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Genetic Parameter Estimation for Milk Fatty Acids in three French dairy Cattle Breeds

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Context

Expectations of consumers evolve:
To improve the nutritional value of bovine milk for human health
Common interest for Dairy industry, breeding and genetic sectors

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Fine milk composition
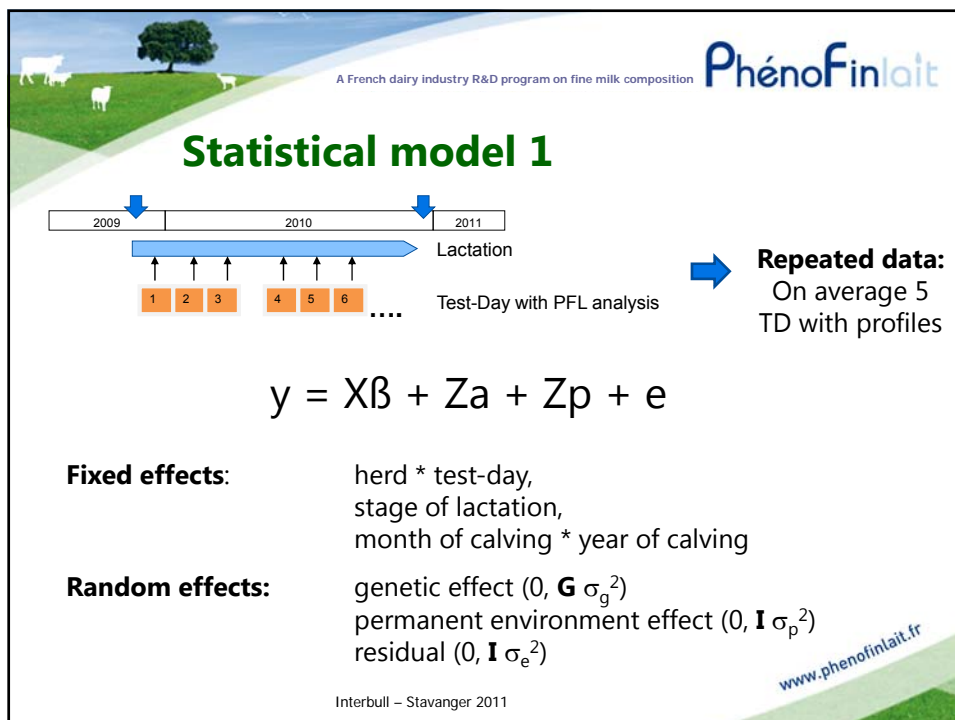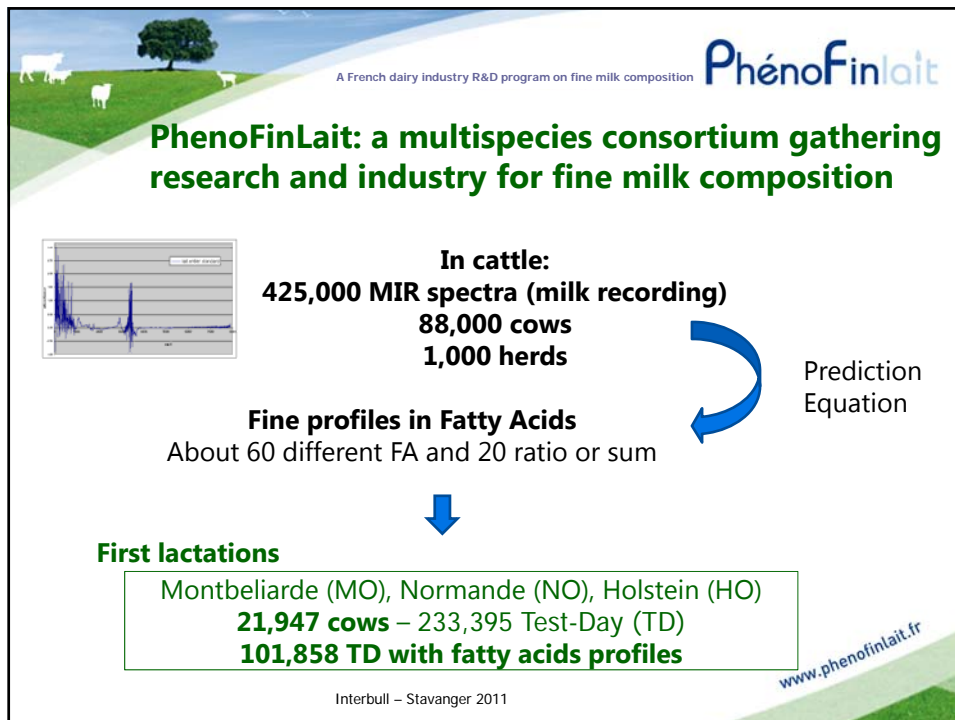Global approach (feeding, genetics…) to develop tools for breeders

Basis for genomic selection

Record the data and estimate the genetic variability

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Slide 1

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PhenoFinLait: a multispecies consortium gathering research and industry for fine milk composition

In cattle:
425,000 MIR spectra (milk recording)
88,000 cows
1,000 herds

Prediction
Equation

Fine profiles in Fatty Acids
About 60 different FA and 20 ratio or sum

First lactations

Montbeliarde (MO), Normande (NO), Holstein (HO)
21,947 cows – 233,395 Test-Day (TD)
101,858 TD with fatty acids profiles

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Statistical model 1

| 2009 | 2010 | 2011 |

Lactation

1 2 3 4 5 6 .... Test-Day with PFL analysis

Repeated data:
On average 5
TD with profiles

$$y = X\beta + Za + Zp + e$$

Fixed effects: herd * test-day,
stage of lactation,
month of calving * year of calving

Random effects: genetic effect $(0, \mathbf{G}\,\sigma_g^2)$
permanent environment effect $(0, \mathbf{I}\,\sigma_p^2)$
residual $(0, \mathbf{I}\,\sigma_e^2)$

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Units and expression: which traits ?

| FA g/100g milk | — Total fat in milk → | FA g/100g fat |

Trait of interest in the **human diet**, but less useful at the cow level.

FA in fat in human diet more dependent on FA in milk than FA in fat.

➡ **All results expressed in g/100g of milk**

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Slide 2

Test-Day heritability estimates

MILK COMPOSITION

POLY
MONO

SAT

Total Fat

$h^2 = 0.18$ to 0.39

1 g/100g milk	MO	NO	HO
C14:0	0.35	0.38	0.29
C16:0	0.32	0.34	0.28
C18:0	0.20	0.18	0.21
Total SAT	0.32	0.34	0.28

MILK COMPOSITION

POLY
MONO

SAT

Total Fat

$h^2 = 0.10$ to 0.24

2 g/100g milk	MO	NO	HO
C18:1c9	0.13	0.16	0.11
C18:2c9t11	0.17	0.14	0.11
MONO	0.13	0.18	0.15
POLY	0.21	0.24	0.22

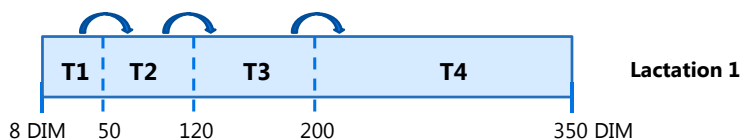**h^2 SAT > h^2 UNSAT**

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Genetic determinism along the lactation

| T1 | T2 | T3 | T4 | **Lactation 1** |

8 DIM   50   120   200   350 DIM

Same model: $y = X\beta + Za + Zp + e$ **Multitrait**

➡ Genetic correlations and 4 h² per fatty acid

➡ h² estimates increase over the lactation.

➡ Correlations tend to **increase** during the lactation.
In many cases, correlations were high accross the 4 traits,
except the **beginning**.

| **T1 is a different trait** |

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Correlations between Fatty Acids

Average lactation measures of fatty acids
TD adjusted for stage of lactation. Fat content as weights.

$y = X\beta + Za + e$ Fixed effects: herd
                                                    month of calving * year of calving
                          Random effects: genetic and residual

⬇

Genetic correlations in Montbeliarde (in g/100g milk)

1	Milk Yield	Total Fat
SAT	-0.15 to -0.40	+0.77 to +0.95
UNSAT	-0.20 to -0.53	+0.42 to +0.51

2	SAT	UNSAT
SAT	0.19 to 0.95	
UNSAT	0.16 to 0.78	0 to 0.69

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Profiles in % fat: some results

h² **higher** when expressed in **milk** than in fat ➡️

Normande	g/100g fat	g/100g milk
C14:1cis9	0.19	**0.34**
C18:2t9cis12	0.10	**0.15**
Total SAT	0.22	**0.38**

Genetic correlations:

Montbeliarde	g/100g fat	g/100g milk
C14:0/C18:1	-0.75	0.24
milk yield/C18:1	0.00	-0.53

Increase SAT = decrease UNSAT in fat and increase UNSAT in milk

Increase milk = no consequence for UNSAT in fat and
decrease UNSAT in milk

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Conclusion

► Results are sound and in agreement with literature.

► MIR spectra provide valuable data for milk composition
Genetic parameters reflect the main FA metabolic pathways.

► Heritability estimates are moderate.
Improving the nutritional value of milk by selection is possible.

► Importance of the unit of expression: %milk or %fat ?
The opposition between SAT and UNSAT is weaker when expressed in milk than in fat.

► Increasing UNSAT for human diet would probably implies a decrease of SAT in fat and a decrease of fat in milk.

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Perspectives

► Test-day random regression model
Multiple lactation
Protein

► 7,500 cows in the PhenoFinLait project were genotyped
QTL detection and genomic selection are under study

► Need for clear direction for the breeding objective.

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Thank you for your attention

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