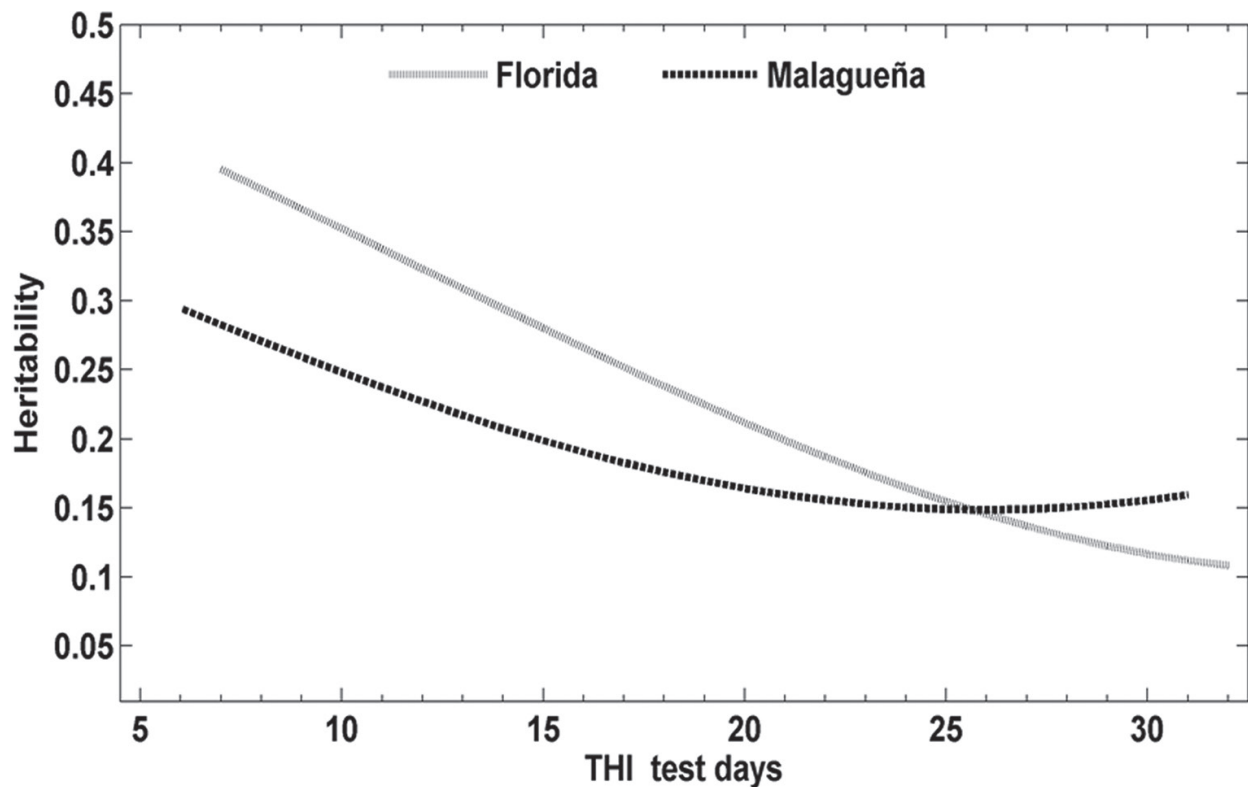
Figure 3. Change of the estimates of h^2 along the scale of values of THI in Malagueña and Payoya breeds (from Ref. [22]).

As a consequence of the differences in the estimates obtained for the variance components and the EBVs along the scale of THI values, any of the studied milk traits cannot be treated as the same trait throughout this scale. This is particularly important in respect to the estimation of breeding values, because the conventional methods of estimation are ignoring these differences and estimating these values at a fixed THI value; therefore, not tolerant animals might be selected. This genetic variability for the response to climatic conditions can be used to select the most adequate animals (tolerant or robust) to cope with future climate changes.

	h^2 comfort	r_g between zones	h^2 stress
Murciano-Granadina			
DMY	0.27–0.30	0.69–0.85	0.22–0.28
DFPY	0.21–0.23	0.71–0.85	0.20–0.22
Payoya			
DMY	0.21–0.22	0.71–0.90	0.22–0.24
DFPY	0.19–0.20	0.72–0.91	0.20–0.21

Table 2. Range of heritability (h^2) values of daily milk yield (DMY) and daily fat plus protein yield (DFPY) in the comfort and stress thermic zones and genetic correlation (r_g) between zones in Murciano-Granadina and Payoya goats (from Ref. [29]).
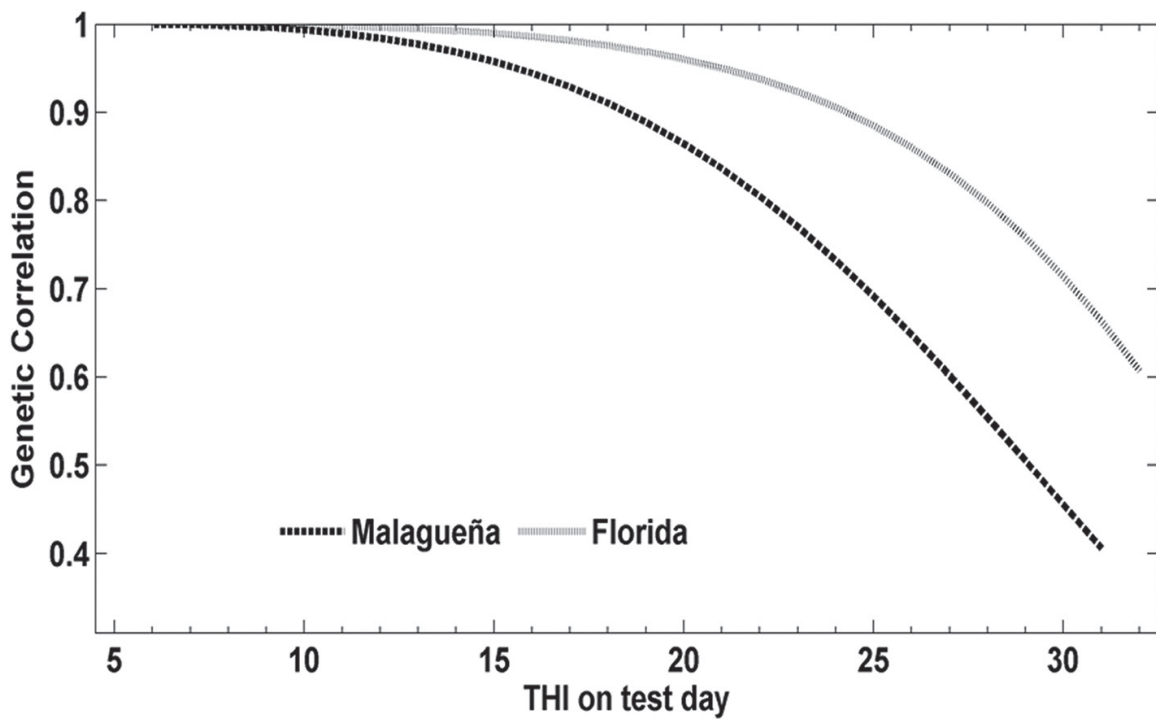
Figure 4. Genetic correlations of daily fat plus protein yields at THI = 7 and the same trait at all other values of THI in Florida and Malagueña goats (from Ref. [22]).
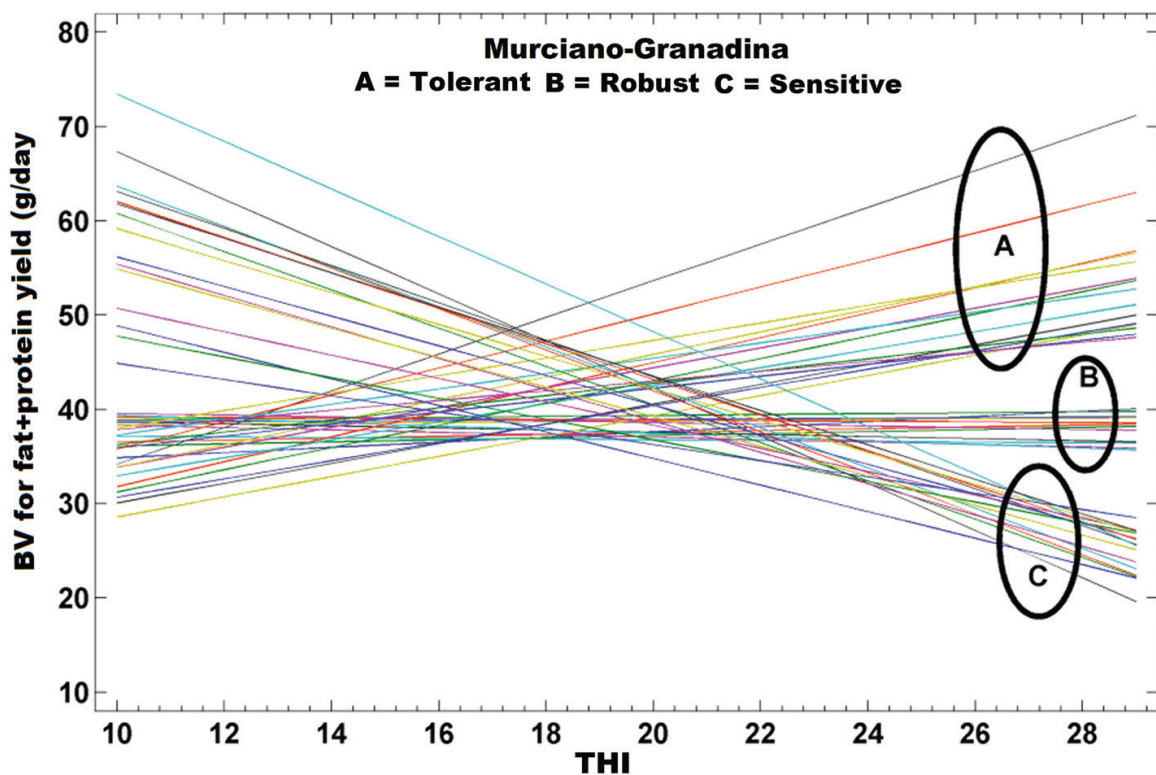

Figure 5. Evolution through the scale of THI values of the EBVs of the 100 animals of Murciano-Granadina breed with the highest EBV at THI = 30 and the 100 animals with the lowest EBV at the same THI (from Ref. [55]).

5. –Omic techniques to analyse the response to heat stress

Quantitative genetic analyses presented earlier have been used for the assessment of the animals' response to HS through its effect on milk production and fitness traits [21]. As a result, we can conclude that the genetic component of response to climatic constraints is not negligible and, therefore, to include traits related to thermotolerance of the animals in breeding programmes may help to face the challenge of climate change on goat production.

The development of -omic technologies has provided some powerful techniques to characterise the response of the animal to HS, either by evaluating (co)-expression patterns of genes in specific tissues [34, 56] or as a tool to understand the complexity of the genetic background of animal's reaction to thermal stress.

Several studies to dilucidate the genetic mechanisms underlying the response to heat stress have been performed using metabolic cages analysing patterns of gene expression occurring in blood and milk with either microarrays or RNA-seq. In blood, Hamzaoui et al. [57] using Affymetrix GeneChip Bovine in Murciano-Granadina goats in late lactation identified 39 and 74 genes whose expression was up- and down-regulated, respectively, by HS ($P < 0.05$). These genes were mainly related to biological processes and, to a lower extent, to molecular functions and cellular components. Moreover, ingenuity pathway analysis detected important pathways related to cell proliferation and death, free radical scavenging, inflammatory response, lipid metabolism and glycolysis/gluconeogenesis. Transcription regulators affected by HS were SATB1 (global chromatin organiser) and PPARD (which might be related to insulin resistance). The HS elicited changes in gene expression related to transcriptional regulation and metabolic processes. On the other hand, gene expression in milk cells has also been studied using RNA-seq by Salama et al. [35]. These authors have showed how decreases in protein and fat in milk composition are accompanied by downregulation in the gene expression of casein, fat and lactose synthesis and upregulation in the expression of genes related to milk cathepsins. This is an evidence of how findings in quantitative studies are the phenotypic expression on the underlying genetic mechanisms.

In parallel to transcriptomic analyses, a number of genome-wide association studies (GWAS) have been run mostly in cattle with the objective of identifying genomic regions associated with the signs of response to HS, based on production traits [58, 59], or physiological signs such as respiration rate or rectal temperatures [60]. Ideally, joining transcriptomic and genomic information together will help to find causal mutations (eQTLs) useful to address an effective selection favouring thermal tolerance in livestock.

A comprehensive review of the main challenges of performing GWAS analysis for HS response in dairy ruminants can be found in Carabaño et al. [61]. These authors highlighted the difficulty of dealing with milk recording data to find a phenotype measuring heat-stress response independent from milk production level in dairy production (cattle, sheep and goats). Separating production level from tolerance to thermal stress is very complex in dairy cattle because both components show a high correlation but not as much in sheep and goats [61]. Principal components analysis can be used to find variables related with heat tolerance independently from production level [59, 62].

A number of studies conducted to detect genomic regions and genes associated with heat tolerance via GWAS, mainly in cattle [58–60], have pointed at genes coding for fibroblast growth factors (FGFs), dehydrogenase-reductase member 3 (DHRS3), involved in the embryonic development in humans, and junctophilin 1 (JPH1), whose expression has been found to be upregulated in the hypothalamus of chickens subjected to HS, as candidate to be associated with HS. Carabaño et al. [61] using a GWAS approach have also validated some of the gene families already found in the literature in relation to HS, such as heat shock proteins (HSP, DNAJ), heat shock protein factors (HSF), mechanisms of immunoresponse (IL and CD) or NADH dehydrogenase (NDUF) families, FMO and FDF coding for growth factor relevant in the remodelling of the mammary gland after lactation. These findings corroborate the complexity of HS effect, involving apoptotic, immunological and metabolic responses.

Less attention has been paid on this topic in goats, as evidenced by the lower number of studies found in the literature. The extensive nature of its production system and the lower production level compared to dairy cattle have led to the belief that HS effects would be lower in this species. Genes found to be associated with response to HS in goats include HSP genes, genes associated with production traits, regulating respiration rate or playing roles in heat generation among others. Thus, Zidi et al. [23], conducting a GWAS analysis in a Spanish local goat, identified an HSP gene, the kappa casein gene CSN3 and some genes encoding enzymes such as malic enzyme (ME1) or acetyl-coenzyme A carboxylase alpha (ACACA). Though candidate genes were coherent with what is expected, the approach followed for this analysis somehow favoured the presence of false-positive signals because the slope used as a pseudo-phenotype in the GWAS analysis was estimated based on EBVs obtained from a reaction norm model without de-regressing them [63]. In another study on Egyptian desert sheep and goats, Elbeltagy et al. [64] found the GRID2 neurotransmitter receptor as genes associated with HS, affecting neuronal apoptosis and PDLIM5 (ontogenesis), or the SLC27, NR2F6 and DRD2 that have been found to be associated with heat generation and detection of temperature stimulus or homeostatic processes. Finally, Carabaño et al. [61] found a relevant signal for fat and protein yields response to heat common to the three dairy species (cattle, sheep and goats) pointing out to a region in Chromosome 6 where a gene encoding a member of the potassium channel-interacting proteins (KCNIP4) that regulate processes of defence against hypoxia and associated to hyperactivity disorders in humans.

Future works on -Omics could contribute to develop powerful tools to select animals not reactive to thermal stress; however, finding phenotypes of thermal response is still a handicap. Genome analysis of HS response should take advantage of the new technologies recently implemented for measuring biomarkers and proxies of thermotolerance in animals.

6. Improving resilience to heat stress

The studies on the genetic variability of the response to HS in dairy cattle [50] opened the opportunity to reduce the unfavourable effects of that stress on milk yields through selection, which represents a relatively cheap way (once milk recording and weather data are

available) that can complement the ways of reducing temperature in farms through costly heat abatement systems. Formerly described results show that applying random regression methods to the data from milk recording, together with the climatic information from the meteorological stations close to the farms, goats can be genetically evaluated for their response to HS and robust or tolerant animals can be selected. Selection criteria can focus on increasing the tolerance threshold or the slope of decay of the considered trait, but the estimation of the genetic value for the threshold of tolerance of each animal in goats is not easy due to the scarce and noisy information available (only six- to eight-test day per lactation) [61]. However, in all studies, in both dairy cattle and goats, it has been found that most of the observed variability of the response is associated to the production level (the intercept coefficient of the response) and only a small fraction of the variation is associated to the slope coefficient. Furthermore, there is an antagonistic relation between the intercept and the slope. Therefore, selecting for a lower decay of yield (lower negative or positive slope) would lead to a negative effect on the level of production. Carabaño et al. [61, 62] have proposed using canonical variables resulting from the eigendecomposition of the additive genetic random regression coefficient (co)variance matrices derived from the norm of reaction models formerly described. The canonical variable explaining the largest proportion of the variation of genetic values of animals across the range of values of THI for milk yield is linked to the production level and only a small proportion of about 10% can be used to select animals tolerant to HS without compromising the level of production. On the contrary, in the case of milk components there is a canonical variable explaining a larger part (up to 25%) of the genetic variation for heat tolerance independent of the production level. This could be a good selection criterion to get heat-tolerant animals for the trait fat plus protein yield, which is the most important trait in goats' selection programmes. According to Carabaño et al. [61], genomic information may play an important role in identifying genomic variants present in animals showing high production levels and a low rate of decay due to HS. Other possible tools to be used for selecting heat-tolerant animals could be the use of single nucleotide polymorphism (SNP) markers, found through GWAS analyses, associated with physiological indicators of the response to HS like rectal temperature and respiration and sweating rate. Biomarkers determined in milk by means of mid-infrared technology, routinely used for milk composition analyses in milk-recording programmes, and other recent discoveries of genetic mechanisms involved in heat tolerance through transcriptomics and proteomics may also contribute to find selection tools to improve the response to HS without impairing production levels [61].

7. Conclusions

Traditionally, it has been considered that goats are better adapted to semiarid and hot climates than cattle and sheep; however, the results of the studies carried out in native Spanish breed formerly describe showed that goats also suffer some physiological effects derived from the exposure to high temperatures with a negative impact on yields.

A negative effect on milk traits of both high and low temperatures was observed in three Spanish native breeds of goats. The effect is higher in high-yielding animals.

Genetic variability for the response to heat stress was observed. Heritability of milk traits and genetic values of animals diminish when heath load increases.

The GWAS and transcriptomic analyses showed some candidate genes possibly associated to the response to heat stress, which evidence the complexity of such a response involving apoptotic, immunological and metabolic process.

Acknowledgements

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