GENE EXPRESSION ASSOCIATED WITH BEEF SENSORY QUALITIES

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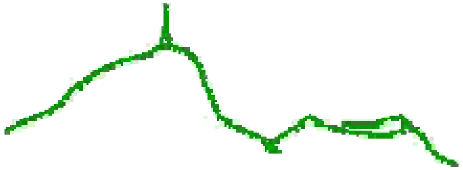
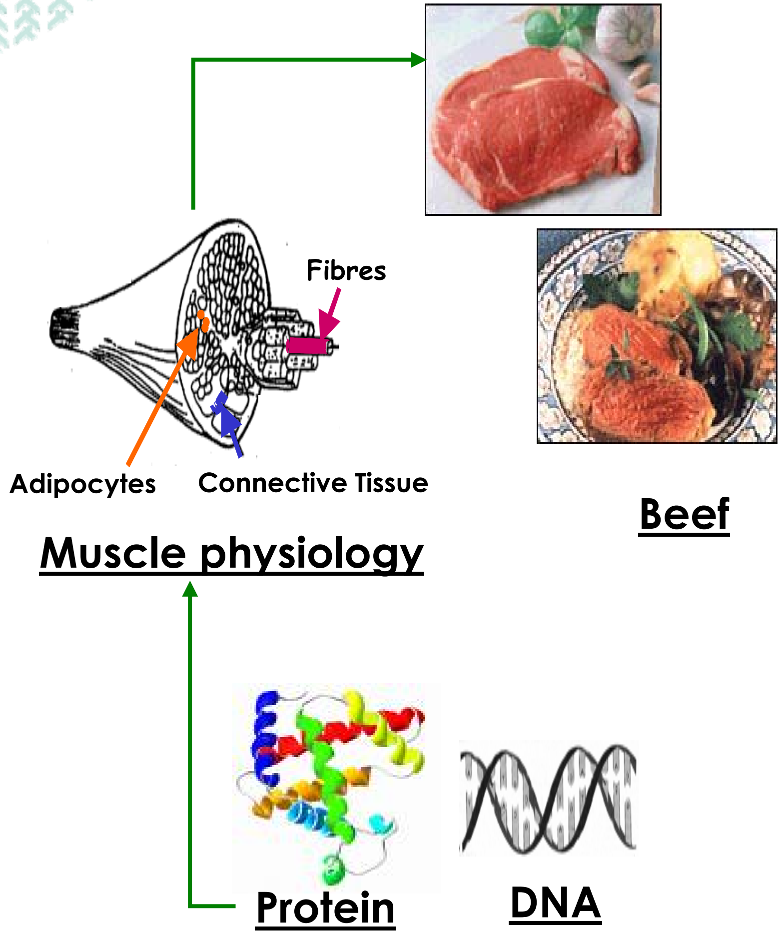


BACKGROUND

- Beef sensory qualities (tenderness, colour, flavour, juiciness) depend on many factors including muscle characteristics

- However, these explain less than 35% of the variability

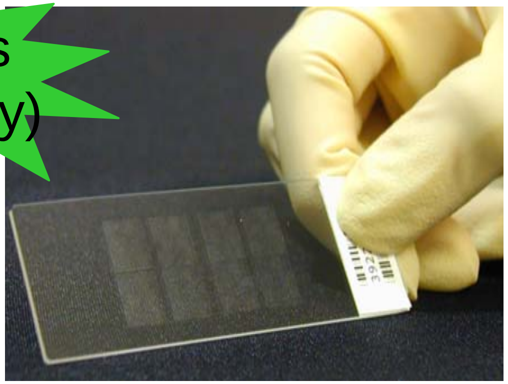


OBJECTIVES

- Identify specific and reliable indicators of beef sensory qualities
- Explore muscle gene expression and identify genes that are differentially expressed between beef meat cuts with variable tenderness, juiciness and flavour

Transcriptomics

Myochips
(oligo-array)



EXPERIMENTAL DESIGN

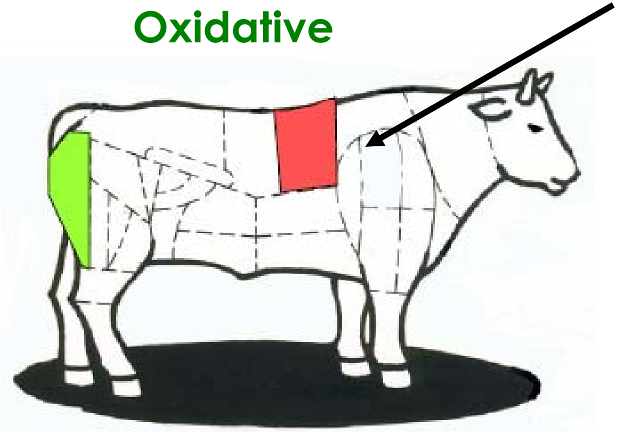
Animals

Charolais bull calves from an INRA experimental herd, weaned at 32 wk, slaughtered at 15 mo (n=13) or 19 mo (n=12)

Samples

***Longissimus Thoracis* (LT)**

Oxidative



Rib steak

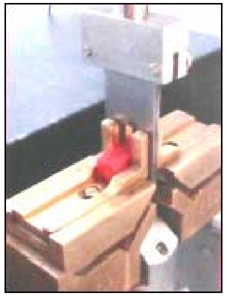
- Muscle Biochemistry
- Meat Quality attributes
- Transcriptomics

MEASUREMENTS

Sensory qualities

Trained panelists : Tenderness, Juiciness and Flavour

Meat texture



Shear force (Warner-Brätzler device)

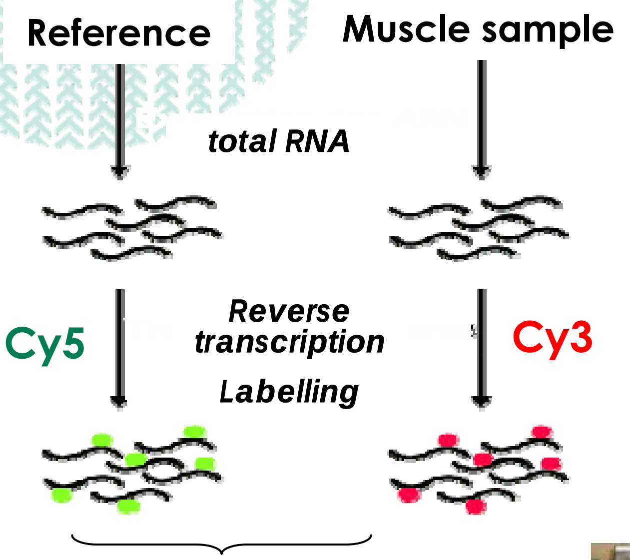
Water loss

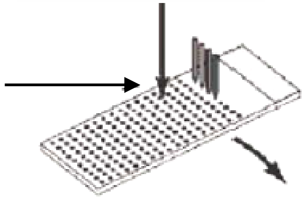
Biochemistry

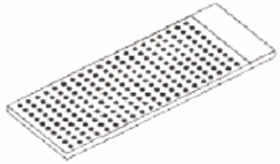
- ✓ metabolic enzymes (COX, ICDH, CS, LDH)
- ✓ lipids (total, TG, PL)
- ✓ total collagen content
- ✓ fibre areas

TRANSCRIPTOMICS

OLIGO ARRAY
6,5K, triplicate
50mers
Human,murine


Reference
Muscle sample
total RNA
Cy5
Reverse transcription
Labelling
Cy3

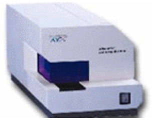


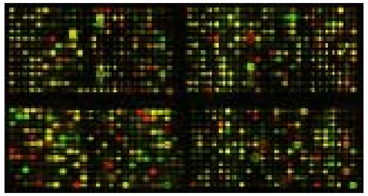


Hybridisation

(n=100)

Array scan





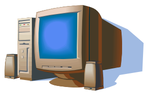
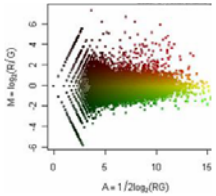


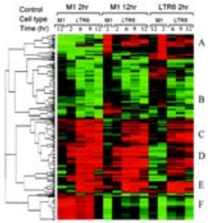
Image analysis

Data analyses

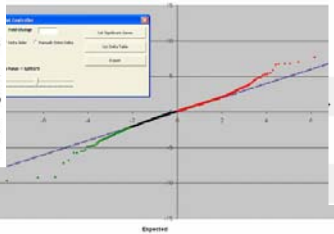
MA plot



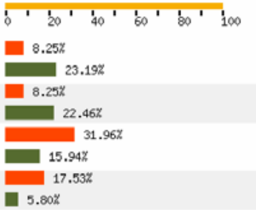
Clustering



SAM



Gene Ontology information



CORRELATION OF SENSORY TRAITS WITH MUSCLE CHARACTERISTICS AND TEXTURE

α = 0,05	COX	CS	ICDH	LDH	Lipids	PL	TG	WB	Water	Collagen
Tenderness	0.37	0.05	0.5	-0.20	0.15	0.15	0.23	-0.36	0.3	0.15
Juiciness	0.30	-0.03	-0.15	0.14	-0.50	-0.03	-0.45	0.02	0.03	0.28
Flavour	0.58*	-0.09	-0.16	0.01	-0.31	-0.35	-0.26	-0.05	0.31	0.44

Tenderness : ICDH, COX (+) , WB (-) → **25%**

Juiciness : Lipids, TG (-), COX (+) → **25%**

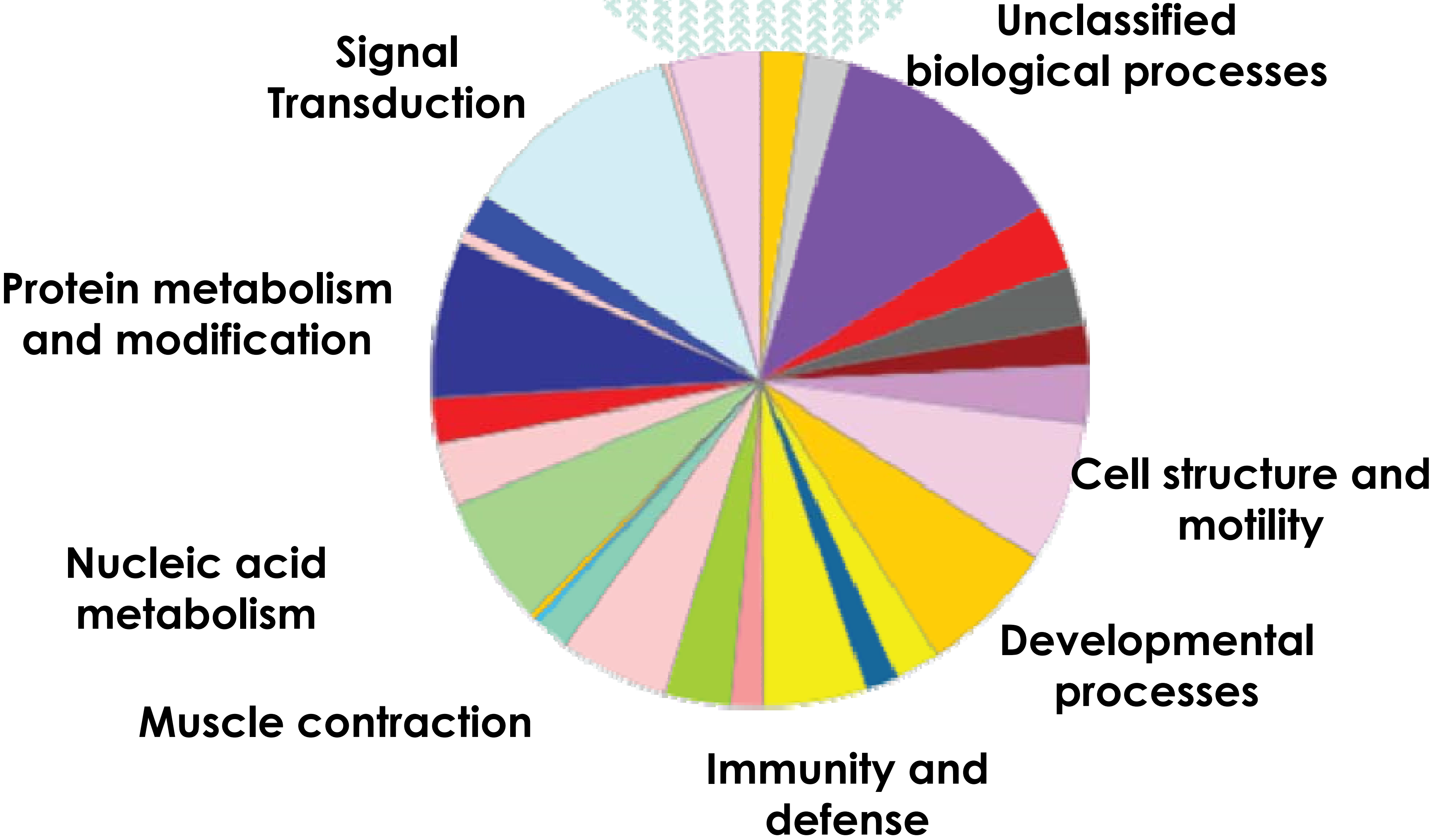
Flavour : COX, Collagen (+) → **33%**

DIFFERENTIALLY EXPRESSED GENES

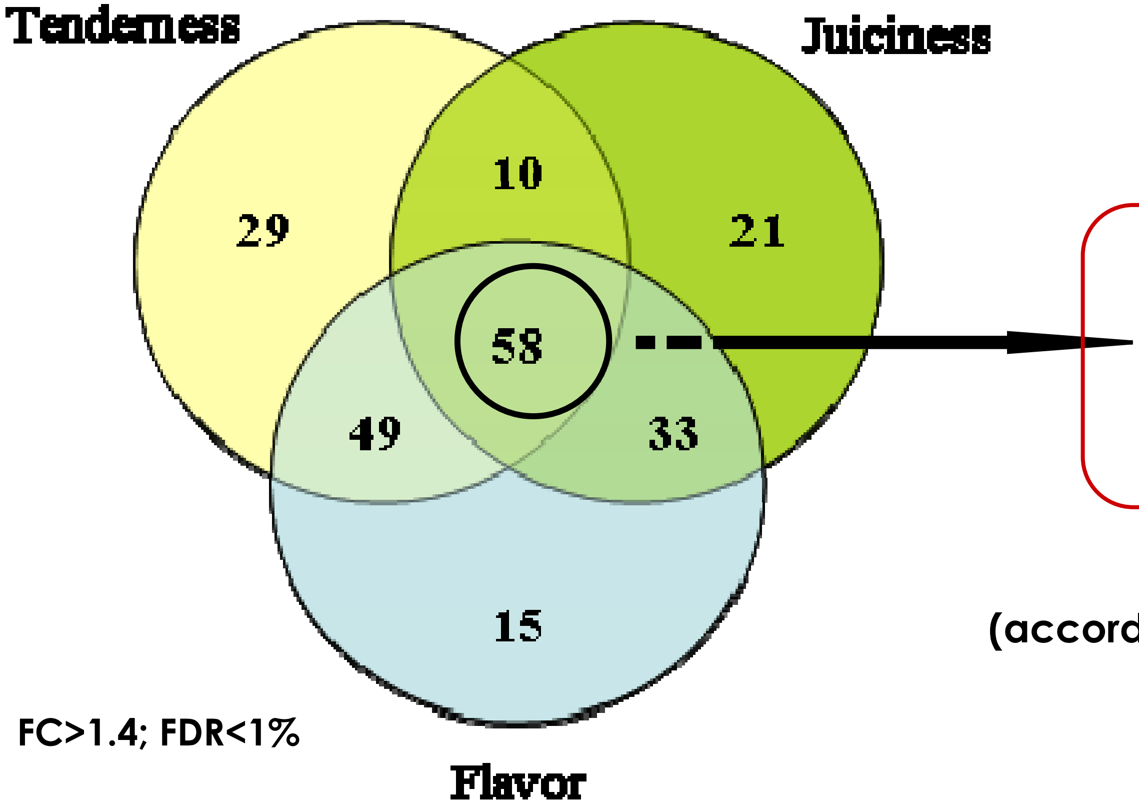
SAM analysis	Tenderness	Juiciness	Flavour
Differentially expressed genes	615	1005	799
Total of genes common to at least 2 sensory traits	1772		
Differential genes (FC>1.4) in at least one trait	146	122	155
Total of differential genes in at least one trait	215		

> 80% homology with bovine genome (genes, EST)

GENE ONTOLOGY INFORMATION



Distribution of the 215 differential genes



FC>1.4; FDR<1%

33 up-regulated
N=10 (15 mo)
+
N=23 (15 & 19 mo)
9 down-regulated

16 variables

(according to the age or the sensory trait)

CORRELATION OF SENSORY TRAITS WITH GENE EXPRESSION

		Tenderness	Juiciness	Flavour
Up-regulated genes	CPT1B	ns	*	*
	Xlkd1	ns	*	*
	NDUFB4	ns	*	*
	JMJD1B	ns	**	**
	LAMA3	ns	*	**
	FLJ12193	*	**	**
	Npm3	*	*	*
	Cyp2c5	ns	ns	ns
	TRIM55	*	**	**
	Cbr2	*	*	**
	C:6970	ns	**	**
	PRRX2	ns	*	**
	OTOR	ns	**	**
	CACNA	ns	**	**
	Ireb2	ns	*	**
	PRKAG1	ns	*	**
	NID1	ns	ns	*
	MPDZ	ns	**	**
	CGREF1	ns	*	**

◄Nineteen of the 23 up-regulated genes belonged to a same expression cluster, and 18 of them were correlated with sensory traits

		Tenderness	Juiciness	Flavour
Down-regulated genes	PDK4	ns	ns	ns
	DNAJA1	** (-)	ns	ns
	CSRP3	ns	*	*
	CRYAB	ns	ns	ns
	THOC3	ns	ns	ns

▲ Five of the 9 up-regulated genes belonged were correlated with a sensory trait

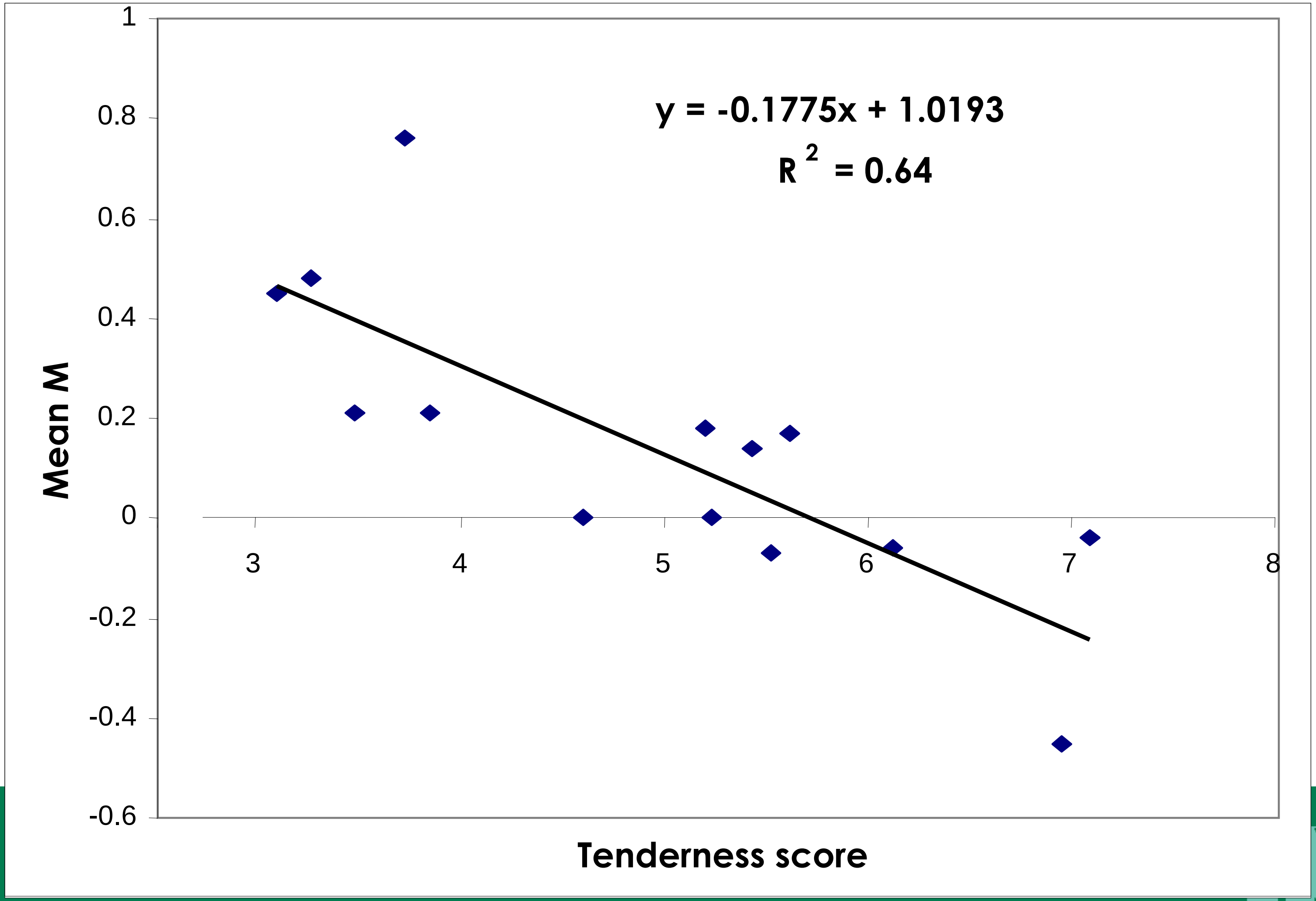
*** : a = 0.05; ** : a = 0.01**

What is DNAJA1?

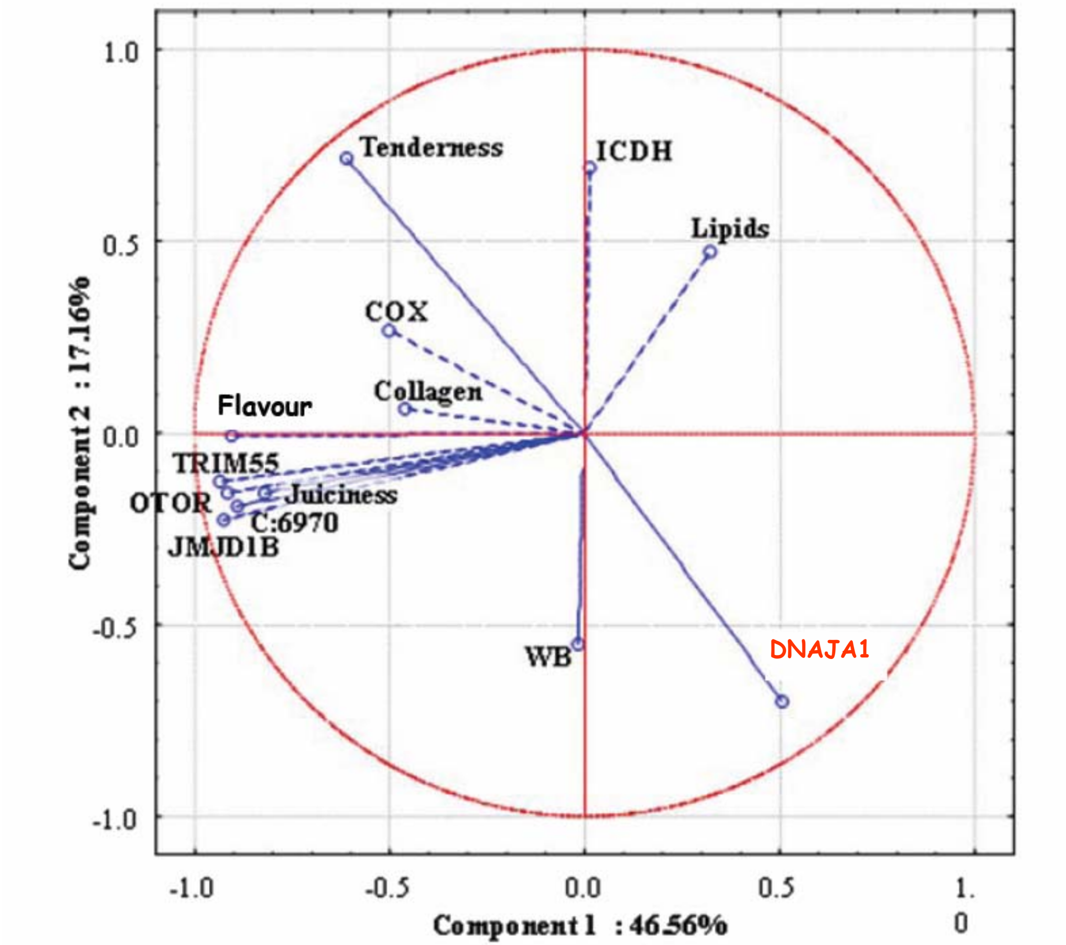
- DNAJA1 encodes a member of the large heat shock 40kDa protein family.
- This protein is a co-chaperone of Hsc70 and could to play a role in protein import into mitochondria.
- Its involvement in beef tenderness remains unknown

IS DNAJA1 AN MARKER OF BEEF TENDERNESS?

Micro array data **N=14 samples** **Confirmed by Real time RT-PCR**



PRINCIPAL COMPONENT ANALYSIS OF BIOLOGICAL AND TRANSCRIPTOMIC DATA



65% of sensory quality variability is explained

CONCLUSION

The study allowed identification of genes whose expression was associated with beef sensory qualities

Of the total differential genes (n=215, FC>1.4, FDR>1%) :

- **42 genes differentially expressed according to the three criteria (tenderness, juiciness and flavour)**
- **33 genes associated with high sensory quality**
  - ✓ **e.g JMJD1B, FLJ12193, TRIM55, C:6970, OTOR and CACNA1B correlated with flavour and juiciness (45 to 60%)**
  - ✓ **e.g. DNAJA1 negatively correlated with tenderness (65%): patent for beef quality prediction**

Thank you for your attention

For any question, send an E-mail to hocquet@clermont.inra.fr or to cassar@clermont.inra.fr