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Session 14 – Abstract 4546

Detection of Quantitative Trait Loci affecting carcass and meat quality in two French beef breeds

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DIET
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ENVIRONMENT



Context of the study

- No routine measure of beef meat quality
→ selection based on records is not feasible
- Implementation of a program Qualvigène which aims at studying meat quality traits:
 - genetic variability
 - genetic polymorphisms
 - functional genomic

In this presentation: QTL detection in two French beef pure breeds: Limousine and Blonde d'Aquitaine
→ mapping genome areas involved in meat quality

The animals

The program is based on three successive years of progeny tests

	Limousine	Blonde d'Aquitaine
Number of sires	3	3
Number of young bulls	248	243
Slaughter age (mo)	15.8	13.9
Hot carcass weight (kg)	394	403



The traits

- Usual traits recorded in the progeny tests
 - average daily gain
 - carcass yield
 - muscle score
 - fatness score ...
- Measures of muscle characteristics
 - pH
 - muscle fibre section area
 - muscle fibre number
 - rib fat content
 - collagen content
 - intramuscular fat content
- Measures of meat quality
 - lightness
 - shear force
 - sensory quality attributes (tenderness, juiciness and flavour scores)

Measures of meat quality

8th and 9th ribs of the Longissimus thoracis muscle

2 steaks of 6 cm thick

14 day ageing at 4°C

Electric grill cooking to an internal temperature of 55°C

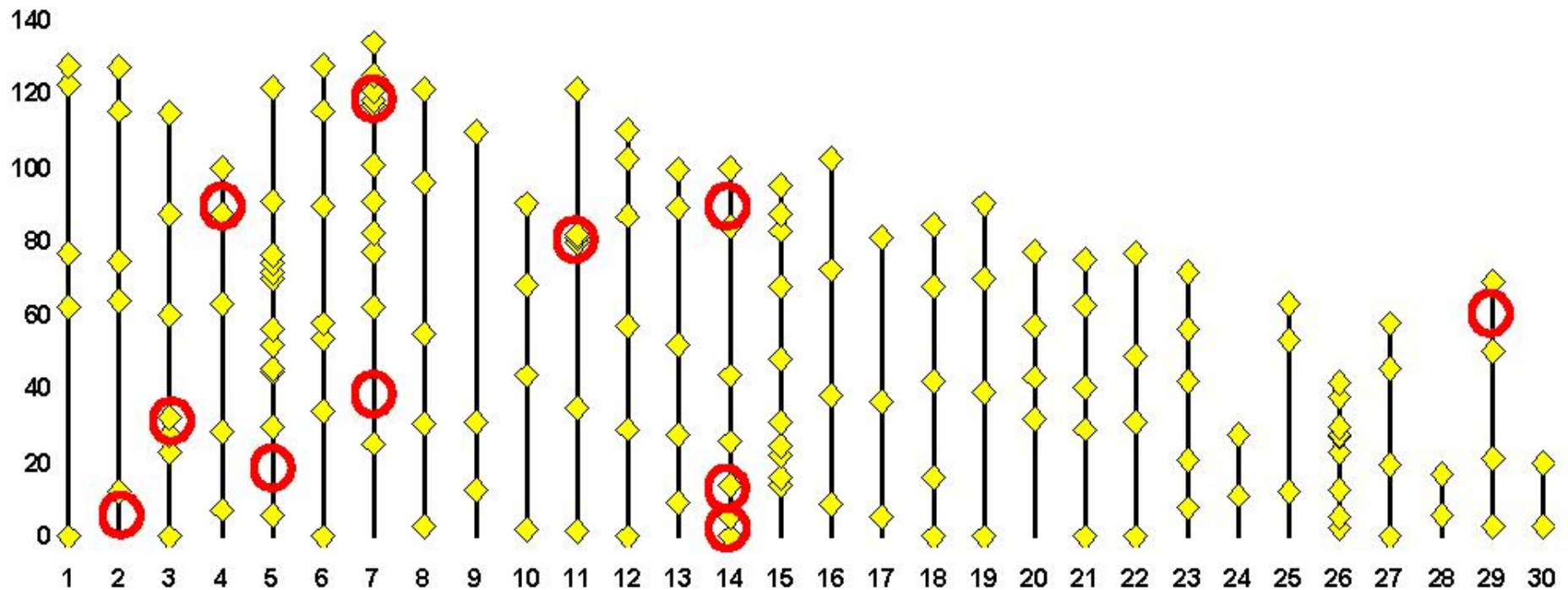
Evaluation by 12 panellists

Tenderness, juiciness and
flavour scores (1/100)

Measure of shear force
(10 repetitions)
Warner-Bratzler method

Shear force (N/cm²)

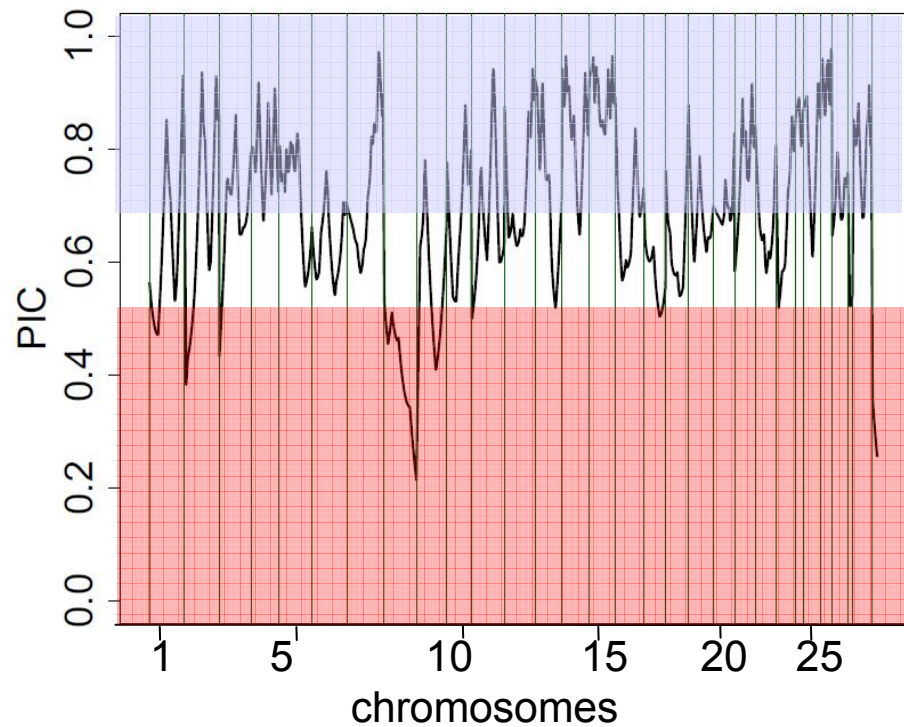
The markers



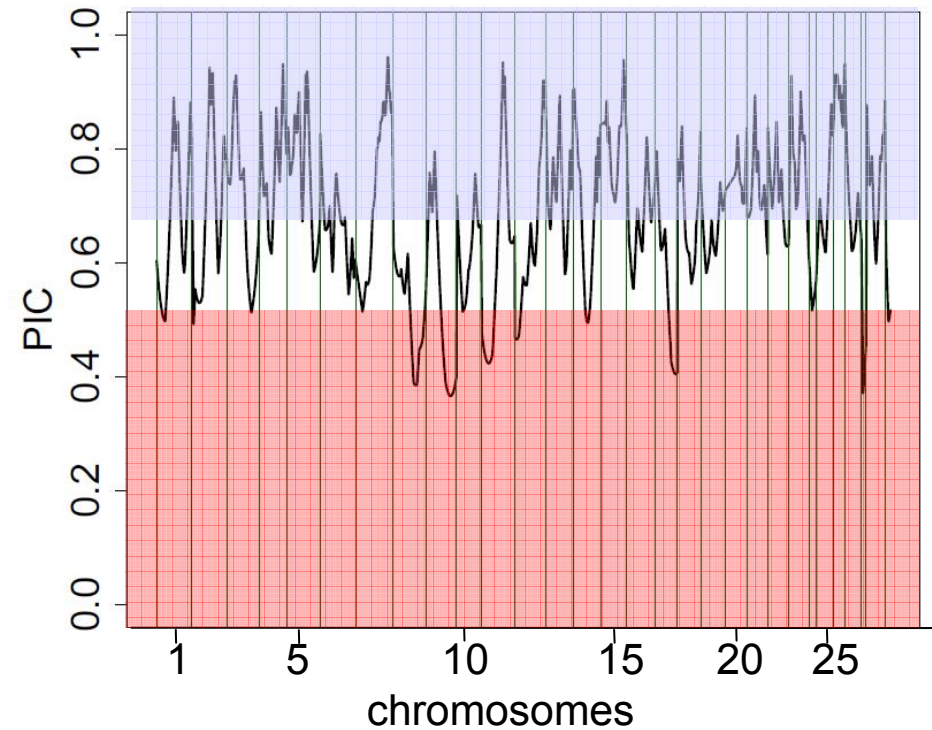
186 markers: 160 microsatellites
 26 SNP in candidate genes

Average interval between markers: 19 cM

Polymorphism Information Content



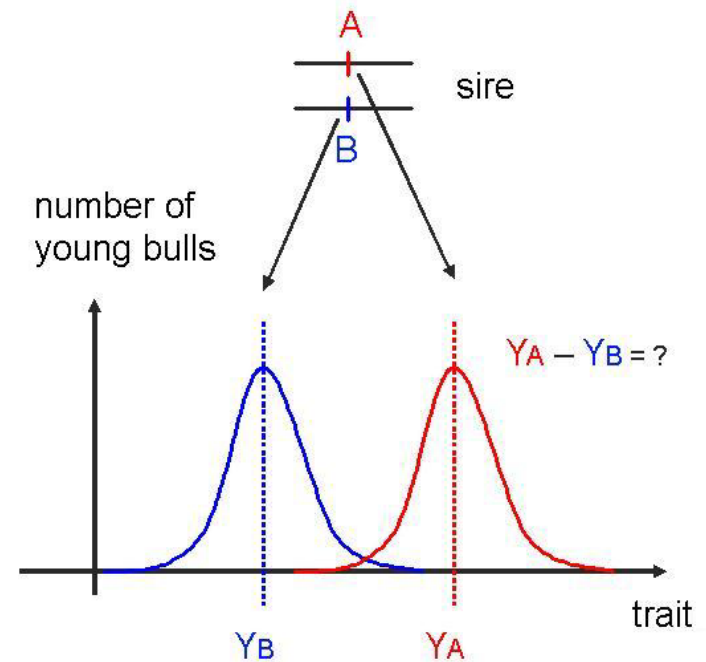
Limousine



Blonde d'Aquitaine

Method of QTL detection

- Traits corrected for fixed effect
- QTLMAP software developed at INRA
- Interval mapping
- 2 steps:
 1. At each position, the probability that each progeny received one or the other chromosomal segment from his sire was estimated
 2. Linear regression in half-sib families
 - Statistical test: LRT (Likelihood Ratio Test)
 - Critical threshold: 10000 rounds of generated performances



→ A one-QTL and one-trait analysis

→ In some chromosomal regions: a multi-traits analysis

→ See QTLMAP presentation of JM Elsen in session 53

Results

groups of traits	number of traits	h^2	number of QTL	
			Limousin	Blonde d'Aquitaine
beef traits	12	> 0.3	29	21
muscle characteristics	8	< 0.3	8	13
meat quality measures	7	< 0.2	13	10

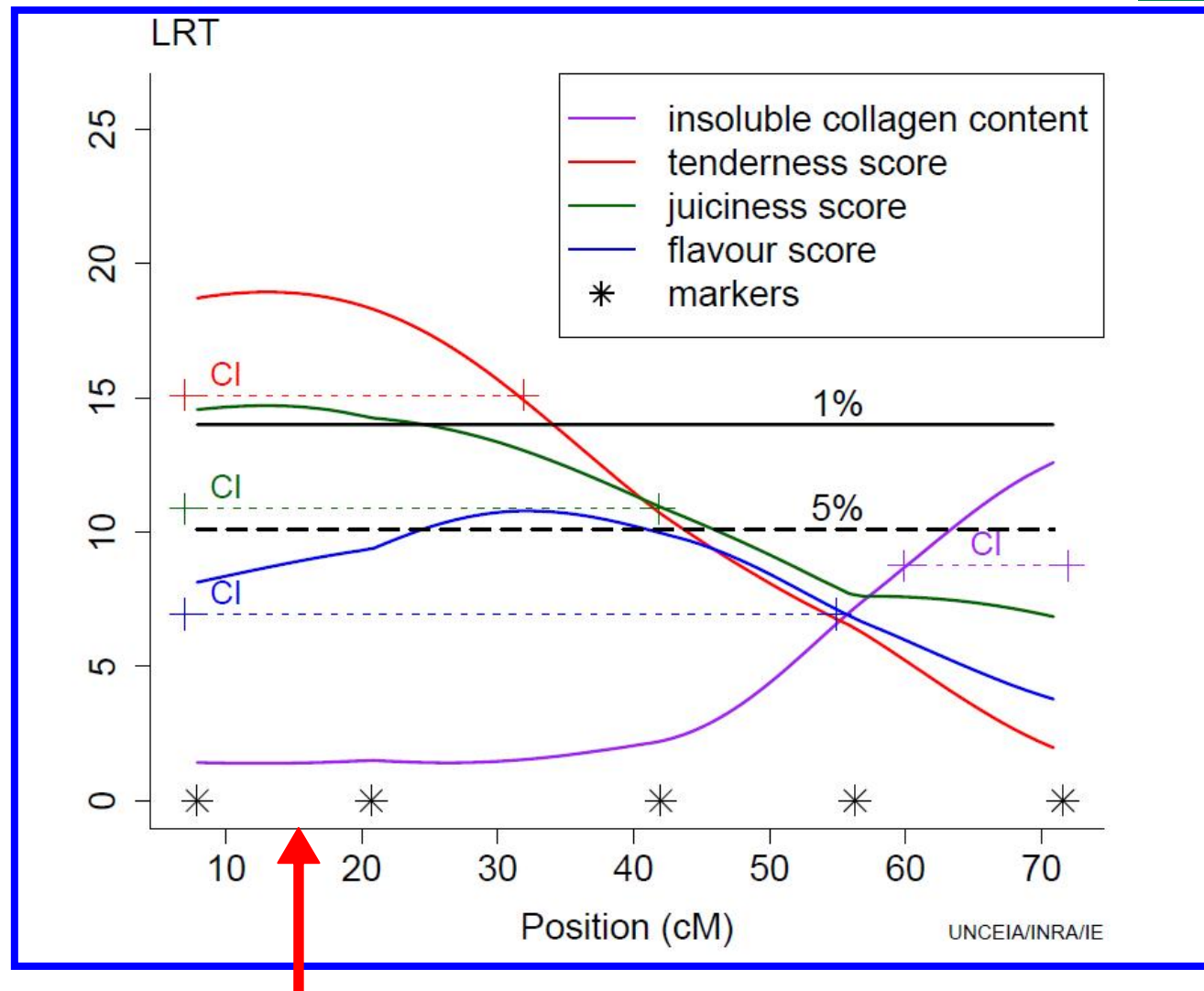
QTL of meat quality

- ➔ QTL effects: 1/5 to 1/3 phenotypic standard deviation
- ➔ Significance at 5% on the chromosome level for most QTL

traits	QTL's chromosome	
	Limousin	Blonde
intramuscular lipids	3, 6, 9	9 , 26
collagen	12, 23	13, 20
muscle fibre	13	8, 20, 23
lightness	12	9
shear force		7, 21
tenderness score	6, 23	7, 10, 23
juiciness score	23	13
flavour score	20, 23	XY

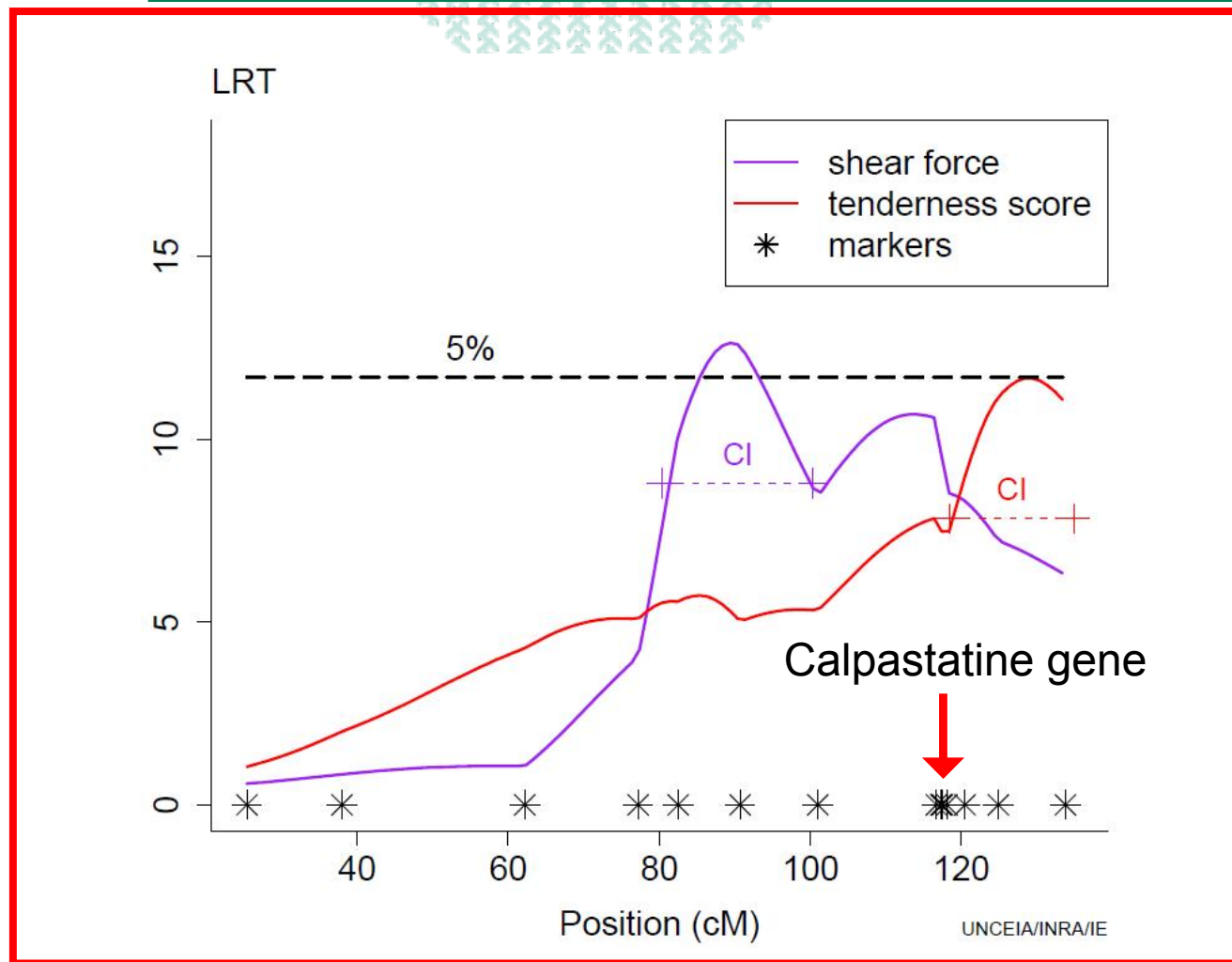
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Chromosome 23 in Limousine



Multi-traits analysis: a significant pleiotropic QTL (tenderness, juiciness, flavour) at position 0.15 M (p-value=0.5%)

Chromosome 7 in Blonde



Multi-traits analysis: 2 different QTL

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Conclusion and perspectives

- A first QTL location in the Limousine and Blonde d'Aquitaine breeds
- Some QTL associated with original sensorial traits
- Few QTL commons → specific breeds
- Few sire families → few QTL
- Few markers → large confidence intervals
- A first step towards fine QTL detection

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