Using QTL studies to screen candidate genes involved in meat quality differences in Avileña Negra Ibérica within a microarray context

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BACKGROUND

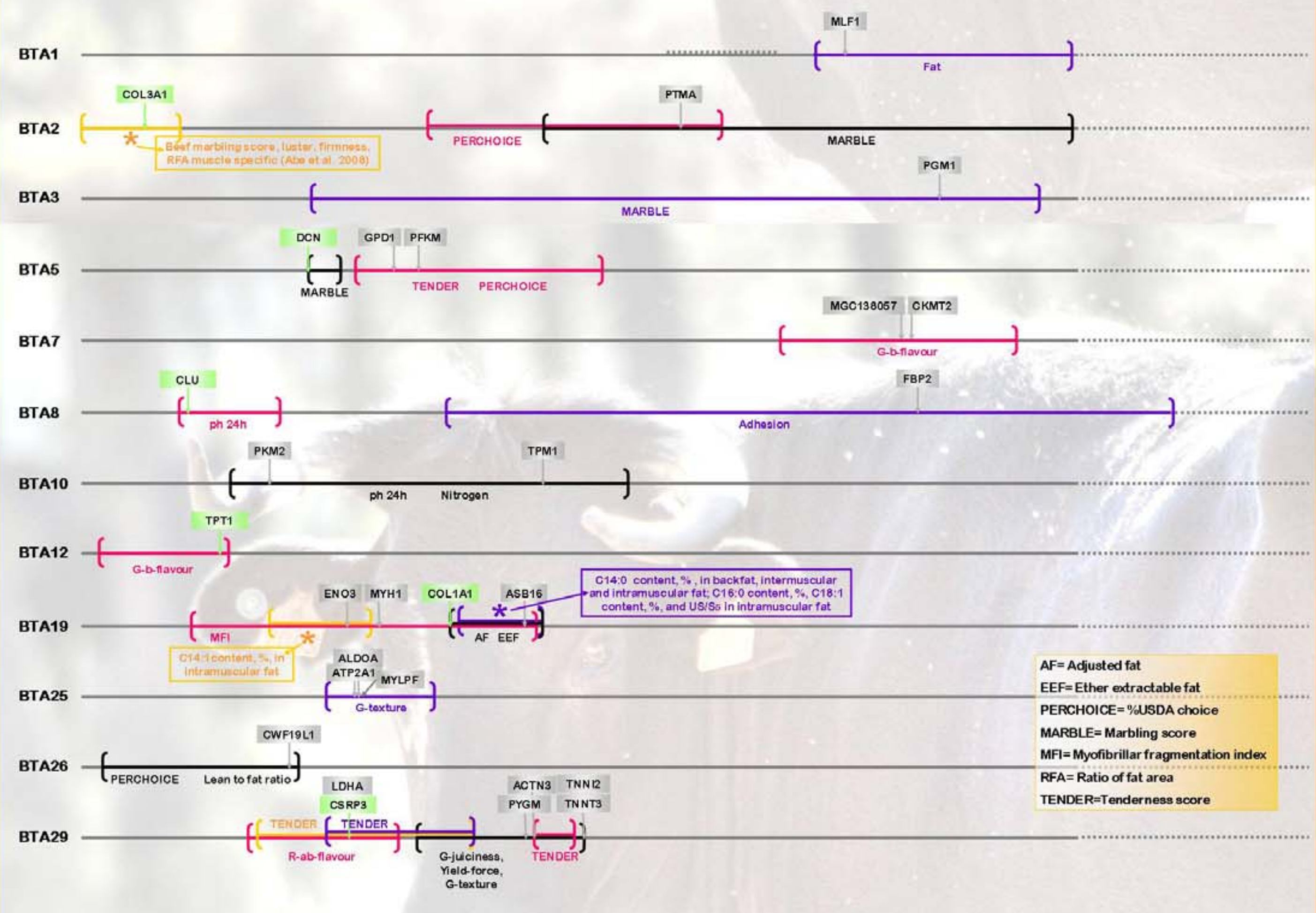
Gene expression and immunohistochemical studies, along with biochemical, instrumental and organoleptic measurements have been accomplished in two muscles (*Psoas major,* PM*,* and *Flexor digitorum,* FD) of Avileña Negra Ibérica calves to investigate the mechanisms underlying meat quality differences among commercial cuts. In a microarray experiment, a total of 84 genes were detected as differentially expressed (DE) between muscles. Positioning the DE genes within previously identified QTL regions of interest would indicate their potential involvement in the biological processes underlying meat quality differences

AIM

To position the DE genes in relation to QTL for meat quality traits in order to identify positional candidate genes with a potential role in meat quality differences between muscles

METHODS

QTL positions were downloaded from available databases (Cattle QTLdb and Bovine QTL viewer), obtained from the literature, and, searched by using STS maps. Gene positions were downloaded from the NCBI database



AF= Adjusted fat
EEF= Ether extractable fat
PERCHOICE= %USDA choice
MARBLE= Marbling score
MFI= Myofibrillar fragmentation index
RFA= Ratio of fat area
TENDER=Tenderness score

Both QTL and gene positions have been made to scale

RESULTS

28 out of the 84 DE genes were located inside 23 significant QTL regions related to traits such as marbling, tenderness, flavour, texture or juiciness among others (above shown). Genes in green (6) were up-regulated in the FD while genes in grey (22) were up-regulated in the PM muscle.

Genes DE in PM or FD did not seem to be associated to specific traits

CONCLUSION

We have identified 28 positional candidate genes with a potential role in meat quality differences

This work was supported by a grant from the "Ministerio de Ciencia e Innovación" of Spain (INIA-FEDER RTA2007-00081-00-00). Authors thank to the"Asociación de Avileña-Negra Ibérica" and to the "Consejo Regulador de Carne de Ávila" for their contribution in the sample collection