

Identification of genomic regions associated with thermotolerance in dairy ruminants

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Summary

Improving the adaptability of animals to the negative effects of Climate Change (CC) is an objective under consideration in various breeding programs in dairy ruminants. Numerous studies have been carried out to define new phenotypes to identify whether an animal has been under heat stress and to what degree, as well as to study the genetic basis of the individual response to heat stress. The present study aimed at identifying genomic regions associated with thermotolerance in dairy ruminants.

For this purpose, genomic (50K SNP chips) and production data from the official test-day control in Hosltein cattle and Assaf and Manchega sheep provided by breeders' associations CONAFE, ASSAF.E and AGRAMA and meteorological data provided by AEMET were used. A mixed-effects model including effects usually used in breeding evaluations in these breeds plus the daily average temperature (T_{ave}) modeled as a cubic polynomial and considered as fixed effect (average population response) and random (individual response) effect nested to the animal was carried out. Slopes under heat derived from individual response curves were used as pseudo-phenotypes in a genome-wide association study. Candidate genes within genomic regions containing SNPs significantly associated with thermotolerance were functionally annotated with DAVID.

Results showed genetic regions containing genes involved in lipid or protein metabolism in both species. This was expected, given the antagonism observed between level of production and heat tolerance (a high correlation between yield level and slope under heat used in this study was found for the three breeds), so the regions found to be associated with thermotolerance will contain some genes involved in yield. In addition to production ability, we observed genes involved in biological processes associated with heat stress response. Some of biological processes were cellular response to heat (PRKACA, TRPM2, SLU7), protein folding (DNAJ Hsp40 family), protein aggregation and organization of endoplasmic reticulum (DNAJB9, CTSZ), DNA repair (DDB1, LIG4, Hsp40 family genes), blood coagulation (HSP6), thermoception and temperature homeostasis (EDN2, RHO, TRPM2) or negative regulation of transcription in response to stress (genes from Hsp40 family and Heat Shock transcription factors). Some of these genes were observed in both species (cattle and sheep) such as the Acetyl-CoA Carboxylase, RHO, HSP? or HSF genes. Next studies will contemplate the use of these genes to improve thermotolerance in dairy cattle and sheep breeding programmes.

Keywords: thermotolerance, GWAS, dairy ruminants