carine.capel@inst-elevage.asso.fr

TRANSCRIPTOMIC MARKERS OF BEEF MEAT TENDERNESS

C. BERNARD-CAPEL[1], I. CASSAR-MALEK[2], G. RENAND[3], J. LEPETIT[4], J.F. HOCQUETTE[2]

(1) Institut de l'Elevage, Service Aptitudes et Sélection des Races Allaitantes, 75595 Paris Cedex 12, France
(2) INRA, UR1213, Unité de Recherche sur les Herbivores, 63122 St-Genès-Champanelle, France
(3) INRA, UMR1313, Génétique Animale et Biologie Intégrative, 78352 Jouy-en-Josas cedex, France
(4) INRA, UR0370, Qualité des Produits Animaux, 63122 St-Genès-Champanelle, France

In Livestock species and more particularly in cattle, meat tenderness is a major factor to help producers to give value to their animals but also to satisfy the consumers. Although there is no genomic selection yet in beef cattle to meet these expectations, many researches have been conducted to get a better understanding of the physiological processes underlying meat tenderness and so to identify genes related to this trait.

OBJECTIVE: Identify key genes associated with beef tenderness by transcriptomic approaches

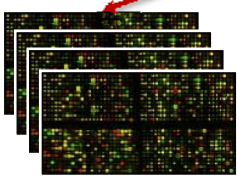
ANIMALS

25 Charolais young bulls
15 or 19 months of age

TRANSCRIPTOMIC ANALYSIS

Muscles:
- ***Longissimus thoracis*** **(LT)**
- ***Semitendinosus*** **(ST)**

Chips: 5 418 to 6 473 oligo



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TENDERNESS EVALUATION

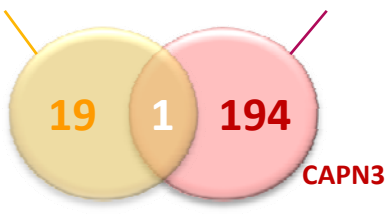
Shear force measurement:
(Warner Brätzler-WB)
55°C grilled meat

COMPARISON OF TRANSCRIPTOME: according to meat tenderness

For each muscle:
Differentially expressed genes were identified by comparing groups of animals selected on the basis of their extreme WB value
Correlations between gene expression level and WB value were determined using all animals data (n=25)

Up-regulated genes in the muscles of animals giving tender beef

LT: 20 **ST: 195**



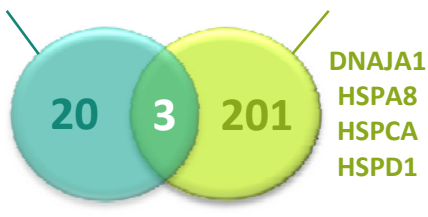
CYP2E1

CAPN3: up-regulated in ST muscle and negatively correlated with the WB value (r=-0,60)

Genes involved in apoptosis (DNAJA1, HSPA8) or genes belonging to the family of Heat Shock Protein (HSPCA, HSPD1…) were down-regulated in ST muscle giving tender beef but their expressions were not correlated with WB value

Down-regulated genes in the muscles of animals giving tender beef

LT: 23 **ST: 204**



HSPB1, ATF3, U2AF1

HSPB1 and ATF3: positively correlated with the WB value in LT muscle (r=0,41 and 0,44)

In conclusion, the transcriptomic markers of beef meat tenderness are specific muscle. These genes are often involved in same pathway (apoptosis) and among them, DNAJA1 and HSPB1 were already shown to be related to beef sensory tenderness. These genes could be good genomic markers of tenderness evaluated by sensory or mechanical analyses.