Global perspectives on trait ontology and phenotyping of livestock: examples from functional genomics and modeling in beef-producing animals

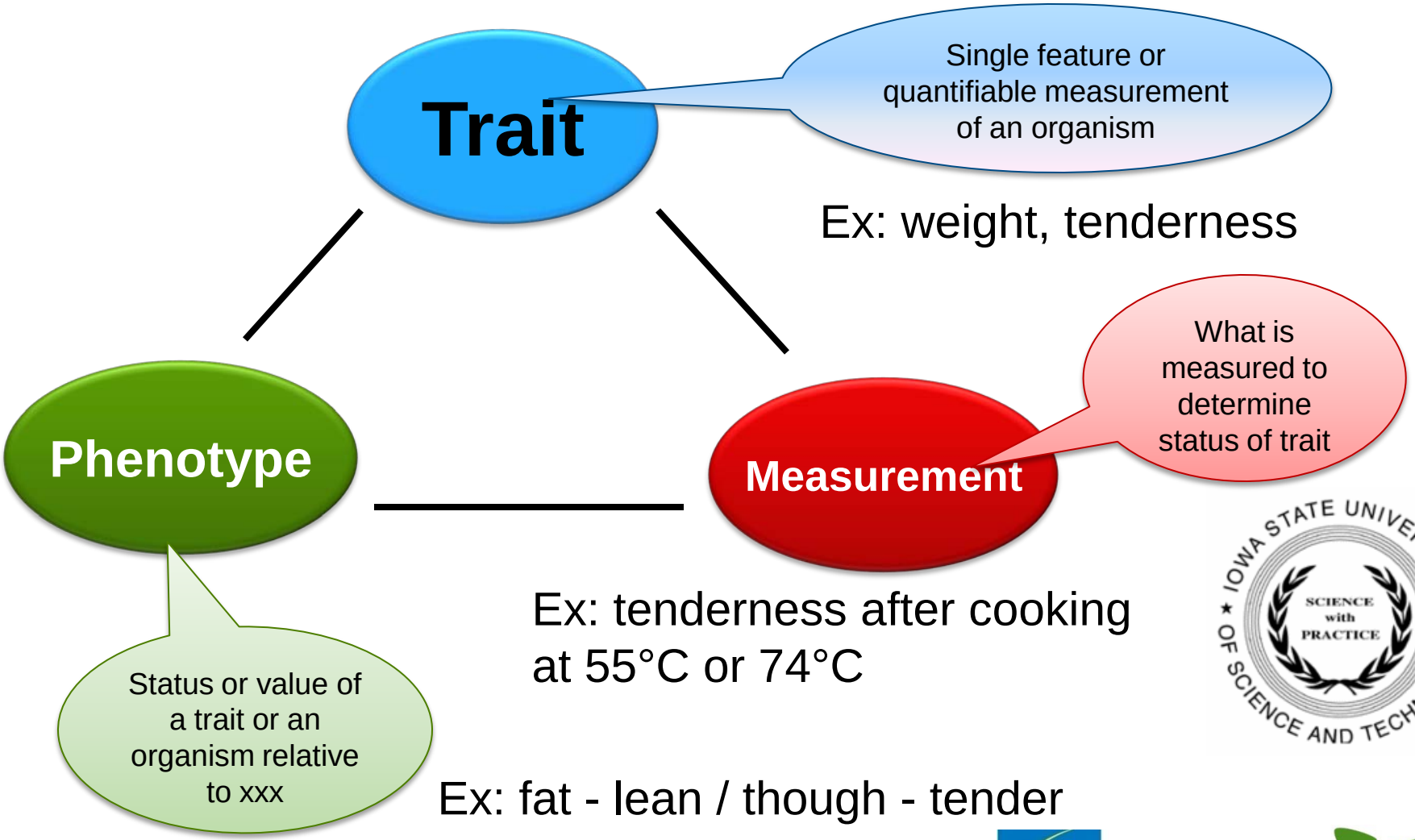
JF Hocquette[1], C Capel[2], M Barbezant[3],
PL Gastinel[2], PY Le Bail[1], P Monget[1], JL Peyraud[1]

[1] INRA, [2] Institut de l'Elevage, [3] UNCEIA

Outline

- ✓ Some definitions and elements of context
- ✓ Challenges about beef quality in genetics
- ✓ Challenges about beef quality in functional genomics
- ✓ Other perspectives

Definitions : trait, phenotype, mesurement « Animal trait Ontology »



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High-throughput phenotyping

- ✓ Measurement of phenotypes using a rapid and repeatable method that can be automated so that the process generates a large number of data
  - 2 components:
    - systematic phenotyping (a few variables on many animals)
    - targeted or deep phenotyping (more variables for a trait family on a small number of animals)

Data bases

- ✓ One challenge: format and access of data.
- ✓ Importance of ontologies

Hrynaszkiewicz *BMC Research Notes* 2010, **3**:235
http://www.biomedcentral.com/1756-0500/3/235

EDITORIAL Open Access

A call for *BMC Research Notes* contributions promoting best practice in data standardization, sharing and publication

Iain Hrynaszkiewicz

ATOL Programme : Animal Trait Ontology of Livestock
(see the presentation of Hurtaud et al)

Output of such research

- ✓ One overall objective is to have efficient, robust and adaptable animals in response to climatic variability
- ✓ Robustness is the capacity of an animal to adapt to environmental challenges: it requires repeated and frequent measurements of phenotypes
- ✓ Genotype-phenotype relationships
- ✓ Development of precision livestock farming
  - To reduce feed costs and waste
  - To reduce labor load

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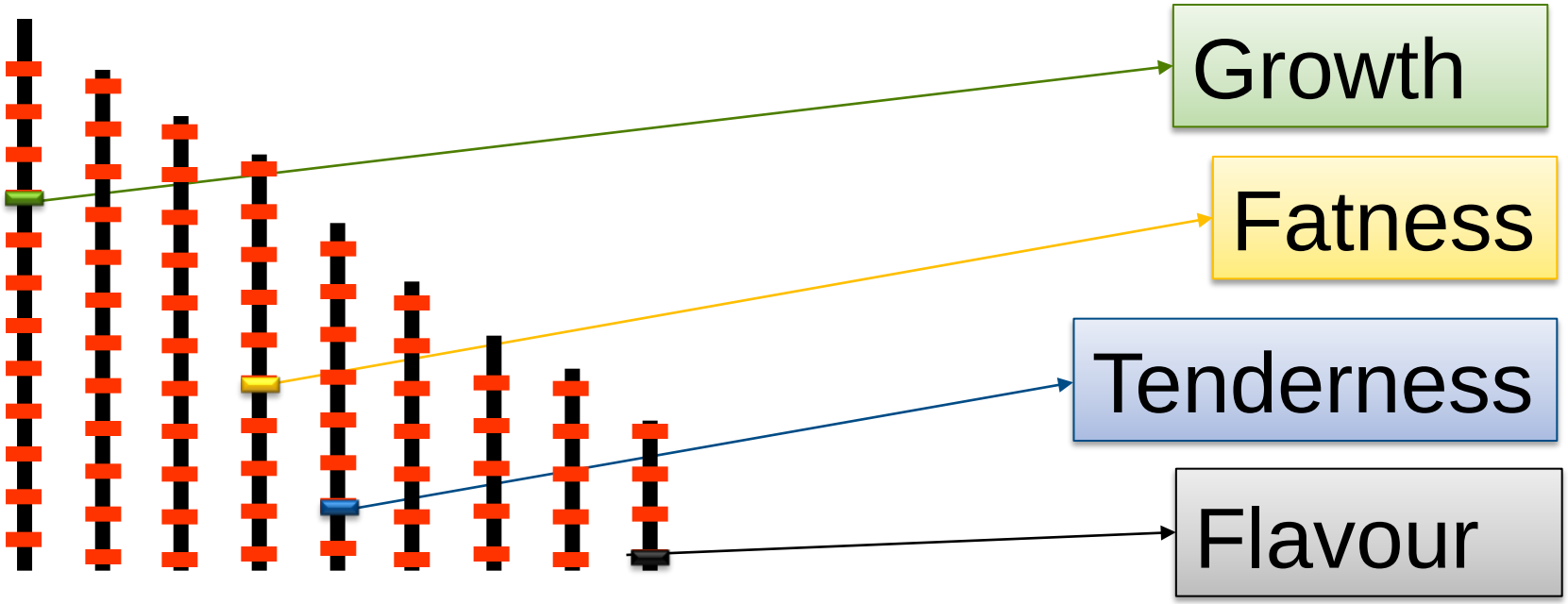
A challenge: the genomic selection

Association studies between genetic markers and phenotypes of interest (*example : beef quality*)



Example : the Qualvigène programme

The French QUALVIGENE programme

- Charolais, Limousin, Blond d'Aquitaine
- 114 sires
- 3349 young bulls

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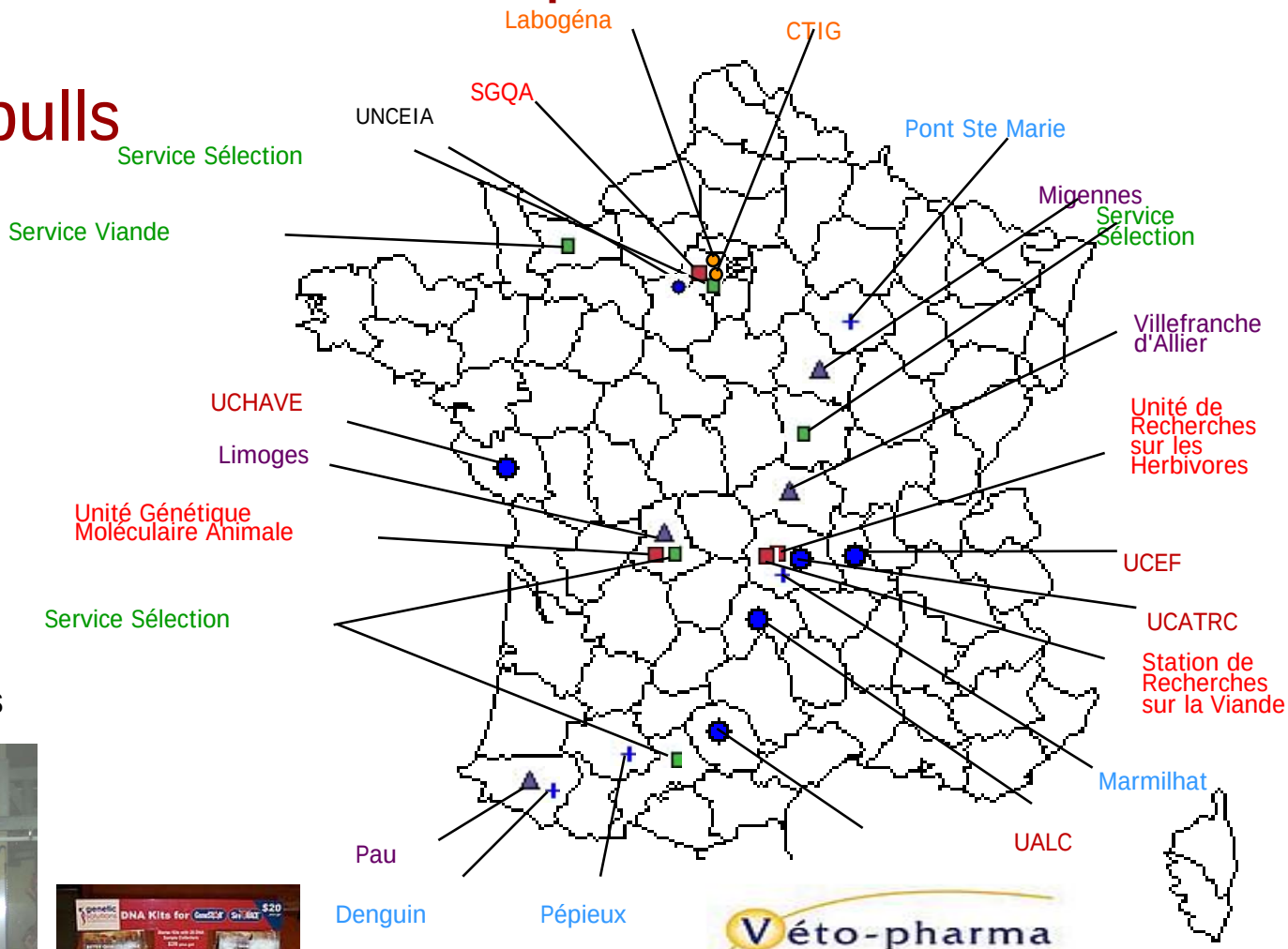
- Breeding Enterprises
- INRA Laboratories
- Livestock Institute
- Abattoirs
- Other
- Progeny Testing Stations



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GeneSTAR

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Material and Methods

➢ Traits measured on the *Longissimus thoracis* muscle

Rib	Sampling	Ageing	Measurements
7th	24 h	0 day	Lipid and Collagen contents Muscle Fibre Section area
8th	24 h	14 days	Warner-Bratzler Shear Force*
9th	24 h	14 days	Sensory attributes* : Tenderness, Juiciness & Flavour scores

* Cooking temperature = 55 °C

Measurement of phenotypes using a rapid (NO) and repeatable (YES) methods that can be automated (NO) so that the process generates a large number of data (YES).

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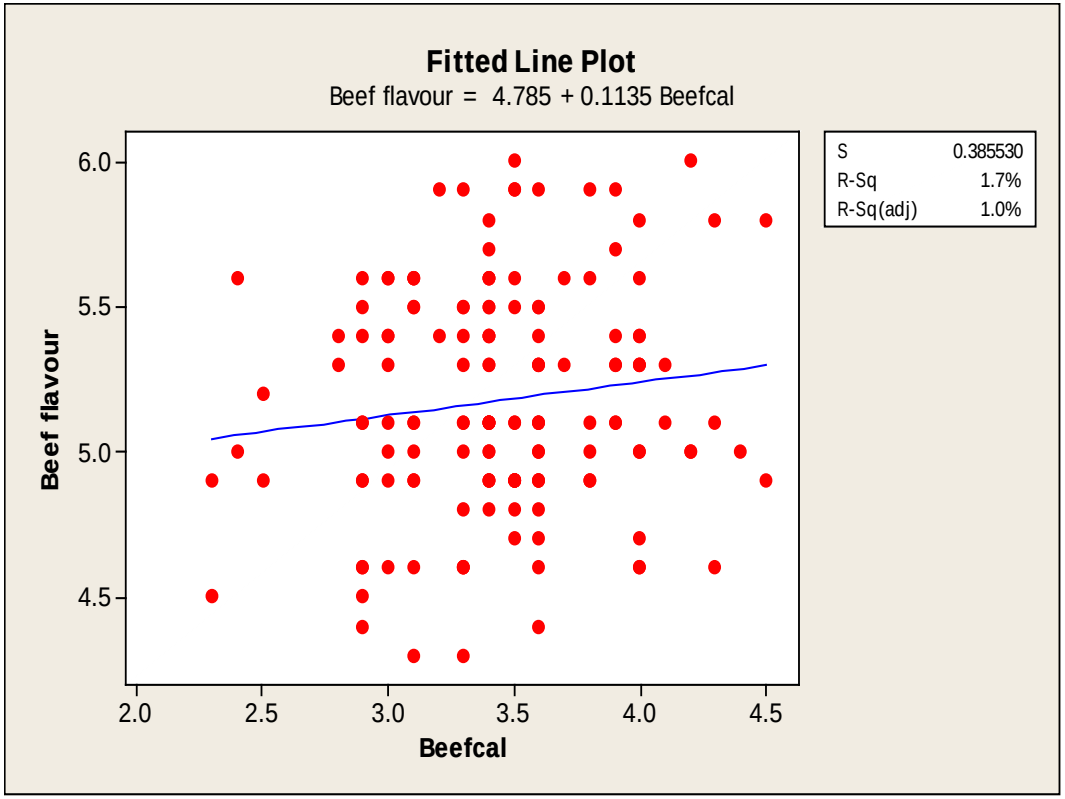
European programme GEMQUAL (Genetics of Meat Quality)

✓ Comparison of the same samples by two sensory panels in Spain and UK.

The measurement of flavour is not repeatable



Calibration results for Beef Flavour

UK + 1.7 = ES Score

Spanish -1.7 = UK Score

(Nute et al., 2006)

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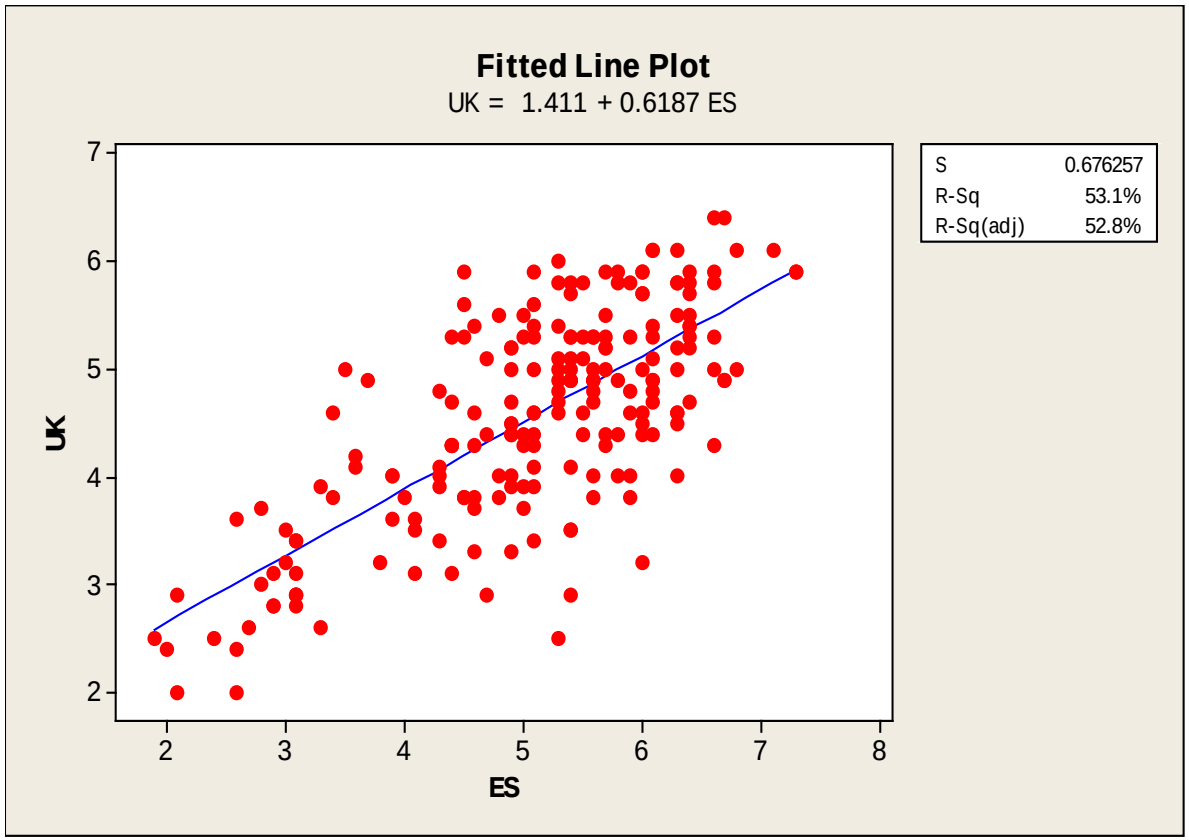
European programme GEMQUAL

The measurement of tenderness is slightly repeatable



Calibration results for texture

UK = 1.4 + 0.6 ES

(n=206 paired values)

(Nute et al., 2006)

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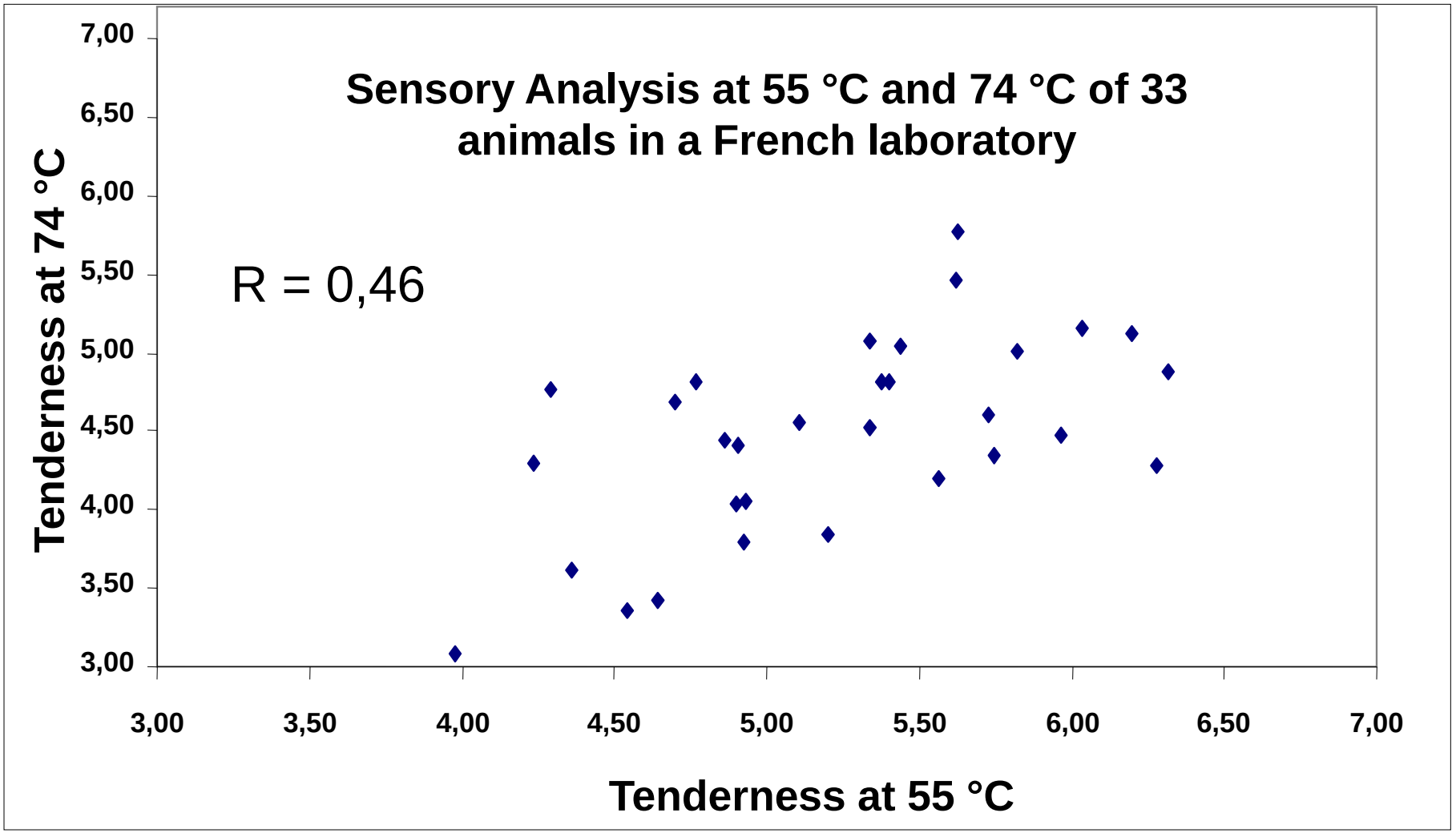
Sensory Analysis at 55 °C and 74 °C



Micol et al., 2011. EAAP

Does imprecision of measurement of phenotypes affect GWAS results ?

- ✓ Values obtained for subcutaneous fat thickness (with the same definition) from two independent working groups were correlated with r = 0.72
- ✓ Differences in GWAS (Genome Wide Association Study)
- ✓ It is recommended that trait values in GWAS experiments be examined for repeatability before the experiment is performed. For traits that do not have high repeatability ($r < 0.95$), two or more independent measurements of the same trait should be obtained for all samples, and individuals genotyped that have highly correlated trait measurements.

Barendse et al., 2011. BMC Genomics 2011, 12:232

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Evolution of research in biology

Large-scale projects in life science are being developed, driven by the desire to explore biology as a whole rather than in pieces

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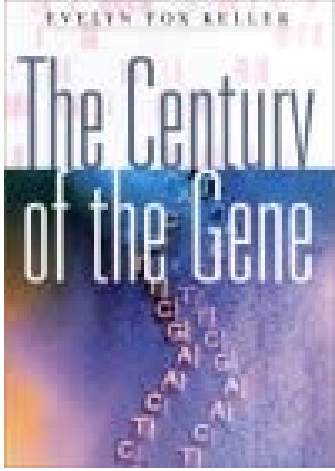
Predictive biology based on modelling is being developed

Fox Keller E (2002)



Genes, the author argues, are merely bit players in the game of life. The concept of the gene has been overused. In future we won't see it as being so important.

We have indeed to look at things differently.

The understanding of biology has reached a turning point.

The central question has shifted from “who are the actors?” [the genes and their products] to “what are the scripts?” [the physiological programmes and interaction between genes].

Specificity of research on beef quality

- ✓ A major criteria is tenderness, the measure of which is little repeatable, neither automatisable nor fast and thus with small sets of data.
- ✓ To solve this problem:
  - development of tenderness measurement on a large scale and in a standardised way (as in Australia)
  - search for predictors, the measure of which could be fast and automatisable

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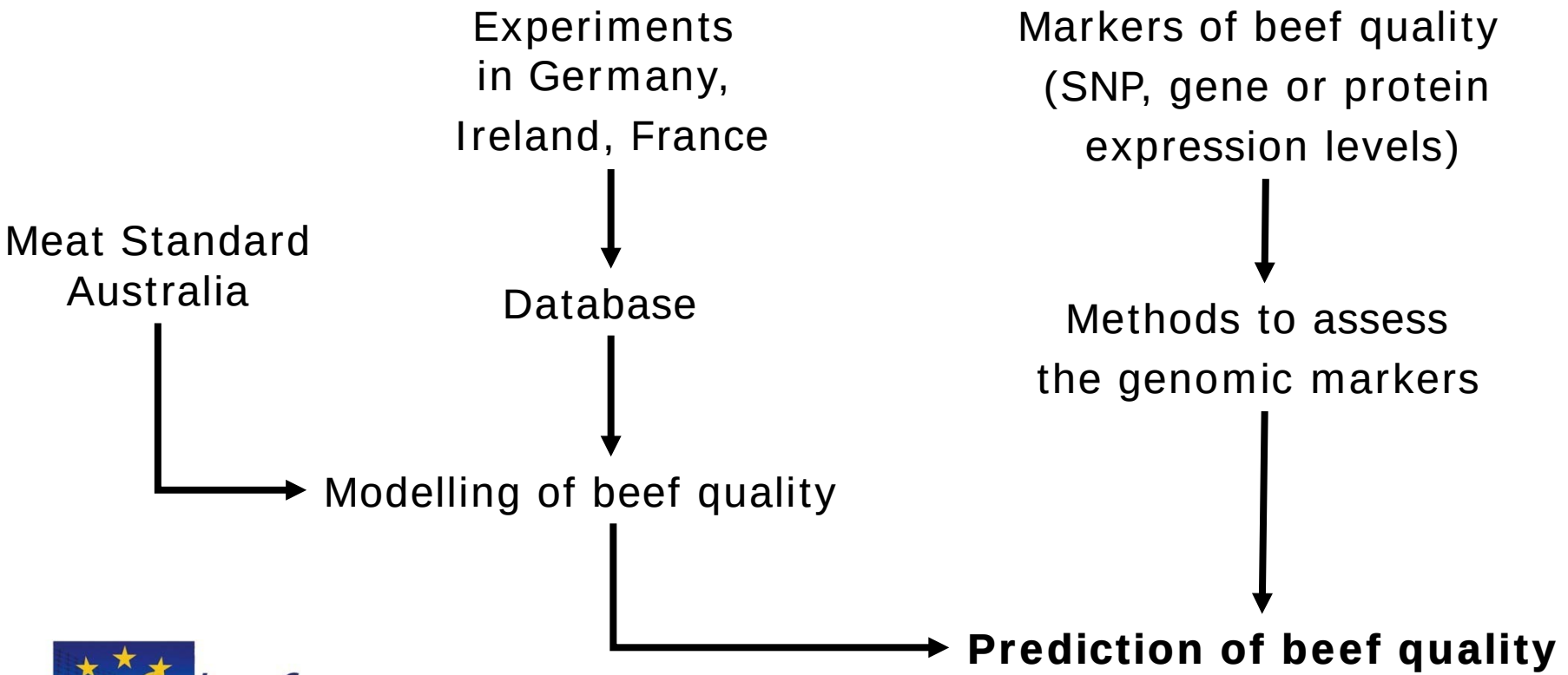
Search for beef quality predictors (ex : EU programme ProSafeBeef)



prosafebeef

SIXTH FRAMEWORK PROGRAMME

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Modelling of beef quality

Consumer tests

- > 530 000 samples
- 40 muscles

MSA2000model®

Hang (AT/TC/TS/TX)	AT
Sex (M, F)	m
Est.% Bos Indicus	0
Hump Height cms	0
Hot Std Carc Weight	200
USDA Ossification	100
Milk Fed Vealer Y/N	N
USDA Marbling	130
Days Aged (min 5)	5
Quarter Point Ribfat	5
Ultimate pH	5.40
AUSMEAT Meat Col.	2
Saleyard? (Y, N)	n
Wght/App.Maturity	1.32

Cut Description	Muscle Reference	Days Aged	Grilled Steak	Roast Beef	Stir Fry	Thin Slice	Cass-erole	Corned Beef
Tenderloin	TDR062		5	4	5			
Cube Roll	CUB045		3	3	3	4		
Striploin	STR045		3	3	3	3		
Oyster Blade	OYS036		4	3	4	4		
Bolar Blade	BLD096		3	3	3	3	3	
Chuck Tender	CTR085			3	3	3	3	
Rump	RMP131		3	3	3	3		
Point End Rump	RMP231		3	3	3	4		
Knuckle	KNU099		x	3	3	3	3	
Outside Flat	OUT005			x	x	3	3	3
Eye Round	EYE075		x	3	3	3	3	x
Topside	TOP073		x	3	x	3	3	
Chuck	CHK078			3	3	3	3	
Thin Flank	TFL051				3		3	
Rib Blade	RIB041				3			
Brisket	BRI056				x	3	3	x
Shin	FQshin						3	

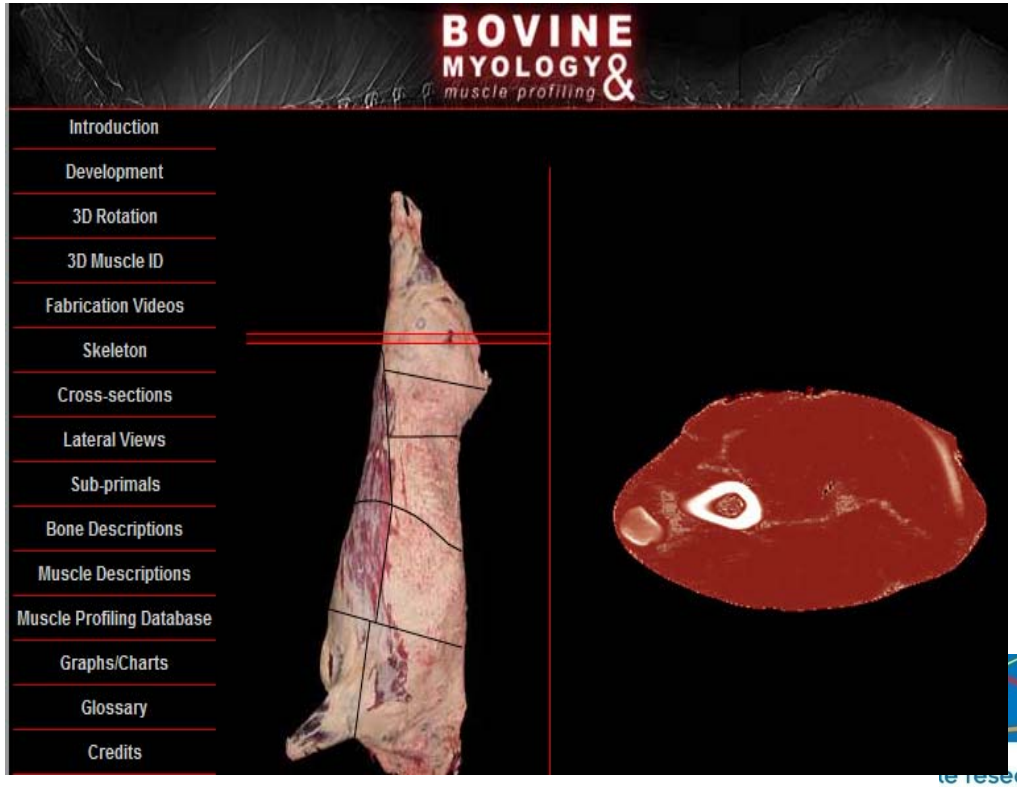
Muscle profiling

Muscle profiling: Characterizing the muscles of the beef chuck and round

Meat Science 71 (2005) 39–51

D.D. Von Seggern [a], C.R. Calkins [a,*], D.D. Johnson [b], J.E. Brickler [b], B.L. Gwartney [c]

[a] *University of Nebraska, Department of Animal Science, A213 AnS, Box 830908, Lincoln, NE 68583-0908, USA*
[b] *University of Florida, Department of Animal Science, Gainesville, FL 32611, USA*
[c] *National Cattlemen's Beef Association, Centennial, CO 80112, USA*



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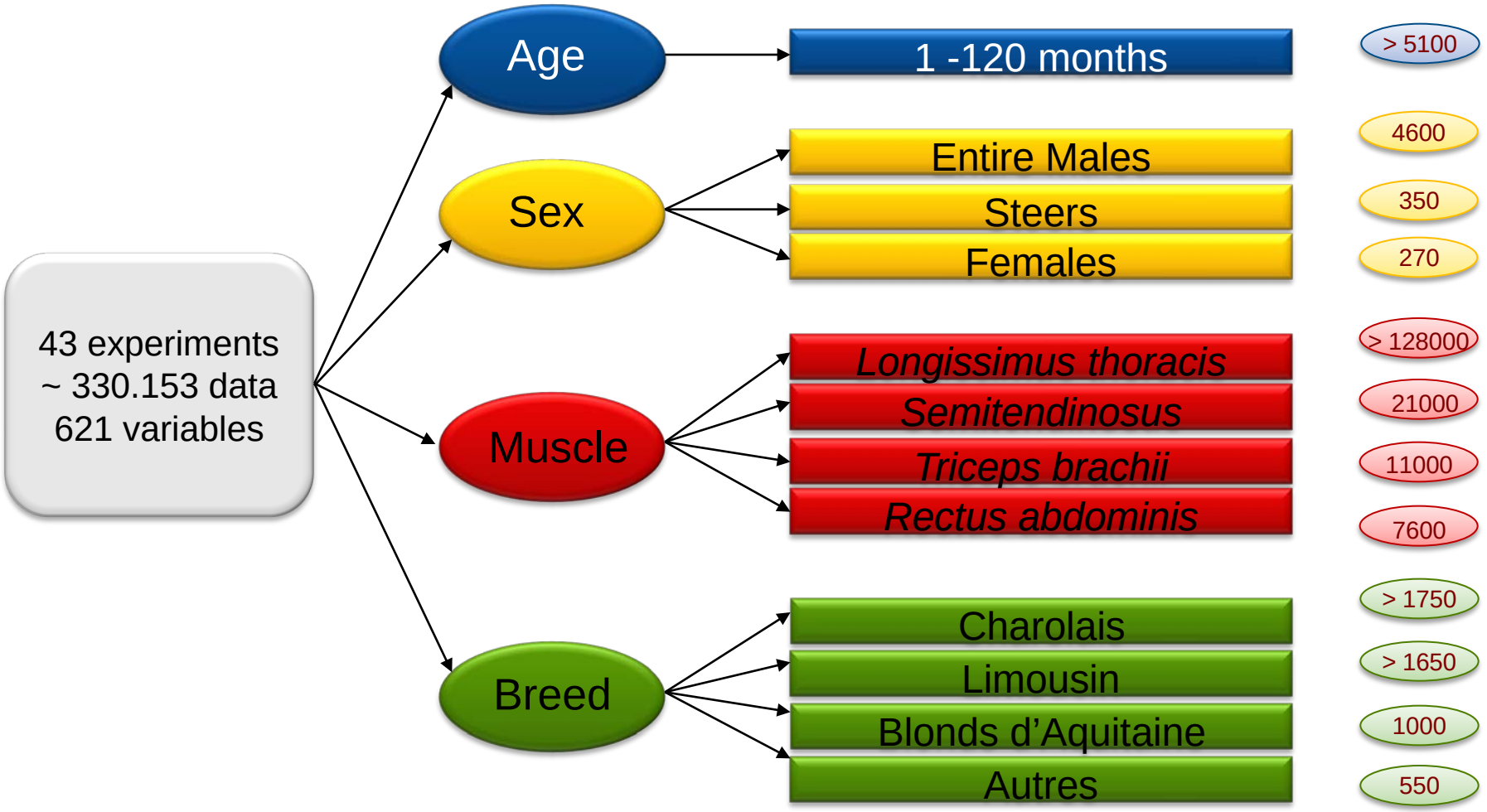
The Whole Data base: BIF-Beef



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Comparison of databases: France & USA

	Muscle Profiling USA	BIF-Beef
Animals	142	5197
Breeds	??	20 (Ch, Li, BA, …)
Sexe	steers ??	mainly young bulls
Variables	colour	colour
	Expressible moisture	
	Ash	Ash
	Fat	Fat, Proteins
		Enzymes (LDH, CS, PFK…)
		Vitamines
		Fibres (% and cross area)
	Emulsion capacity	
	pH	pH
	Collagen	Collagen
	Warner-Bratzler	Warner-Bratzler
		Flavour
		Juiciness
Protocols	standard	variables

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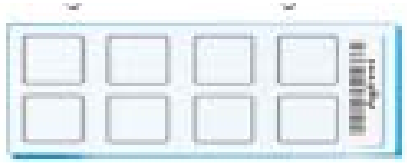
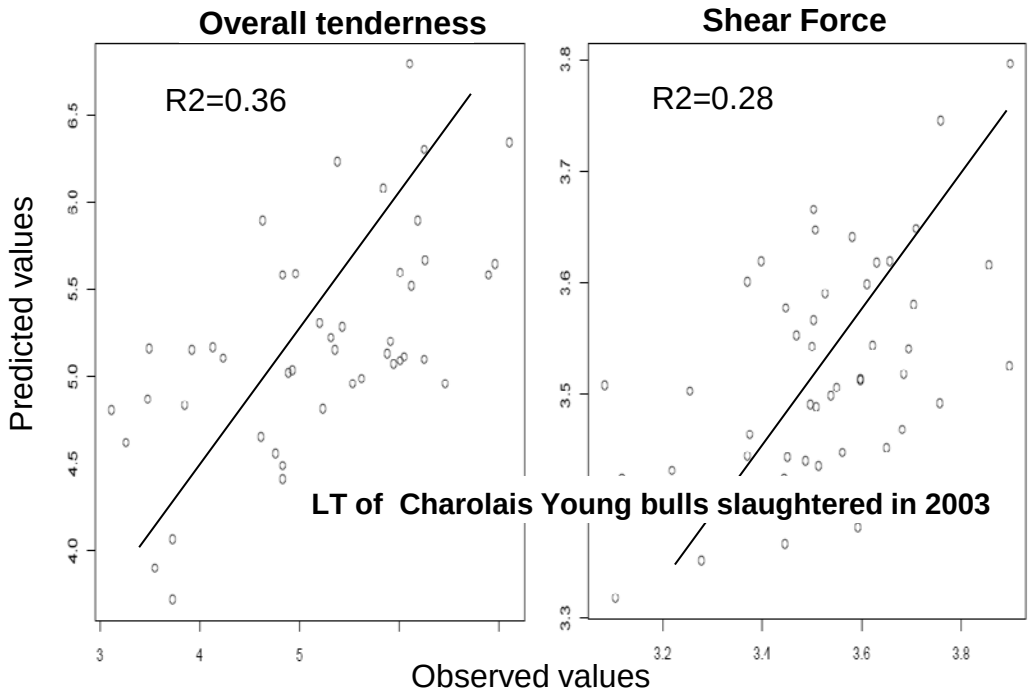
The “meat quality chip”

The GENOTEND programme

- 60 mer Oligonucleotides (in situ synthesis)
- > 3000 genes (selected genes for muscle growth, fibre types and fat metabolism from previous studies)
- Several probes per gene
- 8X15K chip (Agilent technologies)





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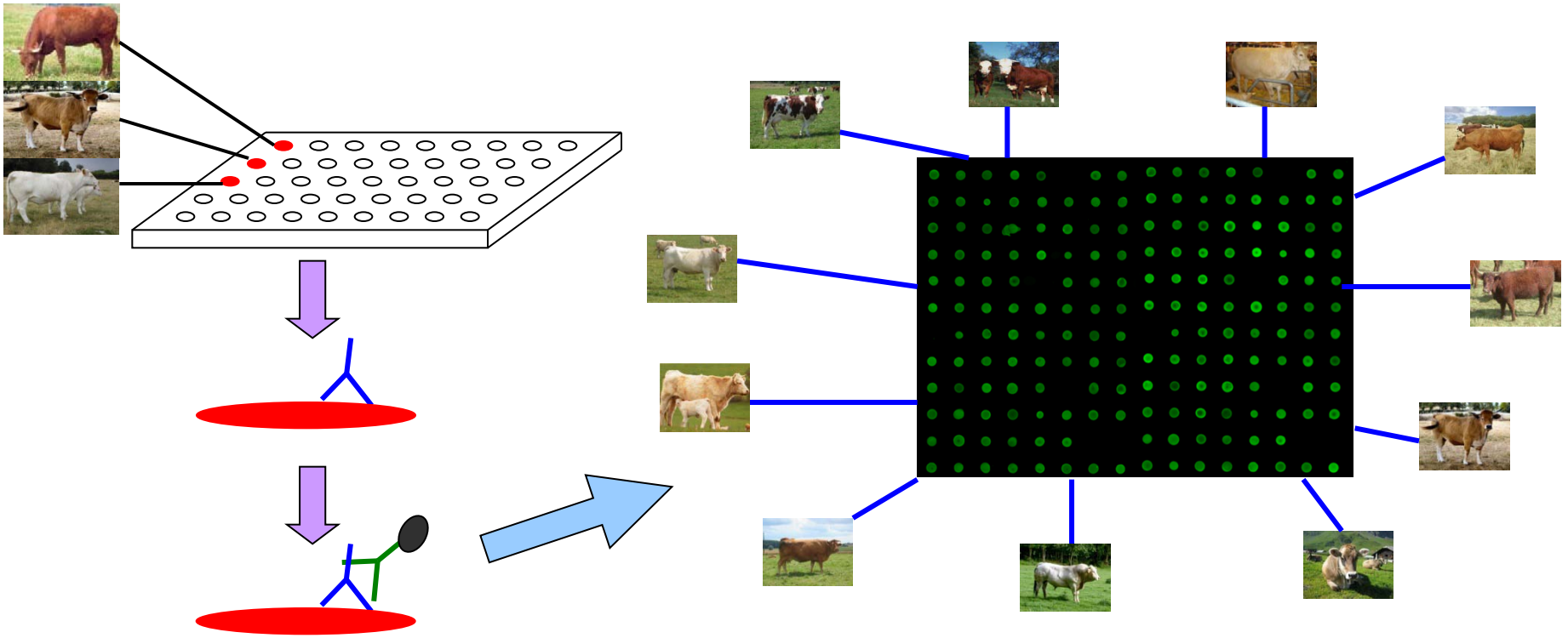
High-throughput protein assay



Guillemin N. et al. 2009. Validation of a dot-blot quantitative technique for large scale analysis of beef tenderness biomarkers. . Journal of Physiology and Pharmacoloy,. 60, 2. 91-97.

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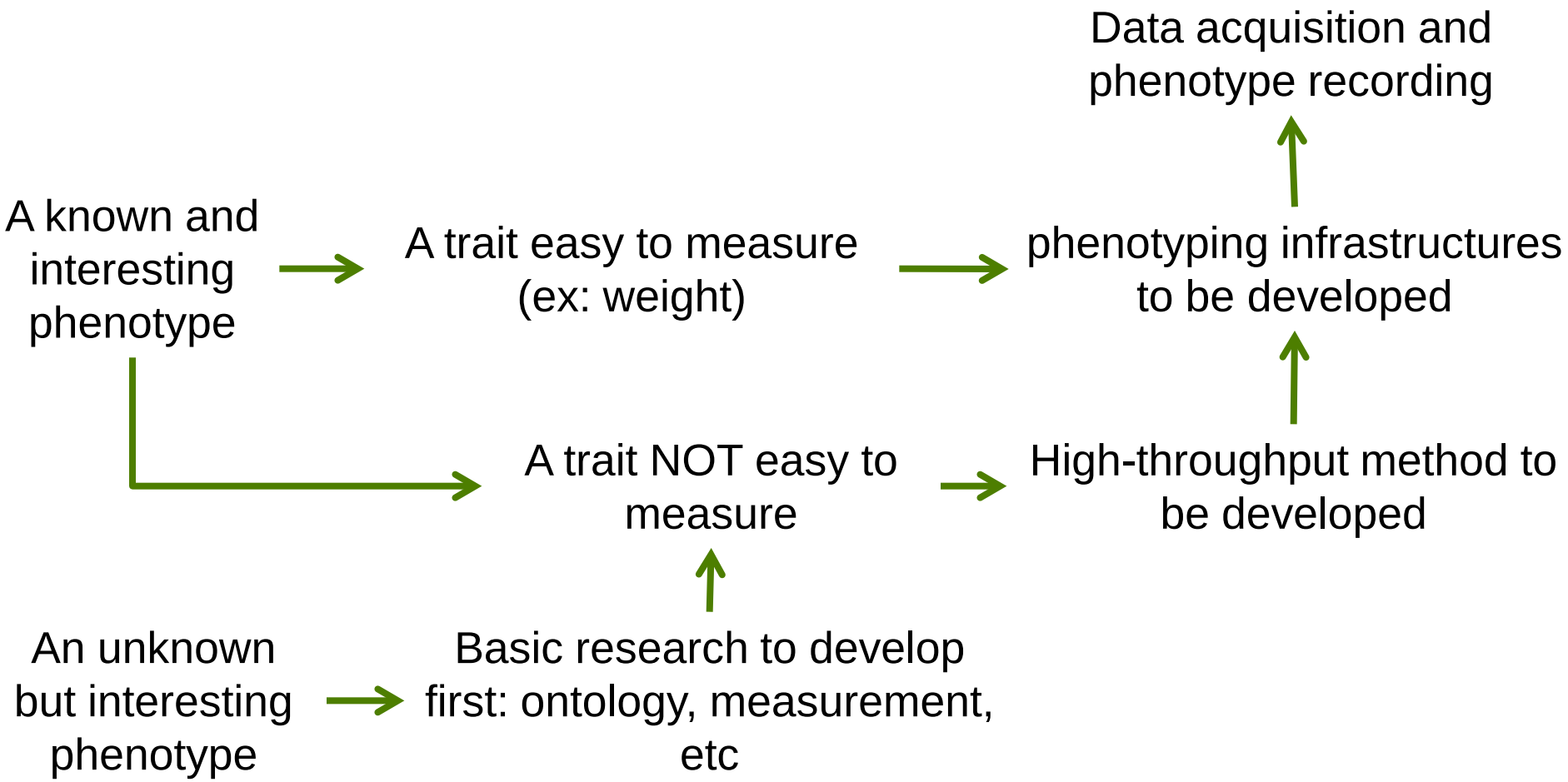
Where does the Efficiency in Australia come from?

- ✓ **Using the best genetics from the bulls to get best growth rates**
- ✓ **Using best pasture to feed the cattle**
- ✓ **Using scientific feeding for profitability in feedlots**
- ✓ **This means best management and this means: MEASURE, MEASURE, MEASURE everything**
- ✓ **Use measurements for bulls, grass, grain**
- ✓ **Measure the cows, measure the calves, measure the time (it takes)**
- ✓ **Only keep the best, kill the rest**
- ✓ **How do Australian Beef producers make good profits ? They measure the cost of everything ; They only use the best feed, genetics, management.**

Geoff Kirton, 2011, Beijing

The French strategy still in discussion



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Trends for the future

- Due to the cost of high-throughput equipments
- Due to the needs of standardized methods and data sharing

✓ We need a network of coordinated, advanced and standardized phenotyping infrastructures :

- Facilities for measuring well-known traits by classic approaches
- Facilities for the development and the measurement of new relevant traits by imaging techniques, and/or comprehensive description of molecular and metabolic patterns
- To develop strategies for multi-level data integration.

Conclusions

- ✓ **Phenotyping : the rate-limiting step in genomic selection**
- ✓ **Phenotyping: the poor partner in integrative biology**
- ✓ **Some technological problems to solve before moving to high-throughput measurements**
- ✓ **A challenge: storage and analysis of data**
- ✓ **Even more difficult in beef production: tenderness is difficult to measure as is robustness**

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