Genes differentially expressed in adipose tissue of dairy cows carrying « fertil+ » or « fertil- » haplotype for one QTL of female fertility located on the BTA3

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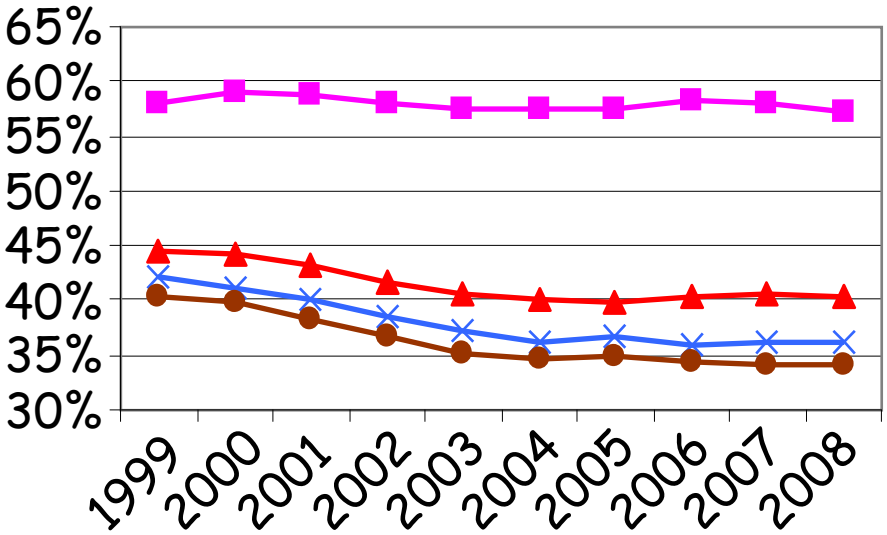
Introduction

Context in France

Success rate at AI1 in Holstein breed



P. Le Mézec, A. Barbat.
French livestock institute

Decline of fertility, between 2000 and 2004:

* All females -3.6 %

* Cows -4.7 %

Introduction

In postpartum:

* beginning of lactation
* negative energy balance / loss of body weight
* insufficient ingestion

=> energy for lactation and not for reproduction

Introduction

* 2001: « fertility » trait in selection index in France
* fertility trait: low heritability (1-2 %)
* Variability: QTLs of female fertility (F-Fert)

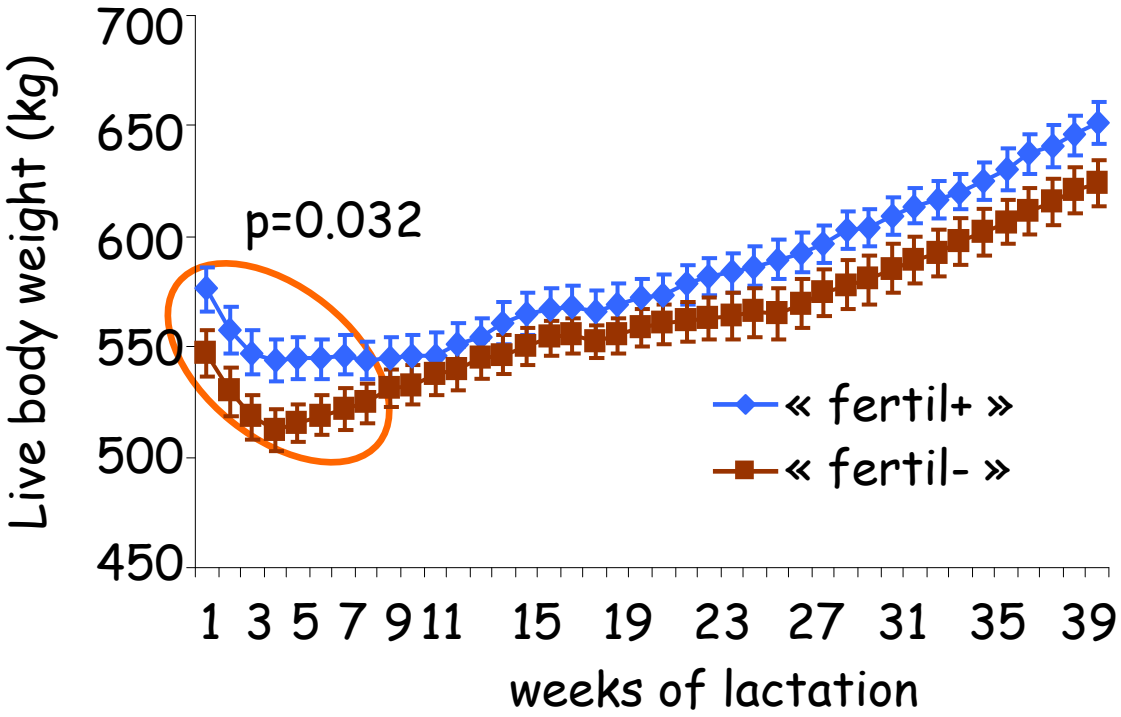
QTL-F-Fert-BTA3
early events of pregnancy

* Homozygous females: 23 **« fertil+ »**
18 **« fertil- »**

- phenotypic characterization

Characterization of « fertil+ » and « fertil- » dairy cows: body weight

Variation of live body weight
(morning weight, first lactation)

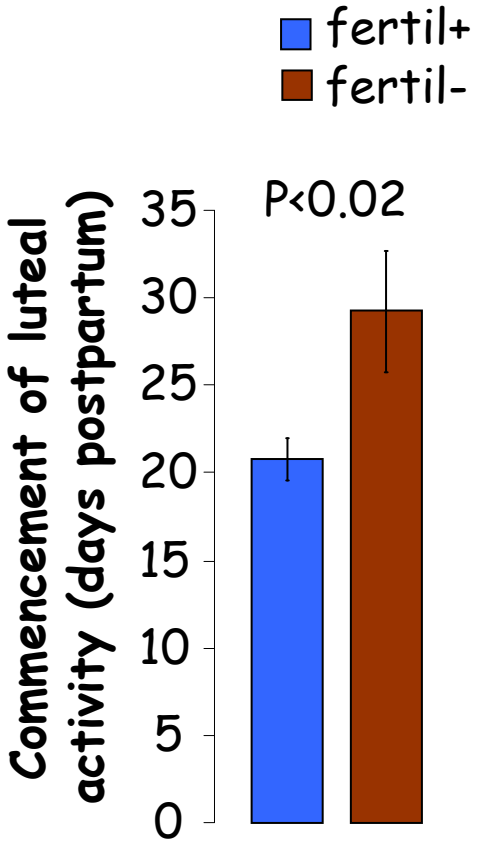


Characterization of « fertil+ » and « fertil- » dairy cows: fertility

Success rate after AI1
(first lactation)

Days after AI1	«fertil+»	« fertil-»	P
35	70 %	39 %	0.05
90	65 %	39 %	0.09

Resumption of cyclicity
(first lactation)



Characterization of « fertil+ » and « fertil- » dairy cows: summary

Differences in

* body weight 1st-8th weeks of lactation **fertil+ > fertil-**
* success rate after AI1 **fertil+ > fertil-**
* resumption of cyclicity **fertil+ < fertil-**

=> Difference in mobilization of fat stores ?

Adipose tissue: role in reproduction *via* adipokines

Variation of gene expression in adipose tissue ?

Aim of the study

Is there a difference in gene expression between « fertil+ » and « fertil- » adipose tissue ?

Tiling Array experiment:

* a 385K array with sequence of the QTL-F-Fert-BTA3

* study of variations in transcripts expression

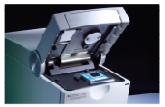
Tiling Array: experimental design

Biopsies of adipose tissue

n=9 per group

Total RNAs extraction & purification

Agilent Bioanalyser



cDNAs synthesis & purification

cDNAs labeling with Cy3

Hybridization on a 385K array 18h, 42°C

Washing and array scanning 532 nm

Analyses

Transcriptional analysis of a known chromosomic region

Results: statistical analyses

Data set : 124 genes of the QTL-F-fert-BTA3

* known coding proteins
* putative coding proteins

Results : 93 genes differentially expressed ($p<0.05$)

* 43 known coding proteins
* 50 putative coding proteins

Results: statistical analyses

15 genes overexpressed in **« fertil- »** females
(ratio 1.03-1.30)

Olfactory receptors

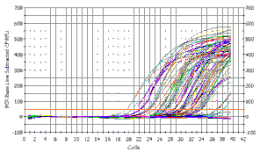
78 genes underexpressed in **« fertil- »** females
(ratio 1.03-2.08)

Immune response

Cytoskeletal organization

Protein metabolism …

Results: real-time PCR confirmation of tiling array

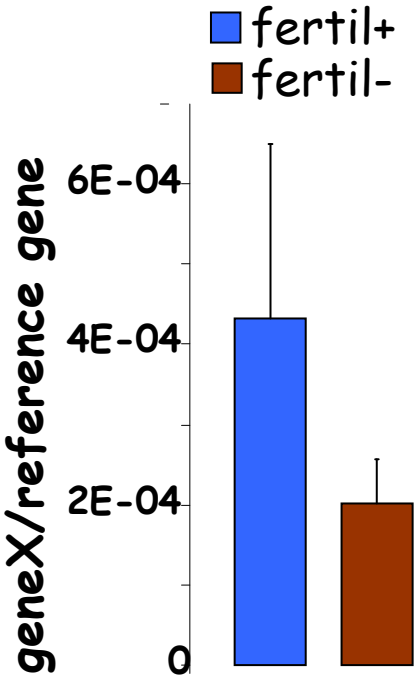


Real-time PCR on adipose tissue (same samples as Tiling array)

10 known genes of the QTL-F-fert-BTA3

* 1 gene differentially expressed (p=0.044)

  - 2 times underexpressed in **« fertil- »**
  - main role: glomerular filtration
  - expressed in mouse/human ovary



Conclusion

Differences between « fertil+ » and « fertil- »:

* live body weight

* fertility

* gene expression in adipose tissue (93 genes)

- Differences are adipose tissue specific ?
- Reproductive tissues ?
- Protein expression ?

Could these genes explain the difference of fertility in our two haplotypes ?

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Thank you for your attention

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