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Towards the Identification of Molecular Markers of Pork Quality



Bénédicte LEBRET and Marie DAMON



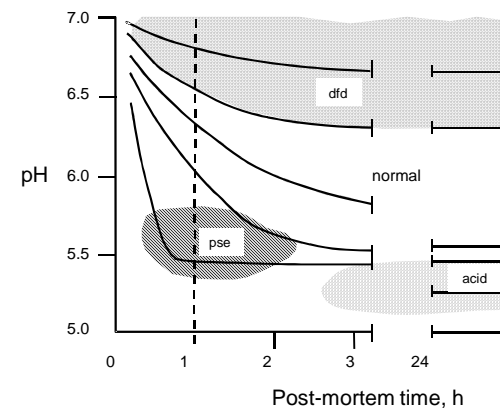
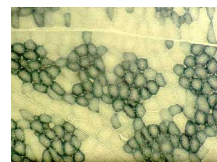
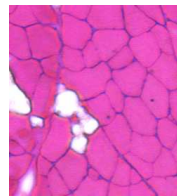
Livestock Production Systems,
Animal and Human Nutrition





Background : Meat Quality - 1

- Pork Quality {
 - Genotype of animals
 - Rearing conditions: feeding, housing,...
 - Slaughter conditions and meat processing
- Factors influencing MQ
 - i.m. fat, glycogen, myofibers, pH decline, proteolysis...





Background : Meat Quality - 2

- But...
 - High variability of MQ
 - Muscle traits → high sensory quality ?



- Q-Porkchains: Identify markers of MQ → control tools using a wide approach : omics methods



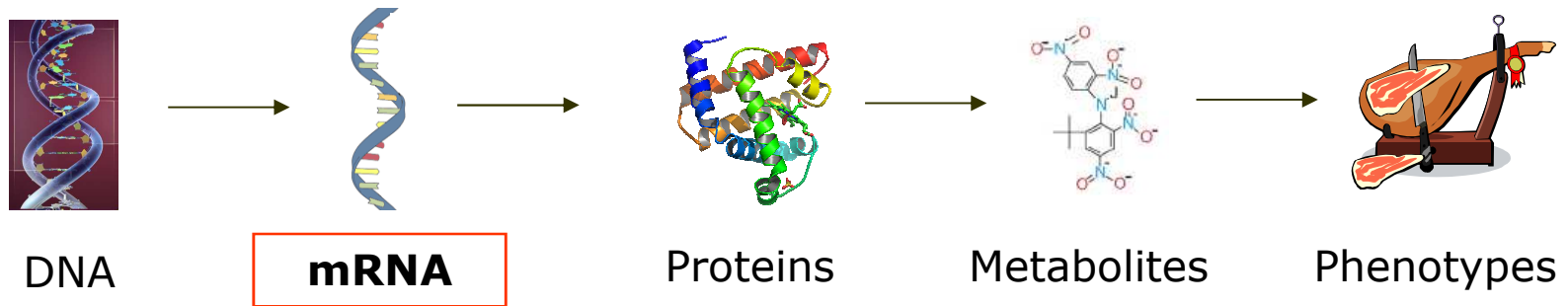
← Biochemistry, expression of target genes

← ***Other genes or proteins involved in MQ?***

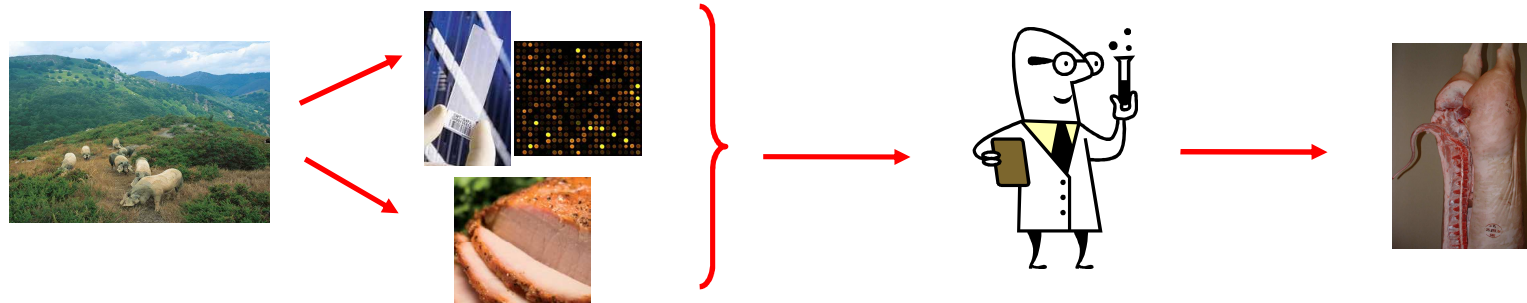


Functional genomics for MQ

- From genes to MQ



- Identify markers of MQ at the RNA level
- Validate on various pork chains



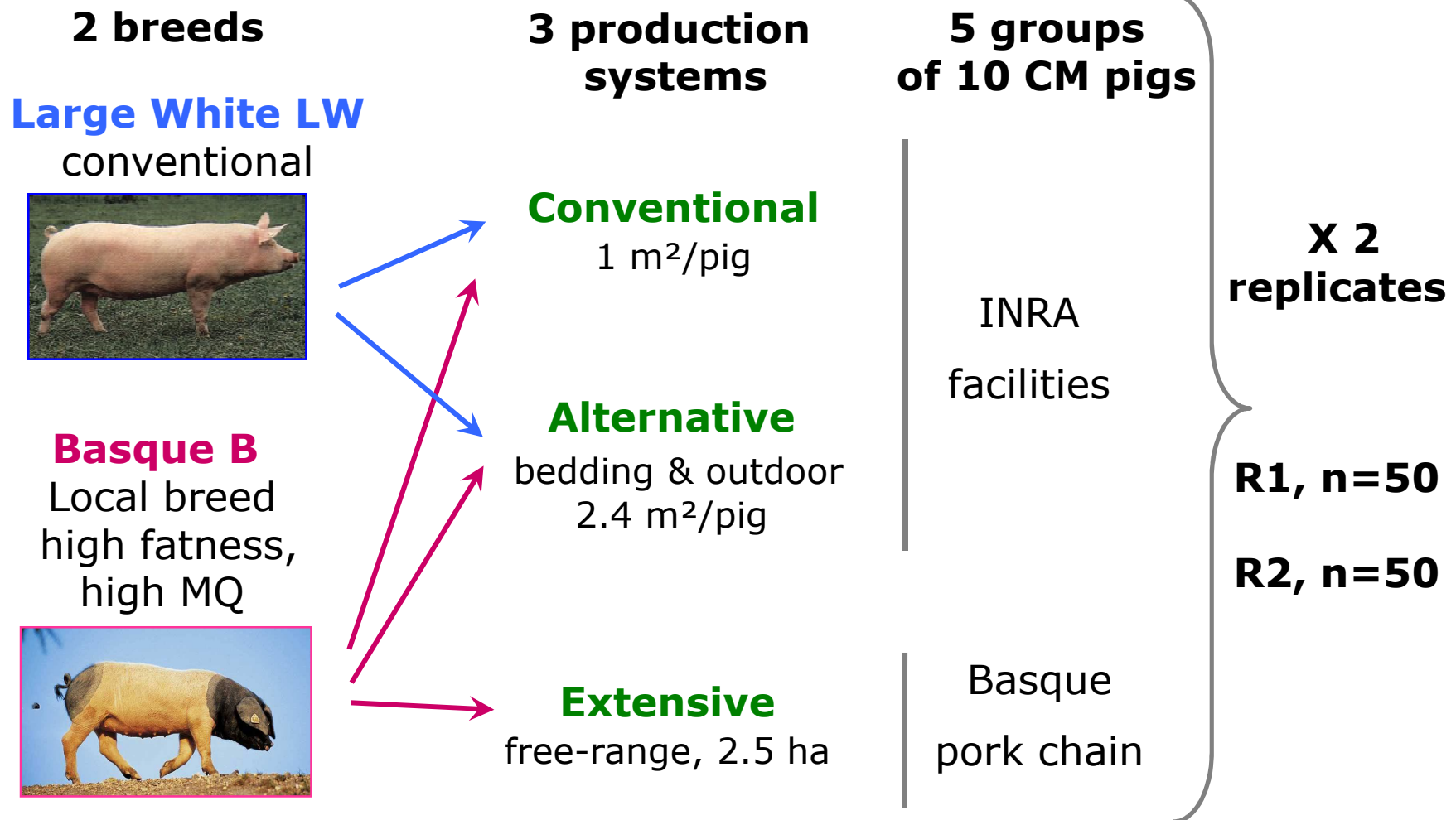


Strategy

- **Step 1 : Identification of markers**
 - 1.1 Data base with high MQ variability
 - Genetic and environmental factors
 - Relationships MQ traits and muscle transcriptome, n=50
 - 1.2 Confirmation : gene expression by PCR – MQ traits
 - Same 50 animals
- **Step 2 : Validation of markers**
 - 2.1 Within-chain validation: other animals, same pork chain
 - 2.2 Wide validation on various pork chains
 - Duroc crossbred, n=40
 - Danish commercial pork chain produced for validation, n=100
 - 2.3 Validation on the whole data set



Step 1. Database set-up - 1





Step 1. Database set-up - 2



Longissimus muscle, 150 kg, Replicate 1



Meat Quality



- pH1, pHu, drip loss, colour (L^* , a^* , b^* , C^* , h°), IMF, glycolytic potential
- Shear Force
- Tenderness, juiciness, flavour

Transcriptome profile

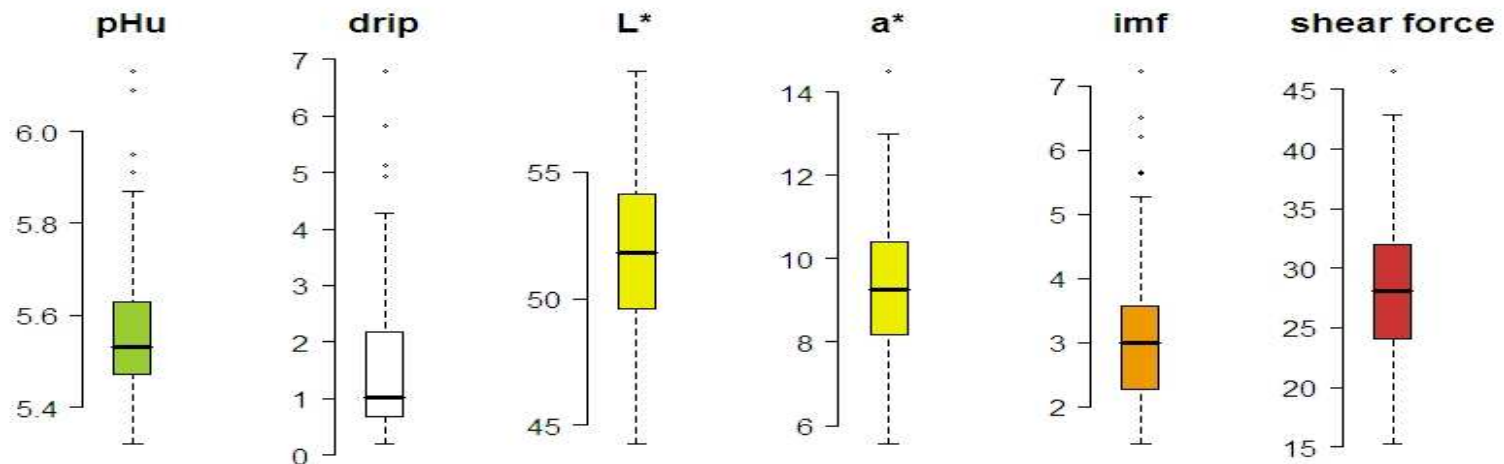


Correlations between gene expression and MQ data:
potential markers



Step 1. Relationships gene expression - MQ

- Database : high variability of MQ traits



N genes	330	354	240	425	156	291
R² max, %	34	33	29	40	27	31

- Many genes correlated to 13 MQ traits, $R^2 \leq 40\%$
- Biological processes of genes related to MQ traits :
drip loss= extracellular matrix, lipid storage, proteolysis,....

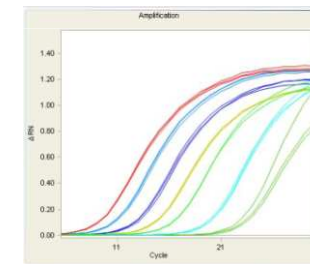


Step 1. Confirmation by PCR

- Numerous correlations found between microarray expression and MQ traits



- Confirmation by **real time PCR**
 - **42 genes**, same 50 animals (R1)



- **174 correlations** between gene expression (PCR) and **13 MQ** were confirmed, $R^2 \leq 36\%$



Step 2. Within-chain validation

- Experimental LW & B, replicates 1 + 2, 100 pigs

MQ trait	n correlated genes, $p < .05$	R^2 max, %
pH1	2	26
pH2	8	22

✓ **58 correlations validated on 100 LW and B pigs**

✓ **25 genes and 13 MQ traits:** pH, drip loss, colour, GP, IMF, shear force, tenderness, juiciness

✓ **R^2 up to 33 %**

Intramuscular fat	8	20
Shear force	2	12

✓ **21 genes, $R^2 \geq 8\%$ chosen for wide validation step**

Juiciness	1	14
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Step 2. Wide validation - 1

- Duroc crossbred, CM and F, 110 kg, n=40
 - MQ traits: pH, colour, drip loss, IMF, tenderness, juiciness

MQ trait	n correlated genes	R ² max, %
pHu	2	14
Drip loss	6	16
Colour: L*	1	13
h°	1	20
Intramuscular fat	3	15

- ✓ **13 correlations validated on a different pork chain**
- ✓ **10 genes and 5 MQ traits**
- ✓ **R² up to 20 %, same range as within-chain validation**



Step 2. Wide validation - 2

- Commercial Danish pork chain - L. Kristensen, DMRI
 - Duroc x Ld x Yorkshire pigs, CM and F, 110 kg n=100

MQ trait	n correlated genes	R² max, %
pH1	2	8
pHu	5	24
Drip loss	5	12
Colour: L*	1	8
b*	1	14

✓ **17 correlations validated on a commercial pork chain**

✓ **9 genes and 8 MQ traits, R² up to 24%**



Step 2. Validation on the whole data set -1

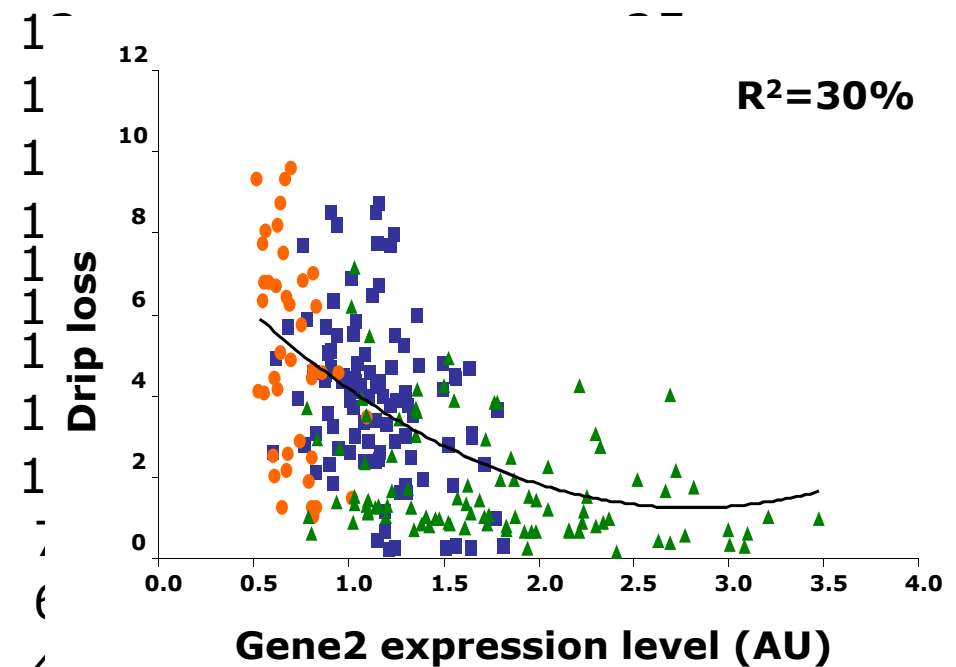
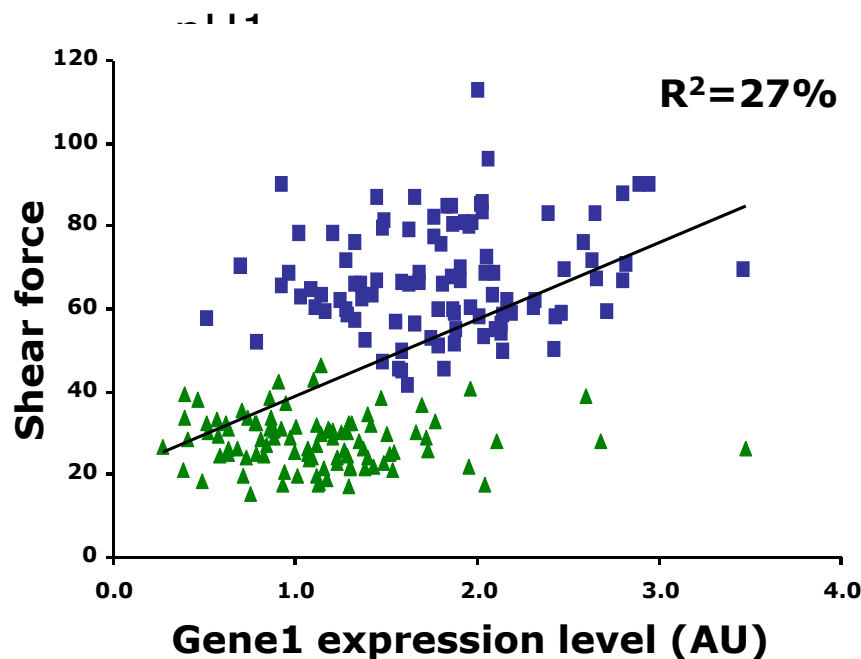
- Correlations: 3 pork chains
21 genes

Experimental LW & B, n=100
Duroc crossbred, n=40
Danish porkchain, n=100

MQ trait

n correlated genes, $p < .05$

R^2 max, %





Step 2. Validation on the whole data set -2

- Multiple regressions: 3 pork chains, all correlated genes

✓ **Models for 12 MQ traits: 3 to 9 genes, $24 \leq R^2 \leq 56\%$**

✓ **Many common genes**

- Multiple regressions: **8 most frequent genes**

MQ trait	n genes	R ² model, %
pH1	6	40
pHu	4	30
Drip loss	2	32
Colour: L*	5	24
b*	4	28
Shear force	7	56

✓ **Models for 12 MQ traits, 2 to 7 genes, $16 \leq R^2 \leq 56\%$**



Step 2. Summary of validation steps

- Experimental LW & B, 100 pigs

58 correlations
25 genes
13 MQ traits

- Duroc crossbred, 40 pigs

13 correlations
10 genes
5 MQ traits

- Commercial pork chain, 100 pigs

17 correlations
9 genes
8 MQ traits

90 correlations
20 genes
12 MQ traits

Regression models
for 12 MQ traits
 $R^2 \leq 56\%$



Conclusions

- Large data base with high variability of MQ
- Confirmation step : gene expression (PCR) – MQ
 - Successful for 42 genes, 13 MQ traits, 174 correlations
- Validation steps
 - Some correlations validated on various pork chains
 - Set of 8 genes : models for 12 MQ traits

- **8 biomarkers** of pork quality have been **identified** and **validated**
- A **combination of markers** should be considered for the development of control tools



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Thank you for
your attention
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