PhenoFinLait

First overview of french farm systems

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Summary

1) Context
2) Material and Methods
3) First results
4) What next ?
5) Conclusions
From animal to product

• 1960’s => bull selection on productivity
• 1980’s => + fat percentage and protein percentage
• From the 1990’s to now => + functional traits (mastitis, longevity, fertility…)

Many traits related to animals or production

Absence of traits related to product : milk
Why considering fine milk composition?

- Fine milk composition = fatty acid (FA) and/or individual protein (IP) profiles of milk
- New phenotypes that give precious help for
  - Consumers (nutrition, flavor...)
  AND
  - Farmers (C18:1t10/C18:1t11 ratio as marker of acidosis)
  - Industries (level of protein phosphorylation, FA profile and milk fat texture)
How fine milk composition can be modulated?

- **Feeding management**
  - In comparison to maize silage diet, pasture, conserved grass and/or some concentrates increase milk mono- and poly-unsaturated FA content

- **Genetics**
  - High inter-individual variability and non negligible heritability make possible selection on fine milk composition
  - QTL for fine milk composition detected: DGAT1, SCD1 and β-lactoglobulin.
The french answer: PhenoFinlait

- Many partners with shared interests for these new phenotypes:

  - **CNIEL** (Dairy industries and farmers)
  - **France Génétique Elevage:** (France Livestock Genetics)
  - **UNCEIA, ANIO and CapGène** (about 10 breeding companies)
  - **FCL and CNBL** (Milk recording organizations)
  - **Actilait and regional laboratories**
  - **INRA** (French National Institute for Agricultural Research) (4 labs, 4 exp. Units, 2 dep)
  - **Institut de l’Elevage** (French Livestock Institute) (4 teams, 3 dep)
  - And about 1 500 farms

26 departments
3 species
7 breeds
A French dairy industry R&D program on thin milk composition

Several objectives

- Develop and control methods to analyze fine milk composition
- High scale analysis of milk composition and development of a huge data base
  - Recording fine milk composition (FA and proteins)
  - Recording diet composition and herd management
  - Taking biological samples (blood for genotyping and milk)
- Understand how genetic and feeding strategies impact fine milk composition
- Promote tools (genetics + feeding strategies) for adapting milk composition to consumers demand and health
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Phenotyping method for FA

GC: milk FA profile

MIR spectra

→ Almost 75 FA and ratio for each species
Improvement of equations accuracy

• By applying selection of variables before PLS regression
• Genetic algorithms already successfully used on IR data (Leardi R. 1998, Gomez-Carracedo 2007)
• Previous study in cow milk with good results (Ferrand, 2009)
Results, precision of FA estimation

⇒ Better estimation for cow and ewe in comparison to goat

⇒ For cow milk, precision of estimation close to Soyeurt et al., 2006
How to deal with spectra differences between analyzers?

- Previous analysis showed spectra differences between analyzers for estimation of milk FA profile.
- Control milks were analyzed frequently on each machine (internal controls).
- We are going to use these internal control for correcting every MIR spectra and FA content estimation.

M. Ferrand (IE), O. Leray (Actilait)
Phenotyping method for proteins

• Difficult to estimate with MIR spectra (many variants)
• Development of a reference analysis method: HPLC-MS
• Creation of reference databases for protein identification
• Analysis of 17,000 samples
• Attempts to link milk protein composition to MIR spectra

P. Martin (INRA)
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## 780,000 MIR Spectra

Recorded in PhenoFinlait database at 2010/09/01

- **Cows:** 406,556
- **Goats:** 244,884
- **Ewes:** 126,290

![Map of France with data recording distribution](image-url)

- **Legend:**
  - < 5,000
  - 5,000 to 20,000
  - 20,000 to 50,000
  - > 50,000

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**M. Brochard (IE)**
7 100 diets composition records
In PhenoFinlait database at 2010/09/01

• Cows : 5 591
• Goats : 600
• Ewes : 936

M. Brochard (IE)
A French dairy industry R&D program on thin milk composition

Animal physiology and milk FA composition

• Lactating stages: decrease MUFA, increase SFA

S. Esvan, A. Varenne (IE)

Pyrenées Atlantique, raw data

East of France, raw data

http://www.phenofinlait.fr
Animal physiology and milk FA composition

- Parity: decrease UFA, increase SFA

East of France, raw data

S. Esvan (IE)
A French dairy industry R&D program on thin milk composition

Milk FA composition

Winter period

Switch between winter and summer periods

S. Esvan (IE)
French farm systems – Winter time

"Maize" diet (>75% of maize in the ration)

581 farms, 68 lactating cows /farm:
- diets in % of farms of the departement

Montbeliarde 7%
Normande 39%
Holstein 54%

M. Brochard, S. Esvan (IE)
French farm systems – Winter time

“Mixed Maize” diet (55-75% of maize in the ration)

228 farms, 77 lactating cows /farm:

- **diets** in % of farms of the departement

**Map showing the distribution of different dairy breeds across the region.**

**Pie chart showing the distribution of dairy breeds:**
- Montbeliarde 15%
- Normande 32%
- Holstein 53%

M. Brochard, S. Esvan (IE)
French farm systems – Winter time

“Mixed Grass” diet (>45% of grass in the ration)

113 farms, 68 lactating cows /farm:
• diets in % of farms of the departement

A French dairy industry R&D program on thin milk composition

M. Brochard, S. Esvan (IE)
A French dairy industry R&D program on thin milk composition

French farm systems – Winter time
“Hay” diet (>90% of hay in the ration)

189 farms, 56 lactating cows /farm:
• diets in % of farms of the department

M. Brochard, S. Esvan (IE)
## Genetic parameters – cows

<table>
<thead>
<tr>
<th>Heritabilities</th>
<th>montbéliarde</th>
<th>normande</th>
<th>holstein</th>
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<tr>
<td>Fat (%)</td>
<td>0.36</td>
<td>0.36</td>
<td>0.23</td>
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<tr>
<td>SFA</td>
<td>0.19</td>
<td>0.32</td>
<td>0.18</td>
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<tr>
<td>MUFA</td>
<td>0.33</td>
<td>0.32</td>
<td>0.20</td>
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<tr>
<td>PUFA</td>
<td>0.31</td>
<td>0.18</td>
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<tr>
<td>C14:0</td>
<td>0.33</td>
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<td>0.35</td>
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<tr>
<td>C16:0</td>
<td>0.25</td>
<td>0.31</td>
<td>0.11</td>
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<tr>
<td>C18:1</td>
<td>0.20</td>
<td>0.33</td>
<td>0.19</td>
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<table>
<thead>
<tr>
<th>Genetic variation coefficient (%)</th>
<th>montbéliarde</th>
<th>normande</th>
<th>holstein</th>
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<tr>
<td>Fat (%)</td>
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<td>5.4</td>
<td>5.7</td>
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<tr>
<td>SFA</td>
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<td>1.2</td>
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<td>PUFA</td>
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<td>2.0</td>
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<td>C14:0</td>
<td>3.5</td>
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<tr>
<td>C18:1</td>
<td>4.0</td>
<td>5.4</td>
<td>7.6</td>
</tr>
</tbody>
</table>

East and west of France, raw data
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What next?

• Milk composition analysis
  – Improve MIR Spectra equations to estimate milk FA profile
  – Work to set equations for FA estimation usable by every milk recording laboratories
  – Analysis of protein composition

• Genotyping of 8000 cows, 3000 ewes and 4000 goats
  – And try to relate markers to milk FA and protein composition

• Have a more precise definition of feeding systems and associate these systems to fine milk composition
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Conclusions

• PhenoFinlait is a huge research program, this year was characterized by:
  – Data collection in the 3 species and 1500 commercial farms
  – First overview of the french farm systems
  – A large diversity of feeding composition

• Many factors have to be taken into account to evaluate fine milk FA profile: lactating stage, parity, feeding strategy, genetic
  ⇒ It is possible to modulate milk FA profile and to select animals on these criteria

• We have to continue the work
  - to perform an analysis method usable by all
  - to valorize these new sets of data
Thanks to every partners of this project

Thank you for your attention!