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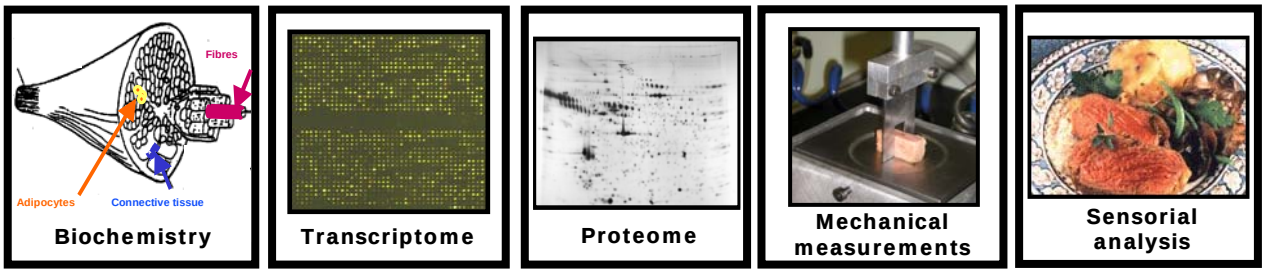
Changes in muscle gene expression in relation to beef tenderness and growth potential in young Charolais bulls

C. BERNARD[1], I. CASSAR-MALEK[2], G RENAND[3], 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, UR337, Station de Génétique Quantitative et Appliquée, 78352 Jouy-en-Josas cedex, France

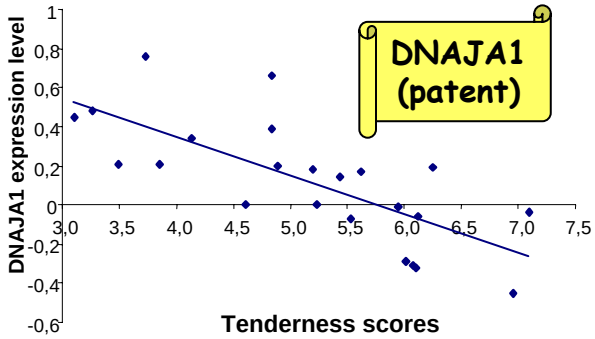
The **objective** of this study, included in the MUGENE program (AGENAE French genomic initiative), was to identify key genes associated with beef tenderness and growth potential by functional genomics approaches.

The expression level of a large number of genes and proteins and the biochemical characteristics were analyzed in the *Longissimus thoracis* (LT) muscle from Charolais young bulls slaughtered at 15 or 19 months of age. The calves were the progeny of 12 Charolais sires divergently selected for muscle growth capacity among 80 progeny-tested sires. The molecular profiles were compared on the basis (i) of tenderness estimated by sensorial analysis or shear force measurement of 55°C grilled meat and (ii) of muscle growth potential.



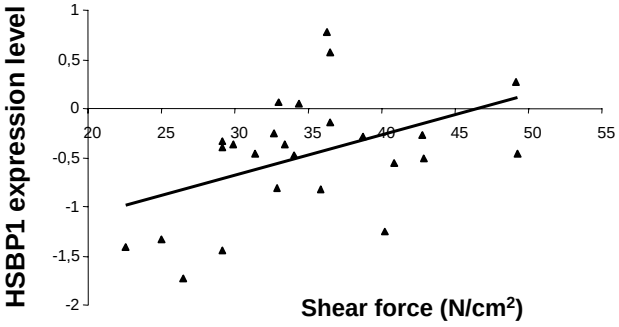
LT muscles were ranked according to tenderness scores and muscle growth potential

SOME RESULTS



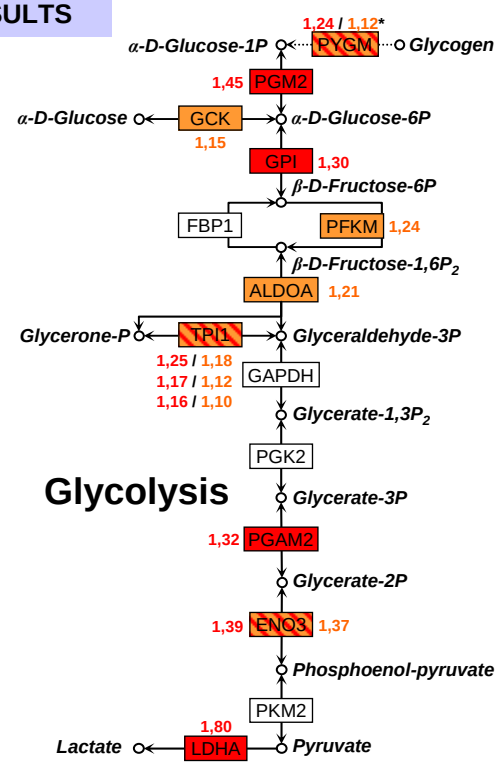
One gene DNAJA1 (Hsp40) showed a strong negative correlation with tenderness after 14 days of ageing

(Genomic marker for meat tenderness. Patent 06 300943.5. 12 /09/06). (Bernard et al., J Agri Food Chem, 2007, 55(13):5229-5237).



Another gene of the HSP family (HSBP1) showed a strong correlation with shear force after ageing.

This was confirmed by proteomic studies.



Transcriptome data revealed that about two thirds of the genes involved in glycolysis were up-regulated especially at 15 months of age in animals with a high muscle growth potential

(numbers indicate fold-changes)

In conclusion, the most original result of this study is the revelation of an important role of proteins of the HSP family in tenderness. These chaperone proteins have anti-apoptotic activity and could decrease apoptosis, an early process occurring after death, and, therefore, meat ageing and its tenderisation during days following slaughtering.

Selection for muscle growth potential is associated with increased expression of genes involved in glycolysis. The gene expression changes which occur with increased muscle growth potential are likely to be dissociated from fat deposition and meat quality.